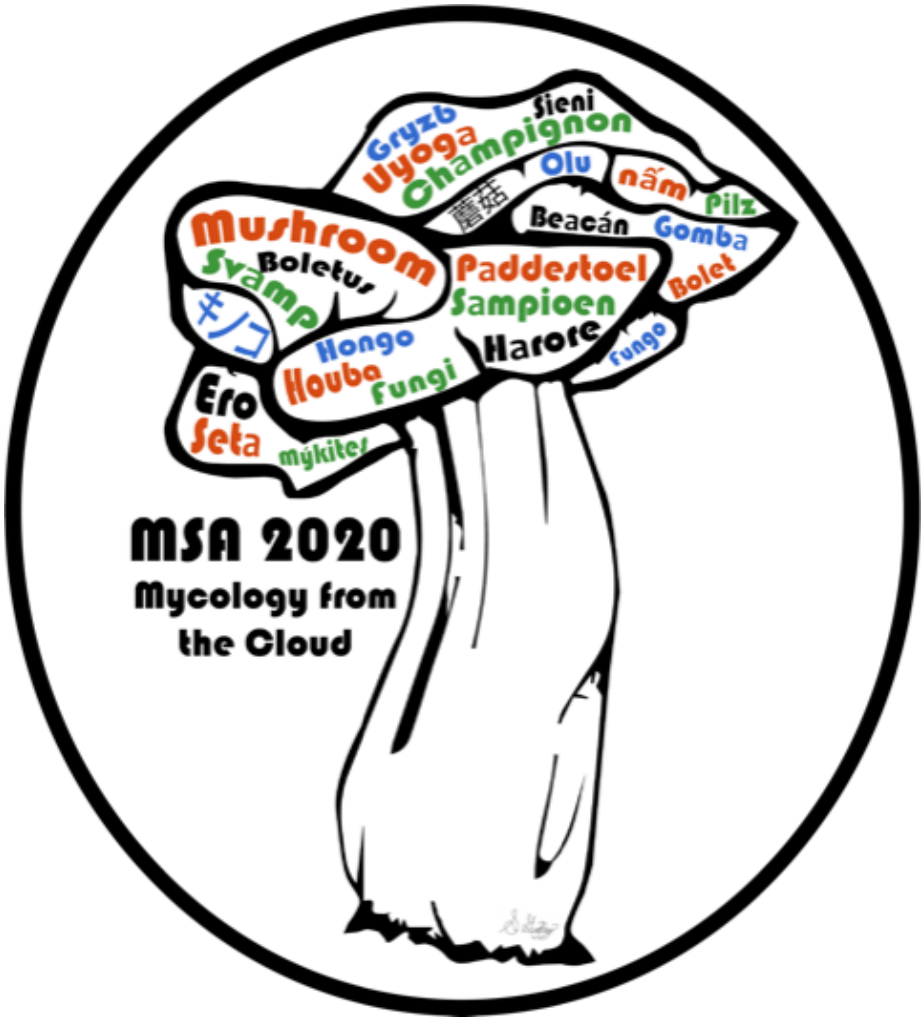
2020 MSA Virtual Meeting

Abstracts



July 21 – 22, 2020

Mycological Society of America 2020 Virtual Meeting: *Mycology from the Cloud* Abstracts
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Presentation ID: 3

First report of *Erysiphe aquilegiae* on *Clematis montana* from Pakistan

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Abstract

The present work was done to investigate, characterize and identify powdery mildew fungus that is infecting *Clematis* plants in different regions of Khyber Pakhtunkhwa province, Pakistan. *Clematis* (Ranunculaceae) is an economically important plant as being source of different types of pharmaceutical compounds. In Pakistan, there are 10-11 species of this genus that are mostly present in the temperate areas of the country and are being reported to be infected by powdery mildew disease. The plants of *Clematis montana* growing in Ayubia, Abbottabad district, KP, Pakistan have been collected to be infected with powdery mildew fungus. Molecular and morpho-anatomical techniques were used to characterize and identify this powdery mildew fungus. After careful observations, the fungus is identified as *Erysiphe aquilegiae* that belongs to the largest genus of Erysiphales including about 50% of all species of family Erysiphaceae. This genus is represented by 378 species worldwide with 19 species reported form Pakistan. *Erysiphe aquilegiae* is new record for Pakistan and is an addition to our fungal flora. This work will not only be a baseline for further such studies in selected site but will also help in selection of means to protect this important plant (*Clematis montana*) as this disease can compromise its economic and esthetic value by reducing the plant's floral output and stunting its growth.

Presentation ID: 6

A new species of bat fly-associated Laboulbeniales revealed by morphology, molecular data, and host association

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Abstract

As a remarkably successful mammalian radiation, bats host many parasitic and pathogenic lineages of arthropods, of which blood-sucking bat flies (Nycteribiidae and Streblidae) are the most conspicuous. Bat flies can in turn be parasitized by Laboulbeniales fungi, a condition termed hyperparasitism, i.e., the parasitism of a parasite. Laboulbeniales forms one of three orders in the class Laboulbeniomycetes, next to Herpomycetales and Pyxidiophorales. All fungi in the class have an obligate association with arthropods, either as microscopic biotrophics (Herpomycetales, Laboulbeniales) or for dispersal (Pyxidiophorales). The names *Laboulbeniomycetes* and *Laboulbeniales* are in honor of French entomologist Joseph A. Laboulbène, who was among the firsts to observe these fungi in the 1840s. Taxonomy of the order Laboulbeniales is confused, and, as a whole, these fungi are vastly understudied in general. With the application of modern approaches, researchers are working to bridge the gaps in knowledge about this group. Four genera of Laboulbeniales are known from bat flies: *Arthrorhynchus* on Nycteribiidae in the Eastern Hemisphere, *Dimeromyces* on Old World Streblidae, *Gloeandromyces* on New World Streblidae, and *Nycteromyces* on Streblidae in both hemispheres. Here we present a new species of *Gloeandromyces* on *Mastoptera guimaraesi* bat flies (Streblidae) collected from *Phyllostomus hastatus* bats in Ecuador and Panama. The new species is supported by a polyphasic taxonomic approach: distinct morphology, phylogenetic reconstruction of a large subunit (LSU) rDNA dataset, and a seemingly strict association with *Mastoptera* bat flies. This is the first known instance of a species of Laboulbeniales on *Mastoptera*.

Presentation ID: 7

Status of genus *Helvella* (Pezizomycetes, Ascomycota) in Pakistan

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Abstract

The order Pezizales is the most diverse group of ascomycetes represented in Pakistan. The Pezizales, the only order of the Pezizomycetes, is characterized by asci that generally open by rupturing to form a terminal lid called operculum. Most of these Ascomycetes are found in Himalayan moist temperate forests which occupy Kashmir, Murree & Hazara hills, Gilgit and Baltistan, Lower Dir, upper part of Khurram Agency and some humid areas of upper Swat, because of moisture and dense vegetation cover. *Helvella* belongs to family Helvellaceae which has worldwide distribution comprising of 59 species specifically recognized by the pileus shape which is saddle like. From Pakistan, 11 species of *Helvella* are previously reported from different northern areas of Pakistan. Fruiting bodies of *Helvella* grow above ground generally; have stems and cap which is irregularly shaped. During present study, by molecular and morphological data, we have described five new species of *Helvella* with their specific location, as the targeted rDNA of the specimen was amplified by using ITSIF and ITS4. The described species are new to science which extended the status of genus *Helvella* in Pakistan. This study suggests that forests of Pakistan are rich in fungal flora and there is need to explore different areas to document and enlist fungi of Pakistan.

Presentation ID: 8

A new and unusual species *Suillelus himalayensis* from Himalayan oak forest Of Pakistan

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Abstract

Pakistan has a huge altitudinal range from sea level to the peak of K2, the second highest mountain in the world at 8611 m, in the Himalayan mountains. The Himalayas, with its vast altitudinal range, contains an incredible diversity of species and ecosystems and there are four biodiversity hotspots found within this region making Pakistan a valuable repository of montane biodiversity with about 60 % of Pakistan considered mountainous. These mountain ranges are major source of floristic diversity and species endesim. The species *Suillellus* Murrill is important ectomycorrhizal fungi in temperate and boreal regions (Singer 1986, Wu *et al.,* 2014). Here we describe a new species *Suillelus himalayensis* collected from Himalayan moist temperate forests of Pakistan. The basidiomata were collected during the July–August late rainy season. The internal transcribed spacer (ITS) and large subunit rDNA (28S) regions were amplified using the primer combination ITS1F/ITS4B and LR0R/LR5 respectively. The ITS and 28S sequences were searched at BLASTn, UNITE and available sequences of other described *Suillules* spp. were downloaded and analyzed for comparison. *Boletus eduils* and *B. pinophilus* were used as the outgroup taxa. Morphological examination and phylogenetic analysis support the Pakistani collection as a new species. The new species is characterized by plane to convex, light yellow to dark brown pileus with whitish or beige patches, ruptured in distinct patches with entire and smooth margin. The basidiospores are boletiod, oblong and sub cylindrical to fusiform. There is need to increase fungal sampling efforts of biodiversity hotspots.

Presentation ID: 10

The Role of Pyrophilous (Burn) Fungi in Soil Stabilization After Wildfire Assessed by an Aggregate Stability Test

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Abstract

Forest fires are an important occurrence in western landscapes where they help drive ecosystem processes and prescribed fires are a common forest management strategy. An initial consequence of fire is burned ground with reduced biodiversity. Numerous studies have documented how forests recover after fire in terms of plant regeneration and animal colonization, but little is known of the ecological roles fungi play in this process. Certain 'pyrophilous' (burn-loving) fungi have been observed to produce large fruitings and copious mycelium on burns following fire. Our hypothesis is that pyrophilous fungi help bind and stabilize soil after forest fires via their extensive mycelial network, thus reducing soil erosion. Four pyrophilous fungi, *Geopyxis carbonaria*, *Pyronema* sp., *Morchella* sp., and *Anthracobia muelleri* were isolated from burn sites and each were grown in 12 jars of burn soil collected from the Ten Mile Fire in Trego, MT. Controls were 12 jars (per species) of burn soil with no fungi added. After assessment at 10, 20, 30, and 40 days, the Soil Aggregate Stability Test showed that the mycelium of the fungi aggregated the soil in comparison to controls, and the rate of aggregation was different and influenced by their respective ecology. Results have important management implications, particularly for erosion in watersheds and on steep slopes. Post-fire activities can disturb delicate soil on burns and our research suggests that such activities might need to be managed post-fire. This is the first direct evidence of pyrophilous fungi aggregating burn soil.

Presentation ID: 16

Survey of Culturable Fungal Endosymbionts in Nova Scotia Intertidal and Subtidal Macroalgae

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Abstract

Marine macroalgae are a polyphyletic group of photosynthetic eukaryotes which play critical roles in oxygen production, as primary producers, and in providing physical habitat structure. They harbor diverse microbial communities, including mutualistic, commensalistic, and parasitic fungi. These fungi may be obligately or facultatively marine and symbiotic. They are being investigated as a promising new resource for bioactive compounds, a wide variety of which likely remain undiscovered. In this investigation algicolous fungi were isolated from marine macroalgal samples collected from five intertidal ecosystems in Nova Scotia and identified using ITS rDNA Barcoding. From 11 species of marine macroalgae, 125 fungal isolates were identified to genus and 89 were identified species, representing 21 genera and 23 species One potentially previously-undescribed fungus was also identified, and multilocus sequencing was undertaken to aid in its confirmation as a novel species.

Presentation ID: 17

A worldwide assessment of herbarium specimens reveals the invasion dynamics of a detrimental plant pathogen

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Abstract

The introduction, spread, and impact of fungal plant pathogens is a critical concern in cultivated, developed, and natural landscapes. In this study, we were motivated by a recently reported decline in *Acer macrophyllum* (bigleaf maple) in the Pacific Northwest, and the sudden appearance of *A. macrophyllum* heavily infected with powdery mildew. In field studies, powdery mildew caused by *Sawadaea bicornis,* was found in several locations in western North America on *A. macrophyllum.* In greenhouse studies, *A. macrophyllum* was significantly more susceptible to *S. bicornis* than nine other *Acer* spp. tested. We then sequenced the ITS and 28S regions of 140 specimens of powdery mildew from throughout the world using both freshly collected and ancient herbarium specimens. Our analyses revealed seven different haplotypes that are phylogenetically split into two separate groups. The high diversity of haplotypes found in Europe coupled with sequence results from a specimen from 1864 allowed us to conclude that *S. bicornis* has a European origin. Furthermore, sequence data from a specimen from 1938 in Canada show that the pathogen has been present in North America for at least 82 years revealing a considerable lag time between the introduction and current epidemic. We believe this is the first study to use herbarium specimens to genetically ascertain the origin, the native host, and the invasion time of a detrimental plant pathogen. Examining genetic data of herbarium specimens can be a useful tool in efforts to decipher the invasion dynamics of non-native plant pathogens, and address ecological, evolutionary and pathological questions related to emerging plant pathogen epidemics.

Presentation ID: 18

Fungal community composition associated with leaves of a *Eucalyptus grandis* half-sib population

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Abstract

Plants provide many different habitats for fungi, which live epiphytically and endophytically in the phyllosphere (i.e., above-ground) and rhizosphere (i.e., below-ground) of plants. Recent developments in high-throughput DNA sequencing have revealed the huge diversity of these fungi that are associated with plants and that the structure of these fungal communities is equally determined by environmental conditions and plant genotype. Furthermore, it has been shown that interactions amongst these plant-associated fungal communities, and amongst these fungal communities and arthropods, can influence plant health. Considering this complexity of biotic interactions and its effect on plant health, the study of the entire plant mycobiome has gained more attention. In this study, we characterize fungal communities associated with 180 *Eucalyptus grandis* half-sib individuals using a metabarcoding approach. The *E. grandis* half-sibs were scored for infestation levels of the gall wasp *Leptocybe invasa*, which causes gall formation on shoot tips and leaves. High fungal diversity was observed across all samples and we were able to identify fungal taxa in Mycosphaerellaceae, Teratosphaeriaceae, and Botryosphaeriaceae, which contain potential pathogens. Furthermore, we observed clustering of the fungal communities according to the severity of *L. invasa* infestations. Ongoing work is now considering the influence of the plant genotype, insect infestation and potential interactions amongst the members of the fungal community.

Presentation ID: 19

Genetic differences among *Teratosphaeria* leaf and stem pathogens of *Eucalyptus*

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Abstract

Teratosphaeria is a fungal genus of predominantly *Eucalyptus*-associated species, many of which cause serious diseases. The *Eucalyptus* hosts of these fungi are cultivated in plantations in many parts of the world, where they are mostly non-native and threatened by disease and pest problems. The majority of *Teratosphaeria* pathogens cause *Eucalyptus* leaf diseases that vary in severity depending on the causal species, but two species cause a stem canker disease. Both the leaf and stem canker pathogens appear to have evolved from a leaf-associated ancestor. In this study, we predicted and functionally annotated genes in the available *Teratosphaeria* genome sequences and compared the gene contents of the stem canker pathogens with those of aggressive and less aggressive leaf pathogens. The results suggest that economically important *Teratosphaeria* pathogens have evolved numerous unique gene families in comparison with their less aggressive counterparts. The expansion of unique gene families was especially pronounced in the stem canker pathogens, which also had a larger complement of secondary metabolite biosynthesis clusters. Unique carbohydrate and amino acid metabolism gene families identified in the stem and leaf pathogens, respectively, could provide clues to the substrate specificity of each group. Overall, the results provide a broad view of gene evolution in *Teratosphaeria* species having different lifestyles and they represent a step towards a more comprehensive understanding of the biology of these important tree pathogens.

Presentation ID: 20

Genomic modifications induced by transposable elements have most likely driven host specialisation of two *Ceratocystis* species

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Abstract

The genus *Ceratocystis* includes important pathogens of great concern to forestry and agricultural industries globally. *Ceratocystis manginecans* causes cankers, wilt and death of *Mangifera indica* (mango), *Acacia mangium* and other leguminous trees. In contrast, *Ceratocystis fimbriata sensu stricto,* a close relative to *C. manginecans*, causes only black rot on *Ipomoea batatas* (sweet potato). Since the genetic factors determining the host specificity of these two species is unknown, our aim was to use genome comparisons to identify genomic differences between *C. fimbriata* and *C. manginecans* that are likely associated with their host specificity. A high overall similarity was found between the genomes of the two species (93% reciprocal alignment) but this was interrupted by large structural variations. Multiple species-specific genes were identified (2-5% of the gene content), including those encoding small secreted effector proteins, nutrient processing proteins and stress response proteins. Nearly 20% of the pathogen genomes consisted of transposable elements (TEs) of which 17% were uniquely distributed in either of the two species. TEs were associated with the structural variants and with species-specific genomic regions and likely facilitated many of these mutational events. Two highly variable effector clusters (11-15 effectors), with unique TEs, were also identified. These clusters could serve as mutation "hot-spots" and contribute to the distinct host associations of the two species. Genome comparisons allowed for the identification of candidate genes likely associated with host specificity in *Ceratocystis.* Planned future functional studies of these genes will confirm their role and their potential for disease control.

Presentation ID: 21

Genome sequencing and development of microsatellite markers for the Eucalyptus pathogen *Calonectria pentaseptata*

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Abstract

Leaf blight caused by Calonectria species (asexual states *Cylindrocladium*) is one of the most important foliage diseases in *Eucalyptus* plantations worldwide. *Calonectria pentaseptata* is the most aggressive of the *Calonectria* species in both *Eucalyptus* plantations and nurseries in southern China. Little is known regarding the population diversity or molecular basis of pathogenecity in *C. pentaseptata*. In this study we generated high quality reference genome sequences for two isolates of *C. pentaseptata* using a combination of illumina and Nanopore sequencing technologies. These assemblies were highly continuous and had the smallest number of scaffolds (18) and highest N50 value (~5.1Mb) when compared to the available genome assemblies of other *Calonectria* spp. Using these genome sequences, 10 pairs of highly polymorphic microsatellite markers were developed for *C. pentaseptata*. These markers will now be used to assess the genetic diversity, population differentiation and gene flow in populations of the pathogen from different locations in China. The high-quality reference genomes generated in this study will also facilitate genomics studies to better understand how *C. pentaseptata* causes disease on *Eucalyptus* species.

Presentation ID: 23

Population structure and reproductive strategy in the *Eucalyptus* foliar pathogen *Teratosphaeria destructans*

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Abstract

The aggressive *Eucalyptus* leaf pathogen *Teratosphaeria destructans* causes widespread damage to plantations in tropical and subtropical *Eucalyptus*-growing regions in South East Asia and South Africa. Little is known regarding the origin, pathways of dispersal or the reproductive biology of this pathogen. The aim of this study was to investigate the mating strategy and population structure of a global collection of *T. destructans* isolates. Using genome sequences, the mating type (*MAT1*) locus was characterized and the distribution of mating type idiomorphs determined for six global populations. Population structure was evaluated by developing and applying polymorphic microsatellite markers. *Teratosphaeria destructans* was shown to have a heterothallic mating system and each investigated population had one dominant mating type. The global collection of isolates grouped in three distinct clusters, generally corresponding to their sampled regions. Populations had high numbers of clones and showed no signs of recombination, highlighting the strong influence of asexual reproduction in *Eucalyptus* plantations. To date, only the asexual state of this pathogen has been found. Low levels of genotypic diversity, high levels of clonality and strong geographic structure suggest independent introductions into all the sampled areas from an unknown source. The results suggest that sexual reproduction plays a minor if any role, where the pathogen occurs in plantations of non-native *Eucalyptus* species.

Presentation ID: 24

A comparative genomics approach to analyse host-specific genes in agriculturally important *Fusarium* species of the American clade of the FFSC

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Abstract

The *Fusarium fujikuroi* species complex (FFSC) contains various agriculturally important pathogens. The genomic sequence information of many of these species is accessible with some assembled into chromosomes. This study aims to identify potential genic factors contributing to host-specificity between *Fusarium* species associated with *Pinus* species (*i.e.*, *F. circinatum*, *F. pininemoral*e and *F. fracticaudum*) and also those *Fusarium* species associated with members of Poaceae (*i.e.*, *F. temperatum*, *F. subglutinans* and *F. konzum*). We identified and functionally annotated 72 and 47 genes potentially involved in host-specificity between and unique to the two sets of species. These genes are suggested to be primarily involved in carbohydrate and protein metabolism. Upon phylogenetic analyses of these two sets of unique genes, we found that they have originated from various ancestral origins. We observed a difference in the frequency distribution of these unique genes between telomeric and non-telomeric regions, with more unique genes residing at telomeric ends. Some of these unique genes also tend to be closely located to each other or cluster together. We identified a chromosome length polymorphism between chromosome 12 of *F. temperatum* and *F. circinatum*. Chromosome 12 of *F. temperatum* are larger in size and possessed more unique genes compared to this chromosome in *F. circinatum*, which likely contribute to niche-specificity amongst *Fusarium* species associated with Poaceae. Our findings demonstrated that *Fusarium* species likely employ several different mechanisms to promote colonisation, infection and disease on their respective plant hosts.

Presentation ID: 25

Nodulose-spored Inocybe from the Rocky Mountain alpine zone molecularly linked to European and type specimens

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Abstract

Inocybe (Inocybaceae) is one of the most diverse ectomycorrhizal genera in arctic and alpine habitats where the primary hosts are *Salix, Betula*, and *Dryas*. Subgenus *Inocybe* is common in these habitats and typically characterized by the presence of thick-walled pleurocystidia. Here we focus on species that have angular or nodulose spores. Historically, over thirty taxa from this group have been reported from Arctic and alpine habitats. Many names have been synonymized, while molecular analysis has revealed new species. Nuc rDNA ITS1-5.8S-ITS2 (ITS) sequence data of 24 type specimens in this group now allows for further taxonomic clarification and comparison across continents of disjunct populations. Here we compare ITS sequence data and the D1–D2 portion of nuc 28S rDNA (28S) from Rocky Mountain specimens with those of types and European reference material. We report ten species from the Rocky Mountain alpine zone, all of which are conspecific with known European boreal, montane or alpine species, and four are described as new; all have intercontinental distributions. Nodulose-spored *Inocybe* that occur in the Rocky Mountain alpine zone include: *I. alpinomarginata* sp. nov*., I. arctica, I. giacomi, I.leonina, I. murina* sp. nov*., I. occulta, I. paragiacomi sp. nov., I. phaeocystidiosa, I. purpureobadia,* and *I. subgiacomi* sp. nov*.* Remarkably, these species occur at elevations up to 4000 m and at latitudes as low as 36^0 N, hundreds of miles from the Arctic, the European alpine, and original type localities. Distributions are explained in part by host distributions and historical glaciation patterns.

Presentation ID: 26

A new genus and species of Coryneliaceae (Coryneliales) causing a serious canker disease on *Araucaria araucana* in Chile

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Abstract

Pewen or the Monkey Puzzle tree (*Araucaria araucana*) is an ancient conifer endemic to the mountain ranges from Chile and Argentina. Its distribution is limited to small populations in the south-central region of the Andes mountain range and Chilean's coastal range, where it is of cultural and economic importance to the indigenous people of the region. In 2015, decline symptoms were observed on *A. araucana* trees throughout most of its distribution. During intensive field surveys, a canker disease associated with the death of branches and young stems of these trees was detected. Samples were collected from symptoms on trees across their natural distribution in Chile. Isolations were made from the margins of freshly formed cankers and directly from black ascomata emerging from older cankers. Cultures having a similar morphology were obtained using both isolation techniques. Morphological and phylogenetic analyses of these isolates showed that the recovered fungus represents a novel genus and species in the Coryneliaceae (Coryneliales). Inoculations conduced on naturally regenerated trees in the field (trees up to 3 metres high), and on young plants in the nursery caused discolouration and girdling symptoms similar to those observed in natural infections. These results confirm that the isolated fungus, which is currently being described, is the causal agent of the cankers observed in the field. The factors triggering the emergence of this canker disease are unknown, however, we believe that climate change is, at least in part, involved.

Presentation ID: 27

The transferability of *Agrobacterium*-mediated transformation technology amongst species from the family Ceratocystidaceae

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Abstract

Performing functional studies requires the establishment of a transformation system in the organism of interest. Numerous transformation systems have been developed and applied to filamentous fungi with varied degrees of success. *Agrobacterium*-mediated transformation is one such system that has shown a lot of success, although this requires extensive optimizations to establish an efficient protocol. Existing protocols are mostly based on model species, making it difficult to apply these to non-model fungi which are often distantly related. For this reason, this study aimed to determine the ease with which an *Agrobacterium*-mediated transformation protocol could be successfully applied to species from different genera among the family Ceratocystidaceae. This fungal lineage is known for its importance to global agricultural and forestry industries, with many members known as tree and plant pathogens. An *Agrobacterium* protocol, recently established in the African fungus *Ceratocystis albifundus*, was adjusted to increase its efficiency in this species. The adjusted protocol was subsequently applied to eight other Ceratocystidaceae species across eight genera, including *Ceratocystis*. Of these, six species (*C. manginecans*, *Berkeleyomyces basicola*, *Chalaropsis ovoidea*, *Davidsoniella virescens*, *Huntiella moniliformis* and *Thielaviopsis cerberus*) were successfully transformed, while transformation of *Ambrosiella cleistominuta* and *Endoconidiophora polonica* failed. All transformed species expressed detectable levels of green fluorescent protein, producing genetically engineered isolates that could prove useful for future studies aimed at tracking host infection processes. The study provides a benchmark for efforts aimed at establishing and optimising *Agrobacterium* transformation in non-model species and demonstrates the transferability of this technology between species of the same family.

Presentation ID: 28

Genetic diversity and population structure of *Chrysoporthe deuterocubensis* in South East Asia

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Abstract

Chrysoporthe deuterocubensis is the causal agent of a serious canker disease of *Eucalyptus* spp. in tropical and sub-tropical areas of Asia. Where the disease occurs, *Eucalyptus* spp. are non-native and the hosts of origin of the pathogen are unknown. The discovery of *C. deuterocubensis* on native *Melastoma malabathricum* growing in the understory of *Eucalyptus* trees in Indonesia raised the possibility that this woody shrub could be the origin of the pathogen and that a host jump could have occurred to *Eucalyptus*. In this study, isolates of *C. deuterocubensis* were collected from *Eucalyptus* and *Melastoma* trees in Indonesia and Malaysia. These were subjected to population genetic analyses using microsatellite markers. The genetic diversity of the populations from *Melastoma* was slightly higher (H = 0.377 and 0.308 for Malaysia and Indonesia, respectively) than those from *Eucalyptus* (H = 0.269 and 0.221). However, these values were not sufficiently enough to be regarded as native populations. The maximum percentage of genotypic diversity was high for all populations of isolates (G_{max} between 60.0 to 74.4 %) irrespective of host. Structure analyses showed admixture within the clusters, regardless of host plant species. Overall, the results failed to show that isolates of *C. deuterocubensis* were native on the indigenous *M. malabathricum*. A more likely hypothesis is that *C. deuterocubensis* has originated from currently unknown host trees in the humid tropics of South East Asia.

Presentation ID: 29

Phylogeny of needle cast pathogens in the *Lophodermella* clade on five-needle pines in the US

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Abstract

Lophodermella species (Rhytismataceae) are known needle cast pathogens on pines. Previously, of the 9 known *Lophodermella*species*,* only *Lophodermella arcuata* was reported to infect five-needle pines in North America. Through molecular information, this study explored a potentially new species of *Lophodermella* sp. associated with needle cast on *Pinus flexilis* in Rocky Mountain National Park, Colorado and its relationship with other *Lophodermella* species. Morphology of *Lophodermella* sp. had significant similarities to *L. arcuata* particularly its microscopic morphometric features such as subhypodermal hysterothecia, tanned hypodermal cells, and colorless clavate ascospores. However, phylogenetic analyses using three gene regions: internal transcribed spacer, large ribosomal subunit and translation elongation factor 1-alpha, revealed that *Lophodermella* sp. was distinct from *L. arcuata* and was consistently nesting within the *Lophodermella* clade composed of *L. arcuata*, *L. montivaga* and *L. sulcigena*. This is a first report on *Lophodermella* sp. infecting limber pine in Colorado apart from the known *L. arcuata*. Further, this study provided more evidence for the reclassification of *Lophophacidium dooksii* (Phacidiaceae)*,* a needle cast pathogen on *P. strobus,* to Rhytismataceae. *Lophophacidium dooksii* sample collected from Maine, USA consistently nested within the *Lophodermella* clade in all three loci phylogenies. Microscopic features of *Lophophacidium dooksii* showed significant similarities to *Lophodermella* species except for its ascospore shape. This study reveals two additional species within the *Lophodermella* clade infecting five-needle pines, *P. flexilis* and *P. strobus*. Our results provide further insights on needle pathogen behavior and ecology causing potential emergence of new diseases on five-needle pines.

