Spring has finally come to Big Pond after a long harsh winter. The snow is beginning to melt in the catchment bringing nutrients into the pond. The ice on the pond has melted so that sunlight can penetrate into the water. The temperature is rising on the surface. Many species of phytoplankton are beginning to resume growth. The surface of the pond is suddenly dusted with pine and sweet gum pollen, which provide substrates for many microorganisms. Mosquito and midge larvae abound feeding on plankton. Tadpoles are beginning to swim along the edge. Birds are diving in to look for fish. However, unnoticed by the casual observer, resistant sporangia of chytrids, which have over-wintered attached to substrates throughout the water column, are beginning to release zoospores. Soon many different substrates will become colonized by chytrid zoospores, and the chytrid epidemic is about to continue on the following page.
begin. This kind of phenomenon occurs in many aquatic ecosystems throughout the world.

The chytrid epidemic appears suddenly as long as substrates are available (Sparrow, 1960). The life cycle of most chytrids is completed rapidly, and many zoospores are released from each sporangium. Therefore, a large increase in population numbers is possible within a very short period of time. For this reason all chytrids are considered to be ruderal in their life histories (sensu Dix and Webster, 1995, p.7).

Nearly fifty years ago Frederick Sparrow (1960, pp. 104-114) defined the chytrid epidemic to include host-parasite interactions involving chytrids (Phyla Blastocladiomycota and Chytridiomycota). Sparrow’s examples considered only phytoplankton and fungi as hosts but zooplankton and larger aquatic animals need to be included as well. According to Sparrow, beginning in early spring, population densities of parasitic chytrids rapidly increase for a short period, then decline due to the loss of available substrates and finally produce resting spores. We would expect to find the same pattern of growth in both parasitic and saprophytic chytrids in aquatic ecosystems.

Donald Barr, Hilda Canter, John Couch, John Karling, Joyce Longcore, Frederick Sparrow, Howard Whisler, Guy Willoughby and many other mycologists have spent their lives recording the presence of parasitic chytrids on aquatic plants and animals and saprophytic chytrids colonizing nonliving substrates in aquatic environments. Sparrow (1960, pp. 1073-1104) provides a long list of substrates reported for the growth of chytrids. Studies on chytrid parasites and saprophytes in freshwater lakes, particularly in northern Michigan, the Netherlands and the English Lake District, have continued for many years. Dix and Webster (1995, pp. 227-231) briefly summarized the roles of chytrid parasites and saprophytes in freshwater ecosystems. Yet, the ecological importance of this group of fungi and its roles in food web dynamics remain unappreciated and are not very well understood. Furthermore, chytrids sometimes have been either totally ignored or wrongly classified in studies on the biodiversity of fresh water ecosystems (Kagami et al., 2007; Lefèvre et al., 2007).

Recently, there has been renewed interest in the ecology of chytrids in aquatic environments. Ibelings et al. (2003) and Kagami et al. (2007) have again examined the large number of species of phytoplankton affected by chytrid parasites. The role of Batrachochytrium dendrobatidis in reduction in size of amphibian populations and in extinctions of species is currently under investigation (Fisher & Garner 2007). Chytridiomycosis is an emerging infectious disease of amphibians world-wide. Kagami et al. (2007) have suggested that chytrid zoospores are an excellent food source for zooplankton and facilitate the transfer of energy to higher trophic levels in food webs. Chytrid zoospores are rich in stored lipids and glycogen. Studies on DNA extracted from water samples from a mountain lake in France have revealed a significant number of ribosomal DNA sequences belonging to known and unknown clades of chytrids (Lefèvre et al., 2007). Chytrid biodiversity is apparently surprisingly high in many freshwater lakes. Research on the ecology of chytrids in freshwater lakes in France is being continued by T. Sime-Ngando and his colleagues and students at Laboratoire Microorganismes: Génome et Environnement, Université Blaise Pascal, 63177 AUBIERRE cedex.

Evidence is emerging that the interactions between the chytrid parasite and its host may involve strong phenotypic selection pressures. A recent study by D. J. Macarthur (unpublished data), funded by the NSW Environmental Trust, involved the inoculation of cultures of the bloom forming cyanobacteria Anabaena circinalis and Microcystis aeruginosa with diatoms infected with chytrids (Fig. 1) and with pure cultures of chytrids in the Rhizophydiales from our culture collection. One of these isolates, SPP, adapted to the new host environments by parasitising both species of cyanobacteria. SPP was isolated into pure culture from a phytoplankton sample containing infected diatoms (by E. Lefèvre) and was tentatively identified as Rhizophydi um sp. These results tend to support the assertion by Kagami et al. (2007) that the host range of chytrid parasites, often thought to be host-specific, could be altered by environmental stress. More interesting, however, was an apparent enhancement of growth and survival of A. circinalis cultures. Clearly, in this case, there are benefits to both the chytrid parasite and the cyanobacteria host. However, more data is required in order to unravel the complicated interactions between the chytrid parasite and its host.

The growth and survival of chytrids are quite sensitive to physical factors, such as moisture, temperature, salinity and dissolved oxygen (Gleason et al., 2007) and possibly toxic chemicals. With global warming and environmental deterioration on the increase, it is high time that more mycologists begin to undertake intensive studies on the ecology of the chytrids in aquatic ecosystems. The survival of many aquatic ecosystems in their present state could even depend on the activities of chytrids along with other groups of microorganisms.
Literature Cited


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MSA BUSINESS

From the President’s Corner . . .

Preparations are well underway for the 2008 Annual Meetings in August at Penn State University. David Geiser has been on top of preparations for several years now so the foray sites have been identified, the lunches have been ordered, and all we need now are some of those big ol’ mushrooms that abound in the forests of central Pennsylvania to get us off to a great start. Jo Taylor and her committee have been hard at work on organizing the program and have selected three gang-buster symposia emphasizing everything from discussions on techniques for measuring fungal diversity to recent advances in live-microscopy tools to take a closer look at the hyphal apex. It’s not too early to start selecting some treasures and novelties for the annual social and auction. Last year we made over $10,000 at LSU and we surely want to reach that mark again. Let Endowment Chair Betsy Arnold know so she can start making a list.