Presentation ID: 30

Botryosphaeriaceae diversity on *Eucalyptus* clones in different climate zones of Indonesia

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Abstract

The *Botryosphaeriaceae* is an important and diverse family of latent fungal pathogens of woody plants, including *Eucalyptus*. These fungi are able to live within asymptomatic plant tissues for an extended time, but cause disease when their host plants are subjected to stress. In this study, we compared the diversity of *Botryosphaeriaceae* in samples from nine different *Eucalyptus* genotypes growing in two areas of Sumatra (Indonesia) having distinct altitude and either a temperate or tropical climate. Samples were taken from asymptomatic trees, as well as those damaged by a sucking insects (Miridae), a wood-boring moth (Cossidae), and a shoot and leaf disease of unknown cause. In total, 215 Botryosphaeriaceae isolates were obtained. These were identified as 14 species based on analyses of rDNA-ITS, TEF-1α, β-tubulin and RPB2 sequence data. These species included seven *Lasiodiplodia* spp. (*L. brasiliensis L. lignicola, L. pseudotheobromae, L. theobromae* and three undescribed species), four *Neofusicoccum* spp. (*N. dianense, N. parvum, N. magniconidium, N. occulatum*), as well as *Endomelanconiopsis endophytica* and *Cophinforma atroviren*s. Twelve *Botryosphaeriaceae* species were found from both asymptomatic trees and those damaged by disease or insects. *Lasiodiplodia brasiliensis* and *L. pseudotheobromae*, were isolated only from disease or insect damaged trees. The results showed a clear pattern of climatic zone occurrence for the 11 *Botryosphaeriaceae* spp. While three species, *L. theobromae, L. brasiliensis* and *L. egyptiacea* were found in both climatic zones, *L. theobromae* was the most common of these species. Future work will include further sampling and pathogenicity tests to determine the role of these Botryosphaeriaceae in disease.

Presentation ID: 31

Ophiostomatoid fungi associated with ambrosia beetles in South Africa, including two new species

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Abstract

Ambrosia beetles are small wood boring Curculionids (Scolytinae and Platypodinae) that associate with one or more primary fungal symbionts and several auxiliary fungal species. Most of these fungi are ascomycetes that reside in a non-monophyletic group collectively known as the Ophiostomatoid fungi (Ophiostomatales and Microascales) and (1) serve as a food source to the developing brood and adults; (2) play a role in brood development; and (3) facilitate the fitness and adaptation of the beetles to different environments. The aim of this study was to collect and identify ambrosia beetles and the Ophiostomatoid fungi associated with them. Beetle specimens were collected using a modified Bamabara beetle trap and isolations were made on Malt Extract Agar (MEA) amended with different antibiotics to facilitate in the isolation of fungi and Ophiostomatalean species. Five species of Ophiostomatoid fungi emerged from the isolations. These were *Raffaelea arxii*, which has previously been recorded in South Africa, *Raffaelea sulphurea,* and *Ambrosiella roeperi* reported here from the country for the first time, and novel species of *Ceratocystiopsis* and *Raffaelea.* This study provides a preliminary foundation for research on ambrosial fungi research in South Africa and it highlights the likely diversity of species yet to be discovered from this niche in the country.

Presentation ID: 32

Novel mating type gene, *MAT1-2-7*, is essential for ascomatal maturation in *Huntiella omanensis*

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Abstract

The saprophyte fungus, *Huntiella omanensis*, harbours two genes at its *MAT1-2* idiomorph. These include *MAT1-2-1*, which encodes a highly conserved protein with a well-characterised HMG-box domain, and *MAT1-2-7*, a novel *MAT* gene that produces a protein with no recognisable functional domains. In this study, we developed a protoplast-based transformation and protein-based CRISPR-Cas9 genome editing protocol. This newly developed method was subsequently used to characterise the novel *MAT1-2-7* gene, particularly with respect to its function in mating. Truncation of this gene resulted in mutant isolates that were capable of producing immature protoascomata when mated with a suitable partner. However, these isolates were incapable of further ascomatal maturation or ascospore production. The mutant isolates also grew significantly more slowly than the wildtype strains. This study thus confirmed that the novel *MAT* gene is essential for sexual reproduction in *H. omanensis* and that it also plays a role in other biological characteristics such as growth. The newly established transformation and genome editing protocols will also be optimised for use in other species of this fungal family and will be used to characterise genes putatively involved in host specificity, virulence and mating.

Presentation ID: 33

Migration and population genetics of the maize fungal pathogen Cercospora zeina in East and Southern Africa

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Abstract

Gray leaf spot (GLS) is a major foliar disease of maize caused by the fungus *Cercospora zeina* Crous & U. Braun. *C. zeina* is reported to be a highly diverse pathogen in maize producing countries globally due to sexual recombination and persistent gene flow. However, these reports are based on analyses of a few isolates, populations, and geographical locations, with no comprehensive population genetics studies of the pathogen in Africa. This study aimed to determine the genetic structure, evolutionary potential, and migration routes of *C. zeina* populations from Kenya, Uganda, Zambia, and Zimbabwe, and South Africa. Analysis of 964 single-spore isolates made from GLS lesions using diagnostic PCR confirmed *C. zeina* as the causal agent of GLS in Africa. None of the isolates were *Cercospora zeae-maydis,* the other GLS-associated pathogen in other continents. Genotyping these isolates using 11 microsatellite markers and a PCR mating-type diagnostic revealed that *C. zeina* is a genetically variable heterothallic pathogen, with high population differentiation between countries and significant linkage disequilibrium. We found directional migration between countries, with South Africa and Kenya being the greatest donors of migrants between regions. Zambia had a distinct population with the lowest number of incoming migrants. Our data indicated that continuous annual maize production in Eastern Africa does not result in a greater diversity of the pathogen compared to a single maize season in Southern Africa. This study lays the groundwork for effective monitoring of the dispersal of *C. zeina* towards improved control of gray leaf spot disease in Africa.

Presentation ID: 34

Repeat-Induced Point mutations in the era of genomics

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Abstract

The increasing availability of fungal genomes that are assembled into chromosome-sized scaffolds allows detailed investigations into the genome-wide effects of the Repeat-Induced Point (RIP) mutation process. RIP is a fungal genome defense mechanism that acts against the deleterious consequences of repeated motifs such as transposable elements (TEs). In this study, we used sliding-window and alignment-based approaches to determine how genome sequence quality and completeness might influence RIP analyses. To this end, the genome-wide RIP statistics were compared for three versions of the *Fusarium circinatum* genome, representing improvements over time as new technologies and more data were used for assembling the genome sequence. Our results showed that the rigor of genome-wide RIP analyses was dependent on the quality of genome data being examined. With an improvement in genome quality, more RIP mutations were detected. Also, more TEs were identified in the more complete genome. However, alignment-based analyses of the highly fragmented assembly provided limited information on the occurrence of RIP, whereas for the same data set, RIP was detected using a sliding-window approach. This limits the feasibility of alignment-based analyses for detecting RIP in less complete, fragmented genomes. Our study showed that a sliding window approach provided information on genomic location of RIP and facilitated identification of regions with extensive RIP. Such information holds valuable clues, not only regarding the RIP-capability of a particular fungal species, but also our understanding of the genetic changes and evolutionary consequences brought about by the RIP process.

Presentation ID: 35

Secreted enzymes and secondary metabolite genes reveal Botryosphaeriaceae adaptation to latent pathogenicity

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Abstract

The *Botryosphaeriaceae* are important plant pathogens, but also commonly establish asymptomatic infections, persisting in their plant hosts for extended periods as latent infections. Very little is known regarding the secretory and secondary metabolite repertoires of the *Botryosphaeriaceae,* which are expected to be involved in these host interactions. Comparative analyses considering secreted hydrolytic enzymes and secondary metabolite biosynthetic gene clusters were performed using available *Botryosphaeriaceae*, as well as selected Dothideomycetes genomes. The *Botryosphaeriaceae* genomes were rich in secreted carbohydrate-active enzymes (CAZymes), proteases, lipases, and secondary metabolic biosynthetic gene clusters (BGCs) when compared to those of other Dothideomycetes. The genomes of *Botryosphaeria*, *Macrophomina*, *Lasiodiplodia*, *Neofusicoccum* and *Neoscytalidium,* in particular*,* had gene expansions in the major constituents of the secretome. These were notably CAZymes involved in plant cell wall degradation and were most similar to prominent necrotrophic plant pathogens, saprobes and an endophytic/latent pathogen in the Pleosporales. The abundant secreted hydrolytic enzymes and secondary metabolite BGCs found in the *Botryosphaeriaceae* are comparable with those of several other studied species of woody endophytes. The general trend in these endophytic species is that they have similar or higher amounts of various secreted enzymes (notably plant cell wall degrading enzymes) or secondary metabolites than closely related plant pathogenic species. The results of this study provide a framework for future comparative genomic analyses and an exploration of the mechanisms underlying host interactions in the *Botryosphaeriacae*.

Presentation ID: 36

Live plant baiting – a tool to understand host specificity in soil-borne *Phytophthora* species

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Abstract

Phytophthora species are important pathogens of several commercial tree species in South Africa. In this study, we used a live plant soil baiting technique together with high-throughput sequencing to identify those *Phytophthora* species that can infect *Eucalyptus grandis* and *Acacia mearnsii*. We hypothesized that the *Phytophthora* species richness associated with roots of the plant baits will be affected by the source of the soils and the host plants associated with them. To test this view, we identified four soil sampling locations in the KwaZulu-Natal (Howick, Melmoth, and Vryheid) and Mpumalanga (Commondale) Provinces of South Africa where plantations of *E. grandis* and *A. mearnsii* were adjacent to natural forests. At each location, we collected two composite soil samples from each environment. Each soil sample was divided into two parts and seedlings of *E. grandis* and *A. mearnsii* that had been established under sterile conditions were planted in each of these soils. After five months of growth in a controlled environment phytotron, roots of the seedlings were harvested and total genomic DNA was extracted. The DNA samples were barcoded using *Phytophthora*-specific primers. The resultant amplicon library was sequenced using the pyrosequencing platform. Statistical analyses of our barcoding data confirmed that *Phytophthora* species richness in the roots was: (i) significantly influenced by the source of the soil, and (ii) higher among the *A. mearnsii* than *E. grandis* seedlings used as live baits. Even though a sub-set of *Phytophthora* species was shared between the tested environments, the majority of species appeared to display host preference.

Presentation ID: 37

Seven novel *Fusarium* spp. associated with ambrosia beetles on *Acacia crassicarpa* in Indonesia

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Abstract

Ambrosia beetles (Curculionidae: Scolytinae and Platypodinae) are wood boring insects, the lifecycles of which are spent almost entirely within the xylem of suitable host trees. They survive in this nutritionally poor ecological niche due to their obligate nutritional symbiosis with fungi. Several ambrosia beetle species have emerged as important invasive pests globally and the diseases with which they are associated, threaten tree species in both urban and commercial forestry landscapes around the world. In this study, several ambrosia beetle species were collected from two to three-year-old non-native and heavily infested *Acacia crassicarpa* trees, located in five geographically separated plantation blocks in Riau, Indonesia. Fungi were isolated from the mycangia and brood galleries of the collected beetles. The beetles and their fungal symbionts were identified based on morphology and DNA sequence data. *Euwallacea similis* and *Euwallacea perbrevis* were the most abundant beetles infesting the trees. Multigene phylogenetic analyses of their fungal associates revealed their non-specific relationship with seven novel *Fusarium* spp. residing in the *Fusarium solani* species complex (FSSC). One novel associate has already been formally described as *Fusarium rekanum* sp. nov (AF-19), while the remaining six novel *Fusarium* spp. are currently being formally described. The ecological role of these novel *Fusarium* species, as well as their pathogenic potential is also under investigation.

Presentation ID: 38

Annual temperature alters recovery time for alpine soil fungi after fires

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Abstract

Though much is known about fungal importance to forest health, there is very little information about factors that impact soil fungal community recovery time after a fire. Soil samples were taken from burn sites within one ecotype of temperate coniferous forest in Utah over a 20-year chronosequence. Sites were selected from available historic burns and were similar in plant community structure, elevation, slope, and aspect. Fungal DNA from these samples was compared to soil from paired unburned sites nearby to measure community similarity and estimate soil fungal recovery rates. Differences between paired burned and unburned sites remained fairly stable over a decadal time scale overall, but fungal community structure was found to recover more quickly in areas with a higher average annual temperatures. A significant positive correlation in community recovery was seen in areas with a difference of as little as two degrees celsius per year. The only other environmental variable that significantly interacted with time since burn was annual mean precipitation. As global temperatures increase, alpine fires are increasing as well, but these results suggest that fungal community recovery time will be shortened under new climate scenarios.

Presentation ID: 39

New species of sequestrate Inocybe from Chilean Nothofagaceae forests

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Abstract

Sequestrate fungi have enclosed hypogeous, subhypogeous or epigeous basidiomes and have lost the ability to actively discharge their spores. They can be distinguished as gasteroid (basidiome fully enclosed with a loculated hymenophore) or secotioid (basidiome with some agaricoid or pileate-stipitate features, but the lamellae are misshapen and unexposed or mostly unexposed at maturity). There are only three described sequestrate taxa within the ectomycorrhizal family Inocybaceae, three from Australia and one from western North America. Recent fieldwork in Nothofagaceae forests in the Chilean coastal range revealed novel sequestrate forms of *Inocybe*. We examined specimens using a combination of morphological and molecular data from nuc rDNA ITS1-5.8S-ITS2 (ITS) and portions of nuc 28S rDNA (28S) and the gene encoding the second largest subunit of RNA polymerase II (*rpb2*). Here we discuss four provisional new *Inocybe*species, *I. ranunculiformis* nom. prov., *I. anfractuosa* nom. prov., *I. illariae* nom. prov. and *I. nahuelbutensis* nom. prov..Results of our phylogenetic analysis resolved the four new species as distinct species-level clades with strong support, suggesting these fungi have convergently evolved sequestrate forms independently. The species described here were all placed among members of the "smooth-spored temperate austral clade", which includes almost exclusively Australasian and South American species of *Inocybe*.

Presentation ID: 40

Molecular markers reveal global genetic diversity and mating strategy in the important plant pathogen, *Calonectria pauciramosa*

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Abstract

Calonectria pauciramosa causes serious diseases on numerous woody, herbaceous and ornamental plants worldwide. An important basis for the control spread of *Ca. pauciramosa* lies in understanding its genetic diversity and mating strategy on different hosts and countries where it occurs. In this study, 15 polymorphic microsatellite markers were developed utilising the whole genome sequences of two *Ca. pauciramosa* isolates from different countries and with opposite mating types. These markers were used to determine the genetic diversity of 145 isolates representing 13 different hosts (12 plant hosts residing in 12 genera, and soil) from 10 countries. In addition, mating type genes were amplified to investigate the mating strategy of the pathogens in these populations using mating type primers designed for *Calonectria* spp. Results revealed that a single dominant genotype of *Ca. pauciramosa* was present in isolates from seven countries across five continents and 11 genera of plant hosts residing in eight families. The MAT1-2 mating type was the most dominant and widely distributed in isolates from 12 different hosts (11 plant hosts and soil) collected in 10 countries. Only isolates from *Eucalyptus* in South Africa and Uruguay contained both mating types. These results provide substantial evidence that *Ca. pauciramosa* has been distributed worldwide, most likely with the global movement of plant material and soil. Keywords: aggressive pathogen, *Cylindrocladium pauciramosum*, population genetics, reproductive mode, dispersal pathways

Presentation ID: 41

Draft genomes and comparative analyses of binucleate *Rhizoctonia* isolates

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Abstract

The *Rhizoctonia* species complex in the family Ceratobasidiaceae is commonly associated with its pathogenic lifestyle causing diseases in crops of economic importance around the world. Within the family, the genera Ceratobasidium and Thanatephorus are teleomorphic stages of *Rhizoctonia*. Classification of this species is based on hyphal recognition and fusion distinguishing different anastomosis groups within two major groups: multinucleate (Thanatephorus spp.) and binucleate (Ceratobasidium spp.). While the genomes of different multinucleate anastomosis groups have been assembled and their pathogenicity mechanisms studied, binucleate isolates have not been equally described. Isolates of different anastomosis groups differ in genome sizes, host specificity and number of secreted proteins, among others, suggesting differences in pathogenesis. Given this diversity and the lack of information for binucleate isolates to date, studying the genome of representatives from all anastomosis groups remains necessary for a better understanding of the species. We assembled and characterized the draft genomes of four *Rhizoctonia* binucleate isolates from Arkansas and other southeastern states using long-read sequences obtained by Nanopore sequencing. The assembly lengths ranged between 72.8 and 82 Mb and the corresponding GC content between 48.35 and 50.81%. Completeness of the genomes was assessed based on BUSCO content and ranged from 75.8 to 81.3% complete genes. Pairwise comparisons of read alignments were performed to understand sequence similarities between anastomosis groups. These preliminary genomic resources provide a framework for future comparative analyses that help understanding the biology of *Rhizoctonia* species.

Presentation ID: 42

Yeast communities associated with a Eucalyptus leaf and shoot disease of unknown aetiology in North Sumatra

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Abstract

During the course of the last two decades, short-rotation plantation forestry has expanded substantially in South-East Asia, and especially in Indonesia. In 2014, a new *Eucalyptus* shoot and foliar disease of unknown aetiology appeared in plantations of North Sumatra. The disease is characterised by black necrotic spots that appear initially on young leaves and petioles. Some infected plants also show mild to severe distortion of infected tissues including small leaves and "feathered" shoots. No fruiting structures typical of leaf and shoot pathogens can be found on the infected tissues. Preliminary observations using scanning electron microscopy confirmed the occurrence of yeast-like cells at the sites of infection. Using culture-dependent methods, a collection of yeast strains was obtained from infected leaf tissues. The isolates were then subjected to phylogenetic analyses using DNA sequence comparisons for the D1/D2 domain of the large subunit (LSU) and the internal transcribed spacer region (ITS) of the ribosomal RNA. From a collection of 79 isolates, eleven yeast genera were identified including *Kalmanozyma*, *Moesziomyces*, *Goffeauzyma, Filobasidium, Kwoniella, Hannaella, Auriculibuller, Saitozyma, Papiliotrema* in the Basidiomycota and *Pseudosydowia* and *Taphrina* in the Ascomycota. The majority (86 %) of the yeasts associated with the disease symptoms were Basidiomycetes. The relatively high diversity of the yeast communities inhabiting the sites of infection suggests that additional studies are required to understand their complex interactions with each other, with their host plants and the role that they could play in disease development.

Presentation ID: 43

Prevalence of *Stachylina* species (Harpellales) in Mayaguez, Puerto Rico

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Abstract

Harpellales fungi are obligate symbionts of arthropods. They need a live host in order to grow and reproduce. They attached without penetration to the gut lining of insect larvae associated with freshwater habitats. One common host family is the Chironomidae (non-biting midges) where we studied the occurrence of Harpellales species in urban sites Mayaguez, Puerto Rico. After sampling and dissecting bloodworm larvae over 12 months, we found two species of *Stachylina* co-inhabiting *Chironomus* sp. larvae. The two species, *S. lentica* and *S. grandispora* represent new records for the island. For *S. lentica* is the first report in the tropics, expanding the known range of the species to the Caribbean region. On average, 38% of the larvae were infected by *S. lentica* reaching a 100% infection in November 2017 and a minimum of 40% in February 2018. For *S. grandispora*, on average, 15% of the larvae were infected reaching a 60% maximum in November 2017 and no infection in February 2018. Interestingly, both fungi reached infection maxima complementarily. We studied correlations between prevalence of each species and abiotic variables (precipitation and temperature). Based on the data analysis, we found no correlation with precipitation, but we detected a weak correlation with temperature for both species, *S. lentica* (0.610929) and *S. grandispora* (-0.61093). This suggests that these species have different optimum temperature ranges that influence their prevalence in the same host. To our knowledge, this is the first time Harpellales species respond to temperature changes.

Presentation ID: 44

Citizen science project contributions to professional mycology

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Abstract

Hibbett et al. (2011) estimated it would take 1170 years to describe 1.4 million fungi. Citizen-science powered projects have started to fill this gap by collecting high quality, vouchered fungal specimens with DNA barcodes. We present recent examples of valuable contributions toward a North American Funga made by citizen-science powered projects. The North American Mycoflora Project (NAMP), The North American Mycological Association (NAMA) forays, Newfoundland & Labrador Foray, Circles de Mycologues Amateurs de Québec, and the 2019 MycoBlitz contributed to professional mycology in numerous ways: 1. The discovery of new species, e.g., *Inocephalus* sp. in Hawaii (Jeff Stallman, NAMP), *Russula* aff. *favrei* in USA (Sigrid Jacob & Steve Russell, NAMP), *Amanita* aff. *vaginata* in Pennsylvania (Garrett Taylor, NAMP), *Gliophorus* sp. in Washington (Steve Ness, NAMP); 2. Contribution of new sequenced specimens of rare species, e.g., *Lachnum halesiia* near the type locality in Georgia (Bill Sheehan, NAMP); 3. The resurrection of North American species previously synonymized with European species, e.g., *Calvatia lilacina ≠ C. cyathiformis* and *Bolbitius variicolor ≠ B. titubans* (Joanne Schwartz, NAMP); *Agaricus lilacifolius ≠ Chromosera cyanophylla (Django Grootmyers & Garrett Taylor, NAMP); 4. Range expansions important for documenting distribution limits of fungi responding to climate change, e.g., the southernmost collections of the circumboreal species, Yuchengia narymica in NW Georgia (Bill Sheehan, NAMP) and Western North Carolina (NAMA Foray). 5. And new occurrence records for North America (e.g., a first record of Pluteus in Hawaii (Jeff Stallman, NAMP); Hygrocybe phaeococcinea, is a record for Western N. America (2019 MycoBlitz).*

Presentation ID: 45

Coker's *Amanita* taxa: 100 years later

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Abstract

Seven Amanita taxa are among the greater than 100 fungal species that Dr. William Chambers Coker described during his career at the University of North Carolina at Chapel Hill. Two Amanita species, *Amanita atkinsoniana* and *A. hygroscopica*, and three varieties, *A. rubescens* var. *alba*, *A. mappa* var. *lavendula*, and *A. spissa* var. *alba,* were published in "The Amanitas of the Eastern United States" (1917, J. Elisha Mitchell Sci. Soc. 33:1-88), as well as two new Amanita species, *A. roanokensis* and *A. gwyniana,* in "New or Noteworthy Basidiomycetes" (1927, J. Elisha Mitchell Sci. Soc. 43: 129-145). All of Coker's four Amanita species and one of his varieties (*A. rubescens* var. *alba*) remain accepted. A second variety has been elevated to the species level as *Amanita lavendula*. The third Amanita variety described by Coker is illegitimate taxonomically, but may still represent a new species or variety. The University of North Carolina at Chapel Hill Herbarium (NCU) boasts a modest Amanita collection of 650 collections representing 80 taxa. Included are 42 type specimens. Coker's *Amanita mappa var. lavendula* (now *A. lavendula*) is of special note given its lavender staining. In recent years, work with Coker's species resulted in the discovery of two additional lavender staining species of Amanita that have been given provisional names. Phylogenetic analysis of the LSU sequences of the three known lavender staining Amanitas and Amanitas featuring similar LSU sequences revealed that lavender staining Amanitas constitute a monophyletic clade.

Presentation ID: 46

Citizen Science for Fungi: Evolution of the North American Mycoflora Project

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Abstract

The North American Mycoflora Project (NAMP) is changing. In August 2020 we will announce a new DNA sequencing partner with new protocols, a more expansive and inclusive vision of engaging citizen scientists and professional mycologists, and a new name and logo. NAMP began at a one-day workshop of professional and amateur mycologists at MSA 2012 at Yale University. The goal was to create a funga for all North American macrofungi. At MSA 2017 at the University of Georgia NAMP was reconceived as a citizen science-driven project. Subsequently, a non-profit organization was created, NAMP, Inc. to help citizen scientists document, sequence & voucher specimens, and post their data online. NAMP, Inc. has more than 160 projects all across the US and Canada, and has sequenced more than 4,000 specimens. Why “reboot”? Fungi don’t get the attention and protection they deserve because most of the world does not yet know that fungi are their own kingdom, equal to plants and animals, and play critical roles in maintaining ecosystems. We are dropping "mycoflora" from our name because it propagates this confusion. Our mission remains unchanged: to equip citizen and professional scientists with the tools to document the diversity and distribution of fungi across North America. Because citizen scientists are more numerous and widely distributed than professional mycologists, they can accelerate our knowledge of macrofungal diversity and distribution and responses to climate change. More: June 2020 Inoculum

Presentation ID: 47

Chromosome length polymorphism (CLP) of a dispensable chromosome in *Fusarium circinatum*

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Abstract

The improvement in sequencing technology allows for improved genome assemblies with scaffold sizes approaching the complete length of individual chromosomes. This has opened up the possibility of genomic comparisons into chromosomal architecture. Resequencing the genome of the pitch canker pathogen, *Fusarium circinatum* isolates FSP34 and KS17, was undertaken using the Oxford Nanopore Technologies (ONT) MinION sequencing platform. These were assembled to chromosomal level with twelve chromosomes obtained for each assembly. Genomic comparisons highlighted the variable nature of chromosome 12, the dispensable chromosome. This chromosome is present in both FSP34 and KS17, yet displays a striking chromosome length polymorphism (CLP), with FSP34 missing large portions from the distal and proximal portions of chromosome 12. These areas are gene poor, have a lower G+C content and contains more repetitive regions, in contrast to the syntenous portion shared amongst FSP34 and KS17, as well as to the core chromosomes. It is hypothesized that these areas implicated in the CLP were formed or expanded by the presence of transposable elements (TEs) in KS17. The association of this disposable chromosome with host-specificity is investigated.

Presentation ID: 48

Hidden species and functional diversity of litter-associated fungi and compositional patterns and distribution on various litter microhabitats in Ozark Mountain forests

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Abstract

Diverse assemblages of macrofungi are associated with the forest floor. Functionally, these organisms are referred to as litter-decomposing fungi, which is a primary component of ecosystem functioning. However, the taxonomic diversity, functional diversity, and community composition of litter-associated macrofungi are seriously understudied. The objectives of the present study were first to identify litter-associated macrofungi using a combination of morphological characteristics and molecular analysis of the nuclear ribosomal internal transcribed spacers (ITS) and then to compare the species richness, function and distribution of these fungi associated with multiple microhabitats on the forest floor at two sites in the Ozark Mountains of Northwest Arkansas. Taxonomically, neither total species richness nor macrofungal productivity was substantially different between the two sites, but the composition of the two assemblages varied. The community patterns comprised of 47 and 42 macrofungal species documented and related to 27 and 24 genera, at least 21 and 17 families for Devil's Den Park and Pea Ridge Park, respectively, with including a group of 16 species belonging to 11 genera recorded in both sites. Diverse functions overlapped various litter microhabitats at both sites, but based on species richness and fruiting productivity, saprotrophs were dominant and appeared to shape the community structure of the guilds present. The leafy litter species formed approximately 62.7% and 60.9% of studied fungal community. The present results documented species that sexually succeed to reproduce, develop, and form fruiting bodies under highly competitive environments between inter and intra populations in fungal diverse community assemblages and other organisms.

Presentation ID: 49

Systematic Analysis of *Russula* in the North American Rocky Mountain Alpine Zone

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Abstract

Russula Pers. (Russulales) is an important ectomycorrhizal fungal genus in alpine and Arctic regions where it occurs in association with *Salix*, *Betula*, *Dryas*, and *Polygonum,* yet an in-depth systematic analysis of the genus in these habitats is lacking. This research compared collections of *Russula* from the Rocky Mountain alpine (CO, MT, WY) to reference specimens from Arctic and alpine habitats, mostly in Europe, using an in-depth morphological study and a systematic molecular analysis of the nuc rDNA ITS1-5.8S-ITS2 region (ITS barcode) and the second largest subunit of the RNA polymerase II gene (*rpb2*). Over 130 *Russula* collections, were sequenced including type material. Eight species are reported for this part of the Rocky Mountain alpine zone, and two from treeline habitats. This is the first formal report of *R. altaica*, *R. saliceticola*, and *R. subrubens* from the Rocky Mountains and of *R. heterochroa* and *R. purpureofusca* in North America. *Russula laevis* is reported for the first time under this name with a voucher, and not as an environmental sample. Previous reports of *R. nana* and *R. laccata* are molecularly confirmed. Two species are reported from subalpine habitats at treeline; *R. montana* with conifers and *R. altaica* with *Betula*. All species have an intercontinental distribution and have been reported in other alpine or Arctic habitats, except for one possible endemic, *R.* cf. *pascua*. A key for the identification of alpine *Russula* in North America is provided. This research contributes data on *Russula* in western North America, and provides baseline data on alpine species threatened by climate change.

Presentation ID: 50

Environmental cues for dispersal in a filamentous fungus in simulated islands

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Abstract

Airborne dispersal is a key part of the life history of many saprotrophic fungi. Theory suggests a transition from growth and resource capture to airborne dispersal at some point as the resource availability in a patch declines, but in the absence of an experimental model system this theory has remained abstract. For saprobes, resources are arrayed in an ever-shifting archipelago of islands with the quality of each island being defined by patch size and resource density. We tracked how *Phacidium lacerum*, a saprotrophic fungus, allocated to dispersal in small and large islands of varying resource density. We found that *Phacidium* altered the timing and rate of dispersal allocation in response to both patch size and resource density. On small resource islands, *Phacidium* drastically increased dispersal allocation after reaching the edge of the patch; if resource density was sufficient, on larger resource islands, *Phacidium* began allocation to dispersal prior to reaching the edge of the island, suggesting an additional absolute total resource level cue. These results are consistent with a two-cue model for the switch to allocation to airborne dispersal: 1) absolute resource level controlled by the fungus, 2) the fungus' perception of patch size. This can be thought of as a mix between a full resource allocation switch (bang-bang) if the fungus perceives the patch is fully occupied with a smaller magnitude early shift (bet-hedging) if absolute resource level crosses a threshold.

Presentation ID: 51

A soil fungal -bacterial biofilm for application in Agriculture

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Abstract

The drive towards sustainable agriculture has sparked the search for natural alternatives to synthetic fertilisers. This study focuses on a species-specific bacterial-fungal biofilm, isolated from the oligotrophic soils of the Cape Floristic Region in South Africa. Initial studies showed that the association between the bacteria and fungal species were very specific, and that the association has the potential to contribute to plant health. This biofilm is capable of fixing atmospheric nitrogen and solubilising phosphates making it an ideal candidate as a biofertilizer. Confocal fluorescence and scanning electron microscopy observations showed that the bacteria associate with the fungal hyphae more readily under nutrient deficient conditions, producing an exopolysaccharide matrix which envelopes the biofilm and potentially provides anaerobic conditions for nitrogen fixation. A second EPS-like formation was found on the fungal hyphae surface in the presence of the bacterial cells, potentially enhancing bacterial attachment. Using a novel encapsulation method, the biofilm was used as a dry biofertilizer in wheat crop field trials. The field trials revealed no significant differences between the treatments and the negative (no fertilizers) and positive (synthetic fertilizer) controls in terms of harvest yield and quality, soil chemical levels and soil microbial community. However, no significant differences were found between the controls themselves, suggesting that the soils were already very nutrient rich as a result of years of agriculture. Future studies will include field trials under nutrient deficient conditions to determine the effectiveness of the biofilm as a biofertilizer.

Presentation ID: 52

Wood-decay -omics data of *Armillaria* reveal patterns of basidiomycete soft-rot

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Abstract

The genus *Armillaria* (Fungi, Basidiomycota) includes some of the most devastating pathogens of temperate forests and saprotrophs that decay wood. *Armillaria* species can efficiently break down all the structural components of wood, making them important players in forest ecosystems and bio-based industries, however, their mechanisms of wood penetration and colonization are poorly known. In order to understand the mechanistic bases of wood-decay by *Armillaria*, we assayed the colonization and decay of autoclaved spruce roots by conifer-specialists *Armillaria ostoyae* and *A. cepistipes* using transcriptomic and proteomic approaches. Transcript and protein levels were altered more extensively in the saprotrophic *A. cepistipes* than in the pathogenic *A. ostoyae* and in invasive mycelia of both species compared to their rhizomorphs. Diverse suites of carbohydrate-active enzyme genes (CAZymes), especially pectinases and expansins, were upregulated in both species, whereas ligninolytic genes were mostly downregulated. *Armillaria* spp. have been discussed as white-rot fungi, however, our gene expression data suggest that unlike white-rotters, they possess and express an atypical wood-decay repertoire, including fewer ligninases, reminding a soft-rot type decay seen in Ascomycota. We propose an evolutionary explanation for the diversity of wood decay types in the Agaricomycetes including *Armillaria* spp, which might have inherited ancestral soft-rot decay machinery from Ascomycota, allowing the fungi to deploy white-rot or soft-rot strategies for wood-decay.

Presentation ID: 53

Metropolitan Fungi: Exploration of woodland soil-fungal communities with urbanization

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Abstract

Soil-fungi play fundamental roles in woodland ecosystem functioning, including driving decomposition and local nutrient cycling. The efficiency of these processes depends not only on which fungi are there, but also how they interact with each other, and their environment. Changes in local environmental factors can drive variation in fungal community composition potentially impacting local ecosystem function. Land-use changes, such as urbanization, can increase resource disruption, heavy-metal deposits, and pollution—all of which have been shown to correlate with soil-fungal diversity and abundance. We assessed soil-fungal community variation across a land-use gradient originating in New York City. We sequenced the ITS1 region of fungal DNA and performed soil elemental and chemical analyses. We predicted that the physicochemical variables associated with variation in land use would correlate with distinct soil-fungal community composition along the gradient. Our results suggest that soil-fungal community composition varied distinctly at sites along the land-use gradient and this change was associated with distance from the urban core. Soil-fungal communities at sites defined as urban and suburban were more diverse than exurban communities and showed a shift in composition towards increased saprotrophs and the phyla Ascomycota and Mortierellomycota. These observations may result from the impacts of land-use change on soils, as seen in our elemental analysis. We observed significant differences in many metals and nonmetals across the gradient ($p < 0.05$), which aligns with results from similar studies in other urban areas. Future research will further explore the abiotic and biotic variables driving this variation in soil-fungal communities.

Presentation ID: 54

Plant-soil feedbacks between Juniperus and Quercus seedlings along a disturbance gradient in Central Mexico

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Abstract

In Central Mexico, *Juniperus deppeana* is frequently used for reforesting areas affected by erosion. The surrounding native forests are dominated by ectomycorrhizal (ECM) plants such as *Quercus spp.* Therefore plant-soil feedbacks between ECM and arbuscular mycorrhizal (AM) hosts like *J. deppeana* can affect seedling survival and impact reforestation projects. We investigated the interactions between fungal communities associated with *J. deppeana* and *Q. rugosa* seedlings along a disturbance gradient, by measuring root colonization and identifying fungal communities using soil and root meta-barcoding of the ITS2 rDNA region. We found that colonization of *Juniperus* roots by endophytic fungi increased with disturbance, while AM fungi colonization decreased. ECM and AM species richness in both *Quercus* and *Juniperus* shifted along the gradient. Fungal community composition in *Quercus* significantly changed in the proximity of *Juniperus*, while the latter was not affected by the presence of *Quercus.* Our findings suggest that oak regeneration is affected by the presence of *Juniperus* with critical implications for forest restoration in ecosystems affected by human activities.

Presentation ID: 55

Density-dependent Fungal Pathogens Associated with Seeds in Three Native Species at Yunque National Rain Forest.

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Abstract

Janzen-Connell hypotheses for the maintenance of tree diversity is derived from host-specific interactions between trees and natural enemies, resulting in plant mortality at high-conspecific densities or near conspecific adults. Since Hurricane Maria affected the Yunque National Forest canopy, our project focused on fungal pathogens, in leaf litter and soil that could affect seed viability at high and low elevation. Tree species were *Shefflera morototoni*, *Guarea guidonia* and *Prestoea acuminata* var. *montana*, species from susceptible to resistant to hurricanes. Overall, 2,880 seeds were collected, 960 from each species. We selected 2 locations at high and 2 at low elevation for each species. Each location had 4 tree-centered plots with 12 bags, 6 bags (2 from each species) filled with forest soil from the same location and buried near the recipient tree, and 6 litter bags were covered and filled with litter from the recipient tree. Each bag had 4 seeds. We evaluated seed viability and fungi by harvesting bags weekly for four weeks. At harvest, seeds were cut in half, and one half was used for viability assessment (tetrazolium chloride) while the other half was divided into two for cultivation. GLM analysis was used in this factorial design to analyze the seed viability data, with source tree species [3], recipient tree species [4], elevation [2], burial duration [4] substrate [2 (Litter and Soil)] and their interactions. Main effects, species, recipient and burial duration were significant. Also, significant interactions were seen. Fungi isolated from the seeds will be identified through Sanger sequencing.

Presentation ID: 56

Potential use of secondary metabolites from *Trichoderma asperellum* (Samuels,Liechfeldt et Nirenberg) T8a against the grey mold *Botrytis cinerea*

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Abstract

The fungus *Botrytis cinerea*, is the pathogen responsible of the grey mold disease. This infectious agent can cause serious losses in more than 200 small fruit crops like grape, strawberry, raspberry or blackberry. The occurrence of multi-drug resistant *B. cinerea* strains, due to the abuse in the use of fungicides and the genetic plasticity of this fungus, has raised the need of new control strategies. An available option is the study of antagonistic fungal microorganisms like *Trichoderma* spp. *Trichoderma* is a genus of necrotrophic, mycoparasitic fungi, whose hosts are fungal plant pathogens. The host range of *Trichoderma* members are wide; they kill the fungal prey by invasion of the hyphae, the secretion of secondary metabolites with toxic effects and the incorporation of the released nutrients. These traits render this group of fungi as biocontrol agents with great value for crop protection from infectious diseases. In this work, the general properties of the secondary metabolites secreted by the *T. asperellum* strain T8a, are studied: the effect of the culture supernatant as inhibitory treatment against the growth of mycelium and early germinated macroconidia of the fungal pathogen *B. cinerea*, and the citotoxicity over two mammal cell lines. The obtained results show that the secondary metabolites contained in the T8a culture supernatant have a clear fungistatic activity against *B. cinerea*, and no significant effects over animal cells. Therefore, the results suggest that the culture supernatant of *T. asperellum* T8a has the potential to be used as an antifungal agent in crops of commercial importance.

Presentation ID: 57

Botryosphaeriaceae from die-back of Eucalyptus in the GuangDong and GuangXi Provinces of southern China

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Abstract

The Botryosphaeriaceae includes important pathogens commonly associated with stem canker, shoot blight and die-back of a range of woody plants, worldwide. Recent field surveys have revealed the common occurrence of die-back in clones of hybrid *Eucalyptus urophylla* × *E. grandis* trees in GuangDong and GuangXi Provinces of southern China. The aims of this study were to identify Botryosphaeriaceae isolates from these die-back symptoms and to evaluate their pathogenicity. The fungi were identified using multi-gene phylogenetic analyses based on DNA sequence data for the internal transcribed spacer and 5.8S regions of the nrRNA gene, partial translation elongation factor 1 alpha, *β*-tubulin, DNA-directed RNA polymerase II subunit, as well as morphological characteristics. A total of 738 *Eucalyptus* die-back samples were collected and these yielded 413 Botryosphaeriaceae isolates. Twenty-one species were identified, including *Botryosphaeria fusispora*, *B. pseudoramosa*, *Lasiodiplodia brasiliense*, *L. chinensis*, *L. citricola*, *L. hormoganensis*, *L. hyalia*, *L. pseudotheobromae*, *L. thailandic*, *L. theobroame*, *Neofusicoccum brasiliense*, *N. kwambonambiense*, *N. parviconidium*, *N. parvum*, *N. sinoeucalypti*, one undescribed species of *Botryosphaeria* and five undescribed *Lasiodiplodia* species. *Lasiodiplodia pseudotheobromae* (27 %) was most dominant followed by *N. parvum* (19%) and *L. theobromae* (12 %). Pathogenicity tests showed that all species were pathogenic to the tested *E. urophylla* × *E. grandis* potted trees and that one of the undescribed species of *Lasiodiplodia* was most aggressive. Overall, the results revealed a high level of Botryosphaeriaceae diversity associated with *Eucalyptus* die-back of in GuangDong and GuangXi Provinces and suggest that some are likely important pathogens.

Presentation ID: 58

Successional trends, community composition and species richness patterns of foliar fungal endophytes within a forest successional gradient

Mathew Harris [1,2], Martin Kemler [3], Bernard Slippers [2,4], Samantha-Leigh Jamison [1], Frederick Witfeld [3], Dominik Begerrow [3], Andreas Brachmann [5], Michelle Greve [1]

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Abstract

Understanding patterns and drivers of succession provides insight into the mechanisms that govern community assembly and provides an indicator of community resilience and stability. Yet, little is known about changes in fungal endophyte communities across environmental gradients. Here we assess whether deterministic succession of the woody vegetation is accompanied by deterministic succession in foliar fungal endophytes. Leaves from three tree species that were abundant across the forest successional gradient were sampled, and the diversity and identity of fungal endophytes were determined using a total amplicon sequencing approach. Unlike the woody plants across the forest successional gradient, fungal endophyte communities showed no consistent evidence of deterministic succession trends. Foliar fungal endophyte composition most strongly predicted by tree host identity and spatial distances between samples, less so by microclimate and not by tree diversity. Host affected endophyte richness, but its effect was dependent on interactions with maximum temperature and with height of the trees from which leaf samples were collected. Additionally, foliar fungal endophyte richness increased as light intensity decreased. Much of the variation in endophyte composition remained unexplained, suggesting the additional contribution of random processes in determining community assembly of foliar fungal endophyte communities.

Presentation ID: 59

Pygmaeomycetaceae, a new root associated family in Mucoromycotina

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Abstract

A new genus, *Pygmaeomyces*, and two new species are described based on phylogenetic analyses, phenotypic and ecological characters. The *Pygmaeomyces* cultures were isolated from the roots of mountain laurel (*Kalmia latifolia*) and pitch pine (*Pinus rigida*) from the acidic and oligotrophic New Jersey Pygmy Pine Plains; however, they likely have a broader distribution because their internal transcribed spacer (ITS) sequences have high similarity with a number of environmental sequences from multiple independent studies. Based on the phylogeny and phenotypical characters, a new family Pygmaeomycetaceae is proposed to accommodate this new lineage in Mucoromycotina. Results from this work will facilitate ecological and evolutionary studies on root-associated fungi.

Presentation ID: 60

Unlocking the Swab: Characterizing Amphibian Skin Fungi

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Abstract

Amphibians play an important role in ecosystems all over the globe. Currently, they are being threatened by the spread of a deadly wildlife disease caused by the fungus *Batrachochytrium dendrobatidis* (Bd). Many studies have shown that certain cutaneous bacteria provide a natural resistance against Bd, as a result of competitive interactions. However, we know little of the fungal diversity that exists on their skin and how those fungi interact with the disease and other cutaneous microbes. To fill this gap, we explored the culturable fungal diversity of the skin microbiome of the eastern redback salamander (*Plethodon cinereus*) at various sites in the New York City area. Individuals were swabbed and plated on PDA and MMN media to maximize culture diversity. Following morphological isolation of the fungal cultures, we extracted, amplified, and sequenced the full ITS region. Our results suggest a diverse fungal community present on the skin microbiome of *P. cinereus*. From 28 individuals, we isolated over 100 morphologically-distinct strains. Twenty-eight of these distinct strains were selected for genomic identification and resulted in 25 OTUs, mainly in the divisions Ascomycota and Mucoromycota. The number of distinct OTUs identified reveal a culturable species-rich fungal microbiome, suggesting the potential for certain strains of these skin-associated fungi to be inhibitory or facilitatory to Bd growth. In the next stage of this project, we will perform challenge assays with these cultures and Bd to determine inhibitory potential and to assess if fungi play a critical role in the microbial defense of amphibians to Bd.

Presentation ID: 61

Advancing Bark Beetle Symbiosis Research by Coordinating, Integrating, and Synthesizing Research Efforts Across Continents

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Abstract

This five-year project aims to critically assess how bark beetles and their fungal associates are studied and recommend ways to improve current research approaches. With over 22 individual researchers representing 17 institutions in five countries, our objective is to coordinate research efforts of forest pathologists, entomologists and symbiologists throughout the world. Bark beetles have evolved symbioses with fungi and their tree hosts that range from highly specific, to loose associations, to asymmetrical dependence. In addition to being interesting, the beetle-fungus relationship has often been hugely destructive, with outbreaks and epidemics reaching record proportions in forests on every continent, costing billions of dollars per year and damaging important ecosystems. Unfortunately, the scientific community is facing a critical shortage of expertise, reliable public databases, research standards, and well-established knowledge flow systems that connect a global community of forest entomologists and pathologists. As a consequence, end-users who make policy decisions concerning international biosecurity, trade, and natural resources protection have incomplete or incorrect information. Entering its third year, the network has hosted eight online and two in-person meetings to prioritize areas of research coordination. Topics included sampling and identification techniques, host plant considerations, genomics, terminology, data mobility and standards, and communication strategies in the context of specific emergent problems that have global impacts (e.g., laurel wilt, invasive shot hole borers). These regular meetings involve additional participation of researchers beyond the network. All meetings and their recordings are freely available at http://www.bbmycobiome.org/.

Presentation ID: 62

Identifying a fungal signature of moisture damage in buildings: targeted and untargeted approaches with mycobiome data

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Abstract

Identifying microbial indicators of damp and moldy buildings remains a challenge at the intersection of microbiology, building science, and public health. Sixty homes in New York City were assessed for moisture-related damage, and three types of dust samples were collected for sequence-based analysis. We applied four approaches for detecting fungal signatures of moisture damage in these buildings. Two novel "targeted" approaches selected specific taxa, identified per *a priori* hypotheses, from the broad mycobiome as detected with amplicon sequencing. We investigated whether (1) hydrophilic fungi (i.e., requiring high moisture) or (2) fungi previously reported as indicating damp homes would be more abundant in water-damaged rooms/homes compared to non-damaged. Two "untargeted" approaches compared water-damaged to non-water-damaged homes for (3) differences between indoor and outdoor fungal populations or (4) differences in presence or relative abundance of particular fungal taxa. Strong relationships with damage indicators were found for some targeted fungal groups in some sampling types, although not always in the hypothesized direction. For example, for vacuum samples, hydrophilic fungi had significantly higher relative abundance in water-damaged homes, but mesophilic fungi, unexpectedly, had significantly lower relative abundance in homes with visible mold. Untargeted approaches identified no microbial community metrics correlated with water damage variables, but identified specific taxa with at least weak positive links to water-damaged homes. These results, although showing a complex relationship between moisture damage and microbial communities, suggest that targeting particular fungi offers a potential route towards identifying a fungal signature of moisture damage in buildings.

Presentation ID: 63

Direct and Indirect Effects of Polycyclic Aromatic Hydrocarbons on Root-associated Partnerships of Saltwater Marsh Grass Species

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Abstract

Contamination of aquatic ecosystems by legacy and emerging pollutants represents a serious hazard to global aquatic ecosystems due to their negative effects on most aquatic organisms. Interestingly, plants can uptake legacy and emerging pollutants into their root tissues, in addition to binding pollutants onto the root epidermis. Little research has been conducted on exploring how these pollutants affect root-associated and root-endophytic partnerships. Herein, root-tissues of *Phragmites australis* and *Spartina alterniflora* were collected from three locations within the Chesapeake bay region, including the Republic Superfund site. Environmental sequencing was completed using surface sterilized (3% hydrogen peroxide for 1 minute) root tissue with 4 replicates per plant with 83 samples in total. Amplification targeted ITS1, ITS2, LSU, and SSU for fungi, V1-V3 and V4 for bacteria, and the standard Achaea region using the Fluidigm Access Array. Preliminary results indicate that the archeal, bacterial, and fungal root-associated and root-endophytic communities are altered at the Superfund site as compared to the two control sites. In addition, the results suggest that the partnerships of *Phragmites australis* were affected more than the partnerships of *Spartina alterniflora.* This research suggests that: 1) direct negative effects on host partnerships can indirectly affect the fitness and productivity of the host, and 2) plant root-associated and endophytic microorganisms have the potential to be leveraged for bioremediation of contaminated sites.

Presentation ID: 64

Experimental Interactions Between a Post-fire Fungus *Pholiota carbonaria* and a Moss Associate *Polytrichum commune*

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Abstract

Wildfires play a critical role in maintaining biodiversity and shaping ecosystem structure in fire-prone regions. There are well known successional patterns involving numerous plant and fungal species in post-fire events. Recently, evidence supporting the "body snatchers" hypothesis, which postulates that some post-fire fungi form endophytic/ endolichenic relationships with plants and lichens, was obtained through culture-dependent and culture-independent methods. However, no direct observation of fungal-moss interactions had been shown to confirm this association. Therefore, the aim of this research was to examine physical interactions between a post-fire fungus, *Pholiota carbonaria*, and a moss, *Polytrichum commune*. Polytrichum spores were plated onto nutrient medium in culture chambers, actively growing *Pholiota carbonaria* mycelium was aseptically added over a period of four weeks, and interactions were examined using standard light microscopy techniques. Microscopic observations indicated that *Pholiota carbonaria* formed appressoria and penetration pegs within the first two weeks of being introduced to live *Polytrichum* protonemata. At six months, fungal mycelium was observed inside older rhizoids. This research supports the conclusion that a fire-associated fungus can form an association with a moss but also raises additional questions as to the extent and longevity of this association.

Presentation ID: 65

Fusarium diversity and roles in conifer tree nurseries of the contiguous U.S.A.

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Abstract

Conifer nurseries serve as reservoirs for a diverse suite of native and exotic pathogens, e.g., *Fusarium* and *Phytophthora* spp. These pathogens can move undetected through asymptomic, infected nursery stock, which can cause mortality in field-planted seedlings and risk pathogen introductions into novel landscapes (e.g., restoration areas). Once introduced, these pathogens can persist in landscapes and harm native plant communities due to costly and inefficient management practices. Broad-spectrum chemical treatments within nurseries and field sites are expensive and affect non-target, beneficial microorganisms in the soil. To mitigate pathogen introductions into field sites, targeted management strategies can be developed for nurseries by determining pathogen composition and pathogenicity/virulence. This project will address to: 1) evaluate the occurrence of *Fusarium* spp. in conifer tree nurseries across the U.S.A.; and 2) identify occurrence patterns among populations of pathogenic *Fusarium*, including host associations, geographic distribution, and potential movement. Because diverse *Fusarium* spp. can cause damping-off and/or root rot diseases of conifer seedlings in tree nurseries, *Fusarium* isolates were collected from western, midwestern, and southern U.S.A. to determine diversity of *Fusarium* spp. Based on DNA sequences of mitochondrial small subunit gene and elongation factor 1-alpha, *F. oxysporum*, *F. commune*, *F. redolens*, *F. fujikuroi*, *F. proliferatum*, *F. solani*, and *F. equiseti* were among the 10 species found from conifer tree nurseries in these regions. This project provides a framework for developing tools to quantify disease pressure by identifying pathogen populations and key mechanisms of disease development (i.e., roles of effector profiles) shared among different *Fusarium* spp.

Presentation ID: 66

Recent projects show the utility of molecular data and community science in understanding Hawaiian macrofungal diversity

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Abstract

Mushrooms are an important yet understudied component of Hawaiian biological diversity comprising endemic species, recently established alien species, popular edibles, deadly poisonous mushrooms, and species that have broader ecological impacts such as facilitating native plant growth or non-native plant invasions. Despite the usefulness of molecular data to identify mushrooms, fewer than 50 Hawaiian macrofungal species had any molecular data available in online DNA repositories prior to 2018. In four recent projects, we collected mushrooms and generated new DNA sequences in order to shed light on their identity and origin. Using both traditional academic research and community science initiatives, combined, we generated approximately 170 new DNA sequences for 140 unique species throughout the Hawaiian Islands. Approximately 50 community scientists participated in this work, enabling us to cover larger areas over longer periods of time and engage interested community members. We found that several species attributed to known taxa are likely misidentified, many Hawaiian taxa have no representative sequences in DNA repositories, and several additional deadly poisonous fungi occur in the islands than previously known. We also identified at least five species that were previously unknown to science. Overall, our work illustrates the need for a better understanding of macrofungal taxonomy for the purposes of conservation and understanding the biological diversity found in the Hawaiian Islands, and argues for the incorporation of community science and molecular data as a model to build capacity towards this goal.

Presentation ID: 67

Host-pathogen-vector dynamics point to complex life cycle of *Exobasidium maculosum*, which causes Exobasidium Leaf and Fruit Spot disease of blueberry

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Abstract

Exobasidium maculosum is a blueberry pathogen that has increased in prevalence in the southeastern United States. The US is the top blueberry producer in the world and Georgia is consistently in the top 5 producing states. Exobasidium Fruit and Leaf Spot can cause significant yield losses, but the complete life cycle of the pathogen is still unknown. Our goal was to investigate whether arthropods play a role in disease transmission and if ploidy variation in the pathogen might be a factor which influences the high level of genetic diversity that is observed. Insect exclusion studies that involved placing covered and uncovered trap plants under diseased bushes and noting differential disease incidence and severity were conducted in Alma and Toccoa, Georgia. Eighty percent of the covered plants had 0-2 leaf spots while uncovered plants had numerous leaf spots. This finding suggests that an arthropod is involved in disease transmission. Ploidy variation was assessed on 15 isolates, equally from three distinct populations, of *E. maculosum* using flow cytometry. Our results show that there is ploidy variation among strains of the pathogen and that aneuploidy exists within its populations. These findings are suggestive of host-pathogen-vector associations that may be more complex than previously thought and that ploidy variation is likely a factor influencing the high genetic diversity observed in the pathogen. Both findings are important in epidemiology of the disease and highlights new factors that should be considered in its management.

Presentation ID: 68

The Rice Blast Fungus and Allied Species: A Monograph of the Fungal Order Magnaporthales

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Abstract

The fungal order Magnaporthales (Sordariomycetes, Ascomycota) includes economically and scientifically important cereal and grass pathogens, such as the rice blast fungus Pyricularia oryzae (syn. Magnaporthe oryzae) and the take-all root rot pathogen of cereals Gaeumannomyces graminis, which are model organisms in host-pathogen interaction studies. Currently, more than 200 species in 38 genera of three families are included in Magnaporthales. We are building an online and print version of a monograph, in order to provide a comprehensive taxonomic overview of Magnaporthales that includes both historic records in literature and recent advancements. Morphological descriptions, illustrations, type designation, geographical distribution, host range, and gene or genome accessions are provided for representative taxa, especially the type or economically important species.

Presentation ID: 69

Investigating trade-offs or complementarity between functional leaf traits and foliar endophytic fungi in the defense against natural enemies of tropical woody plants.