Our goal to increase the amounts in the mentor travel funds is doing well, but again we ask for your support of your favorite mentor so we can get all the funds over $10,000 and be able to assist young mycologists in attending our annual meetings. Our mentor research funds did get a tremendous boost from long-time member and all-around good guy Tom Volk who donated $10,000 in honor of medical mycologist John Rippon. We have an article detailing Dr. Rippon’s career in this issue of Inoculum. Tom added another $500 on top of that to make sure the funds were awarded this year. I hope you all saw the criteria for the award that was sent in an email blast to the membership and on the webpage. With a symposium in cell biology and research awards in medical mycology, we hope to get more mycologists in these fields back in the fold and participating in the annual meetings.

The council will hold its annual mid-year meetings at University of California at Berkeley in late March. I just couldn’t talk anyone into the trip to Hawai’i. Thanks go to John Taylor for making local arrangements. If any of you have issues you would like to have brought up at the mid-year meetings, please email me or secretary Cathie Aime as soon as possible and we’ll make sure they get on the agenda.

And while I’m at it, don’t you all think the Inoculum issues are just terrific! Kudos go to Jinx Campbell for a job well done. If you appreciate her efforts as much as I do, drop her an email and give her a pat on the back.

—Don Hemmes
President
MSA Council has completed two email polls since my last report, approving the following:

- MSA Full Council poll 2008-01: Council approved the establishment of a new Graduate Research Award in the name of John W. Rippon for research in Medical Mycology. The Award was established by a generous donation from Tom Volk and will be presented for the first time this year at the 2008 Annual MSA meeting at Penn State.
- MSA Exec Council poll 2008-02: MSA council approved the allocation of an additional $1500 to supplement the symposium budget for the 2008 Annual Meeting at Penn State. This will allow Program Chair Jo Taylor to provide support for three top-notch symposia this year.

New Members: It is my pleasure to extend a warm welcome to the following new (or returning) members. New memberships will be formally approved by the Society at the Annual Business Meeting at Penn State in 2008.

- Canada: Kevin J Beiler, Laura Biggs
- China: Meichun Xiang
- Colombia: Maria Camila Pizano
- Gambia: Felix C. Onyemachi
- Germany: Martin Strohmeyer
- Panama: Meike Piepenbring

Emeritus candidates: I have received two applications for emeritus status by long standing members Jack Fell (Key Biscayne, FL) and F Brent Reeves, Jr. (Fort Collins CO). Emeritus status is conferred upon retired or retiring members who have at least 15 years good standing with the Society.

REMINDER: MSA Directory Update: Is your information up-to-date in the MSA directory? The Society is relying more and more on email to bring you the latest MSA news, awards announcements and other timely information, and our newsletter. To ensure that you receive Society blast emails and the Inoculum as soon as it comes out, and so that your colleagues can keep in touch, please check the accuracy of your email address and contact information in the online directory. This can be accessed via our website at www.msafungi.org. If you need assistance with updating your membership information, or help with your membership log-in ID and password, please contact our Association Manager at Allen Press, the always-helpful Kay Rose at krose@allenpress.com.

—Cathie Aime
MSA Secretary
maime@agcenter.lsu.edu

Inoculum Editor’s Note

You will notice we have some great new changes to Inoculum. From this issue there is an expanded list of contents. This list is hyperlinked so you can click on the article you want to read and jump straight to it. No more scrolling through looking for a specific page! Also all web sites are hyperlinked so you can click on them direct from Inoculum and be taken through cyberspace to the webpage directly. Additionally, email addresses have been hyperlinked so one click on those will open up a new mail message window with the recipient’s address.

If you have any comments or suggestions to improve Inoculum or some content you wish to see added, please let me know. If you would like to submit an article or have any news or classifieds etc for Inoculum, please send your materials to me at jinx.campbell@usm.edu. Do not send materials to Kay Rose at Allen Press. All submissions should be sent as attachments, preferably in Word. If you submit pictures, these need to be sent as separate JPGS or GIFFS, not embedded in the word document. Please do not send your submission in the body of the email as copy often has to be cleaned of extraneous symbols, brackets, etc and reformatted for use. My concern is that on reformatting and cleaning up, typographical errors may occur that could alter the context of your submission.

Inoculum is published in odd numbered months (January, March, May, July, September, November). The deadline for submitting is the 15th of even numbered months: February, April, June, August, October, except December, which is the 10th.

If you would like to review a book or CD, please contact Amy Rossman at Amy.Rossman@ars.usda.gov. She will send it to you, you write the review, and then you can keep the book. Titles for review can be found in the Mycologist’s Bookshelf section.

—Jinx Campbell
Inoculum Éditeur
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Antrodiella luteocontexta

For rarely collected species (e.g. *Fomitopsis*), complete ITS, the 3'-end of the LSU, EF-1 alpha, beta-tubulin, and partial sequences from DNA of the following five nuclear genes: the species using multigene phylogenetic analysis. The analysis is based on &B. Most of the strains are not identified. We examine the lineage of *Cytosporin A*, *B*, & *C*, *Cytosporone D* & *E*, and *Grahamimycin A*, *A1*.

University, East Lansing, MI 48824, USA. gadams@msu.edu. A multigene phylogenetic analysis of species of *Valsa* revealing lineages of medically important strains. *Valsa* is a cosmopolitan genus of fungi in the Diaporthales. Species in the genus cause cankers on woody angiosperms and gymnosperms and occasionally parasitize herbaceous plants. Identification of *Valsa* species based on morphology has long been problematical. Species discovery has been ongoing yet description of new species has foundered on the lack of distinguishing features. Members of the Diaporthales are recognized as a profitable resource for drug discovery. *Valsa* contains several strains that have received U.S. Patents because they produce unique compounds with important medical properties. The compounds include Cytosporanic Acid, Cytosporon A, B & C, Cytosporone D & E, and Grahamimycin A. A & B. Most of the strains are not identified. We examine the lineage of the patented strains in relation to clades containing well-characterized species using multigene phylogenetic analysis. The analysis is based on partial sequences from DNA of the following five nuclear genes: the complete ITS, the 3'-end of the LSU, EF-1 alpha, beta-tubulin, and histone H3. Poster

Aime, M. Catherine, 1 Henkel, Terry W. 2* and Ryvarden, Leif. 3 1USDA-ARS, Systematic Botany and Mycology Lab, Beltville, MD 20705, USA, 2Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA, 3Department of Botany, University of Oslo, Blindern, N-0316 Oslo, Norway. twh5@humboldt.edu. Polyporoid fungi of Guyana: diversity, new species, and ecological roles. Seven years of field work in a remote region of Guyana have uncovered a diverse assemblage of polypores associated with mixed and/or ectotrophic *Dicymbe corymbosa* (Caesalpinioideae)-dominated rainforests in the Pakaraima Mountains. As a result, the total known species of polypores in Guyana has nearly doubled, from 55 to 91, including nine new species in seven genera of the Polyporales, *Hyphonochaetales* and Russulales (*Amauroderma*, *Ceriporia*, *Dichomitus*, *Fomitopsis*; *Coltricia*, *Coltriciella*; *Wrightioporia*) and new distribution records for rarely collected species (e.g. *Antrodiaella dentipora*, *Antrodiaella lateocentexa*, *Junguhuitia minuta*). We report new species that expand current generic and family concepts, such as *Amauroderma coltricioides*, which is the first known species in the Ganodermaaceae with smooth basidiospores. In addition to describing a variety of wood-decay strategies among these polypores, we provide habitat, morphological and molecular evidence supporting an ectomycorrhizal nutritional mode for *Coltricia* spp. and examine the ecological consequences of *Phellinus* heart rot in *D. corymbosa* forests. Contributed Presentation

Alexander, Mark* and Baird, Richard. Plant Pathology, P.O. Box 9655, 206 Dorman Hall, Mississippi State, MS 39762, USA. MAlexander@plantpath.msstate.edu. Baseline data on pathogenic and ectomycorrhizal fungi associated with old growth eastern hemlock in the GSMP and effects of imidacloprid on rhizospheric fungi and future restoration efforts. At its current rate of spread the exotic Hemlock Wooly Adelgid (HWA) will infest and devastate the entire native range of eastern hemlock within the next 2 decades. Baseline data on all associated fungal organisms must be obtained before forest habitat succession occurs. The effects of the loss of hemlock on associated soilborne fungal communities and on subsequent hemlock seedling establishment and regeneration are unknown. Select stands are being preserved using the systemic insecticide imidacloprid. The current application method, soil drenching, has an unknown impact on belowground fungal communities. Two study sites were selected in the Great Smoky Mountains National Park at two elevations within pure stands of mature hemlock. Twenty mature trees randomly selected at each site were subjected to one of 5 imidacloprid treatments varying rate and frequency and replicated 4 times at 2 elevations. Effects of treatments were analyzed by collecting a 120cm root sample from each replicate tree for identification of fungi using cultural techniques and molecular sequence data. Baseline data on fungal population diversity and abundance were compared among treatments and controls. In addition, all terrestrial macrofungi within the plots were collected monthly. Ectomycorrhizal fungi were isolated from fresh sporocarps and cryogenically stored in a fungal repository. Poster

Alspaugh, Andrew. Dept. of Medicine, Duke University School of Medicine, Durham, NC, USA. andrew.alspaugh@duke.edu. Transcriptional profiling in the human fungal pathogen *Cryptococcus neoformans*. Similar to other microbial pathogens, *Cryptococcus neoformans* must coordinate the expression of many genes to adapt to the environment of the infected host. We have previously demonstrated that the cAMP signal transduction pathway coordinately regulates the expression of genes required for capsule and melanin production. Using whole genome microarrays, we have begun to explore the transcriptional network controlled by the cAMP pathway. Several transcription factors act downstream of this conserved pathway, including the Nrg1 protein. In addition to capsule and melanin production, *C. neoformans* must also control subtle morphogenic events to retain full virulence. The cytoskeletal changes required for altered morphogenesis are regulated by Ras signaling pathways. Gene microarray studies have also demonstrated the role of Ras-dependent gene expression in morphogenesis. Transcriptional profiling of targeted *C. neoformans* mutant strains with altered virulence has begun to demonstrate the complex ways in which a microbial pathogen develops an adaptive cellular response to the host environment. Symposium Presentation

Arnold, A. Elizabeth. Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA. arnolda@ag.arizona.edu. Barcoding endophytic fungi: lessons, limitations, and links with muliticlone data sets. Drawing from surveys of endophytic fungi from (1) all major

Continued on following page
lineages of land plants and (2) biogeographic provinces ranging from the arctic to the tropics. I will explore the degree to which a large-scale, single-locus (bar-code) data set based on the nuclear ribosomal internal transcribed spacer (ITS) can further our understanding of fungal diversity and ecology. Specifically, I will (1) address patterns of geographical distributions, taxonomic makeup, host specificity, and diversity of endophytic fungi using a data set of over 6000 ITS sequences from cultures and environmental samples; (2) explore empirical approaches for delineating meaningful taxonomic units from ITS data alone; (3) highlight a variety of limitations imposed by the single-locus and ITS-specific approach, and demonstrate that such issues vary in intensity among clades of Ascomycota and among different geographic sites; (4) discuss the degree to which ITS data are congruent and incongruent with inferences based on multi-locus datasets; and (5) describe several new methods for visualizing ITS data in spatial and phylogenetic contexts, with the goal of critically evaluating the biological realism and inferential strength of the bar-code approach for studies of highly diverse fungi. 

Symposium Presentation

Atkinson, Toni J.,* Orlovich, David, A. and Miller, Andrew N. Section for Biodiversity, Illinois Natural History Survey, 1816 S. Oak St., Champaign, IL 61820, USA. Department of Botany, University of Otago, P.O. Box 56, Dunedin 9054, New Zealand. toni@botany.otago.ac.nz. *From the Land of the Long White Cloud to the Great Smoky Mountains: New Zealand and Appalachian diversity among woody decay pyrenomycetes. The New Zealand archipelago, a temperate, oceanic island group 1600 km south-east of Australia, forms the largest landmass in the south Pacific. Island biotas are usually considered ‘depauperate’ when compared with those of continents. New Zealand does have fewer plant and animal taxa than a continent, but its biota has long been noted for its uniqueness. Recent research among woody decay pyrenomycetes in New Zealand, while finding a high level of endemism, nonetheless shows that families, genera, and species are shared with the continental northern hemisphere. From knowledge to date, we will discuss the striking morphological and molecular similarities and differences between New Zealand and Appalachian members of the Lasiophialaceae, Chaetosphaeriaceae, and Helminthosphaeriaceae. 