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Abstract

Leaf traits, such as leaf chemistry, lifespan, toughness, and leaf mass per area are a plant's first line of defense against herbivory, yet foliar endophytes may also play a role in plant defense. Our overarching hypothesis is that endophytes alter leaf defense (i.e. functional leaf traits) in the tripartite interaction between endophytes, leaf traits, and plant enemies (i.e. herbivores and pathogens). To that matter, we inoculated seedlings from 7 tropical tree species with natural and diverse endophyte communities and clarified endophyte inoculation and community structure with culture assays and Illumina sequencing. To test our general hypothesis, we performed assays with 7 tropical tree species that were challenged by a generalist herbivore (*Atta colombica*) and a generalist fungal pathogen (Calonectria sp.). We predicted that (1) *A. colombica* would remove less plant material from leaves with higher endophyte (E+) abundance and richness compared to leaves with lower endophyte levels (E-), yet this could be contingent on specific leaf traits (e.g. leaves with longer lifespans could be less attractive to leaf-cutting ants; (2) pathogen damage will decrease in leaves with high (relative to low) endophyte loads (abundance, richness); and (3) Endophyte-mediated defense against both herbivores and pathogens will be most important in short-lived leaves, as long-lived leaves are expected to rely more on intrinsic defense.

Presentation ID: 70

Identification and pathogenicity of *Calonectria* species from soils in *Eucalyptus* plantations and adjacent natural forests in FuJian Province

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Abstract

To meet the growing demand for wood and pulp products, *Eucalyptus* plantations have expanded rapidly during the past two decades to become an integral part of the southern China landscape. *Calonectria* species which cause leaf blight threaten the sustainability of these plantations. To better understand the diversity, distribution and pathogenicity of these species we undertook surveys in six regions of FuJian province. Soil samples were collected from *Eucalyptus, Cunninghamia lanceolata* and *Phyllostachys heterocycle* plantations as well as from natural forests adjacent to *Eucalyptus* plantations and used to bait for *Calonectria*. A total of 101 *Calonectria* isolates were obtained and these were subjected to species identification based on comparison of multilocus DNA sequence data of the β-tubulin (*tub2*), calmodulin (*cmdA*), histone H3 (*his3*) and translation elongation factor 1-alpha (*tef1*) gene regions as well as morphological characteristics. A total of twelve *Calonectria* species were identified including four known taxa (*Ca. arbusta*, *Ca. pentaseptata*, *Ca. pseudocolhounii* and *Ca. pseudoturangicola*) and eight novel species. *Calonectria arbusta* is the most dominant species which was found in all five surveyed regions and accounted for 47 % of all the isolates.

Presentation ID: 71

Unidirectional mating-type switching confers self-fertility to *Thielaviopsis cerberus*, the only homothallic member of the genus

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Abstract

Heterothallism in ascomycetes is underpinned by a single genetic mechanism, whereas homothallic behaviour originates from various strategies distinguished through genetic analysis. Among the six species in the genus *Thielaviopsis* (family Ceratocystidaceae, order Microascales), five are heterothallic, while strains of *T. cerberus* can sexually reproduce in isolation and are classified as homothallic. This study aims to elucidate the genetic mechanism underlying the homothallism observed in *T. cerberus*. A draft genome sequence of *T. cerberus* was produced and used to identify and annotate the mating-type locus. Single ascospore progeny were recovered from a self-fertile *T. cerberus* isolate, yielding self-fertile and self-sterile cultures. The structure of the mating-type locus for both progeny types was investigated using PCR and Sanger sequencing, and RNA sequencing was used to confirm gene models. The mating-type locus of self-fertile *T. cerberus* isolates has four known mating-type genes, *MAT1-1-1, MAT1-2-1, MAT1-1-2* and *MAT1-2-7*. The *MAT1-1-1* gene is split into two fragments bordered by two 114 bp direct repeats and the other three mating-type genes. In the self-sterile progeny, only a fused *MAT1-1-1* gene containing a single direct repeat was present. The presence of self-fertile and self-sterile mating-type isolates that differ in the structure of their mating-type locus, and direct repeats bordering a region of deletion, are distinctive characteristics of unidirectional mating-type switching, a form of homothallism known from several other Ceratocystidaceae species. *Thielaviopsis cerberus* utilizes this sexual strategy, which likely evolved through an aberrant crossover event between the two mating-type idiomorphs present in the heterothallic sister species.

Presentation ID: 72

A new species of *Rugonectria* detected in South Africa: evidence for host-jump by a "sleeper" pathogen

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Abstract

Botanic gardens are valuable sites for sentinel research and the detection of newly emerging invasive forest pathogens. They also provide a link to the past, with collections capturing the historical exchange of plants undertaken during the Victorian Plant Collecting frenzy. Founded in 1849, the Durban Botanic Gardens (DBG) is the oldest surviving botanic garden in Africa. In the late 1800s, links between the Royal Botanic Gardens, Kew, and other gardens in the then British Empire, resulted in the introduction of plant material to DBG from gardens of other colonies, including those in India, Hong Kong and the Malayan Peninsula. In May 2017, cankers were detected on two specimens of *Hymenaea verrucosa* (East African Copal, Fabaceae, Mozambique) in DBG. *Cylindrocarpon*-like isolates were recovered from canker margins of both trees. A subsequent survey identified *Rugonectria*-like perithecia on cracking bark of *Albizia chinensis* (Chinese False-thorn, Fabaceae, Tropical Asia). When cultured, isolates were morphologically identical to those from copal. Sequences of the ITS and *BenA* gene regions confirmed the isolates from the two hosts as a single undescribed species of *Rugonectria.* This genus resides in the Nectriaceae and currently accommodates five species, including the canker pathogen *R. castaneicola.* Although pathogenicity has yet to be tested, all indications are that the new *Rugonectria* sp. is the cause of the cankers. We propose that the fungus was accidentally introduced into the DBG with plant material of East Asian origin, possibly *A. chinensis*, and after a long period of latency has jumped to a novel host, causing extensive disease.

Presentation ID: 73

Signatures of optimal codon usage predict metabolic ecology in budding yeasts

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Abstract

Reverse ecology is the inference of ecological information from genomic variation. One rich source of ecologically-relevant genomic information is codon optimality or adaptation. Bias toward codons that match the tRNA pool is robustly associated with high gene expression, suggesting that codon optimization could identify highly expressed, ecologically relevant genes. We examined the relationship between optimal codon usage in the classic galactose metabolism (*GAL*) pathway and known ecological niches for 329 species of budding yeasts. We find that optimal codon usage in the *GAL* pathway is positively correlated with quantitative growth on galactose, suggesting that *GAL* codon optimization reflects increased capacity to grow on galactose. *GAL* optimal codon usage is also positively correlated with human-associated ecological niches in yeasts of the CUG-Ser1 clade and with dairy-associated ecological niches in the family Saccharomycetaceae. For example, *GAL* optimal codon usage is ≥ 85% of all genes in the major human pathogen *Candida albicans* (CUG-Ser1 clade) and ≥ 75% of genes in the dairy yeast *Kluyveromyces lactis* (family Saccharomycetaceae). We further find a correlation between optimization in the thiamine biosynthesis and *GAL* pathways. As a result, optimal codon usage in thiamine biosynthesis genes is also associated with dairy ecological niches in Saccharomycetaceae, which may reflect competition for extracellular thiamine. This work highlights codon optimization as a tool for gaining insights into the metabolic ecology of microbial eukaryotes. This may be illuminating for studying fungal dark matter—species that have yet to be cultured in the lab or have only been identified by genomic material.

Presentation ID: 74

Mitochondrial evolution and inheritance in *Amanita phalloides*–using the forgotten pieces from whole genome sequencing

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Abstract

Whole genome projects typically aim to assemble and annotate the nuclear genome, whereas organellar genomes are often left out. While working with the nuclear genomes of 88 Californian (invasive) and European (native) *Amanita phalloides* mushrooms collected between 2004 and 2015, we took advantage of an extremely high sequencing depth to also assemble and annotate mitochondrial genomes. Except for three, all of these genomes were assembled into single circular contigs, providing an opportunity to study the organization, diversity, evolution and even inheritance of these important organelles. Most mitochondrial genomes of *A. phalloides* are similar in size: genomes house 49 protein-coding genes, including 15 genes considered essential to mitochondrial function, 15 homing endonuclease genes, 2 genes not essential to mitochondrial function and 17 as yet functionally unidentified, hypothetical genes. The genetic diversity of Californian mitochondria derives primarily from two dominant haplotypes. Nucleotide diversity is similar in the native and invasive ranges, suggesting little founder effect or multiple introductions to California. In addition, the nucleotide diversity of the mitochondrial genome is greater than the diversity of the nuclear genome, supporting the hypothesis of a higher mutation rate in mitochondrial genomes. We also detected signals of recombination at a low rate, suggesting the possibility of biparental inheritance of mitochondria. However, the limited evidence of heteroplasmy in our genome collection suggests biparental inheritance is either rare or transient.

Presentation ID: 75

Using Harpellales as a model to study insect-fungus symbiosis and genome evolution of gut-dwelling fungi

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Abstract

Harpellales (Kickxellomycotina, Zoopagomycota) are universal fungal symbionts living in the digestive tracts of immature aquatic insects, including black flies, midges, and mosquitoes. The symbiotic relationship between Harpellales and the lower Diptera has recently been estimated to emerge since the Permian (~270 million years ago) and co-occurred with the complete metamorphosis of the Diptera hosts. Their long-term association also left genomic hallmarks, which are invaluable resources for us to study the insect-fungus symbiosis and the fungal evolutionary history through epochs. Currently, we have nine whole-genome sequences of Harpellales fungi that are publicly available. Preliminary investigations suggest that Harpellales genomes are featured with low GC content (26-37%) and the *Zancudomyces culisetae* is able to code mosquito-like polyubiquitin chains possibly via horizontal gene transfer events. Phylogenomic analyses and comparative genomics also revealed potential whole-genome duplications within Harpellales. Allele frequency analyses suggest that most Harpellales species are diploid although the snow fly gut symbiont, *Capniomyces stellatus,* is haploid. The production of Harpellales genomes also leads to the discovery of the 21st amino acid (selenocysteine) in Harpellales, which may be related to their ancient lifestyle in cryptic niches. The first batch of Harpellales genomes already proved their value in helping us understand the differences and similarities between insect-associated fungal commensals and pathogens. The increasing effort to produce more genomic resources of Harpellales in the near future will help us better understand the natural history of gut-dwelling fungi and the dynamic boundaries between insect commensals and pathogens.

Presentation ID: 76

Fungal diversity associated with sunflower and soybean seeds in South Africa

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Abstract

Sunflower and soybean are important crops for South Africa. Its high protein and fibre content makes these ideal as animal feed but is also consumed by humans. The safe usage of these seeds is threatened by the presence of mycotoxins produced by storage fungi. *Aspergillus, Fusarium,* and *Penicillium* are the most common mycotoxigenic genera and are responsible for producing five of the globally regulated mycotoxins. Even though they play a major role in South African food and feed quality, their true diversity in South Africa is largely unknown. This study explored the fungal diversity associated with sunflower and soybean seeds. A total of 322 fungal strains belonging to *Aspergillus* (103)*, Fusarium* (122) and *Penicillium* (97) were isolated. Strains were grouped based on morphological characters and representatives from each group were sequenced. The identification markers calmodulin (*CaM)*, translation elongation factor 1-α (*TEF*) and β-tubulin (*BenA*) were sequenced for the identification of *Aspergillus, Fusarium,* and *Penicillium* respectively. Identifications yielded 17 *Aspergillus* (2 major mycotoxin producers); 6 *Fusarium* (2 major mycotoxin producers) and 19 *Penicillium* (1 major mycotoxin producer) species. Amongst the isolates, 1 new *Penicillium* species was found from sunflower seeds. Multigene phylogenies based on *ITS, BenA, CaM* and *RPB2* showed that the new species belongs to section *Fasciculata* series *Viridicata*. During this survey, several mycotoxigenic fungi were isolated. Further studies is needed to determine the impact of fungi on these important crops.

Presentation ID: 77

Diversity and structure of soil fungal communities across experimental Everglades tree islands

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Abstract

Fungi play prominent roles in ecosystem services (*e.g.*, nutrient cycling, decomposition), and thus have increasingly garnered attention in restoration ecology. However, it is unclear how most management decisions impact fungal communities, making it difficult to protect fungal diversity and utilize fungi to improve restoration success. To understand effects of restoration decisions and environmental variation on fungal communities, we sequenced soil fungal microbiomes from 96 sites across eight experimental Everglades tree islands ~15 years after restoration occurred. We found that early restoration decisions can have enduring consequences for fungal communities. Factors experimentally manipulated in 2003-2007 (e.g., type of island core) had significant legacy effects on fungal community composition. Our results also emphasized the role of water regime in fungal diversity, composition, and function. As relative water level decreased so did fungal diversity, with a ~25% decline in the driest sites. Further, as water level decreased, the abundance of the plant pathogen-saprotroph guild increased, suggesting low water may increase plant-pathogen interactions. Our results indicate that early restoration decisions can have long term consequences for fungal community composition and function and suggest that a drier future in the Everglades could reduce fungal diversity on imperiled tree islands.

Presentation ID: 78

Four-way interactions in the plant holobiont: How does plant viral disease alter fungal and bacterial community assembly?

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Abstract

Plant viruses can be extremely damaging to the productivity of many crops. The feedback between a plant's microbiome and the plant's infection with a disease-causing virus is potentially complex and unobserved. Because viral infection influences resource allocation and immune defenses of the host plant, virus-infected hosts may have altered microbiome assembly by bacterial and fungal endophytes. We aimed to characterize the effects of infection of *Brachypodium distachyon* by Barley Yellow Dwarf Virus (BYDV, *Luteovirus*) and endophytic bacteria (*Enterobacter ludwigii*) and fungi (*Fusarium solani* sp. complex). Plants were fed on by virus-containing or virus-free aphids, followed by aphid removal and co-inoculation of both bacteria and fungi or mock inoculation. Plants were harvested 21 days post-inoculation, and measurements of leaf area, shoot and root biomass, and plant height were performed. Root DNA was extracted, and qPCR was used to quantify relative amounts of bacterial, fungal, and plant DNA. While both virus infection and endophyte infection have independent effects on plant phenotypes, we did not observe interaction between virus and endophyte infection status. Bacterial infection of roots was significantly decreased in virus infected plants, possibly due to decreased phloem availability. Four-way interactions of plants, viruses, bacteria, and fungi will require further factorial experiments to identify directions and sizes of impacts, and improved applicability of experiments with growth conditions and microbial communities.

Presentation ID: 79

Diversity of fungi associated with *Stipagrostis* in the Namib desert "fairy circles"

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Abstract

So-called "fairy circles" are mysterious barren, almost circular patches surrounded by lush tufts of *Stipagrostis* species (Poaceae) growing at their margins. They typically occur in the Namib desert, but some are present in the Northern Cape of South Africa and south Angola. There are many hypotheses relating to the origin of these circles, and they remain the subject of significant debate. A recent study has suggested that microbes including plant pathogens could be involved in causing *Stipagrostis* spp. at the centres of the circles to die. In this preliminary study, we considered the fungal diversity associated with *Stipagrostis* roots and shoots from the centres and peripheries of the circles. Three sampling regions were selected, and two circles were sampled at each location. Roots and shoots were surface-disinfested and plated onto Fusarium Selective Media (FSM), Malt Extract Agar (MEA) and Dichloran-Glycerol (DG18), supplemented with chloramphenicol and streptomycin. Isolates were identified to genus level and preserved in glycerol. The resulting isolates were mainly species of *Alternaria, Aspergillus, Aureobasidium, Chaetomium, Fusarium, Hormonema, Paecilomyces, Penicillium, Pleosporales, Sclerotia, Talaromyces,* and *Trichoderma*. Future studies will include identification of the isolates to species level and a consideration of their possible role, if any, in the development of the "fairy circles".

Presentation ID: 80

The *Pluteus nanus* complex: Dealing with unclear species boundaries in a hyperdiverse lineage of agarics (Pluteaceae, Agaricales)

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Abstract

The taxonomy of the brown, grey and olive colored *Pluteus* species in section *Celluloderma* remains largely unresolved. This morphological group has proven to be extremely species-rich across the Holarctic region, and it includes widely used names such as *P. nanus, P. phlebophorus, P. cinereofuscus* and *P. cyanopus* and also many validly published names of unclear taxonomic status, including: *P. brunneoater, P. homolae, P. griseoluridus, P. laevis, P. luctuosus, P. ludovicianus, P. mammifer, P. olivaceus, P. satur, P. spinosae* and *P. suzae*. The problematic taxonomy is a consequence of the lack of clarity on how to apply older names, the overlapping intra- and interspecific morphological variation, and the limited value of the fungal barcode (ITS) to separate closely related taxa. We studied over 200 collections, spanning across the Holarctic region, revised available type collections, and generated molecular data for them when possible. A total of 212 ITS sequences were analyzed, mostly newly generated for this study. We also generated and analyzed 98 *tef1* sequences, to help clarify species boundaries when ITS lacks resolution. A total of 43 Holarctic species can be recognized in the phylogenies, but only 10 taxa can be assigned names based on sequencing of type collections and/or modern collections from the type locality. The rest of the species are either candidates to keep some of the older names in this group, or represent potentially undescribed taxa. There are high levels of cryptic diversity, even in relatively well-studied areas (Europe, Eastern North America).

Presentation ID: 81

Are endophytes tolerated or hiding? Insights from the *Botryosphaeria dothidea* – *Eucalyptus grandis* pathosystem

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Abstract

Fungal endophytes are immensely diverse and ubiquitous in plants. *Botryosphaeria dothidea* is a well-known plant pathogenic fungus, that can also persist as an endophyte in many important woody plant species. This fungus can infect its plant hosts without resulting in symptoms but how it avoids triggering a host-defence response is unknown. The infection process of *B. dothidea* on *Eucalyptus grandis* leaves was examined with scanning electron microscopy and qPCR analysis of inoculated, asymptomatic *E. grandis* leaves that confirmed the infection had occurred. Using dual RNA-sequenced data, the molecular responses of *B. dothidea* and *E. grandis* were characterized at 24 hours, 48 hours and 7 days post-infection. A weak host-defence response was observed at 48 hours post-infection (hpi) which was characterised by only 129 differentially expressed genes. This included the up-regulation and down-regulation of key defence genes such as the jasmonate/ethylene transcription factor, *MYB15*, and the potential salicylate receptor, *NPR5*, respectively. Analysis of the *in planta B. dothidea* transcriptome suggested that the fungus is metabolically active during the infection process, envinced by the expression of genes involved in nutrient acquisition, detoxification and cell wall degradation. No fungal effector transcripts were detected. Despite evidence of a weak defence response at 48 hpi, transcriptome analysis suggested that *B. dothidea* is recognized by *E. grandis* but this is an interaction of tolerance.

Presentation ID: 82

Real-Time PCR Detection of Clarireedia spp., the Causal Agents of Dollar Spot in Turfgrasses

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Abstract

Dollar spot is one of the most economically important diseases of turfgrasses. Recent taxonomic revisions have placed the dollar spot fungal pathogens in the new genus Clarireedia, with five species described. The main goal of this study was to develop a quantitative real-time polymerase chain reaction (qPCR) molecular detection assay based on the internal transcribed spacer (ITS) of the ribosomal RNA genes to quantify the abundance of Clarireedia species from environmental (field) samples. The qPCR assay was able to detect isolates of the four tested Clarireedia species but did not cross react with non-target fungi, including closely related taxa, other turfgrass pathogens, or other fungal species commonly isolated from turfgrass. The assay is capable of detecting as little as 38.0 fg (3.8 x10-14 g) of Clarireedia genomic DNA in three hours. The qPCR assay detected Clarireedia in both symptomatic and asymptomatic creeping bentgrass (Agrostis stolonifera) foliar tissue. Clarireedia species were rarely detected in the thatch or soil, indicating that these pathogens are not widely distributed in these areas of the environment. The fact that the pathogen was detected in asymptomatic tissue suggests that creeping bentgrass may be able to tolerate a certain quantity of the pathogens in leaves before disease symptoms appear; however, further research is needed to validate this hypothesis.

Presentation ID: 83

Holistic appraisal of soil fungal communities reveals high functional and taxonomic diversity in a Mexican pristine montane cloud forest

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Abstract

Montane cloud forests are listed among the most threatened ecosystems globally, in spite of their relevance in the maintenance of biogeochemical and hydrological cycles, biodiverse biotic communities, and as reservoirs of numerous endemic species. However, insufficient baseline information on key, yet neglected components of diversity such as microfungi limits the environmental quality monitoring and conservation efforts. We present an extensive evaluation of the soil fungal diversity, community structure and ecological patterns of a pristine montane cloud forest in Mexico, using culture-based methods, ITS rRNA gene amplicon Illumina sequencing and soil biogeochemical profiling. Our results revealed a diverse soil fungal community within nine phyla, outnumbering former figures in Mexico, and representing the 13.4% of the overall fungal diversity reported in this ecosystem. At the functional level, we identified >10 guilds, with saprobes as the dominant component. This biodiverse fungal community is linked to an extraordinarily heterogeneous environmental setting, providing room for functional redundancy at small spatial and temporal scales. In this system, deterministic assembly processes largely operate at a small spatial scale, where patchy ecoenzymatic activities and fungal aggregation patterns denote characteristic functional entities at a site level, in accordance with metabolic capacities to efficiently access nutrients. This significant attribute should be considered in management plans, and when identifying priority areas for conservation.

Presentation ID: 84

Clones of Fusarium circinatum display different phenotypes

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Abstract

Fusarium circinatum is an important *Pinus* pathogen. In the commercial forestry setting, it causes pitch canker on plantation trees and root disease in nursery seedlings. Although this fungus is heterothallic, its sexual stage has only been observed in laboratory experiments. Population genetic data from regions where the fungus has been introduced also suggest that it reproduces asexually. In this study we aimed to determine whether members of the resulting clones display similar phenotypes. For this purpose, we used three isolates (from different locations and plant tissue types) with the same 10-locus microsatellite-based genotype. Their virulence was assayed with standard inoculation on *P. patula* seedlings. We also analysed the chemical responses of the seedlings towards the isolates using gas chromatography-mass spectrometry. We observed differences among the lesion lengths and the terpenoid oleoresin induced by the three isolates on the seedlings. Interestingly, quantities of the three major sesquiterpenes in pine (caryophyllene, humulene, germacrene D) correlated broadly with the lesion lengths induced by the isolates. These observations may have two possible explanations. One is that the clonal isolates differ phenotypically due to differences in gene regulation and expression, the analysis of which could provide valuable insight into the *F. circinatum-Pinus* interaction. The other possibility is that the isolates were genetically different because the initial genotyping method did not provide sufficient resolution for identifying true clones. Our future research will therefore seek to shed light on these issues by making use of genomic and transcriptomic approaches.

Presentation ID: 85

2020 Best Poster Winner

Azole-resistance profiles of *Aspergillus fumigatus* on commercial products

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Abstract

Cases of invasive aspergillosis are rising due to increasing numbers of immunocompromised patients. The primary class of drugs used for treatment of invasive aspergillosis is triazoles. However, patients have begun presenting with pan-azole resistant strains of *Aspergillus fumigatus* prior to treatment. Pan-azole resistance is most often caused by tandem repeats of 34 and 46 base pairs in the promoter region of the *cyp51A* gene The use of triazoles to combat plant-pathogenic fungi in agricultural settings provided the selective pressures required to develop these mutations. Our goal is to identify azole-resistant *A. fumigatus* on agricultural commercial products commonly treated with azoles. One hundred and eighty-two isolates have been recovered from grapes, peanuts, and pecans. Forty-four isolates were found to be resistant to itraconazole via selective media plating. Minimum inhibitory concentration experiments (MICs) were performed on 39 isolates to confirm azole-resistance. Eighteen isolates from grapes and peanuts were found to have intermediate resistance to tebuconazole (2µg/mL). Two additional isolates from peanuts displayed a pan-azole resistant phenotype (≥ 2µg/mL itraconazole, tebuconazole, and voriconazole, and ≥ 0.5µg/mL posaconazole). This indicates that there are likely mutations such as the TR34 or TR46 alleles present in these two isolates. An in-progress review of relevant literature also found azole-resistant *A. fumigatus* on commercial products such as tulip bulbs, daffodil bulbs, compost, soil, and seeds. This indicates that interacting with these products may pose a risk of azole-resistant aspergillosis. Further testing on other commercial products would be useful to determine the extent of azole-resistance in the environment.

Presentation ID: 86

Fungal isolates have unique physiology under differing nitrogen environments

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Abstract

Human generation of nitrogen pollution and the subsequent deposition of nitrogen on soils is a phenomenon of changing environments and a potentially enormous stress on organisms and their ecosystems. Fungi are critical to biogeochemical cycles, but because individuals grow hidden in substrates, fungi are difficult to observe or manipulate in natural contexts. Measuring adaptation is difficult, and the ability of fungi to adapt their metabolisms to nitrogen stress is unknown. I am testing physiological functional traits of decomposer fungi which have experienced nitrogen pollution for multiple decades, and will compare those to closely related fungi which have not experienced nitrogen pollution. I aim to demonstrate whether fungi experiencing nitrogen pollution have adapted to grow differently in nitrogen rich environments. Fungi were isolated from the Long-Term Ecological Research (LTER) Chronic Nitrogen Amendment study (CNAS) at the Harvard Forest, and grown in the lab in minimal nutrient liquid culture at three concentrations of nitrogen, mimicking the CNAS plots. Each isolate was grown in shaking culture and biomass was destructively harvested daily to measure growth rate and other physiological functional traits. I am reporting growth rate here, and I am currently measuring respiration and nitrogen in biomass to garner a more complete understanding of the fungal physiological response to nitrogen pollution. By quantifying physiological functional traits for isolates of the same species exposed or not exposed to nitrogen pollution, I am testing whether adaptation has occurred, a key to understanding how evolution will impact decomposition in contexts of global change.

Presentation ID: 87

Rediscovery of *Ancylistes closteri* (Ancylistaceae, Entomophthorales) and its phylogenetic position

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Abstract

The genus *Ancylistes* is an endoparasite of green algae (*Closterium* or *Netrium*) and includes three described species. Currently, *Ancylistes* is placed in the family Ancylistaceae (Entomophthorales, Entomophthoromycotina, Zoopagomycota) along with *Conidiobolus*. However, DNA sequences of *Ancylistes* have never been obtained, and its phylogenetic position is unknown. The phylogenetic position is important to resolve nutritional evolution in the group, because other members of the Entomophthorales are primarily animal associated. In the present study, we established a dual culture of *Ancylistes closteri* and its host alga, *Closterium* sp. We characterized the culture based on precise microscopic observation and clarified its phylogenetic position based on the molecular phylogenetic analysis using 18S and 28S rDNA sequences. Morphology and life cycle of our culture are as below. The fungus develops as hyphae in the host cell and consumes the host cytoplasm. The hyphae are divided into several segments by septation, and one hypha emerges from each segmented cell and extends to the outside of the host cell. The external hyphae reach a new host cell and a new infection occurs via an appressorium. When the infected cells are on the surface of water, external hyphae form conidiophores to produce forcibly discharged conidia. Secondary conidia arise from the primary conidia. The conidia possess multiple (> 10) nuclei. Under dark conditions, the fungus produces resting spores by sexual reproduction in which fusion of two hyphae occurs. In our phylogenetic tree, *Ancylistes closteri* was sister to the clade of Entomophthoraceae + *Conidiobolus* spp., and Ancylistaceae was paraphyletic.