Avis, Peter G.,* Leacock, Patrick and Mueller, Greg M. Department of Botany, The Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago IL 60605, USA. pavis@fieldmuseum.org. Scale dependent responses of ectomycorrhizal fungal communities to simulated nitrogen deposition in oak forests of the Chicago region. Nitrogen deposition can dramatically impact the diversity and species composition of ectomycorrhizal communities, but it is uncertain at what level of added nitrogen or at what spatial scale these responses occur in temperate deciduous ecosystems. We tested the impact of projected realistic increases in nitrogen deposition levels in the Chicago region by measuring the response of ectomycorrhizal fungi to nitrogen fertilization at two oak dominated forests. We systematically surveyed ectomycorrhizal sporocarps in treatment and control plots from 2003-2006, but did not detect any significant differences in either abundance or species richness of ectomycorrhizal mushrooms. Belowground, we measured ectomycorrhizal fungi colonizing roots by morphological and molecular methods including terminal restriction length fragment length polymorphisms and sequencing. We detected significant differences between treatment and controls in species richness and composition at the scale of the treatment plots but not at the scale of the soil core or individual roots. Such responses indicate that realistic future increases of nitrogen deposition could impact ectomycorrhizal communities, especially at larger spatial scales. 

Baucom, Deana*, Romero, Marie and Creamer, Rebecca. New Mexico State University, Las Cruces, NM 88003, USA. dbaucom@nmsu.edu. Morphological and genetic characterization of new fungal endophytes of locoweed found in six western states. Toxic locoweeds (Astragalus and Oxytropis spp.) found throughout the western USA are accountable for significant losses to grazing animals. Fungal endophytes of locoweed are responsible for production of the toxic alkaloid swainsonine and have been shown to cause symptoms of locoweed toxicity outside of the plant environment. Fungal endophytes of locoweed have been characterized previously from only a few of the many species of Astragalus and Oxytropis. To further expand our understanding of this endophytic fungus, we examined culture morphology and genetics of fungi isolated from nine locoweed species collected from six states. Although all isolates were typically slow growing in culture, as indicative of the locoweed fungal endophyte, we found novel morphological characteristics that were not seen in the previously limited examination of locoweed species. Genetic differences were also observed in nucleic acid sequences of the ITS (internal transcribed spacer) and gpd (glyceraldehyde phosphate dehydrogenase) regions of the different isolates. The morphological and genetic differences we found illustrate the diversity of the fungal endophyte and allow us to distinguish between isolates collected from a number of different locoweed species. 

Beard, Charles E. Department of Entomology, Soils, and Plant Sciences, Clemson University. Clemson, SC 29634, USA. cbrd@clemson.edu. Trichospore shapes of the trichomycete fungus Harpella melusinae. The trichomycete fungus Harpella melusinae is a common symbiote in the midgut of larval black flies. The variation and wide distribution of Harpella melusinae probably represents the existence of a species complex, but limited morphological characters are available for discriminating possible cryptic species. The asexual spores (trichospores) of the fungus vary from coiled to straight. Straight and coiled or curved trichospores have not been found on the same thallus. Straight-spired thalli might represent a species or genotype distinct from coiled- or curved-sporiform thalli. We are testing the heritability of spore shape by allowing horizontal transmission of the fungus from field-collected larvae to lab-reared trichomycete-free larvae. The straight spore shape (from Simulium innoxium) carries over to the new host (Simulium vitatum). Coiled spores are more difficult to collect and horizontal transmission is less successful, suggesting that the lab-reared larvae are less competent hosts for the coiled spores from field-collectet larvae (Simulium tuberosum grp.), or that the coiled spores are less infective in this study. Spore shape might be related to other parameters such as host physiology. We also demonstrate that horizontal transmission between host species occurs. 

Bechara, Mark A.,* Heinemann, Paul,1 Walker, Paul N. and Romaine, C. Peter,2 1Department of Agricultural and Biological Engineering, 249 Agriculture Engineering Building, The Pennsylvania State University, University Park, PA 16802, USA. 2Department of Plant Pathology, 211 Buckhout Laboratory, The Pennsylvania State University, University Park, PA 16802, USA. mab568@psu.edu. The development of non-composted grain-based substrates for mushroom production. Two different systems for Agaricus bisporus (button mushroom) production are proposed as alternatives to the traditional environmentally problematic mushroom production system that relies on composting of plant and animal organic matter. Each system involves processing grains into suitable mushroom substrates. The first system proposes the use of commercial grain spawn, the vehicle typically used to inoculate traditional substrates, supplemented with high protein delayed-release supplements. In this system, grain spawn producers supply mushroom producers the entire substrate for mushroom production. The second system consists of producing mushrooms on sterilized grains supplemented with oilseeds. In this system, an aseptic processing system would be located on-site at the mushroom production facility to sterilize grain substrates. For the second system, mushroom producers would need to get their inoculum from grain spawn producers to inoculate the sterilized substrates. The highest yield of mushrooms for the commercial grain spawn substrate supplemented with delayed-release supplements was 13.7 kg/m², whereas yield from substrates composed of cereal grains and oilseeds was 16.9 kg/m². A discussion about the advantages and disadvantages of each alternative mushroom production system will be addressed.

Contributed Presentation

Beard, Charles E. Department of Entomology, Soils, and Plant Sciences, Clemson University. Clemson, SC 29634, USA. cbrd@clemson.edu. Trichospore shapes of the trichomycete fungus Harpella melusinae. The trichomycete fungus Harpella melusinae is a common symbiote in the midgut of larval black flies. The variation and wide distribution of Harpella melusinae probably represents the existence of a species complex, but limited morphological characters are available for discriminating possible cryptic species. The asexual spores (trichospores) of the fungus vary from coiled to straight. Straight and coiled or curved trichospores have not been found on the same thallus. Straight-spired thalli might represent a species or genotype distinct from coiled- or curved-sporiform thalli. We are testing the heritability of spore shape by allowing horizontal transmission of the fungus from field-collected larvae to lab-reared trichomycete-free larvae. The straight spore shape (from Simulium innoxium) carries over to the new host (Simulium vitatum). Coiled spores are more difficult to collect and horizontal transmission is less successful, suggesting that the lab-reared larvae are less competent hosts for the coiled spores from field-collectet larvae (Simulium tuberosum grp.), or that the coiled spores are less infective in this study. Spore shape might be related to other parameters such as host physiology. We also demonstrate that horizontal transmission between host species occurs. Contributed Presentation

Bechara, Mark A.,* Heinemann, Paul,1 Walker, Paul N. and Romaine, C. Peter,2 1Department of Agricultural and Biological Engineering, 249 Agriculture Engineering Building, The Pennsylvania State University, University Park, PA 16802, USA. 2Department of Plant Pathology, 211 Buckhout Laboratory, The Pennsylvania State University, University Park, PA 16802, USA. mab568@psu.edu. The development of non-composted grain-based substrates for mushroom production. Two different systems for Agaricus bisporus (button mushroom) production are proposed as alternatives to the traditional environmentally problematic mushroom production system that relies on composting of plant and animal organic matter. Each system involves processing grains into suitable mushroom substrates. The first system proposes the use of commercial grain spawn, the vehicle typically used to inoculate traditional substrates, supplemented with high protein delayed-release supplements. In this system, grain spawn producers supply mushroom producers the entire substrate for mushroom production. The second system consists of producing mushrooms on sterilized grains supplemented with oilseeds. In this system, an aseptic processing system would be located on-site at the mushroom production facility to sterilize grain substrates. For the second system, mushroom producers would need to get their inoculum from grain spawn producers to inoculate the sterilized substrates. The highest yield of mushrooms for the commercial grain spawn substrate supplemented with delayed-release supplements was 13.7 kg/m², whereas yield from substrates composed of cereal grains and oilseeds was 16.9 kg/m². A discussion about the advantages and disadvantages of each alternative mushroom production system will be addressed. Poster
Compared the foliar endophyte biodiversity of black spruce (Picea mariana) and Pseudotsuga menziesii trees. We investigated the structure of mycorrhizal networks (MNs) formed between roots of *P. mariana* (*P. menziesii*) trees in British Columbia. Structure was determined based on DNA obtained from tuberculate mycorrhizas sampled within a 30m x 30m plot, and tree needles obtained from trees inside and within 10m of the plot. Microsatellite regions of DNA were used to distinguish both tree and fungal individuals, and to match the identities of tree roots in mycorrhizas with trees above ground. This data was used to model MN structure from the phylogenetic perspective with trees as nodes and *R. vinicolor* (*R. vesiculosus*) genotypes colonizing >1 tree as links. Based on 210 mycorrhizas collected among 55 trees, we recovered 21 *R. vesiculosus* genets, 22 *R. vinicolor* genets, and 77 tree genotypes, 69 of which were linked to other trees through shared fungal genets. The degree of tree-node connectivity ranged from 0 to 30, with an average of 1.4 fungal genets and 5.7 linkages per tree. Thus, there is a high degree of connectivity between Douglas-fir trees and *R. vesiculosus* / *R. vinicolor* genets in this site, with an uneven and clustered degree distribution. Continuing work will resolve the MN structure by integrating spatial data with genetic and network analyses.

Berube, Mary L. Department of Botany, University of British Columbia, Vancouver BC, V6T 1Z4, Canada. berbee@interchange.ubc.ca. **What makes a fungus? Fungal specific genes and the origin of chitinous cell walls.** The Chytridomycota and Zygomycoma include ancient fungal lineages that may have originated hundreds of millions of years before fore-forests invaded land. Complete genomic sequences are now available for species in both groups. We have been studying genes that distinguish the fungi from other kingdoms. Among the fungal specific genes, genes involved in wall cell construction, notably chitin synthases and chitin deacetylases were diverse among fungi and divergent compared with their closest paralogues in other organisms. Both chitin synthases and chitin deacetylases were more numerous in the basal fungi than in the Ascomycota, where the genes have been best characterized. While most filamentous ascomycete species have ~7-8 paralogues of the chitin synthases, the zygomycete *Rhizopus oryzae* has 25; the chytrid *Batrachochytrium dendrobatidis* has 16 and an EST library of *Batrachochytrium dendrobatidis* has 8 different chitin synthases. Suggesting that diverse chitin synthases, genes involved in cell wall construction, notably chitin synthases and chitin deacetylases were diverse among fungi and divergent compared with their closest paralogues in other organisms. Both chitin synthases and chitin deacetylases were more numerous in the basal fungi than in the Ascomycota, where the genes have been best characterized.

Berube, Jean A. and Stefini, Franck O.P. Canadian Forest Service, 1055 du PEPS, P.O. Box 10380, Quebec City, QC, G1V 4C7, Canada. CRBF, Faculte de foresterie et de geometique, Universite Laval, Quebec City, QC, G1K 7P4, Canada. jberube@cfl.fostry.ca. **Foliar endophyte biodiversity of cloned needles versus plated needles.** We compared the foliar endophyte biodiversity of black spruce (*P. mariana*) cloned needles versus the endophytes recovered in Petri plated needles. Three-years old asymptomatic healthy needles were collected in Valcartier near Quebec City, surface sterilized and then plated on nutrient agar or DNA extracted, ITS PCR amplified and cloned. Twenty-three plated needles yielded only three foliar endophyte species and never more than one endophyte per needle, whereas six cloned needles yielded 11 endophyte OTUs, with an average of 6 OTU’s per cloned needle. The most common foliar endophyte from plated needles was also found in cloned needles but the other two rare foliar endophytes from plated needles were not found in cloned needles. Cloned needles yielded 9 new foliar endophytes, of which eight seem to be new fungal species. In this sampling protocol, one single cloned needle yielded more foliar endophyte OTU’s than the normal sampling effort of plated needles from a spruce stand. Cloning needles also lead to the discovery of 9 new foliar endophytes never recorded before as foliar endophytes using traditional plating methods.

Blackwell, Meredith, Suh, Sung-Oui and Nguyen, Nhu H. Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803, USA. Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720, USA. mblackwell@lsu.edu. **Yeasts across the gulf divide.** More than 1000 yeasts were isolated from mycoplagous insects in Panama and the southeastern USA over a seven-year period; the isolations resulted in the discovery of about 500 taxa of which almost 250 had not been described previously. Our data indicate that few yeast species span the geographical region between Panama and the southeastern USA. In a few cases when species do occur in both regions, populations display genetic variation consistent with the region. Collection data, including repeated isolation of yeasts from specialized gut pouches of beetles and recovery of certain yeasts from different life stages of the same beetle species, have been taken as evidence of close association between yeast and insect, rather than yeast and fungal host. Many potential basidiomycete hosts (e.g., *Tinctoporellus epimiltinus*, *Pycnoporus sanguineus*, other polypores, species of Hymenochaetaceae) occur throughout the Caribbean and Gulf of Mexico coastal plain spanning both collecting regions, but the beetle hosts have more restricted distributions. Now, phylogenetic evidence lends additional support for a hypothesis that isolation occurs in association with the insect host. Certain beetle genera are associated with yeast clades that have diverged independently with related beetles in either Panama or in the southeastern USA.