Presentation ID: 89

Aggressiveness and Deoxynivalenol Production of Nebraska Isolates of *Fusarium boothii* and *F. graminearum*

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Abstract

Significant losses in wheat result from Fusarium head blight (FHB) and its associated mycotoxin deoxynivalenol (DON). The predominant FHB pathogen in North America is *Fusarium graminearum*. *F. boothii* was recently confirmed for the first time in the United States as a causal agent of FHB in Nebraska wheat fields. This greenhouse study compared the aggressiveness and DON production in wheat among 13 *F. graminearum* and three *F. boothii* isolates from Nebraska. Spikes of the susceptible spring wheat cultivar Wheaton at anthesis were spray-inoculated with spores of the isolates. Severity data were used to calculate the area under the disease progress curve (AUDPC). DON concentration in the grain was quantified by gas chromatography/mass spectrometry. *F. graminearum* isolates were more aggressive and produced more DON than *F. boothii* isolates. Mean AUDPC values were 1,171 and 885 percent days for *F. graminearum* and *F. boothii*, respectively. Mean DON values were 41.0 and 13.6 µg/g for *F. graminearum* and *F. boothii*, respectively. Although only three available *F. boothii* isolates were used, the results are in agreement with previous studies that found *F. graminearum* be more aggressive and toxigenic in wheat than *F. boothii*.

Presentation ID: 90

Experimental pyrocosms demonstrate key features of the autecology of *Pyronema domesticum* and *Lyophyllum aff. anthracophila*

Thomas Bruns , Akiko Carver , Krya Stillman , Catharine Adams

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Abstract

Pyrophilous fungi fruit prolifically after fire and are generally restricted to post-fire environments. Although they have been known for over a hundred years, most elements of their autecology remain unknown. To explore the behavior of these fungi in post-fire soil environments we have used small experimental units termed “pyrocosms” to control soil heating and incubation conditions. Earlier work with pyrocosms showed that one genus of pyrophilous fungi, Pyronema spp., can develop rapidly in these systems, but the generality of this response was unknown, and growth of other pyrophilous fungi did not occur. Here we used soils from multiple forest, meadow, and agricultural sites to test the generality of the Pyronema response and we varied incubation conditions and lengthened the incubation period to attempt to stimulate additional pyrophilous fungi. Similar to previous studies, we found that post-fire communities had lower species richness and diversity, and we found that post-fire response was driven by a small subset of species. Pyronema domesticum was the most dominant OTU in the first few weeks after fire; all forest soils contained it. Most meadow soils also contained them, but generally at lower levels. Several other known pyrophilous fungi occurred but only Pyronema domesticum and Lyophyllum aff anthracophila had extraordinary high responses (>40%). Lyophyllum aff anthracophila was stimulated by vernalization and was most abundant is forest soils. Varying other parameters of fire and incubation are likely to simulate additional species.

Presentation ID: 91

Peroxisomes, lipid droplets and early endosomes carpool on fast rides along microtubules in *Neurospora crassa* hyphae

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Abstract

Fungal peroxisomes (POs) have a role in primary and secondary metabolism, in sexual and asexual development, as well as, in protection against mechanical damage. In *Aspergillus nidulans* and *Ustilago maydis* POs are co-transported on early endosomes (EEs). The EEs are multipurpose carriers to transport a variety of cargo, such as, proteins, mRNAs, ribosomes, and other organelles such as endoplasmic reticulum (ER) and lipids droplets (LD). This endosomal transport is mediated by the microtubule-dependent molecular motors kinesin and dynein. Here, we have analyzed whether POs move by hitchhiking on EEs in *Neurospora crassa*, a filamentous ascomycete with some of the highest growth rates and largest hyphae displayed among the commonly studied model fungi. In addition, we have studied the co-transport of POs with ER and LDs. First, the subcellular location of POs was determined by fusion of the peroxisome targeting sequence (PTS1) with the TagRFP fluorescent protein. Hyphae co-expressing TagRFP-PTS1 and markers of other organelles tagged with fluorescent proteins or stained with fluorochromes were analyzed by confocal microscopy. Partial co-localization of rapid mobile POs and microtubules (MT), EE and LD was observed. These results allowed the construction of a "pero-endo" transport model in *N. crassa*, where peroxisomes that are co-transported together with EE and LD undergo rapid and directed movement via MT.

Presentation ID: 92

Soil nutrient amendments alter foliar fungal endophyte phenotypes and phylogenetic composition

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Abstract

Foliar endophytes influence plant health and productivity in natural and agricultural environments, but their response to commonly applied nutrient inputs is not well understood. We studied the response of foliar endophyte communities in a natural grassland to eight years of annual nitrogen, phosphorous and potassium (NPK) amendment. Fungi were isolated from healthy leaves (n = 6 per treatment, NPK-amended or control) of the prairie grass *Andropogon gerardii.* A random collection of isolates (n = 120, 10 from each leaf) were assigned to genus using ITS2 sequence similarity and characterized for nutrient utilization using 95 single carbon substrates (Biolog SF-P2 plates). Fungal community composition and nutrient utilization phenotypes varied between NPK and control treatments. There was a greater number of fungal genera, families and orders found in NPK-amended plants ($P \leq 0.02$), and phylogenetic analysis showed both intra- and intergenic differentiation between treatments. Mean fungal niche width, or the number of individual carbon compounds used, was significantly lower in NPK-amended leaves ($P = 0.007$), and the growth efficiency of fungi from the NPK treatment was lower across five of seven carbon classes. Functional and phylogenetic differentiation occurred within each of three genera common to both treatments (*Aspergillus*, *Penicillium* and *Trichoderma*), and the correlation between pairwise phylogenetic and functional distances was small (r = 0.08), indicating that the differences observed in niche width and growth efficiency were not explained by changes in phylogenetic composition. These results show widely applied soil nutrients alter both the structure and function of foliar endophytic communities.

Presentation ID: 93

Population structure and diversity of *Dothistroma pini* in Europe suggests human mediated movement of the needle blight pathogen

Ariska van der Nest [1], Michael J. Wingfield [1], Dušan Sadiković [2,3], Martin S. Mullett [4], Valentin Queloz [5], Katarina Adamčíková [6], Kateryna Davydenko [7,8], Irene Barnes [1]

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Abstract

Dothistroma pini is one of two species that cause the important disease of pine known as Dothistroma needle blight. In contrast to the closely related, well studied and cosmopolitan *D. septosporum*, *D. pini* has been reported only from Europe, the Northeastern USA and Russia. Very little is known regarding the population structure or genetic diversity of *D. pini*. As part of the collaborative DIAROD COST action, a collection of 345 *D. pini* isolates were collected from twelve countries on eight different hosts. These isolates were screened with sixteen microsatellite markers and species-specific mating-type markers to investigate the population diversity and structure, as well as to determine the mode of reproduction for these populations. Of the 109 multilocus haplotypes detected, eight occurred in multiple and often non-bordering countries. Variable population diversity was found in populations of *D. pini* in Europe. High levels of genetic diversity were observed in populations from France, Spain and Ukraine. There was evidence for some newly emerging populations, such as those in Slovakia, Slovenia and Switzerland due to high clonal fractions and the presence of single mating types in each of the sampled locations in Slovakia and Slovenia. Both mating types were detected in isolates from France, Serbia, Slovakia, Spain, Switzerland and Ukraine. Evidence for sexual recombination was statistically supported only for the population from Spain. The observed population structure and several shared haplotypes between non-bordering countries of Europe, suggests that human activities have played a major role in the dispersal of the pathogen on the continent.

Presentation ID: 94

Unidentified barcode sequences: novel fungal diversity or artifacts of incomplete databases?

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Abstract

Ecological studies that rely on sequence-based identification have proliferated rapidly, generating millions of barcode sequences for fungi from diverse settings. Metabarcoding typically uses the first or second nuclear ribosomal internal transcribed spacers (ITS1 or ITS2), and culture-based surveys often use the ITS1, ITS2, and 5.8S (ITS rDNA) to delimit operational taxonomic units and estimate taxonomic identity. Together these data highlight the massive scale of unknown fungal biodiversity. However, when sequences have low similarity to reference sequences, ecological studies cannot be linked to phylogenetic, taxonomic, or phenotypic data, and insights into the scale of biodiversity are limited: do such sequences represent novel fungal biodiversity, or do they represent known fungi that are poorly represented in databases, have limited taxonomic annotations, or are only coarsely identifiable due to a lack of a robust phylogenetic context? We examined 61 difficult-to-identify barcode sequences of Pezizomycotina identified as 'most wanted' taxonomic orphans by the UNITE database team. We obtained cultures corresponding to those sequences from the living endophyte collection in the Gilbertson Mycological Herbarium. We sequenced the ITS and partial LSU rDNA for each culture and inferred placement via phylogenetic and integrative taxonomic methods. Our analyses show that a small number of isolates represent putatively novel lineages not placeable within currently described classes or orders. However, the majority were identifiable to the order level or below with phylogenetic approaches and rich taxon sampling. This work highlights the continuing importance of biodiversity repositories, and their capacity to facilitate integration of ecological and taxonomic disciplines in mycology.

Presentation ID: 95

Evidence for two types of sporangia in the life cycle of *Coelomomyces utahensis*, a parasite of mosquitoes in the rock-pools of Utah

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Abstract

Coelomomyces species are heteroecious obligate fungal parasites which form an ephemeral gametophyte stage in microcrustacean hosts that alternates with a sporophyte stage producing thick-walled resistant sporangia in mosquito hosts. In *Coelomomyces utahensis* this association is maintained under the greatly varying environmental conditions found in rock-pools in Utah. In this study larvae of *Culex tarsalis* and *Aedes epactius* infected with *C. utahensis* were collected, dissected, and examined with light microscopy and scanning electron microscopy. Two distinct types of sporangia were observed in both hosts: thick-walled resistant sporangia with punctate walls as in the original description of the species and smooth-walled sporangia. Differences between the two sporangium types were not easily observable with brightfield microscopy but significant differences became readily apparent when sporangia were observed with phase-contrast optics and scanning electron microscopy. To determine if the observed dimorphism could be attributed to different *Coelomomyces* species, we sequenced the 18S rDNA regions of both punctate resting sporangia and smooth-walled sporangia and found their sequences to be identical. The smooth-walled sporangia were similar in some respects to thin-walled sporangia reported in a small number of African and Asian *Coelomomyces* species but differed from them in having pigmented walls that were approximately equal in thickness to punctate resting sporangia. Presumably the dimorphic condition is a response to the unstable environmental conditions in temporary rock pools with punctate resting sporangia being an adaptation for survival during periods of drought and the smooth-walled sporangia a mechanism to ensure rapid reproduction following a flooding event.

Presentation ID: 96

Species of Diaporthe can survive as Endophytes on Sunflower

Nabin K. Dangal [1], Samuel G. Markell [2], Robert M. Harveson [3], Nathan Braun [1], Clay Carlson [3], Bryan Hansen [2], Jessica Halvorson [2], Brian Kontz [1], Tyler Patrick [3], Allison Rickey Rickey [3], Febina M. Mathew [1]

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Abstract

Phomopsis stem canker, caused by multiple species of *Diaporthe,* is an economically important disease of sunflower (*Helianthus annuus* L.) globally. Field trials were conducted in the U.S. states of Nebraska, North Dakota and South Dakota in 2019 to assess the prevalence of endophytic *Diaporthe* in sunflower. Commercial hybrids were planted at a seeding rate of 18,000 to 20,000 seeds/A in eight plots (four-row; 50 ft long by 10 ft wide) at one location each in each state. Six plants were randomly collected from the middle two rows of all plots beginning from early vegetative to early reproductive growth stages of sunflower development every two to three weeks. The leaves and stems of the plants were cut into small pieces, surface-disinfested and incubated on potato dextrose agar for 10 to 14 days at 22ºC. Fungal cultures were identified using morphology, DNA sequencing, and quantitative polymerase chain reaction assays. At all locations, eight fungal genera were identified occurring as endophytes on sunflower, among which members of the *Alternaria*, *Fusarium* and *Diaporthe* genera were frequently isolated. To evaluate the overall prevalence of endophytic *Diaporthe* in the three U.S. states, the relative importance (RI) index of *Diaporthe* were computed as a percentage of the most frequently isolated genus, *Alternaria*. The *Diaporthe* genus had an overall RI of 11% in Nebraska, 24% in North Dakota and 47% in South Dakota. Results suggest that research on the endophytic survival of *Diaporthe* and how they affect deployment of resistance to Phomopsis stem canker in sunflower is needed.

Presentation ID: 97

Fungal communities in *Schizachyrium scoparium* roots do not differ between restored and native prairie sites

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[1]Kansas State University, Manhattan, KS, USA. [2]University of Kansas, Lawrence, KS, USA

Abstract

Conversion to row-crop agriculture has left less than 4% of the North American tallgrass prairie remaining. Restoring prairie vegetation after long periods of agriculture is challenging, as is measuring restoration effectiveness. Evaluating restoration has historically focused on plant communities, but microbial communities are increasingly recognized as important to maintaining remnant prairie diversity and facilitating restoration. To assess fungal restoration, we contrasted root and leaf fungal communities from restored and remnant prairies at two sites in eastern Kansas. From plants sampled in four replicate plots in paired remnant/restored areas at two sites, we extracted DNA from roots and leaves of the dominant grass, *Schizachyrium scoparium*. We then used Illumina MiSeq to assess fungal community richness, diversity, and composition. Root-associated fungal communities were indistinguishable between plants from remnant and restored prairies. In contrast, leaf-associated fungal communities were distinct, with remnant prairie communities being significantly more diverse than those from restored prairies. Though restoration of the root-associated fungal community seems to have been successful, restoration of leaf-associated communities was less clear. Evaluating multiple aspects of hidden fungal biodiversity can improve the ways we use them to evaluate the effectiveness of restorations of prairies and other threatened ecosystems.

Presentation ID: 98

Standardization of two nested PCR assays to detect resistant isolates of *Aspergillus fumigatus* directly from soil

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Abstract

Aspergillus fumigatus is a ubiquitous fungus, saprophyte of plants, and an opportunistic pathogen of humans. The agricultural industry uses azole fungicides to control pathogens of crops, and azoles are also used as a first line of treatment for Aspergillosis. The continued exposure of *A. fumigatus* to azoles in the environment has led to azole resistance in the clinic where infections result in high levels of mortality. Azole resistance in environmental isolates is associated with tandem-repeat (TR) mutations containing 34 or 46 base pair repeats in the *cyp51A* gene. Since the detection of resistance is important for public health, PCR-based techniques have been developed to detect TR mutations in clinical samples. We are interested in identifying agricultural environments conducive to resistance development, but environmental surveillance of resistance has focused on labor-intensive isolation of the fungus followed by screening for resistance. Our goal was to optimize an assay for rapid detection of azole-resistant *A. fumigatus* directly from soil. i) the DNA extraction using a commercial soil kit was optimized by using the supernatant of a suspension of soil and saline solution, ii) two nested-PCR targeting the TR mutations were standardized, and iii) sensitivity and specificity were tested using *A. fumigatus* DNA from wild type and resistant isolates and then with soils spiked with conidia of the same isolates. The nested-PCR assays allowed us to detect thirty cells of *A. fumigatus* without cross-reaction with DNA from other soil microorganisms. These assays will allow the surveillance of resistant isolates directly from the agricultural environments.

Presentation ID: 99

Microbial diversity in deep-sea hydrothermal vents in the south Gulf of California: Insights into fungal-bacterial *in vitro* interactions

Abril Hernandez-Monroy [1,2], Laura Espinosa-Asuar [3], Luis A. Soto [4], Diana L. Salcedo [2], Luis E. Eguiarte [3], Valeria Souza [3], Patricia Velez [2]

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Abstract

Hydrothermal vents are deep-sea ecosystems with extreme environmental characteristics including abrupt temperature gradients (4°C - <300°C), high hydrostatic pressures, and lack of sunlight energy. Prokaryotic cultivable diversity has been well studied in these ecosystems since their discovery. Nevertheless, fungal cultivable diversity and ecological capacities in response to interactions with further members of the microbial community remain poorly understood. The aim of this work was to 1) characterize the fungal and bacterial cultivable diversity in three deep-sea hydrothermal systems at the south Gulf of California, Mexico, and 2) identify *in vitro* biotic interactions between members of this microbial community. We isolated and identified microfungi and bacteria from sediment cores collected in three hydrothermal systems: Pescadero Basin, Pescadero Transform Fault, and Alarcon Rise, Gulf of California, Mexico. Selected members of the community (four fungi and five bacteria) were chosen for *in vitro* cross-kingdom bioassays in order to characterize ecological interactions using growth indexes. Within the microfungi, members of Aspergillaceae predominated, while *Bacillus* and *Paenibacillus* were the most abundant bacterial genera. In terms of ecological interactions, antagonism and competition prevailed. Nevertheless, time scale changes were detected. In accordance with the Microbial Market Theory, we identified both: variable and stable interactions, which depended on the interacting genotypes and presumably the resources being used or exchanged. These results show a glimpse of the importance of cross-kingdom interactions in deep-sea hydrothermal vents in shaping the microbial community.

Presentation ID: 100

Masters of the manipulator? A comparative genomics study of two new hyperparasite species of the Zombie Ant Fungus.

Brittany Lebert [1], João Araújo [2], Sara Linehan [1], Andreas Brachmann [3], Charissa de Bekker [1]

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Abstract

Although several hyperparasites of *Ophiocordyceps* species have described, little research has been done to determine their effects on *Ophiocordyceps* or gain insight into their lifestyles. The purpose of this study was first to formally describe two new fungal hyperparasite species of the behavior-manipulating parasite, *Ophiocordyceps camponoti-floridani*. From there, we investigated their life history and potential effects on *O. camponoti-floridani* through a longitudinal field study. Finally, we aimed to confirm that these species indeed have a hyperparasitic lifestyle through sequencing their genomes and comparing them to the genomes of saprophytes, mycoparasites, phytopathogens, and animal pathogens. Through phylogenetic analysis we found that both hyperparasites are distinct, new species within the order Hypocreales. One of the new hyperparasite species places within the genus *Polycephalomyces*, while the other matches most closely with the genus *Akanthomyces*. Additionally, our field study found that, of all the observed *Ophiocordyceps* infected ants, only 6.5% were hyperparasatized. Of these hyperparasatized samples, nearly 75% were infected by the *Polycephalomyces* species and only 25% were infected by the *Akanthomyces* species. We also observed that hyperparasites showed up as early as a week and as late as nine months from the first time a manipulated ant cadaver was noted. Our comparative genomics with other fungal lifestyles indicated that both of these new hyperparasite species uniquely shared more genes with mycoparasites and animal pathogens than saprophytes and phytopathogens. They also both had a greater percentage of unique genes than any other species in the study, of which they shared ~20% with one another.

Presentation ID: 101

Are symbionts of invasive grasses a key to their ecological dominance in grasslands of southern Arizona?

Robin Bradley , Jeffrey Fehmi , Craig Rasmussen , A. Elizabeth Arnold

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Abstract

Lehmann's lovegrass (Eragrostis lehmanniana) was introduced to southern Arizona over a century ago to improve livestock grazing. In the semiarid grasslands where it became established, it now displaces native grasses and dominates the landscape. Diverse hypotheses have been proposed to explain its success, focusing on its phenology and its tolerance of drought and fire. Lehmann's lovegrass harbors diverse fungal endophytes in its introduced range, many of which complete their life cycles in litter and soil. Here we tested the prediction that endophytes of Lehmann's lovegrass could promote dominance of that species by negatively impacting seed germination of native species. We selected 19 endophytes isolated from healthy E. lehmanniana in Arizona. We placed surface-sterilized seeds of E. lehmanniana and five native grasses on mycelial lawns on malt extract agar (MEA) and evaluated seed germination and seedling vigor over four weeks. Plates containing MEA but no fungi served as controls. We found that endophytes from Lehmann's lovegrass increased seed germination of that species but decreased germination of all native grasses that germinated during the experiment, including species of Bouteloua, Leptochloa, and Sporobolus. The potential for endophytes of an invasive grass to limit germination and establishment of diverse native species highlights a cryptic but important aspect of plant invasions. Future work should evaluate the impacts of such fungi in the field and examine mechanisms by which seed germination is inhibited or enhanced. Overall this study helps illuminate a microbial contribution to the success and dominance of Lehmann's lovegrass.

Presentation ID: 102

2020 Best Poster Winner

Intraspecific variation in the infectivity of *Laccaria trichodermophora* in *Pinus montezumae* roots

Valeria Stephany Flores-Almaraz , Rodolfo Enrique Ángeles-Argáiz , Camille Truong , Roberto Garibay-Orijel

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Abstract

Ectomycorrhizal (ECM) associations play major roles for the availability of nutrients in temperate and boreal forests. Therefore the use of ECM fungi in reforestation programs has been proposed to improve the productivity and survival of re-introduced plants. *Laccaria trichodermophora* is an ECM fungal species with a high potential as ectomycorrhizal inoculant in Mexican reforestation programs, due to its wide distribution range, dominance in young forest stands, rapid growth in culture and prevalence in the roots of inoculated seedlings. Previous ecological, genomic and biotechnological studies demonstrated the high genetic and phenotypic variability among different strains of this species. We performed a microcosm experiment by inoculating *Pinus montezumae* seedlings with four *L. trichodermophora* strains. These strains showed strong differences in their ability to colonize pine seedlings, since only one of them successfully colonized the roots. We also found that strains that showed the highest biomass production in liquid media were not necessarily able to colonize roots successfully. Such characteristics must be taken into account during germplasm selection of ECM inoculants for biotechnology applications.

Presentation ID: 103

Citizen Science Discoveries within *Hygrophoraceae*

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Abstract

Objective: Our goal has been to gain a better understanding of the family *Hygrophoraceae* through citizen science and undergraduate initiatives. Our ongoing collection of data in the Pacific Northwest has helped contribute to our contemporary knowledge of the range, habitat, and phylogeny of several Waxy Cap species across the world as well as characterize new species. Summary: The "*Hygrophoraceae* of the Lower Puget Sound" was registered in 2017 under the North American Mycoflora Project and furthered with the help of the South Sound Mushroom Club and the Evergreen State College's Myco-Collective. Members of these groups were instructed on collection protocols including completion of field vouchers, photographing and drying specimens, and uploading their findings onto the iNaturalist project page for sorting and prioritization. Active members of the project carefully select which collections to send in for genetic sequencing of the ITS regions at various institutions across the country. The subsequent results are then entered into NCBI's GenBank and compared to other global fungal sequences via BLAST. This process has yielded an abundant influx of new information that has aided in the academic restructuring of taxonomy within *Hygrophoraceae*. In collaboration with mycologists from several countries, citizen scientist efforts of this project have led to the discovery of new species, expanded ranges, and has confirmed distinctions and overlap between Amphi-Atlantic species and coastal North American species.

Presentation ID: 104

Penicillium and Talaromyces from a biodiversity hotspot

Cobus M. Visagie [1], Jos Houbraken [2], Neriman Yilmaz [1]

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Abstract

South Africa is a biodiversity hotspot containing many undescribed fungi. During the morphological era, a trend started of not identifying local *Penicillium* or *Talaromyces* to species level. DNA sequencing combined with a published accepted species list changed this, resulting in 35 new species described from South Africa in recent years. The goal of this project was to update the identifications of strains accessioned in the National Collections of Fungi (PPRI) and the Medical Research Council (MRC). A total of 358 PPRI and MRC strains (283 *Penicillium* and 75 *Talaromyces*) were revived and examined. To identify them, Beta-tubulin sequences were generated for these strains and compared to a locally curated sequence database. For putative new or rarely found species, we added sequences from the ITS, calmodulin and RPB2 gene regions. We generated 593 new reference sequences which were submitted to GenBank. Strains were classified into 97 *Penicillium* and 25 *Talaromyces* species. Amongst these, 12 represents new species (8 *Penicillium* and 4 *Talaromyces*). Morphological characterization and comparisons with close relatives confirmed the novelty of these species. South Africa can make significant contributions to a better understanding of these important genera. Not only were rare and new species discovered, but additional infraspecies variation for well-known species were captured. Capturing this infraspecies variation is critical to aid future identifications and further exploring diversity in these genera.

Presentation ID: 105

First report of *Lecanosticta pharomachri* on exotic pine hosts in Colombia

Cheyenne A. Theron [1], Michael J. Wingfield [1], Carlos A. Rodas [2], Irene Barnes [1]

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[2]Forest Health Protection Programme, Smurfit Kappa, Valle, Colombia

Abstract

Commercial forestry in Colombia includes plantations of non-native *Pinus* spp., mainly originating in Mesoamerica. Brown spot needle blight (BSNB), thought to be caused by *Lecanosticta acicola*, has been known in Colombia for 40 years. A disease resembling BSNB has recently emerged in Colombian plantations of *Pinus* spp. The taxonomy of isolates previously identified as *L. acicola* from Mesoamerica has recently been re-evaluated based on DNA sequence data (van der Nest et al. 2019; IMA Fungus 10: 2) and is now recognised as representing several different species. The aim of this study was to identify the fungus causing the new outbreaks of needle disease resembling BSNB. Isolates collected from various plantation farms in Colombia were characterised based on morphology and DNA sequences data for the internal transcribed spacer region (ITS) and the translation elongation factor 1-α gene (*TEF*1). All isolates emerged as the newly described species, *Lecanosticta pharomachri*. In addition, examination of the fruiting structures on *Pinus patula* revealed, for the first time, the sexual state of this fungus. This study represents the first report of *L. pharomachri* outside the native range of *Pinus* spp. in Central America. It also includes important new hosts *Pinus maximinoi* and *P. patula* for this apparently emerging pathogen.

Presentation ID: 106

New Fusarium and Bisifusarium species from rhizosphere soil of the Jurassic relic Welwitschia mirabilis

Neriman Yilmaz [1], Pedro Crous [2], Mike Wingfield [1]

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[2]Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands

Abstract

Welwitschia mirabilis, discovered in 1859, is the only member of the family *Welwitschiaceae* and endemic to hyper-arid desert regions of Western Namibia and Southern Angola. Some of the specimens are estimated to be between 1000 to 1500 years old and is thus considered "living fossils". In nature, the seeds collected from the wild female cones are often heavily contaminated with spores of *Aspergillus niger* which severely reduces seed viability and causes it to rot. Regarding the fungal diversity associated with *Welwitschia* and the surrounding area, very little information is available. In this study, samples were collected from the rhizosphere of *W. mirabilis* and the surrounding bulk soil. During the survey, *Aspergillus* was the predominant genus isolated from the soil followed by *Alternaria*, *Aureobasidium*, *Bisifusarium*, *Cladosporium*, *Curvularia*, *Fusarium*, *Myrothecium*, *Neocosmospora* and *Phoma*. Amongst these, two new species are discovered in *Bisifusarium* (previously known as the *Fusarium dimerum* species complex) and *Fusarium chylamydosporum* species complex, respectively. Two new species will be described and illustrated using morphological and multilocus molecular analyses. Further studies will be needed to determine the new species' ecological role in relation to *W. mirabilis*.

Presentation ID: 107

A forest *Saccharomyces* population is robust to environmental changes

Primrose Boynton [1,2], Doreen Landermann [2], Rahul Unni [2], Dominika Wloch-Salamon [3], Eva Stukenbrock [2,4]

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Abstract

Microorganisms, including yeasts, evolve remarkably quickly in laboratory environments. But do observations of rapid evolution in the laboratory apply to wild microbial populations? We investigated the response of a wild *Saccharomyces paradoxus* population to environmental changes in its native forest environment. *S. paradoxus* is the wild sister species of the model laboratory organism *S. cerevisiae*, and is an emerging model organism for ecology and evolution. The wild *S. paradoxus* population was robust to seasonal abiotic environmental changes and intraspecific competition: over the course of four seasons, the population's structure did not change and secreted intraspecific toxins did not select for resistant strains. The forest *S. paradoxus* population was also inbred, and we speculate that *S. paradoxus* individuals are well adapted to their changing environments such that monthly environmental changes are not effective selective pressures for the wild *S. paradoxus* population.

Presentation ID: 108

Incursion into a new bio-based material development using marine Ascomycota mycelium from some sandy beaches of the Mexican Pacific coast

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Abstract

A current problem that represents a global environmental threat is the accumulation of plastic waste in the world. Due to the increasing need to produce biodegradable and sustainable materials scientists have developed bio-based materials from fungal mycelium. Usually, *Basidiomycota* from temperate forests are used. However, in the intertidal zone of the marine beaches, a distinctive group of *Ascomycota* exists that show adaptations to the adverse conditions of this ecotone, making them interesting candidates for the production of these bio-based materials, as they can grow in a wider range of conditions and substrates. Therefore, the aim of the study is to isolate, identify, and test the physical properties of the mycelium of the marine *Ascomycota* species that can be used to produce bio-based materials. The sampling was done in September 2019, establishing five points of sampling along the Manzanillo Bay, Colima. To obtain the marine fungi *sensu stricto* the method of incubation in humid chambers of organic remains was followed. All the isolates obtained were characterized morphologically and those that show potential for developing a bio-based material with the mycelium were selected. As expected, *Corollospora maritima* was the predominant species found. Currently, we are testing the following physical properties: swelling, rugosity, hydrophobicity, mechanical performance, and thermal resistance to characterize the material for potential industrial uses.

Presentation ID: 109

Genetic and genomic insights into the successional patterns and reproduction methods of fire-associated *Morchella*

Annie Schauster , Thomas Volk , Todd Osmundson

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Abstract

Burn morels are among the earliest-emerging post-fire organisms in western North American montane coniferous forests, occurring in large numbers the year after a fire. Despite their significant economic and ecological importance, little is known about their duration of reproduction after a fire or the genetic and reproductive implications of mass fruiting events. I addressed these unknowns using post-fire surveys in British Columbia, Canada and Montana, USA in May/June of 2019. To assess fruiting duration, I collected specimens in second-year sites, where burn morels were collected the previous year, and identified them using DNA sequencing. Results demonstrated a predominant shift from burn to non-burn morel species, suggesting rapid changes in soil conditions and/or significant ecological differences between species. To address the implications of mass fruiting, I surveyed first-year post-fire sites, using whole-genome sequences to reveal the spatial extent of individuals and assess population genetic structure within and between sites for two species. Although gene flow appears more inhibited in *Morchella sextelata* than *M. eximia*, both species appear to disperse widely by ascospores and form populations characterized by large numbers of small individuals that persist as dormant structures between fires. My results will lead to a better biological understanding of these commercially and ecologically important mushrooms.

Presentation ID: 110

Effects of Salinity on Environmentally Driven Halotolerace in Root-Associated Ascomycetes

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Abstract

Communities of animals, plants, and micro-organisms are commonly differentiated along precipitation gradients, yet it remains uncertain whether individuals within species are similarly ecotypically selected, particularly for microbes. In order to recognize environmentally driven adaptations of Ascomycota fungi to environmental conditions, we analyzed stress tolerance for five ascomycete species, with 6 unique individuals per species for a total of 30 individuals selected from sites that experienced up to two-fold differences in mean annual precipitation (MAP) across the central United States. Utilizing fungal isolates previously acquired from past research and from a multitude of locations differing in ranges of MAP were categorized as either arid (<600 mm MAP) or mesic (>600 mm MAP). We used quadrant Petri plates amended with sodium chloride (NaCl) at four concentrations (0g/L, 25g/L, 50g/L, 100g/L). Analyses of estimated NaCl concentrations that reduced the fungal growth by 50% (ED_{50}) indicated that, although the fungal isolates varied in their halotolerances, ecotypic adaptation to prevailing environmental conditions at the site of their origin was limited. Our data suggest physiological plasticity in fungal populations adapted to environments with multiple potential stressors. Further experiments using conspecific isolates that vary significantly in their environmental tolerances to NaCl will aim to identify the underlying proteomic, genomic, and functional traits of haloial stress tolerance in fungi.

Presentation ID: 111

Exploration of marine lichenized fungi as bioindicators of coastal ocean pollution in the Boston Harbor Islands National Park

Liam Nokes , Donald Pfister

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Abstract

This preliminary exploration of marine lichenized fungi (lichens) as bioindicators of water pollution examined the distribution of intertidal lichen communities in the Boston Harbor Islands National Park with respect to recorded pollution throughout the harbor. We found significant negative associations between pollution measurements and the health of the lichen community based on cover and species richness. We observed significant differences in species composition between areas of higher pollution and areas of lower pollution, though there are not enough data to establish the pollution sensitivity or tolerance of individual species. We note that difficulties in the collection and identification of marine lichens hamper efforts to use them broadly as bioindicators. This study suggests that marine lichens could prove useful as bioindicators, but more research is needed to understand the differential effects of pollution on individual species as well as to establish practical procedures both for quantifying marine lichen community health and for widespread bioindication using marine lichens.

Presentation ID: 112

Control Cross Inoculation Experiment: The discovery of new hosts susceptible to Snake Fungal Disease and Yellow Fungal Disease

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Abstract

Snake Fungal Disease (SFD, *Ophidiomyces ophiodiicola*) and Yellow Fungal Disease (YFD, Nannizziopsis guarroi) afflict reptiles and, until now, were thought to only infect snakes and lizards, respectively. We sought to test if *O. ophiodiicola* is capable of infecting other animals, potentially causing disease in naïve wild populations and exacerbating spillover effects into domestic populations of reptiles. We ran a cross-inoculation experiment using the two fungal pathogens, and two animal hosts, corn snakes (*Pantherophis guttatus*) and bearded dragons (*Pogona vitticeps)*. Each fungus was capable of infecting both corn snakes and bearded dragons, expanding the known host range of both pathogens. Bearded dragons inoculated with *O. ophiodiicola* exhibited a range of clinical signs in response to infection and histological analyses revealed evidence of epidermal invasion by fungal elements (hyphae or conidia), confirming *O. ophiodiicola* can infect animals other than snakes. Corn snakes inoculated with *N. guarroi* never developed thickened scales or gross lesions. However, as with bearded dragons, histological analyses revealed epidermal invasion of fungal elements, confirming *N. guarroi* can infect animals other than lizards. Our experiment is the first to reveal *O. ophiodiicola* is capable of infecting hosts other than snake species, suggesting a much larger host range exists than previously thought, which validate concerns of spillover effects into domestic reptile populations. Furthermore, our experiment is the first to confirm *N. guarroi* as a causative agent of disease in bearded dragons, as the experiment simultaneously fulfills Koch's postulates, and shows that YFD is capable of infecting hosts other than lizards.

Presentation ID: 113

Cultivation protocols of *Pycnoporus sanguineos* in lignocellulosic biomass system for mycelial mass and antibacterial bioactives extraction.

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Abstract

Pycnoporus sanguineos when decomposing wood, synthesizes pigments wich produces an orange-red mycelial structure, one of them is Cinabarina, a well-known antibacterial substance. Protocols for cultivation and quantitative extraction of this bioactive have been developed. Thus, the strain was grown in potato dextrose agar and variations with addition of peptone, and/or maltose, compared to a lignocellulosic biomass system containing sawdust from Pinus, rice bran, and oats. Aliquots were removed every 7 days until the 28th day of growt. The bioactives of the filtered mycelia were extracted with organic solvents (acetone, ethyl acetate, methanol, ethanol and propanol). Antibacterial activity was evaluated in an agar diffusion assay. The lignocellulosic biomass system obtained an average of 5 times more mycelial mass, compared to other crops. An opposite result, of the broth and/or variations, which did not show significant influence on the achievement. In general, the extracts obtained with ethyl acetate after the 20th day, obtained greater antibacterial activity, against *Staphylococcus aureus*, when compared to the other solvents. However, all extracts had low action against *Escherichia coli*, and no action on *Pseudomonas aeruginosa*.

Presentation ID: 114

Different Fire Severities Result in Distinct Soil Fungal Community Trajectories

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Abstract

Wildfires have increased in occurrences and severity. These fires create landscape mosaic of varying burn severities. We created experimental fires that differed in severity to mimic such landscape mosaics. We established ten pairs of plots in the Pringle Falls Experimental Forest in Oregon, USA. For each pair, one plot served as a background control (low severity burn), whereas another included logs piled in 1.5m x 8m x 1m structure for intense whole log combustion (high severity burn). The soils were sampled from 0-10cm depth within each plot before the burn, a week after the burn, as well as 2, 4, and 6 years after the burn. DNA was extracted from these soil samples and ITS2 barcode amplicons Illumina MiSeq sequenced to compare community richness, diversity, and composition among the severity treatments over time. We found that high and low severity fires differently impacted the fungal communities.

Presentation ID: 115

2020 Best Poster Winner

To explore the effects of habitat fragmentation on soil microbiomes and how these microbial communities affect early growth and germination

Kasey Kiesewetter , Michelle Afkhami

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Abstract

Anthropogenic habitat fragmentation is a key driver of biodiversity loss. While studies have analyzed fragmentation effects on macro-organisms, we are just beginning to understand these effects on microbial "hidden players" whose ecosystem services can span multiple levels of biological organization. Our study uses the highly fragmented South Florida Pine Rockland ecosystem to describe the effects of fragmentation on soil microbial communities. We collected soil from 14 Pine Rockland fragments to characterize their microbiomes and test their effects on native plant performance. We sowed seeds from 3 native plant species in the presence and absence of microbiomes from each of the 14 fragments (14 fragments x2 microbial treatments x3 replicates x 3 species). We measured germination and plant performance parameters. Soil microbiomes were characterized using ITS and 16S barcode regions targeting fungi and bacteria (respectively). Patch and connectivity metrics explained variation in both fungal and bacterial community composition. Further, the variation in microbial community composition affected plant performance and allocation. Variation in fungal communities primarily affected plant performance traits (e.g. days to germination, leaf growth) while variation in bacterial community composition primarily affected plant allocation (i.e. root:shoot ratio). These relationships also vary in strength and direction depending on plant species identity. Our results suggest that habitat fragmentation has complex effects on species interactions between plants and microbes. This work will inform our general understanding of complex, native microbiomes and provide some of the first insight into how fragmentation's impact on microbial communities affects species interactions and primary production.

Presentation ID: 116

FunCore: A Database for Fungal Core Genes

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Abstract

Recent observations of biosynthetic gene cluster (BGC) characteristics of fungal secondary metabolites (SM) point toward specific resistance-gene-based hypotheses leading to accurate BGC prediction. The resistance hypotheses suggest that there are resistance genes within the BGC against the SM which are potentially harmful of an organism. In the target-based strategy, duplicated copies of an essential gene within BGC can provide excess targets of SM, hence give greater tolerance against the SM. While the current database for fungal essential genes contained only a few numbers of fungal genomes. The aim of this study is to construct an exhaustive fungal core gene database for accurate the BGC prediction in fungi. A total of 774 fungal genomes were collected and used for identifying potential fungal core gene clusters. We used a large-scale genome comparison followed by a network-based clustering prediction using Louvain Algorithm. The 442 million predicted core gene clusters were ranked by the probability scores using generalized linear model with the network statistical parameters. Our top predictions of core genes are significantly enriched with the known fungal essential genes. The data can be visualized on a web-based GUI with dynamic 3D network plots which allow users to browse the entire core gene networks and their functions. The FunCore database contains the largest numbers of fungal genomes, using a novel network biology prediction and statistical modelling, giving a full list of fungal core genes. Based on FunCore, we will be able to implement the resistance-gene based hypotheses for the prediction of fungal BGC.

Presentation ID: 117

Loop-mediated isothermal amplification (LAMP) is specific and sensitive for the detection of the White-nose syndrome fungus, *Pseudogymnoascus destructans*

Jasmine Grey , Hannah Reynolds

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Abstract

Pseudogymnoascus destructans (*Pd*) is a fungus that is causing the White-nose syndrome epidemic in bats in North America. We have developed a protocol for the reliable and cheap detection system called loop-mediated isothermal amplification (LAMP) to identify infected bats in early stages of infection and to test bat habitats for *Pd*. This method must be highly specific due to the presence of closely related, non-virulent *Pseudogymnoascus* species in bat habitats. LAMP has been successfully implemented in other systems such as malaria, *Candida auris,* and SARS-CoV-2 in humans, and Flavescence dorée in grape vines, indicating the versatility and value of this technique. The advantages of using LAMP over other PCR techniques are the isothermal conditions, a low cost, and the on-site capabilities due to a color change indicator. First, we generated and screened nine primer sets that were based on barcoding and virulence genes with no success. Then, we generated ten additional primer sets for regions of the genome consisting of a window of 100 base-pairs with at least six single nucleotide polymorphisms in *P. destructans* when compared to ten strains of *Pseudogymnoascus spp.* Of these, one primer set was highly specific, sensitive, and rapid (25 minutes) for the detection of *Pd.* This primer set can be used with the WarmStart® Colorimetric LAMP 2X Master Mix to result in a color change, with pink being negative and yellow being positive. The LAMP method is faster, more specific, and more accessible than current methods for the detection of *Pd*.

Presentation ID: 118

Patterns and drivers of occurrence of *Neonectria faginata* and *N. ditissima* across the range of beech bark disease

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Abstract

Beech bark disease (BBD) is a cankering disease of American beech (*Fagus grandifolia*) in North America that is caused by an invasive scale insect and two presumptively native fungal pathogens, *Neonectria faginata* and *N. ditissima*. *Neonectria ditissima* has been observed as the dominant pathogen in stands within the killing front of the disease where the beech scale, *Cryptococcus fagisuga*, is actively spreading. Conversely, *N. faginata* can become dominant in aftermath forests. The drivers of this observed pattern have not been rigorously examined, however. Additionally, nearly all assessments to date have relied on spore size from field-collected perithecia which could introduce detection bias. Here we characterized the distributions of *N. faginata* and *N. ditissima* using ITS-metabarcoding of beech phloem from ten sites across the range of BBD, and used joint species distribution modeling to understand species associations with disease severity and climate. Both pathogens occurred across the range of BBD, co-occurring within sites, trees, or even 1cm phloem disks. *Neonectria faginata* was associated with longer-duration infections supporting the idea that it becomes prevalent in aftermath forests, however there was no significant relationship between *N. ditissima* and infection duration. Trees with more extensive crown dieback had greater *N. ditissima* prevalence irrespective of BBD stage. The two species had opposite responses to climate, with *N. faginata* and *N. ditissima* associated with warmer and cooler sites, respectively. Together, our results suggest that the distribution and relative frequencies of these two important pathogens vary systematically with BBD range expansion, but that range-wide climate patterns may contribute to differing outcomes for tree and forest stand health.

Presentation ID: 119

Variation in predicted secondary metabolite profiles of fungal species in Botryosphaeriaceae

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Abstract

The family Botryosphaeriaceae contains endophytic, plant pathogenic, and saprobic species of filamentous fungi. As research into fungal secondary metabolite (SM) diversity expands, there has been interest in discovering how these molecules function in plant pathogenesis. Using the SM prediction pipeline antiSMASH (v5.1.2), the nuclear genomes of 11 fungal species in Botryosphaeriaceae were examined to identify putative biosynthetic gene clusters (BGCs). Total predicted BGCs ranged from 20 in *Diplodia sapinea* to 65 in *Macrophomina phaseolina*. The number of BGC types ranged from 1 to 147 with type 3 polyketide synthases (T3PKS) and type 1 polyketide synthases (T1PKS) representing the least and most frequently predicted BGCs, respectively. To further investigate possible BGC variation, the genomes of 10 isolates of *M. phaseolina* (genome sizes ranging from 45.8 Mb to 98.7 Mb) from 10 different hosts representing five plant families were analyzed. The isolate of *M. phaseolina* from castor bean, which had the largest genome (98.7 Mb) among the isolates, had approximately two-times the number of T1PKS, terpene, non-ribosomal peptide synthetase (NRPS), and NRPS-like BGCs compared to the other isolates. In contrast, isolates from alfalfa, bushclover, corn, jute, sorghum, soybean, strawberry, sunflower, and switchgrass had similar genome sizes (45.8 Mb to 52.5 Mb) and similarly predicted numbers and types of BGCs. These results will inform future research on the diversity and predicted SM function in Botryosphaeriaceae fungi and may provide insight into the relative contribution of the SM profile variation in *M. phaseolina* to host range expansion.

Presentation ID: 120

Abundance of Actinomycetes on Decomposing Pine Ectomycorrhizae

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Abstract

Actinomycetes are filamentous bacteria that make up one of the largest groups in the domain Bacteria. They are found in a wide range of environments, although mainly in the soil. Actinomycetes are well known as producers of important secondary metabolites, such as two-thirds of all known antibiotics, other pharmaceutical compounds, fungicides, and pesticides. For this reason, they are highly sought after as sources of new pharmaceuticals and bioactive agents. Actinomycetes are important in the soil as nitrogen fixers and efficient decomposers of chitin, keratin, and lignocellulose. Actinomycetes are also found in association with ectomycorrhizae and may be involved in tripartite plant-fungal-bacterial symbioses. However, their ability to digest chitin and lignocellulose may also allow them to digest mycorrhizae. The objective of this study was to monitor actinomycete abundance after severing ectomycorrhizal root systems. An increase in actinomycetes over time may be indicative of a role in mycorrhizal decomposition, whereas a decrease may indicate a mutualistic relationship. Alternatively, shifts in actinomycete DNA over time could also show seasonal trends in abundance of actinomycetes and ECM. Actinomycetes associated with ectomycorrhizae formed by *Cenococcum geophilum* on the roots of *Pinus strobus* were quantified by real-time quantitative PCR (qPCR) at different time points over a 9-month decomposition period. Actinomycete abundance appears to be highest in the undisturbed samples, suggesting that actinomycetes have a closer association with healthy, rather than decomposing ectomycorrhizae.

Presentation ID: 121

DIVERSITY OF MYCORRHIZAL TYPES ALONG ALTITUDINAL GRADIENTS IN MONTANE TROPICAL FORESTS OF NORTHERN SOUTH AMERICA

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Abstract

Mycorrhizal fungi play key roles in the functioning of terrestrial ecosystems. The main types of mycorrhizal associations are: arbuscular mycorrhizas (AM), ectomycorrhizas (EcM), ericoid mycorrhizas (ErM) and orchid mycorrhizas (OM). Previous studies have shown that the abundance of AM, EcM and ErM plants change gradually along latitudinal and altitudinal gradients driven by the effects of climate on decomposition, reflected in the accumulation of carbon and nutrients in the soil. The Colombian Andean mountain range reaches altitudes over 5,000m becoming a great system to test the effects of altitude in tropical ecosystems. We aimed to understand how altitude and climatic and soil conditions shape the distribution patterns of mycorrhizal types in plant species distributed along this region. To test this, we used a herbarium plant record database and assigned mycorrhizal type based on the available literature. We also used bioclimatic and soil variables at a resolution of 10 km. We calculated the proportion of each of the different mycorrhizal associations types per grid cell and created a diversity index to explore their spatial distribution and their association with abiotic factors based on GLMs. We found that the diversity of mycorrhizal associations increases with altitude and soil carbon stock. We also found that the abundance of EcM and OM plants peaks around 2,000m and the abundance of ErM peaks around 2,300m, while AM plants preferred lower elevations (1,700m). Our results suggest that climate change can alter the distribution of mycorrhizal types in tropical mountains with consequences for ecosystem function.

Presentation ID: 122

Characterization of the Roles of the Monothiol Glutaredoxin, Grx4 in the Cell Biology and Virulence of *Ustilago maydis*

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Abstract

The corn smut fungus, *Ustilago maydis*, is the premier basidiomycete model for studying plant-pathogen interactions. Monothiol glutaredoxins are central regulators of cellular functions such as iron homeostasis, cell wall integrity and the redox status of fungal cells. The roles of glutaredoxins in the pathogenesis of plant pathogens have yet to be characterized. In this study we investigate the novel role of the monothiol glutaredoxin Grx4 in the pathogenesis of *U. maydis* on its host, *Zea mays*. Mutant strains expressing a conditional allele of *grx4* under the control of the arabinose-induced/glucose-repressed promoter P_{crg} exhibit significantly decreased virulence on maize. When grown in glucose, these strains exhibit increased susceptibility to reactive oxygen species, cell membrane stressors and cell wall stressors; additionally, they demonstrate altered abilities to utilize exogenous iron sources. These data suggest that glutaredoxins play an important role in the virulence of plant pathogenic fungi, in addition to their established roles as key regulators of fundamental cellular processes.

Presentation ID: 123

Finding a phylogenetic home for a beautiful leaf inhabiting fungal fossil

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Abstract

Comparing the morphology of living and fossil fungi on leaves offers an opportunity to track the evolution of fungal lineages through time. Fossils in the genus *Callimothallus* have been recorded frequently over the past 65 Million years, together with other fly-speck fungi. To infer the relationships of *Callimothallus*, we first need to estimate the relationships of its likely extant relatives. These comprise the known radiate fly-speck fungi, all of them in Dothideomycetes. We added four-locus data from 65 species to a published tree from 101 fungal genomes. We coded eight morphological characters for *Callimothallus* and for 86 of the extant taxa that we selected for further analysis. We used the molecular tree trimmed to our 86 taxa as a constraint for a branch-and-bound morphology-based parsimony search for the position of *Callimothallus*. In all of our analyses, *Callimothallus* appeared most closely related to Muyocopronales. Asexual Muyocropronales most frequently produce cells aggregated in a plate-like scutellum, each bearing raised pores for conidiation. In some taxa, those asexual scutella may be radiate, as in *Mycoleptodiscus venezuelensis*. Trees that were one step longer showed *Callimothallus* with non-radiate Muyocopronales or with Microthyriales. Microthyriales sexual scutella share hyphal branching patterns and margin type with *Callimothallus*. Since the scutellum cells in Microthyriales are not porate, we interpret the oldest occurrence of *Callimothallus*, from the Maastrichtian of Colombia (72–65Ma), as ancient, asexual Muyocopronales. The available record of *Callimothallus* species through geological time suggests that Muyocopronales could have survived the last mass extinction event.

Presentation ID: 124

The mycobiome of Nova Scotia vineyard grapes

Adele Bunbury-Blanchette [1], Lihua Fan [2], Gavin Kernaghan [3], Marcia English [4], Kaylee Boyle [3]

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Abstract

Winemaking is a burgeoning industry in Nova Scotia, with many new opportunities for research into biological interactions within its vineyards. While *Saccharomyces cerevisiae* is usually added to grape juice (must) to induce wine fermentation, many native yeasts reside naturally on grape skins and can noticeably influence wine flavour (the "microbial terroir"). However, it is unclear how factors such as grape variety and vineyard management practices influence native yeast communities. We analysed yeast communities before and after the spontaneous fermentation of pressed juices from five Nova Scotia vineyards using next generation ITS sequencing (Illumina MiSeq). Vineyards grew white and red grape varieties, and used conventional or organic management practices. Regardless of grape variety or vineyard management type, musts from vineyards with better tasting and more efficient fermentations tended to contain *Saccharomyces cerevisiae*, while those with somewhat lower taste scores and slower fermentations were more likely to be associated with other yeasts, such as *Saccharomyces uvarum.* These results may allow Nova Scotia winemakers to begin experimenting with native yeast communities in order to highlight the distinctive qualities of their individual vineyards.

Presentation ID: 125

Comparative genomics of the mitochondrial genomes of fungal species in the Ceratocystidaceae

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Abstract

The small, relatively conserved, and uniparental inherited mitochondrial genome can offer important insight into evolutionary history of an organism. Currently a large number of whole genome sequences are available for species in the Ceratocystidaceae, a fungal family which consists of plant pathogens of great economic importance. However, little is known regarding the mitochondrial genomes and their conservation in these species. The aims of this study were to assemble and to compare the mitochondrial genomes of species of the Ceratocystidaceae. Using the available genomics data, we assembled, annotated and compared mitochondrial genomes of 11 species residing in 8 different genera of the Ceratocystidaceae. The results show that these genomes were highly variable in terms of size, which ranged from 99 Kb in *Ceratocystis manginecans* to 224 kb in *Endoconidiophora laricicola*. Despite the large variation in genome sizes, the number of genes and their order were highly conserved across the species investigated. However, the number of introns and their sizes varied greatly across different species and genera and accounted for the variation of the overall genome size observed. Current research focuses on studying the evolutionary relationship of the mitochondrial genes and comparing that to the nuclear genes in order to gain further insight into the evolution of these important fungi.

Presentation ID: 126

From plants to ants: *Leucoagaricus gongylophorus* modifies plant lipids for delivery to leaf-cutter ant mutualists

Lily Khadempour [1], Jennifer Kyle [2], Bobbie-Jo Webb-Robertson [2], Carrie Nicora [2], Francesca Smith [2], Richard Smith [2], Mary Lipton [3], Cameron Currie [1], Erin Baker [4], Kristin Burnum-Johnson [3]

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Abstract

Leaf-cutter ants cultivate a mutualistic fungus *Leucoagaricus gongylophorus*, which enzymatically digests fresh plant material that the ants provide, and in exchange, provides the ants with a food source in the form of specialized hyphal swellings called gongylidia. Here, using global lipidomic analysis, we characterized and quantified lipids in fresh leaf material, through layers of the fungus garden, and in the gongylidia. Interestingly, the lipids identified in sample types and garden regions varied significantly. The top of the fungus garden was similar in lipid content to the fresh leaves, both of which were enriched in lipids containing alpha-linolenic acid (18:3). These lipids became less dominant as leaf material moved down through the middle and bottom of the fungus garden. The gongylidia were dominated by lipids containing linoleic acid (18:2). We conducted a behavior experiment to test the ants' response to these different lipids. We found that leaf-cutter ants were attracted to the gongylidia-associated lipids (18:2) but acted aggressively toward the leaf-associated lipids (18:3). The 18:2 lipids found in the gongylida may be serving as mode of communication between the co-evolved ants and their fungal cultivar.

Presentation ID: 127

RNA-seq of cell populations during the early development of *Coprinopsis cinerea* reveals intensive reprogramming of hyphal growth patterns

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Abstract

The fruiting body is the most complex multicellular structure in fungi which shows three-dimensional organization and develops many tissue types. Several studies have examined fruiting body development, yet genetic background of early development and tissue differentiation is incompletely known. Here, we explore fine-scale gene expression patterns of the development of *Coprinopsis cinerea* strain A43mutB43mut, by sequencing mRNA of cell populations (tissues) through early developmental stages isolated using laser-capture microdissection (LCM). We first adapted and modified LCM and RNA-seq methods to *C. cinerea* achieving a reliable wet-lab protocol (RNA integrity number > 6 and 80% coverage of reads on the reference genome). We examined seven developmental stages and nine tissue types but here we focused on the first two steps of development: the transition from vegetative mycelium (VM) to primary hyphal knot (H1) and from H1 to secondary hyphal knot (H2). We found that a high number of genes were upregulated in H1 (1,293 genes), the H2 universal veil (2,050), and the H2 nodulus (2,590). By annotating and manually curating the protein functions of upregulated genes using public and in-house databases we found a preponderance of genes associated with cell division and hyphal growth pattern. We also found 75 upregulated genes with glycoside hydrolase activity suggesting that CAZy could have an important role in morphogenesis besides wood degradation. Finally, we identified many tissue-specific gene expression patterns indicating that the low-input RNA-seq method gave higher resolution than is possible using traditional techniques and the importance of fine-scale genetic analysis.

Presentation ID: 128

Informative markers for delineating species boundaries in *Ceratocystis*

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Abstract

The genus *Ceratocystis* includes many plant pathogens of economic significance. As such many species are on the quarantine list of countries around the globe. A solid taxonomic foundation and rigorous species recognition of these fungi is crucially important for effective quarantine measures. Currently species recognition in *Ceratocystis* is problematic which is mainly due to the lack of an informative set of markers for species recognition in these fungi. The aim of this study is to use available whole genome sequence data for species in the *Ceratocystis* and other genera in the Ceratocystidaceae and develop a set of informative markers which can be used for recognizing species boundaries in these fungi. Whole genome sequence data for 26 species in the Ceratocystidaceae were used to construct a species tree for these species. Using this species tree as a guideline, a set of informative markers were selected out of the 3571 shared single copy orthologous genes present in all 26 species. These markers are currently being tested for their usefulness for species recognition in *Ceratocystis*. The set of novel makers identified in this study will facilitate and unify the species recognition in *Ceratocystis* and also in other genera in the Ceratocystidacaee.