Binkova, Olga*, Feldman, Tracy and Walker, Nathan. 246 NRC, Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK 74078, USA. blinkova@biochem.okstate.edu. **Mycoviruses in symbiotic plant-fungal interactions.** Mycoviruses or fungal viruses have frequently been reported from fungi and often associated with symptomless infections. Several examples of virus regulation of hypovirulence in the pathogenic fungi are known from the many investigations. However, the effect of mycoviruses on mutualistic interactions, especially in the natural ecosystems, is practically unknown. We are investigating the biodiversity and ecology of endophytic fungi and their mycoviruses from a dominant grass, big bluestem (*Andropogon gerardii*) collected from 2004 - 2006 from plots periodically burned at the Tallgrass Prairie Preserve, Pawhuska, OK. This study showed that the root fungal endophyte community is very diverse: most fungi are from the classes Dothideomycetes and Sordariomycetes, the predominant fungal genera...
were *Peroncia*, *Gaumannomyces*, *Fusarium*, *Anguillospora*, and many unknown species. We found that many of the fungi are infected by viruses. The majority of these viruses may be newly discovered and previously unknown. Future studies will aim to understand the role of the discovered mycoviruses on the character and intensity of plant-fungus interactions and possibly how disturbances, such as fire, can influence virus-fungal-plant interactions. **Poster**

Boerstler, Boris*, Raab, Philipp and Redecker, Dirk. Institute of Botany, University of Basel, Helbestr.1, CH-4056 Basel, Switzerland. boris.boerstler@unibas.ch. **Mitochondrial large ribosomal subunit sequences as potential marker for population studies of *Glomus intraradices*.** Arbuscular mycorrhizal fungi (AMF) form symbioses with the majority of land plants. *Glomus intraradices* is a widespread member of this group which was found in an extremely broad range of habitats, indicating a high tolerance for a multitude of environmental factors. Despite this ecological versatility, almost nothing is known about the local and geographic structure of this fungal species which might reveal specialized ecotypes. As the well-established marker genes of the nuclear-encoded rDNA subunits and internal transcribed spacers (ITS) display sequence heterogeneity even within single fungal spores we have developed a nested PCR approach for the mitochondrial rDNA large subunit (mtLSU). These sequences display no intra-isolate heterogeneity but different haplotypes can be distinguished among isolates of *G. intraradices*. The development of highly specific primer sets makes it possible to obtain mtLSU sequences of *G. intraradices* from colonized roots. The varying content of introns in the analyzed gene region represents a further feature to distinguish genotypes. Therefore mtLSU has the potential to be a highly sensitive marker for population studies of *G. intraradices*. **Contributed Presentation**

Bogale, Mesfin*, Wingfield, Michael J., Steenkamp, Emma T. and Wingfield, Brenda D. Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa. mesfin.bogale@fabi.up.ac.za. **Characterization of *Fusarium oxysporum* isolates from Ethiopia using SSR, AFLP and DNA sequence analyses.** *Fusarium oxysporum* is known for the wilt and rot diseases that it causes in many plant species. However, little is known regarding the genetic diversity of this fungal species in Ethiopian agriculture. We used SSR, AFLPs and DNA sequence analyses to study 32 Ethiopian isolates. For comparative purposes, we also included strains representing 18 *formae speciales*, and GenBank sequences representing the three phylogenetic clades in this species. The three methods separated the strains into three lineages, which corresponded with the three clades known to reflect groups in *F. oxysporum*. Five translation elongation factor-1 alpha nucleotide sites were found to be fixed differently among the lineages, further supporting the separation of the lineages. Thirty of the Ethiopian isolates grouped in Lineage 2, whereas the remaining two isolates grouped in Lineages 1 and 3. The genetic diversity observed among the Ethiopian isolates was also low. This most probably reflects the nature of the Ethiopian agricultural system that heavily relies on local crop varieties, thereby restricting the introduction of new genotypes of the fungus via infected seeds. The 18 *formae speciales* did not separate according to host, with any of the three DNA-based techniques used. This confirmed that pathogenicity of isolates does not necessarily correlate with phylogenetic grouping. **Contributed Presentation**

Bogale, Mesfin*, Wingfield, Michael J., Steenkamp, Emma T. and Wingfield, Brenda D. Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa. mesfin.bogale@fabi.up.ac.za. **Species-specific primers for *Fusarium redolens* and a PCR-RFLP technique to distinguish among three clades of *Fusarium oxysporum*.** The presence of strains with intermediate macroconidial sizes between *F. redolens* and *F. oxysporum* makes morphological differentiation of these species problematic. The PCR-RFLP technique developed to differentiate these species does not distinguish *F. redolens* from *F. hostae*. Grouping of isolates into the three phylogenetic clades of *F. oxysporum* requires DNA sequencing and inclusion of strains/sequences representing each clade. DNA sequencing is, however, not available to most plant pathologists, especially to those in the developing world. To solve these problems, we used nucleotide sequences from the translation elongation factor 1 alpha (TEF-1 alpha) genes of these species and their close relatives. We aligned these sequences to design *F. redolens*-specific primers, and to identify restriction sites that discriminate among the three clades of *F. oxysporum*. The *F. redolens*-specific primers distinguished this species from all others included in the study based on the presence of an amplification product only in *F. redolens*. Restriction of *F. oxysporum* TEF-1 alpha products with endonucleases *MseI* and *AluI* resulted in three TEF-1 alpha-RFLP patterns. These PCR-RFLP patterns corresponded with the three clades of *F. oxysporum*. These techniques provide simple and inexpensive diagnostic methods for the identification of *F. redolens* and members of the three clades of *F. oxysporum*. **Contributed Presentation**

Bonito, Gregory* and Vilgalys, Rytas. Duke University, Durham, NC 27708, USA, gmb2@duke.edu. **Molecular ecology of truffles (*Tuber*) and their mycorrhiza.** Truffles belonging to the genus *Tuber* are mycorrhizal fungi characterized by belowground fruitbody production and a northern hemisphere distribution. Of the 100 or so described species of *Tuber* worldwide, a dozen or so species have economic value and are harvested commercially. This has stimulated interest to better understand truffle ecology. DNA sequencing is a common component in systematic and ecological studies of mycorrhizal communities. The public database Genbank includes approximately 30 unidentified ectomycorrhiza submissions that BLAST closest to *Tuber*, and another 30 accesses from unidentified *Tuber* sp. sporocarps. Our research on the phylogenetic relationships within the genus *Tuber* has resulted in a *Tuber* phylogeny and has resolved 7 well-supported clades. In this study, we analyzed unidentified *Tuber* collections and mycorrhiza from our field studies and from Genbank accessions in a phylogenetic framework to determine the identification of unidentified samples and to ascertain the prevalence of ‘novel’ and undocumented lineages. Our results show that the majority of unidentified *Tuber* sequences belong to non-economically important (and less studied) species within the *Tuberulum* and *Maculatum* clades. Further ecological insights into host, habitat, and geographical ranges of these species are discussed. **Poster**