Presentation ID: 129

Elucidating the growth of *Fusarium circinatum* towards *Pinus patula* root exudates.

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Abstract

The criticality of the interaction between roots and fungal pathogens in research is increasingly recognized. There are chemicals secreted from these pathogens and roots that act as signals and when they are recognized the process of communication and interaction takes place. Studies have shown that the sex pheromone receptor Ste2 can facilitate these interactions between the fungal pathogen such as *Fusarium oxysporum* and its host plant. The objective of our research was to determine whether Ste2 is involved in recognition of root exudes by the pine pathogen *Fusarium circinatum.* To achieve these goals, a quantitative plate assay was developed to investigate the growth of *F. circinatum* toward the *Pinus patula* root exudates. The results indicated that the wild type strains produced significantly more germlines growing toward the root exudates than the Ste2 deletion mutants. In other words, *F. circinatum* does not only exhibit a positive response to the root exudate of its plant host, but that the sex pheromone Ste2 is involved in the process. Data suggest that the pheromone receptor Ste2 is involved in the recognition pathway for some chemicals in pine root exudates.

Presentation ID: 130

Genetic mechanisms of context dependency: Identifying gene families with putative roles in arbuscular mycorrhizal symbiosis

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Abstract

Outcomes of species interactions are almost universally context-dependent, but the mechanisms that underpin these context-dependent responses remain unclear. To investigate how context dependency regulates interactions, I used the symbiosis between arbuscular mycorrhizal fungi and plants as a model system because of the rich literature describing how it shifts along a mutualism-to-parasitism continuum and extensive genomic resources of host plants. Specifically, I phylogenetically grouped proteins from 32 mycorrhizal and 10 non-mycorrhizal plants and found 493 of 28756 candidate gene families that likely have undergone genetic decay in non-mycorrhizal plants because they lack selective pressure to maintain the symbiosis. To confirm that these candidate families are involved in mycorrhizal symbiosis, I confirmed genes previously identified as essential for mycorrhizal symbiosis, common symbiosis genes, are enriched in the candidate families (7/10, null=1.7%, p=4.99*10-11). I am also analyzing promoter sequences of candidate families to identify transcription factor binding sites of transcription factors associated with environmental regulation that separate family members into different groups and RNA sequencing data of Medicago truncatula in the presence/absence of drought stress to directly tie differential expression of candidate symbiosis family members with water stress (a known abiotic factor important for AM symbiosis). My results will inform future work identifying these families' roles in mycorrhizal symbiosis and how they are regulated in different contexts.

Presentation ID: 131

Drivers and implications of distance decay differ for ectomycorrhizal and foliar endophytic fungi across an anciently fragmented landscape.

Elizabeth Bowman [1,2], A. Elizabeth Arnold [1]

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Abstract

Fungal symbionts of forest trees often decrease in community similarity with increasing geographic distance between sampling areas (i.e., they demonstrate distance decay). In the southwestern USA, forests typically occur in disjunct mountain ranges separated by warmer, drier biomes with taxonomically and evolutionarily distinct plants and fungi. These disjunct forests are similar in climate to one another, offering an opportunity to examine the drivers of distance decay against a backdrop of ecologically similar but disparate landscapes with a long history of separation. We examined ectomycorrhizal and endophytic fungi associated with a dominant forest tree (*Pinus ponderosa*) across mountain ranges spanning ca. 550 km in Arizona, USA. Although both functional groups of fungi showed distance decay, drivers differed for each: ectomycorrhizal fungi appear to be constrained primarily by dispersal limitation, whereas widespread endophytes are constrained by specific environmental conditions. Ultimately the strong signature of dispersal limitation in ectomycorrhizal symbioses, and strong environmental selection for endophyte symbioses, suggests that regional-scale perspectives are needed to (1) establish baseline estimates of the diversity of fungi associated with forest trees at a landscape scale, and (2) frame hypotheses regarding their sensitivity to increasing fragmentation, decreasing areas of suitable habitat, disturbance, and related impacts of climate change.

Presentation ID: 132

Monetary value of Citizen Science: The 2019 MycoBlitz

Bitty A Roy [1], Eric Chandler [2], D Jean Lodge [3]

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Abstract

Citizen Science has both intellectual and monetary value for mycology. In this poster we focus on the monetary. For the 2019 Mycoblitz, Chandler kept track of the number of miles driven (264), which was used to calculate fuel (@3.02/G) and maintenance costs (0.18/mi), combined with the number of hours a single person put into the foray and post-foray identification(95.5. We estimated a mycologist earns about 34$/hr. on average. There were 219 participants. When all these numbers are multiplied out, we end up with a value of 698,500.50 for citizen science contributions for a single foray. The value, of course, is much more than that because the intellectual contributions are incalculable.

Presentation ID: 133

Genomic diversification of the parasite *Escovopsis* across the evolutionary history of the attine ant-microbe symbiosis

Gotting Kirsten [1], Daniel May [1], Lily Khadempour [1,2], Aileen Berasategui Lopez [3], Quimi Vidaurre Montoya [4], Shelby Sanstrom [1], Caitlin Carlson [1], Ted Schultz [5], Andre Rodrigues [4], Monica Tallarico Pupo [6], Tim Bugni [1], Nicole Gerardo [3], Cameron Currie [1]

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Abstract

Close symbioses drive species diversifications, with the interplay between host and symbiont shaping one another's evolutionary trajectories. Fungus growing ants have been in a mutualism with agaricaceous fungi for over 65 million years. Over this time, the ants and their fungal cultivars extensively coevolved; ants and fungi in the leafcutter symbiosis exhibit reciprocally evolved genomes that reflect their obligate co-dependency. An Ascomycete fungus in the genus *Escovopsis* parasitizes this mutualism. While the genomic coevolution between the ants and their cultivar has been characterized, we know little about the evolutionary trajectory of the parasite and whether it similarly coevolved with its host. We combined genomes from seven previously reported strains with 18 newly sequenced strains to show that the genome-scale phylogeny of *Escovopsis* tracks its ant host cultivation strategy. In addition, we find genome reduction in protein coding DNA in all *Escovopsis* genomes compared to sister taxa in the Hypocreaceae. Only 8% of identified orthologues were unique to *Escovopsis* spp., these consisting mainly of virulence factors, signaling molecules, and resistance genes. Detection of biosynthetic gene clusters (BGCs) revealed their varied distribution across *Escovopsis* strains, with this category of genes showing the largest increase in unique genes. The products of several BGCs were confirmed by metabolomics. One such group of molecules, the shearinines, are known for their adverse effects on insect hosts. Our results demonstrate how long-term symbioses impact the evolutionary trajectories of specific partners and, in particular, how a parasite evolves to adapt to selective pressures from the host.

Presentation ID: 134

A new genus sister to *Apophysomyces* (Mucoromycota: Mucorales), isolated from fungus-feeding millipedes

Angie Macias [1], Brian Lovett [1], Chase Mayers [2], Derreck Carter-House [3], Jessie Uehling [4], Lindsay Kasson [5], Teresa Pawlowska [2], Matt Kasson [1], Jason Stajich [3]

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Abstract

Four unidentified fungal isolates with identical culture morphology were collected in Oklahoma, USA in 2016 from the fungivorous millipede *Brachycybe lecontii.* ITS barcoding revealed that these isolates were closely related to but likely distinct from *Apophysomyces*, a genus of soil saprotrophs that are also facultative human pathogens. Morphological studies recovered sporangia containing slightly trapezoidal to ellipsoid sporangiospores, similar to those produced by several *Apophysomyces* species. Unlike known *Apophysomyces* species, which can grow at or above 40 °C, the new isolates were not able to survive temperatures of 35 °C with growth significantly inhibited above 33 °C. Genomic studies identified an endohyphal bacterium (*Mycetohabitans* sp.) from two of four isolates investigated. Interestingly, growth of isolates lacking endohyphal bacteria was greater at 33 °C, possibly indicating an interaction between endohyphal colonization and thermotolerance. The cultures lacking evidence of endohyphal bacteria were the only strains that sporulated. Follow-up studies found that the new isolates represent a novel, genealogically exclusive lineage sister to *Apophysomyces*. Phylogenetic and phylogenomic trees generated using 3 loci and 422 conserved orthologous protein sequences, respectively, had long branches separating novel isolates and *Apophysomyces*, indicating they may represent a novel genus. Finally, a pathogenicity assay against *Brachycybe* millipedes, from which these fungi were recovered, found that isolates of the novel genus were not pathogenic. Future efforts will build upon existing morphological, genomic, and thermotolerance data to complete a formal taxonomic description of the novel genus and species, and will contribute to continuing efforts to identify and visualize putative endohyphal bacteria.

Presentation ID: 135

A new basidiomycete fungus that is pathogenic on *Ligustrum*

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Abstract

In the fall of 2019, we identified mortality, blight symptoms, and signs of white mycelium on ornamental *Ligustrum japonicum* in Gainesville, Florida. To determinate the causal agent, isolations and in-vitro experiments were performed with two replicates. We identified an unknown basidiomycete (G19-1738) based on morphological characteristics (rhizomorphs and clamp connections) and sequences of the ITS and LSU-rDNA. Sequences of the LSU region were subjected to BLAST analysis. We then constructed a nucleotide alignment of diverse Agaricales fungi and performed Maximum likelihood phylogenetic analysis. Based on our analysis we determined that the unknown basidiomycete (G19-1738) is related to resupinate and cyphelloid fungi in the Marasmioid clade. To determinate the pathogenicity of the unknown fungus, in-vitro experiments were carried out with *Ligustrum* leaves on water agar medium. Leaves were inoculated with mycelium plugs of G19-1738, a Trichoderma sp. as a positive control, and water agar as a negative control. Blight and white mycelium were present in the leaves inoculated with G19-1738 and the symptoms and signs were consistent among replicates. A greenhouse experiment will be performed in the Summer of 2020.

Presentation ID: 136

Investigations into the boletes of south Florida

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Abstract

Much of Florida remains critically under-sampled with respect to fungi. An overwhelming majority of fungi collections are from the north Florida region, and very few have been collected from southern Florida. In the past few years, we have been inventorying macrofungi from Everglades National Park and Dagny Johnson Key Largo Hammock Botanical State Park, with a particular focus on the boletes (Boletales). We have discovered several Caribbean boletes from these areas, including *Austroboletus* sp. nov., *Boletellus cubensis*, *Boletus projectelloides, Fistulinella gloeocarpa*, *Neoboletus antillanus*, *Tylopilus griseiolivaceus*, and *Xerocomus olivaceus*. The novel species of *Austroboletus* closely resembles *A. subflavidus. Fistulinella gloeocarpa* is possibly synonymous with *F. jamaicensis*, an earlier name probably misapplied to a species in Texas. Singer did some work in south Florida, describing a few new boletes species that will need to be closely compared with our recent material. We have noted variation in stipe reticulation on *Tylopilus griseiolivaceus*, indicating it may not be as morphologically distinct from *T. rhoadsiae* as thought. Preliminary sequencing of the internal transcribed spacer (ITS), widely considered the DNA-barcoding locus, has already been undertaken on these bolete specimens. Future work will include phylogenetic analyses of additional loci, including LSU, RPB1, RPB2, and TEF.

Presentation ID: 137

White pine blister rust in the rocky mountains: linking endophyte assemblage, treeline dynamics, and island biogeography

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Abstract

The plant microbiome has been identified as an important component of plant health and success for the critically distressed whitebark pine (*Pinus albicaulis*). A keystone species at high elevations in the northern Rocky Mountains, whitebark pine populations have diminished dramatically over the last 20 years, culminating in candidacy for endangered species protection. The long-term pattern of decline is attributed to invasive white pine blister rust (*Cronartium ribicola*), the mountain pine beetle, habitat loss, and altered climate patterns. *Cronartium ribicola,* the most destructive force on whitebark pine populations, infects pines by growing through the needle stomata, into the branch and vascular system where it parasitizes the tree until its lifecycle is complete. Given the close spatial interaction of needle endophytes during the critical first stage of blister rust infection, and initial research suggesting that needle endophytes are a possible first line of defense against blister rust, this remains a promising area of study. Previous studies have examined the endophytic fungal communities of whitebark pine in common gardens, suggesting that certain endophytes may prevent or reduce the impact of blister rust. As whitebark pine populations plummet across the western US host availability for endophytes is equally diminished. Inversely, at the northern and high elevation range edges, climate shifts are increasing availability of suitable habitat for stands to establish. Given the ecological importance whitebark pine, understanding elements of dispersal, ecology, pathogen resistance and endophytic communities are of critical importance for future predictions of habitat use and ecosystem health.

Presentation ID: 138

Extra-heavy crude oil degradation by *Alternaria alternata* isolated from deep-sea sediments of the Gulf of Mexico.

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Abstract

At present, fossil fuels and petrochemicals are mainly obtained worldwide from conventional light crude oil, but these reserves are quickly running out. Heavy crude oil represents 70% of the total petroleum world reserves, and its extraction will be the only available option to obtain petroleum products in the next decades. In the unfortunate event of an oil spill, bioremediation would become the most suitable technique to transform the recalcitrant petroleum fractions into harmless metabolites. However, studies focused on the prospection and use of microorganisms capable of degrading extra heavy oils are still scarce. In this work, *Alternaria alternata*, *Cladosporium halotolerans*, *Penicillium chrysogenum, P. corylophilum,* and *Stemphylium* sp. were isolated from sediment samples of the Gulf of Mexico. Conidia from each fungal strain were inoculated into liquid medium containing light (40°API), heavy (16-20°API), or extra-heavy (7-10°API) crude oils as a sole carbon source. The presence of hyphal growth in the cultures was scored as an indicator of the use of petroleum as a sole carbon source by the fungi. While all the species were able to grow with light crude oil, *Stemphylium* sp. and *A. alternata* were the only ones that grew with heavy crude oil. Notably, *A. alternata* was the only species able to grow with extra-heavy crude oil. The extent and preferences of degradation will be assayed by gas chromatography coupled with mass spectrometry and SARA fractional chromatography, respectively. This study identifies *A. alternata* as a marine-derived cultivable fungus with an extraordinary bioremediating potential of extra-heavy crude oils.

Presentation ID: 139

Foliar fungal endophyte communities shape leaf functional traits of tropical trees

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Abstract

Leaves of tropical plants exhibit trade-offs in leaf lifespan associated with growth vs. persistence: short-lived leaves grow fast with few structural defenses, while long-lived leaves grow slowly and invest resources into defense. Functional traits, such as leaf mass per area (LMA), punch strength, and leaf thickness underpin these tradeoffs. Leaves of tropical trees are infected by foliar fungal endophytes (FE) starting at leaf emergence, but the roles of FE in shaping leaf traits remains underexplored. We evaluated how FE influence leaf trait development in 7 tropical tree species. Seedlings of species ranging in life-history strategies were inoculated with a natural FE community (E+) and measured 1, 2, and 3 weeks post-exposure. Control plants (E-) were not inoculated. We predicted that E+ leaves would become denser and tougher over time relative to E- leaves, and that this difference would be more evident in shorter-lived leaves. For three species, LMA was greater in E+ vs. E- leaves over time, but two of these species had a long leaf lifespan. One short-lived species had a greater punch strength in E+ leaves. Greater leaf thickness in E+ over E- leaves was observed in three species, of which two had short leaf lifespans. Our results show that exposure to an endophyte community can lead to denser and tougher leaves relative to E- leaves, but that these cannot be predicted easily by leaf lifespan. We anticipate that effects may be driven by particular species or functional groups of endophytes, the focus of future work.

Presentation ID: 140

Traits along the Leaf Economics Spectrum predict functional traits of fungal endophytes

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Abstract

The Leaf Economics Spectrum (LES) describes functional traits that link physiology, morphology, and ecological traits of leaves worldwide. The LES ranges from thick, tough, long-lived leaves with limited nitrogen (N) to thin, soft, short-lived leaves rich in N. Closely related and co-occuring trees in tropical forests can represent opposite ends of the LES, with LES-related traits explaining variation in endophyte communities that is unresolved by spatial proximity, environmental factors, or phylogenetic relatedness of hosts. In lowland forests in Panama, endophytes in leaves of common trees are dominated by Xylariales (a lineage with evolutionary ties to saprotrophy) and Botryosphaeriales (with evolutionary ties to pathogenicity). These orders differ in their occurrence with respect to the LES: Xylariales are markedly more common in less-dense leaves with more N and less carbon (C), whereas Botryosphaeriales are more common in denser leaves with more C and less N. We examined whether traits of favored leaves may predict functional traits of the fungi themselves. Bioactivity assays with 106 representative isolates showed that Xylariales were significantly more likely to degrade cellulose, chitin, and proteins than Botryosphaeriales. Such degradative traits are associated with antimicrobial defense, consistent with a potentially defensive role of Xylariales in the softer, lower-C leaves with limited structural protection in which they frequently occur. Antipathogen assays *in vitro* corroborated this interpretation. Together our data suggest that leaf traits along the LES filter endophyte communities with respect to functional traits, which may in turn extend or complement the phenotypes of leaves in which they occur.

Presentation ID: 141

Comparison of rDNA markers for environmental sampling with an emphasis on recovery of early diverging fungal groups

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Abstract

Metabarcoding is an important tool for understanding fungal communities. The internal transcribed spacer (ITS) rDNA is the accepted fungal barcode but has some known problems. The large subunit rDNA (LSU) has been used in tandem with ITS in order to investigate differences in the fungal community detected by these markers. Many studies have found that ITS and LSU detect similar community structure but differ in taxonomic composition. Numerous LSU primers have been developed for metabarcoding, but these were mostly designed to target Dikarya with little attention paid to early diverging fungi (EDF). We compared the ITS1 and two different segments of LSU using the primer sets ITS1F/ITS2, LROR/LR3, and a modified version of LR22 paired with LR3. We focused on the Zoopagomycota as an example of EDF by creating a mock community comprised of only Zoopagomycota. We collected environmental samples from California and Florida and sequenced them with the three primer sets using Illumina MiSeq. EDF occur in a wide variety of habitats, so we sampled soil mud, water, and microinvertebrates from each site. We used AMPtk to assemble and taxonomically identify OTUs using two different methods . Fungal community composition was evaluated with non-metric multi-dimensional scaling plots, betadisper and Adonis analyses, Mantel tests, and sample richness differences between site and sample type. Our results show that all primer sets had challenges with amplifying and identifying EDF sequences, but LSU recovered some EDF taxa that were missing in the ITS1 data. Further metabarcoding investigations of EDF may require specialized methods.

Presentation ID: 142

Global characterization of the fungal community associated with the seagrass, *Zostera marina*

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Abstract

Seagrasses are marine flowering plants that are foundation species in coastal ecosystems worldwide. Previously we sequenced the ribosomal internal transcribed spacer (ITS) region to characterize the fungi associated with the seagrass, *Zostera marina* (ZM) from Bodega Bay, CA. We found that there were many fungal taxa for which a taxonomic assignment could not be made associated with ZM and that many of these taxa were close relatives of Chytridiomycota lineages. In an effort to further expand knowledge of ZM-associated fungi and marine fungi more generally, we collected leaves, roots and sediment from twelve ZM individuals from sixteen sites across the Northern Hemisphere. We then sequenced the ITS region and the 18S ribosomal RNA gene to characterize the community associated with ZM globally. We found that the fungal community was significantly different between sites ($p < 0.001$) and observed a weak, but significant pattern of distance decay ($p < 0.001$). Variability between sites was too high to define a global mycobiome, even at low prevalence rates (e.g. 20%). However, when we investigated the distribution of differentially abundant amplicon sequence variants (ASVs) across tissue types (e.g. leaves vs. sediment), even though the majority of ASVs were only found at one or a few locations (e.g. due to local adaptation, dispersal limitation or seasonal bloom events), some were more ubiquitous across all locations suggesting a global distribution. This work highlights a need for further studies on marine fungi and the potential importance of these understudied communities to the seagrass ecosystem.

Presentation ID: 143

Endophytes fungi present in purple passion fruit (*Passiflora edulis* Sims f. *edulis*), potential for promoting plant growth and controlling Fusarium oxysporum.

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Abstract

Purple passion fruit is a climbing plant native to South America. In Colombia, has the fourth place of export. To satisfy the demand for markets, it is important to increase its yield and reduce losses due to phytosanitary factors such as vascular wilt caused by Fusarium oxysporum (FO). As a management alternative, in this research, endogenous purple passion fruit fungi were isolated and characterized. Plants from three places (Sutamarchán-Boyacá, Pasca and Granada-Cundinamarca) were collected and endophytic fungi were isolated from different organs. Subsequently, its ability to produce indole acetic acid (IAA), solubilize phosphorus, promote seedling growth and inhibit a pathogenic FO strain in-vitro was evaluated. Sutamarchán had the greatest diversity of endophytic fungi. In IAA production, were important the strains: Xylaria sp., Fusarium equiseti, Sterile mycelium, Epicoccum nigrum, Stemphylium vesicarium, Diaporthe passiflorae. The strains with the highest capacity to solubilize phosphorous were: F. equiseti, F. solani, Fusarium sp., Trichoderma asperellum. It was also found that endophytic fungi T. asperellum generate in FO a percentage inhibition of radial growth (PIRG) greater than 50% in-vitro in dual culture, and up to 30% by the action of organic compounds volatile. As a for growth promotion, Curvularia penniseti produced a slight increase, not significant, in fresh weight of the stem, root, leaves, and total fresh weight. It is concluded that the purple passion fruit is a reservoir that presents endophytic fungi in all its tissues, with different abilities to promote growth and biocontrol of the pathogen FO in-vitro, with potential application in bioprospecting.

Presentation ID: 144

PACBIO Multi-locus Sequence Typing (MLST) of MSA Post-Conference Collecting (WI & MI) Contributes to Rediscovery of North American Species of Russula as well as New Species

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Abstract

Following the 2019 Mycological Society of America Annual Meeting in Minneapolis, MN, a collection trip was undertaken in an attempt to recollect species of *Russula* described by Dr. Charles Kauffman and Dr. Robert Shaffer from Michigan and Wisconsin. Over 80 collections were documented over a week's time, including photographs, spore prints, detailed descriptions, and macrochemical tests. We were able to recollect species described by Charles Kauffman (*Russula borealis*) and Robert Shaffer (*Russula xantho, Russula michiganensis*), as well as European taxa (*Russula atrorubens*, *Russula vinosa*) and putative new species. The specimens were sequenced using a multi-locus sequence typing (MLST) approach using the PacBio Sequel II system to assess the applicability of this technology for generating multi-locus barcode sequences for *Russula*. Three loci were amplified and multiplexed using PacBio barcodes. The tef1 and ITS loci were the most successful for both polymerase chain reaction (PCR) amplification (100% success rate) and sequencing through the PacBio Sequel II system (97% & 99% respectively). The *rpb2* locus was less successful for PCR amplification (85%) and saw a steep drop-off in sequencing success (45%). Even with an incomplete success rate for amplification, cost per sequence was determined to be cheaper than traditional Sanger sequencing. When generating consensus sequences for the internal transcribed spacer (ITS) region, it was observed that polymorphic sites were not consistent within reads, indicating that sequence variation within samples were not due to haplotypes. It is unknown what the cause of this variation is, unless it is due to ITS variants within the genome.

Presentation ID: 145

Evolution of *Pneumocystis* Host Niche in New World Rodents (Neotominae)

Spenser Babb-Biernacki [1], Li Peng [2], Jamie Rothenburger [3], Claire Jardine [4], Jacob Esselstyn [1], Liang Ma [2], Vinson Doyle [5]

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Abstract

As the world is increasingly impacted by emerging infectious diseases, understanding how pathogen host niches evolve and expand is critical to protect human and wildlife health. An excellent system with which to study host niche evolution is the fungal genus *Pneumocystis*, an obligate lung symbiont that is ubiquitous in all groups of mammals. Here, we investigate the systematics of *Pneumocystis* in New World rodents of the subfamily Neotominae. Although dogma holds that *Pneumocystis* evolution is dominated by strict host specificity and cospeciation, this rapidly diversifying clade challenges this. Based on a phylogeny inferred using mitochondrial ribosomal DNA (mt rDNA) from *Pneumocystis* in eight Neotomine species, we demonstrate that *Pneumocystis* diversification cannot be explained simply by cospeciation. We identify five potential novel *Pneumocystis* species in these eight hosts, implying that a promiscuous host niche and host switching are important in the evolution of this genus. To further explore the early stages of divergence in *Pneumocystis,* we collected geographically dispersed samples from two Neotomine sister species: *Peromyscus leucopus* (white-footed mouse) and *Peromyscus gossypinus* (cotton mouse*).* Although the *Pneumocystis* mt rDNA of these samples contained no population structure, sequencing nuclear rDNA revealed two populations corresponding to host identity, but not geography, which may represent the first step of the speciation process. Further study of Neotomine *Pneumocystis* has the potential to inform our overall understanding of host-symbiont evolutionary dynamics.

Presentation ID: 146

Just the sum of its parts? Dual-mycorrhizal hosts as model systems for testinglinkages between mycorrhizal types and ecosystem processes

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Abstract

Populus species host a diversity of arbuscular mycorrhizal, ectomycorrhizal and endophytic fungal root associates. This diverse root microbiome makes *Populus* an ideal model system to study how fungal root associates respond to environmental and biotic factors. In one experiment, I will be documenting changes in the *Populus* root microbiome during the first few years of growth in a controlled bioassay experiment. *P. tremuloides* and *P. trichocarpa* were inoculated with live field soil from *P. tremuloides* stands in southern Utah. Pots will be non-destructively repeatedly sampled to collect roots for sequencing of LSU transcripts and to sequence amplicons from individual root tips. So far, data from the five month time point has documented nine ectomycorrhizal morphotypes colonizing the roots, including *Tuber*, *Hebeloma*, *Cenococcum*, *Wilcoxina*, *Meliniomyces*, and *Hygrocybe*. Additionally, root have been observed to be extensively colonized by arbuscular mycorrhizal fungi and endophytes. Sequencing of LSU transcripts from bulk roots will provide a quantitative measure of the activity of these respective fungal guilds. In a second experiment, I plan to evaluate how root-associated fungal communities of *P. tremuloides* varies across 1000 meter elevation gradients in the Uinta Mountains of Utah. Past work has shown that arbuscular mycorrhizal fungi increase in abundance on dual-mycorrhizal hosts in drier soils or at lower elevations, with ectomycorrhizal fungal colonization increasing in moister, organic-rich soils found at higher elevations. This study will also provide insight into the role of mycorrhizal fungi in driving latitudinal patterns of plant host distribution, with altitude serving as a proxy for latitude.

Presentation ID: 147

Viability quantification and three-dimensional visualization of cell in *Aspergillus niger* biofilms treated with sodium hypochlorite

Aswathy Shailaja , Julia Kerrigan , Terri Bruce , Patrick Gerard

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Abstract

Biofilm cells are encased within and bound by an extracellular polymeric substance that is responsible for adhesion to a surface and for the cohesion of the biofilm. These characteristics contribute to their prevalence and resistance to antimicrobial agents. Previously, we developed a protocol to grow *A. niger* biofilms in a controlled reactor under low-shearing force to reflect those that form in the built environment. To evaluate the cell viability of these biofilms, we developed a staining protocol with molecular probes, using a combination of SYTO9 and propidium iodide. Images are analyzed with COMSTAT, a computer program that quantitatively measures biofilm accumulation from digital image stacks. The purpose of this study was to evaluate the efficacy of an antifungal agent, sodium hypochlorite (bleach), on *Aspergillus niger* biofilms. Biofilm samples were treated with different concentrations of a disinfecting cleaner with bleach, standard bleach, and buffer for the control, and cell viability was quantified in proportion to biofilm volume. Biofilms treated with the disinfecting cleaner with bleach had significantly fewer viable cells compared to those treated with bleach at equal sodium hypochlorite concentrations, as well as the controls, indicating the higher efficacy of this disinfecting solution. Some differences were also observed based on where the sample was collected, indicating the importance to sample from different locations within a biofilm. With this system in place, future research involves evaluating natural products, such as essential oils, for their antifungal activity against biofilms.