Branco, Sara. University of Chicago, Chicago, IL 60637, USA; The Field Museum, Chicago, IL 60601, USA. sbrano@uchicago.edu. **Is there a serpentine ectomycorrhizal community?** Serpentine soils are extreme environments rich in heavy metals and poor in nutrients that host depauperate plant communities with high rates of endemism. I am investigating whether the symbiotic fungal communities from serpentine forests follow the same pattern seen for plants. I surveyed the ectomycorrhizal (ECM) communities from serpentine and non-serpentine oak forests in northeastern Portugal using the rDNA Internal Transcribed Spacer (ITS) region and found enormous diversity. All three forests showed very different and rich communities with very low ITS type overlap. Additionally, sampling of fungi in the same forest in consecutive years revealed a tremendous ITS type annual turnover. The pattern of species-poor communities found for plants does not seem to hold for ECM fungi and the existence of endemic ECM serpentine species is still unclear. However, the detection of many ITS types restricted to the serpentine forest is an indication of putative endemics. A few ITS types were detected in serpentine and non-serpentine forests, suggesting the existence of plastic species tolerant to both soils. These results document high ECM diversity associated with Mediterranean oak forests. Further investigation is needed to clarify the existence of particular ECM communities specifically associated with serpentine soils and determine the role of this extreme habitat in the evolution of symbiotic fungi. **Contributed Presentation**

Brooks, Micheal C., Powell, Martha J.*, Blackwell, Will H., Letcher, Peter M. and Wakefield, William S. Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487-0344, USA. mpowell@biology.as.ua.edu. **Detection of chytrid fungi involved in...**

Continued on following page
the degradation of chitin in Lake Lurleen (Tuscaloosa County, Alabama). Chitin is one of the most abundant biopolymers in aquatic habitats and is a bait commonly used to retrieve chytrid fungi from environmental samples. Current ecological models for the role of microorganisms in the degradation of chitin in aquatic habitats, however, largely ignore chytrids. The purpose of this study is to use culture and culture-independent nucleic acid techniques to detect through multiple seasons the diversity of chytrids on chitin from Lake Lurleen, a reservoir in the Black Warrior River Basin. In the first phase of this study, ribosomal genes are sequenced for all chytrids cultured, generating a reference database of molecular diversity detected with direct culture techniques. This study will be the foundation for continued studies where total DNA from chitin incubated in traps in the same lake site and from floating particulate matter along the lake shore will be isolated and ribosomal genes sequenced. This approach provides baseline data for (1) determining if direct culture methods and identifications based on morphology adequately monitor the diversity of chytrids in the lake; (2) recognizing culture-independent organisms and potential novel chytrid clades; and (3) elucidating chytrid diversity in chitin biodegradation in a freshwater habitat. Poster

Brown, Matthew, W. 3 and Spiegel, Frederick, W. Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville, AR 72701, USA. mwbrown@uark.edu. Assessment of protostelid diversity in Ozark Plateau oak-hickory forests in south central USA. Protostelids are unicellular amoeboid slime molds commonly found on dead plant substrates. To assess protostelid species distribution and assemblages, 164 samples were collected in uplands and riparian habitats in oak-hickory forests in the Arkansas Ozarks. Ninety-two percent of samples yielded at least one protostelid. A total of 22 described species of protostelids and one myxymycete, Echinostelium bisporum, were found during this study. If the variants of Protostelium mycophaga are considered, then there were 27 species, the highest species richness yet recorded for a temperate habitat. Microhabitat distributions of protostelids indicate that Protostelium mycophaga and Soliformovum irregularis are the most abundant species in ground and aerial litter microhabitats. Three other species were commonly encountered on the ground litter. Four species were frequently encountered in bark microhabitats. Species composition between upland and riparian forest types is different. Though Protostelium mycophaga and Soliformovum irregularis were well represented in the two habitats, some species, e.g. Echiosteliosis oligospora and Protostelium arachisporum, are markedly different, especially for ground litter microhabitats. Six species were found on all microhabitat types and also found in all habitat types. Overall, species’ microhabitat distribution is consistent with other studies. Poster

CANCELED Bushley, Katharyn E. 1, and Turgeon, B. Gillian. Cornell University, Department of Plant Pathology, Plant Science Building, Room 343, Ithaca, NY 14853, USA. ke45@cornell.edu. Evolution of chemical arsenals in filamentous fungi: rapidly evolving NRPSs among closely related taxa. Non-ribosomal peptide synthetases (NRPSs) are multimodular enzymes, found in ascomycete fungi and bacteria that make non-ribosomal peptides (NRPs) through a thioester peptide mechanism independent of ribosomes. NRPs are structurally diverse and often bioactive small molecules with biological functions ranging from antibiotics to immunosuppressant drugs. Previous studies suggest that genes encoding NRPSs are rapidly evolving and have highly discontinuous distributions even among closely related taxa. Various evolutionary processes could explain this pattern: 1) gene duplication and differential loss, 2) recombination, 3) gene conversion, 4) diversifying selection, and 5) horizontal gene transfer. We are investigating diversity and evolution of NRPSs among closely related species utilizing data from genome sequencing projects as well as data generated from a suite of closely related Cochliobolus species and in order to address which of these mechanism(s) are involved in generating novel NRPS genes. We are also exploring the relationship between NRPSs and their chemical products by addressing the roles of both modular domain architecture and amino acid residues involved in substrate recognition in shaping the chemical structure of the NRP peptide product. Poster