Presentation ID: 148

Comparative genomics provides insight into ecological specialization in the class Geoglossomycetes

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Abstract

Despite their global presence and ubiquity, members of Geoglossomycetes (Pezizomycotina, Ascomycota) are understudied both systematically and ecologically. These fungi have long been presumed saprobic due to their occurrence in leaf litter on the forest floor and lack of apparent association with other organisms. Based on observations of their fruiting near ericaceous shrubs, there is an alternative hypothesis of a mutualistic ecology, either ericoid mycorrhizal or ectomycorrhizal. This claim, however, has yet to be confirmed via microscopy or amplicon-based studies examining root communities. As a result, our current understanding of their ecology is based on cursory observations.In this study, we present a comparative genomic analysis seeking genomic signatures related to ecological niche. We compared the carbohydrate-active enzyme (CAZyme) and secondary metabolite content of our newly sequenced Geoglossomycetes to fungi of known ecologies across Pezizomycotina. Our analysis reveals patterns in both CAZyme and secondary metabolite content consistent with other ectomycorrhizal (EcM) members of Ascomycota, including *Elaphomyces* (Eurotiomycetes) and *Tuber* (Pezizomycetes). Specifically, we found a reduction in CAZyme content in Geoglossomycetes and other members of Pezizomycotina exhibiting an EcM lifestyle. These results suggest a mutualistic ecology of Geoglossomycetes and improve our understanding of these understudied fungi. Our work represents the first functional genomics study of Geoglossomycetes and builds the foundational knowledge of the ecology and evolution of the class.

Presentation ID: 149

A new species of *Rhizophagus* with dimorphic spores

Brian Lovett [1], Greg Boyce [1], Joseph Morton [1], Bill Wheeler [1], Chase Mayers [2], Teresa Pawlowska [2], Matt Kasson [1]

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Abstract

A dimorphic species of arbuscular mycorrhizal fungi, Rhizophagus dimorphicus, was recently discovered. The two spore phenotypes were so different they were thought to be distinct species; however, repeated in vivo culturing of each phenotype yielded mixed cultures containing both at a consistent ratio of 4:1 (dark:white) spores regardless of strain or whether the fungus was in planta or in storage. Interestingly, single phenotype inoculations also uncovered delayed onset of colonization and spore production in white spore inoculations with production of new spores completely absent at 8-weeks post-inoculation (wpi), but abundant by 16 weeks-post-inoculation. Analysis of 28S rDNA resulted in the grouping of the two phenotypes into a single genealogically exclusive clade, aligning closely with R. dunense. Both dark and white morphotypes form globose to subglobose spores with three distinct layers ranging in size from 60-160 µm and 60-120 µm, respectively. In addition to phylogenetic and morphological analysis, omics-based approaches were applied to better understand both morphotypes. A global proteomics analysis revealed a truncated proteome was expressed in the white morphotype compared to that of the dark morphotype. The global metabolomics showed a similar pattern, with the metabolome of the white spores lacking many of the secondary metabolites found in dark spores. Repeated attempts to identify endosymbiotic bacteria common across AMF from both phenotypes revealed that no such relationships exist in R. dimorphicus. Overall, the differences of each spore morphotype suggest a potential compartmentalization of distinct metabolic processes not seen in other AM fungi.

Presentation ID: 150

New insights into the wheat seed mycobiome: an *in silico* approach

Lindsey Becker , Marc Cubeta

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Abstract

Wheat (*Triticum aestivum* L.) is grown on more acres than any other crop worldwide and accounts for 19% of total available calories globally. During wheat seed development, physiological changes are likely to shape the microbial community of the seed, however little is known about the mycobiome of the developing wheat seed. The recent release of the wheat genome allows for examination of microbial communities of seeds and facilitates targeted isolation of seed associated fungi. Here we took an *in silico* approach to examine fungal diversity associated with developing wheat seeds. Our dataset included publicly available RNAseq reads from internal wheat seed compartments sampled at 10, 20, and 30 days post anthesis. Quality filtered reads were mapped to the reference wheat genome to remove host reads. The remaining microbial reads were assembled in rnaSPAdes. Using kraken2, our community analysis predicted 57, 57, and 59 fungal species associated with the wheat seed mycobiome for 10, 20, and 30 days post anthesis, respectively. We identified 52 predicted fungal species across all seed developmental stages, including *Zymoseptoria tritici*, *Botrytis cinerea*, *Fusarium pseudograminearum*, *Neurospora crassa*, and *Schizosaccharomyces pombe*. Our findings enable us to utilize a targeted isolation approach that will expand our fungal culture collection for future synthetic community experiments.

Presentation ID: 151

Suilloid fungi are major drivers of early seedling establishment in Florida slash pines

Elena Karlsen-Ayala , Romina Gazis , Matthew E Smith

University of Florida, Gainesville, USA

Abstract

The south Florida pine rocklands, characterized by an open canopy of south Florida slash pine trees (*Pinus elliottii var. densa*), is a critically endangered ecosystem due to habitat fragmentation and invasive species. While ample studies in the western USA demonstrate the importance of ectomycorrhizal fungi "spore banks" in early pine seedling establishment, little is known about spore banks in naturally occurring tropical and subtropical pine forests in the Southeastern USA. Understanding the diversity and community structure of ectomycorrhizal fungi in Florida pine ecosystems will be critical for restoration initiatives. The aim of this research was to document broad patterns in the diversity and community structure of ectomycorrhizal fungi during early seedling establishment. We used a bioassay approach with soils sampled across a gradient from Florida's tropical southern pine rocklands to the subtropical northern pine forests. Bioassay soils were sampled from 23 sites in 7 different forests. We used Illumina MiSeq of ITS1 to assess the pool of ectomycorrhizal fungi in the soils at each site. We then planted six aseptically germinated slash pine seedlings in soils from each site. Seedlings were grown for 7 months in a greenhouse and then sampled for ectomycorrhizal fungi. Representatives of each morphotype from each seedling were sequenced using primers ITS1F and ITS4. Illumina Miseq data from the soil show unique habitat level differences in the total fungi in each community. Approximately 22 OTUs were recovered from seedling root tips representing 9 different ECM lineages. *Rhizopogon* was the most abundant across all sites in Florida.

Presentation ID: 152

2020 Best Poster Winner

Treeline white spruce are more nutrient-limited than trees at the valley bottom in the western Brooks Range of Alaska

Megan Keller [1], Rebecca Hewitt [2], Patrick Sullivan [1]

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Abstract

The mechanism constraining tree growth at treeline is controversial. The carbon (C)-sink limitation hypothesis argues that photosynthesis can occur at a wider range of temperatures than cell division, thus growth at treeline is limited by cold temperatures. Alternatively, the C-source limitation hypothesis argues that photosynthetic capacity is limited, potentially by nutrient availability. To test for greater nutrient limitation at treeline than at lower elevations, fertilizer was applied to white spruce trees at an upland treeline, an adjoining forest, and a riverside terrace in northwestern Alaska. Air temperature varied little across the sites, but growing season soils were colder at the treeline and forest than the terrace. Growth declined from terrace to forest to treeline. Three years of applying nitrogen (N) fertilizer alone had little effect on growth. After three years of applying nitrogen-phosphorous-potassium (NPK) fertilizer, growth increased strongly, with greater proportional increases at the treeline and forest than on the terrace. The proportion of root length colonized by ectomycorrhizal (ECM) fungi was greatest on the terrace, where soils are warmest and tree growth is greatest. NPK fertilization led to an overall decrease in ECM fungal colonization and eliminated differences in colonization that were present across sites among control trees. These results support the C-source limitation hypothesis; growth at the treeline and forest is more nutrient-limited than on the terrace. Nutrient uptake at treeline could be diminished by the effects of cold soils on nutrient availability, root growth, water uptake, reduced ECM fungal foraging efficiency, and/or reduced ECM colonization.

Presentation ID: 153

SEGREGATING THE PALM RUST GENUS *CERRADOA* FROM *EDYTHEA*

MARIA SANTOS [1], MALTE EBINGHAUS [2], CHARLES BARNES [3], JOSÉ DIANESE [1]

[1]UNIVERSIDADE DE BRASÍLIA, BRASÍLIA, Brazil. [2]RHUR BOCHUM UNIVERTITY, BOCHUM, Germany. [3]USDA FOREST SERVICE, SAN BERNARDINO, CA, USA

Abstract

The genus *Cerradoa is* the only rust fungus on palm trees kowon in its uredinial and teliial states. Since 1983 *Cerradoa* has been treated as a synonym of *Edythea.* Our morphological (LM and SEM documentation) and phylogenetic analyses based on *nuc*LSU and COX3 sequences, showed that the two fungi are not congeneric, although both belong to family Pucciniaceae. Thus, the reinstament of the genus *Cerradoa* is here shown to be appropriate.

Presentation ID: 154

GUAC AT RISK: HOW A BEETLE-FUNGUS SYMBIOSIS IS THREATENING THE AVOCADO INDUSTRY

Pedro Pablo Parra , Jonathan Crane , Bruce Schaffer , Romina Gazis

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Abstract

Most beetle-fungus symbiosis do not represent a threat to ecosystems; however, few beetles are able to inoculate their fungal symbiont into healthy plants, causing disease. This is the case of *Raffaelea lauricola* (RL), which causes a deadly vascular fungal disease known as Laurel Wilt (LW) in over 30 species of Lauraceae. Since its introduction in 2002, RL has killed over 500 million trees, including 140,000 avocado trees. LW has spread rapidly across the U.S. and is now present in 11 states, approaching the major avocado-producing areas in California and Mexico. The Florida avocado industry, second largest in the U.S, is being threatened by LW, which has already caused more than $100 million in losses to avocado growers and associated industries. Early detection and eradication are currently the primary recommendations to contain outbreaks. Our research group has optimized the standard PCR-based detection technique and confirmed its reliability in detecting the pathogen directly from infected vascular tissue. This detection method represents an important tool for diagnostic laboratories and a baseline for developing more sensitive detection technologies that can be implemented in surveillance programs. Progression of LW varies depending on pathways of transmission, inoculum concentration and host genotype. Therefore, we are conducting large-scale greenhouse and field inoculation experiments to address the efficacy of diverse management practices and document disease development in multiple cultivars from different avocado races and rootstock-scion combinations. Data collected from these trials will inform future approaches and research directions to protect the avocado industry in Florida and other producing regions.

Presentation ID: 155

Saprotrophic fungi associated with the decomposition of dominant salt marsh grass Sporobolus pumilus

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Abstract

Salt marshes are critical ecosystems for maintaining coastal biodiversity and perform a range of ecosystem services, but their ecology is poorly understood in Northern climates. In particular, the decomposer communities associated with the salt marsh grass *Sporobolus pumilus* (*Spartina patens*) have been largely ignored despite this being the dominant primary producer in Northeastern salt marshes. To address these gaps, this study characterizes the biodiversity of saprotrophic fungi associated with *S. pumilus*, as well as the dynamics in their biodiversity over time. Decomposition rate will also be measured over an 8 month period which will be used to contextualize temporal trends in biodiversity. Above-ground and below-ground decomposition will be quantified using a litter bag experiment in tandem with the Tea Bag Index. Samples were collected monthly from June to November 2019. Fungi were identified morphologically using material derived from the litter bags, some of which was transferred to moist chambers and allowed to incubate. 21 morphospecies were found, of which only 4 could be reliably identified to the species level. The most abundant fungi are two Phaeosphaeriaceous anamorphs somewhat resembling the genus *Stagonospora*, *Phoma spp.* s.l., an apparently unnamed species of *Phaeosphaeria*, and *Pseudohalonectria halophila.* To further understand their taxonomy, multigene phylogenies will be constructed for all fungal species collected.

Presentation ID: 156

Worldwide diversity and distribution of freshwater fungi in Dothideomycetes with their morphology and phylogeny

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Abstract

Freshwater fungi are defined as "all fungi that occur on submerged or partially submerged substrates in aquatic habitats". To study worldwide diversity and distribution of freshwater fungi in Dothideomycetes, we review each genus with freshwater fungi in Dothideomycetes, and construct a phylogenetic tree for all freshwater Dothideomycetes which have molecular data, as well as introducing nine new genera and 38 new species. As the largest class of Ascomycota, Dothideomycetes includes the largest number of freshwater fungi, with a total of 405 species in 144 genera, 43 families and six orders (i.e. Jahnulales, Kirschsteiniotheliales, Minutisphaerales, Natipusillales, Pleosporales and Tubeufiales). The order with the largest number of freshwater Dothideomycetes is Pleosporales (230 species), followed by Tubeufiales (98 species) and Jahnulales (33 species). Within Pleosporales, Dictyosporiaceae (32 species) and Lindgomycetaceae (23 species) are the two families with the most freshwater Dothideomycetes. Among 144 genera, 46 genera (32%) occurred exclusively in freshwater habitats, of which *Lindgomyces* is the largest with 14 species. Among 35 countries where freshwater Dothideomycetes are reported, China has the largest number (147 species), followed by Thailand (139 species). Twelve species, distributed across all six orders except Kirschsteiniotheliales, commonly occur in different countries, and are likely to be cosmopolitan taxa. Morphological characters of freshwater Dothideomycetes are highly diverse, with a range of hyphomycetous and coelomycetous asexual morphs. In their sexual morphs, these fungi are characterized mainly by asci with two wall layers (bitunicate asci) and often with fissitunicate dehiscence. A new website (https://www.freshwaterfungi.org/) is built to providing online resources with high quality illustrations for freshwater Ascomycetes.

Presentation ID: 157

The road to a stable classification of the Leotiomycetes.

Alisha Quandt [1], Tina Melie [1], Danny Haelewaters [2]

[1]University of Colorado, Boulder, USA. [2]Purdue University, West Lafayette, USA

Abstract

Leotiomycetes (Pezizomycotina, Ascomycota) encompasses many fungi that were historically classified as inoperculate discomycetes. The class includes economically important pathogens (e.g., powdery mildews on various plants and the causal agent of the white-nose syndrome of bats), mycorrhizae formers, endophytes, and many saprobes. Systematics within Leotiomycetes has lagged behind other groups. Initial molecular phylogenetic studies indicated that many current higher and lower taxonomic level taxa are polyphyletic, and loci that are commonly used in fungal phylogenetics have proven uninformative for resolving many nodes within the Leotiomycetes. Here, we present a new preliminary hypothesis of the relationships among major orders of Leotiomycetes, based on genomic-scale data and increased sampling of several clades including two orders that previously had no available genome data.

Presentation ID: 158

How are the ectomycorrhizal fungi *Hebeloma cylindorosporum* and *Paxillus ammoniavirescens* involved in potassium uptake of Loblolly pines?

Hannah Frank , Kevin Garcia

North Carolina State University, Raleigh, USA

Abstract

Ectomycorrhizal relationships are critical ecological mutualisms involving plant hosts and fungal symbionts to utilize their respective advantages to obtain necessary nutrients from their symbiotic partner. The role of ectomycorrhizal fungi in plant potassium uptake has yet to be investigated as thoroughly as nitrgoen and phosphorus uptake. The aim of this research is to better understand the role of the ectomycorrhizal fungi *Hebeloma cylindrosporum* and *Paxillus ammoniavirscens* in potassium transport to Loblolly pines (*Pinus taeda*). This project has three components: First, using rubidium, an effective potassium tracer, to track K transport to the plants through the fungal hyphae. The second component is tracking carbon allocation from the plant to the fungus through carbon-13. A split-root system has been developed to have two separate sections of root colonized by fungi with access to different levels of K. And finally, RNA sequencing of seedling roots colonized with the fungi and grown in high/low K conditions to identify potassium transporter candidates from *P. taeda* seedlings. A better understanding of these relationships and their mechanisms holds potential for respecting their ecological significance and utilizing their nutrient optimization.

Presentation ID: 159

Diversity of cultivable fungi from deep-sea sediments of the Gulf of Mexico

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Abstract

The deep-sea of the Gulf of Mexico (GoM) is a harsh environment, harboring a wide diversity of fungi, previously characterized by metagenomics. This study aims to identify the cultivable fungi from deep-sea sediments of the GoM with desirable biotechnological potential. Sediments from nine stations ranging from 1,156 to 3,739 m below sea level, were collected with a multi- or box-corer in 2019 during the oceanographic campaign XIXIMI 7. Surface (top 10 cm of the sediment) and subsurface (30 to 60 cm from the top layer) samples were processed. Serial dilutions were spread onto different media, containing 3.2% sea salts and used at 1/5 strength to simulate the low nutrient conditions of deep-sea sediments. The plates were maintained in darkness for up to 90 days at 23 ºC and 4°C. Isolates were first identified morphologically and confirmed by amplicon sequencing (ITS for filamentous and 26S for yeast strains). A total of 125 isolates were recovered: seven yeasts and 118 filamentous forms. In addition, 12 filamentous fungi were recovered from media supplemented with 1M and 3M NaCl. The most commonly recovered genera were *Penicillium* and *Cladosporium*, and with lesser frequency *Aspergillus*, *Curvularia* and *Acremonium*, all of them filamentous Ascomycota. Among yeast forms, two Basidiomycetes, *Cryptococcus* and Exobasidiales, and an Ascomycete, the black yeast *Neophaeotheca triangularis*, were identified. Dixon´s medium proved to be the best one for isolation of marine fungi. Unexpectedly, isolation was greater from the subsurface than from the surface samples, both in terms of abundance and halotolerant species.

Presentation ID: 160

Investigations of the mycoflora inhabiting the bark of *Juniperus ashei* (Cupressaceae) in central Texas

Jessica Bernardin [1], David Rodriguez [2], Dittmar Hahn [2], David Lemke [2]

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Abstract

Juniperus ashei (Cupressaceae) is a common evergreen tree in central Texas with a range extending from Arkansas to northern Mexico. A notable feature of these trees are conspicuous white patches that occur on the bark of the trunk and branches that have been identified as a parasitic fungus, *Robergea albicedrae*. This fungus, along with others that inhabit the bark of Ashe juniper, remains understudied and ambiguous in terms of morphology and possible symbiosis. The goal of this study was to sequence the ITS region of the 18S gene, document the mycoflora of *J. ashei* bark, and to document key morphological features to determine if it could undergo optional lichenization. Samples of bark were excised from the trunk, branches, and twigs of *J. ashei* in San Marcos, Texas and ten other sample sites along the Edward's Plateau and Southern Oklahoma. Experiments included culturing and sequencing the mycoflora of *J. ashei* bark using media and culturing experiments. Lastly, the partial nuSSU and full ITS region of the 18S gene for *R. albicedrae* was sequenced and compared to other species in the same genus and family using cloning and Sanger sequencing. Preliminary results demonstrate that the mycoflora on *J. ashei* bark is more diverse than anticipated. Culturing techniques used in this study were successful in eliminating contamination and simulating nutrients needed for fungal growth on bark.

Presentation ID: 161

Population Genomics Reveals Single Domestication Event of *Aspergillus sojae* from *Aspergillus parasiticus*

Kimberly Acevedo , John Gibbons

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Abstract

Domestication refers to the genetic modification of a species by breeding a subset of individuals in isolation from its ancestral population in an effort to enhance its utility to humans. Domestication was one of the most influential technological innovations of the last 13,000 years, as it led to the rise of modern civilizations, shaped global demographics, and provides the majority of our present day food. Though the vast majority of research has focused on plant and animal domestication, archeological, molecular, and genetic evidence also supports the domestication of fungi (e.g. yeast and molds) for their utility in food preservation, flavoring, aroma, and texture. *Aspergillus sojae* is a filamentous fungi used for its flavor enhancing properties and enzymatic production to produce several Asian fermented foods (*e.g.* soy sauce, miso, and mirin). It has been hypothesized that *A. sojae* is domesticated from *Aspergillus oryzae*, an aflatoxin producing agricultural pest, though insufficient data exists to investigate this relationship. Here, we generated and analyzed whole-genome sequence data from a diverse collection of 13 isolates of *A. sojae* and 10 isolates of *A. parasiticus* in an effort to illuminate the evolutionary relationship of these species. We identified 73, 291 SNPs across the 23 genomes, which we used to perform phylogenetic and population structure analysis. Phylogenetic and population structure analysis suggests the existence of 2 distinct genetically distinct populations, including one population with little genetic variation consisting entirely of *A. sojae* isolates. Our analysis suggests a single domestication event of *A. sojae*followed by a clonal expansion.

Presentation ID: 162

Reassessing the relative impact of *Lasiodiplodia* species on the health of cacao in the Philippines

Johnny Balidion [1,2], Caleb Bollenbacher [1], Marc Cubeta [1]

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Abstract

A predominance of *Lasiodiplodia* spp. was observed and recorded in a survey conducted in 2016-2017 from 20 cacao-growing provinces in the Philippines to characterize symptom expression in Vascular Streak Dieback (VSD), an endemic disease of cacao in Southeast Asia reported to be caused by *Ceratobasidium theobromae*. Fifty three percent of the leaves and petioles sampled (n=1170) exhibited marginal necrosis and chlorosis with epidermal cracks on the leaf midrib while 10% of the samples exhibited characteristic chlorotic leaf spotting symptoms typically associated with VSD disease. A PCR-based detection assay using ITS specific primers with 30 petiole samples exhibiting VSD symptom revealed 100% and 73% detection frequency for *Ceratobasidium theobromae* and *Lasiodiplodia* spp., respectively. An examination of intact cacao twigs representing five types of symptoms showed that 58% of the leaf segment samples across symptom types were positive for *Lasiodiplodia* spp., 5% for *C. theobromae* with 16% co-occurrence of both fungal species. Morphological and multi-locus sequence analysis of ITS, *tef1-α, tub2, rpb2*, and *cmdA* for randomly selected isolates sampled from cacao plants with VSD symptoms identify majority of them as *L. theobromae* and possibly some *L. pseudotheobromae*. Growth of *Lasiodiplodia* species at different incubation temperatures indicate optimum temperature from 25 to 30C with growth inhibition below 20C and above 37C. Water activity influenced vegetative hyphal growth with inhibition observed at –3 MPa and complete growth inhibition occurring above -6 MPa. Our results indicate that these *Lasiodiplodia* species play a significant role in the observed variation in VSD disease symptoms in the field.

Presentation ID: 163

Langdonia walkeria sp. nov., causal organism of smut, on *Aristida* species in a longleaf pine-grassland ecosystem in the southeastern USA.

Abeer Alqurashi [1], Julia Kerrigan [1], Joan Walker [2], Kyryll Savchenko [3], Guido Schnabel [1], Steven Jeffers [1]

[1]Clemson University, Clemson, USA. [2]USDA-Forest Service, Southern Research Station, Clemson, USA. [3]Butler University, Indianapolis, USA

Abstract

Langdonia walkeria sp. nov. was designated the causal organism of smut on *Aristida beyrichiana* and *A. stricta* in longleaf pine-grassland ecosystems in the southeastern United States. The morphology of *L. walkeria* differed from other species of *Langdonia* by its solitary teliospores that do not form in spore balls, teliospore size, and teliospore wall ornamentation. The combined analysis of DNA sequences from three regions—ITS, LSU, and EF-1 α—demonstrated a distinct separation of this species from other species of *Langdonia*. A field study was conducted to determine if the infection occurs during the flowering stage. Inflorescences of 64 plants of *A. beyrichiana* in three sites were dipped on Abound® flowable fungicide (a.i. azoxystrobin) solution. Each treated plant was paired with a non-treated control plant. During the seed production stage, a significant decrease ($p < 0.0001$) was found in treated plants than control, providing evidence that the infection occurs during the flowering stage. To fulfill Koch's postulates, plants in the greenhouse and in the field were inoculated during the flowering stage with a sporidial suspension containing a mixture of *L. walkeria* isolates. Sori bearing teliospores formed on greenhouse and field inoculated plants. Teliospores were cultured, and morphological and phylogenetic examinations confirmed that the fungus is the same species isolated from *Aristida beyrichiana* and *A. stricta* in longleaf pine forests.

Presentation ID: 164

Shotgun Metagenomics Analysis of Pulque Yeast Diversity

Katherine Chacon-Vargas [1], Martha Giles-Gomez [2], Julian Torres [3], Adelfo Escalante [2], John Gibbons [1]

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Abstract

Pulque is a culturally important 4,000-year-old traditional Mexican fermented drink. It is produced by adding fresh aguamiel to mature pulque, resulting in a mixture of microbial communities and chemical compositions. We performed shotgun metagenomic sequencing of five stages during fermentation to characterize yeast taxonomic diversity. Yeast relative abundance were assessed with MetaPhlAn and Kaiju. Two main fungal genera were identified in pulque, *Saccharomyces* and *Kluyveromyces*. MetaPhlAn detected only *Saccharomyces* with only one species, *S. cerevisiae.* Kaiju detected both genera and 15 species within *Saccharomyces*. Both pipelines showed that only *Saccharomyces* had high abundance (over 1%) across fermentation while *Kluyveromyces* remain low (less than 1%). We evaluate correlation between the abundance of both genera and the amount of metabolite production of alcohols and sugars. We found that Only *Kluyveromyces* was positively correlated with metabolism of fructose and production of ethanol but only this last comparison was statistically significant. Finally, we found that *S. cerevisiae* was the most abundant yeast which progressively increased during fermentation. We compared pulque *S. cerevisiae* strains to other available strains. We performed metagenomic assembly and binning with Automate and MetaBat2. We retain contigs with more than 2000pb in length and used Augustus to perform annotation and Orthofinder to identify orthologous groups and infer phylogenetic relationship among our *S. cerevisiae* pulque strain and additional 156 strains isolated from different environmental sources. Overall, our analysis suggests that pulque is produced, in part, by a diversity of yeast species that may contribute to overall chemical composition and sensory characteristics.

Presentation ID: 165

Imidacloprid movement into fungal conidia is lethal to mycophagous beetles

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Abstract

Applications of systemic pesticides can have unexpected direct and indirect effects on nontarget organisms, producing ecosystem-level impacts. We investigated whether a systemic insecticide (imidacloprid) could be absorbed by a plant pathogenic fungus infecting treated plants and whether the absorbed levels were high enough to have detrimental effects on the survival of a mycophagous beetle. Beetle larvae fed on these fungi were used to assess the survival effects of powdery mildew and imidacloprid in a factorial design. Fungal conidia were collected from treated and untreated plants and were tested for the presence and concentration of imidacloprid. Survival of beetles fed powdery mildew from imidacloprid-treated leaves was significantly lower than that of beetles from all other treatments. Imidacloprid accumulated in fungal conidia and hyphae was detected at levels considered lethal to other insects, including coccinellid beetles. Water-soluble systemic insecticides may disrupt mycophagous insects as well as other nontarget organisms, with significant implications for biodiversity and ecosystem function.

Presentation ID: 166

Landraces and Hybrid maize fungus diversity assessed through metabarcoding

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Abstract

One of the most dominant farming systems in agriculture is the "**milpa**", this is a traditional agroecosystem where the main products are corn, squash, and beans. Farmers have contributed to obtaining and preserving different local varieties of corn. Thanks to the cultivation process and preserving part of the yield to use as **maize landrace seeds** in the next agricultural cycle. These practices cause natural selection to operate on genetic variants, so an evolutionary process leads to local adaptation. Also, an artificial selection is happening. There are also **hybrid seeds**, these are sold to farmers and are not stored for the next agricultural cycle, these are produced under optimal environmental conditions and the selection is made by relatively few people, as a consequence we have less genetic diversity. Most land plants live in association with symbiotic fungi. Fungi play a critical role in the carbon and nutrient cycling of terrestrial ecosystems, therefore the question arises: The use of maize landraces and Hybrid maize in a milpa, the interaction between plants and associated fungi can affect their diversity? This work seeks to evaluate the diversity of fungi from samples in the soil cultivated with hybrid and native corn seeds. Using a DNA metabarcoding analysis, the ITS2 nuclear region was selected as a barcode to capture fungal diversity. Our preliminary results show that for the alpha diversity there is a significant difference between the fungal communities under the both treatments. The richest phylum is Ascomycota followed by Basidiomycota. Further analysis is still being performed.

Presentation ID: 167

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Abstract

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