CANCELED Cabanelas, Marivic V. 1, 2, Smitana, Prasartporn 1, To-An, Chaiyawat 1, Jeewon, Rajesh 1 and Hyde, Kevin D. 3 Chiang Mai University, Department of Plant Biotechnology, Laboratory of Plant Pathology, Chiang Mai, Thailand; 2Mushroom Research Centre, 128 Moo3 Ban Phadeng, Pa Pae, Mae Taeng, Chiang Mai 50150, Thailand; 3University of Hong Kong, Department of Ecology and Biodiversity, The University of Hong Kong, Pokfulam Road, Hong Kong. mvc0206@yahoo.com. Biodiversity of freshwater fungi in Paoy Lake, the Philippines and the Mushroom Research Centre, Thailand. This study is focusing on the fungi on submerged wood samples collected from Paoy Lake, in the Philippines and MRC Lake, in Thailand. Wood or bamboo samples that have been submerged for several months have been collected from both lakes and examined for fungi following incubation in a moist chamber. The fungal communities are compared. This project is important to understanding the biodiversity of freshwater fungi. This is the first study of fungi at Paoy Lake and one of the few studies of fungi in the Philippines, which has been poorly studied for fungi. Fungi identified so far from MRC Lake are Annullatasca biatriisporus, Dactylaria plomerovensis, Digitodesmium hep- tasporn, Sporochisma saccardoi, and Sporochisma unisepatu and Savoryella lignicola, S. aquatica, Kirschsteiniothelia elaterascus, Annulastacus triestipatus, Anipodera triestipata have been identified from Paoy Lake. A new genus of freshwater ascomycetes, Paoyen- sistis lignicola collected from Paoy Lake in Ilocos Norte, in the Philip- pines is described and illustrated and compared with analogous taxa. Paoyenistis lignicola is characterized by immersed, slightly erumpent ascospore which fuse into a single ostiole. Asci are uniminate, clavate and short pedicellate with a discoid refractive apical ring and as- cospores are lemoniform, brown to dark brown and with a unique germ slit. Characters suggest that the genus should be placed in the Sordari- ales, possibly Sordariaceae. Molecular based phylogenies support morphological based assumptions. 185rDNA sequence data indicates a close relationship to Xylomelasma sordida and Ceratostomella pyre- na whose taxonomic placement is still insecure. 285rDNA based phy- logenies, on the other hand, depict a close affiliation with members of the Annulatacaceae which are freshwater ascomycetes. An appropri- ate familial placement for Paoyenistis lignicola is still unknown (Sor- dariozymetes incertae sedis). Contributed Presentation

Cai, Guo-hong 1, 2, Myers, Kevin 1, Hillman, Bradley L. 2 and Fry, William E. 1 1Department of Plant Pathology, Cornell University, Ithaca, NY 14853, USA; 2Department of Plant Biology and Pathology, Rutgers University, New Brunswick, NJ 08901, USA. gc228@cornell.edu. Identification of viruses in Phytophthora infestans. Phytophthora infestans continues to be a threat to potato and tomato production worldwide – more than one and a half centuries after the Irish famine. Recent migrations of diverse, virulent populations into many parts of the world has rendered the disease more difficult to control. These populations contain individuals of A2 as well as A1 mating type. Additionally, molecular genetic studies remain very difficult in P. infestans. In order to explore additional potential control measures and to enable development of an efficient system for gene expression/silencing in P. infestans, we are searching for viruses in this oomycete. Viruses might have a role in biocontrol, and they might also have potential to be engineered into vectors for gene expression/silencing. We have therefore screened P. infestans isolates for virus-like double stranded RNAs (dsRNAs), and to date (spring 2007) have found five dsRNAs in four patterns. Sequencing of a doublet showed that it has the characteristics of the replicative form of a single-strand RNA virus. The first RNA (RNA1) encodes an RNA dependent RNA polymerase (RdRp, pfm 00680) and the second (RNA2) encodes a putative trypsin-like serine protease. Preliminary sequence data indicate that the other three dsRNAs also have characteristics of viruses. Contributed Presentation

Campbell, Jinx. Department of Coastal Sciences, University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, Mississippi 39564, USA. Continued on following page

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The public is simply unaware that fungi are indispensable components of ecosystems. Growing interest in marine and estuarine habitats in recent years has led to an increase in studies on marine fungi. Although the first marine fungi were described in 1846, the existence of fungi entirely confined to a marine environment was not recognized until about 40 years ago. Marine and estuarine environments occupy 75% of the globe. However, marine fungi occur mainly in intertidal habitats such as sandy beaches, jetties, saltmarshes and mangroves. Compared with terrestrial fungi, the number of higher marine fungi is small. To date only 600 fungi have been described. Marine fungi can be saprophytes, symbionts or parasites on plants or animals. All are microscopic; the largest being only 4-5mm in diameter. Saprophytic fungi are important decomposers of cellulose, in the form of driftwood, pilings, mangrove roots, marsh plants, algae and seagrass leaves. They are also found on the exoskeletons, shells and protective tubes of animals and fish where they degrade chitin, keratin, tunicin and calcium carbonate. Marine fungi are able to form several types of symbiotic associations: lichenoids which have phototrophic partners, usually microscopic cyanobacteria or green algae, that can also occur in a free-living state; true marine lichens that form obligate associations between a mycobiont and a photobiont; and mycophycobioses that are obligate symbioses between systemic fungi and a dominant marine macroalga. Of the known parasitic species of marine fungi, all but two paralyze algae: one has been found on the carapace of crabs and the other on proproots of mangroves. Marine fungi have often been overlooked as participants in coastal ecological processes. However as interest has grown in the existence of a marine mycota, so has the quest for knowledge of what are they doing there and how are they doing it. Marine fungi play a role in some of the major coastal ecosystem processes. They are important in driving or controlling the mineral and energy cycling within the ecosystem as well as influencing the community composition of other organisms within the ecosystem.

**Symposium Presentation**

Cantrell, Sharon A. and Perez-Jimenez, Jose R. School of Science and Technology, Universidad del Turabo, Gurabo, PR 00778, USA. scantrel@uatgm.edu. Fungi thrive in hypersaline microbial mats. Microbial mats are a laminated consortial system, functionally integrated and self-sustained that harbor specific microbial communities. Three layers are formed during the formation of the microbial mat (surface oxic - green, a redox transition - pink and lower anoxic – black). The objective is to document the fungal community within microbial mats using molecular tools. Sampling was conducted in April (dry season) and October (wet season) of 2006. We extracted DNA with MoBio Soil DNA kit. For TRFLP, the ITS region was amplified using FAM-ITS1/ITS4. Amplicons were digested with Hae III, cloned with TopoTA, sequenced with Big Dye Terminator and analyzed in an ABI 3130. TRFLP showed higher diversity in the wet season (49 phylogenotypes vs 25) particularly in the transition layer probably due to decrease in salinity and increase in oxygen. Unique phylogenotypes were observed in the green layers due to entrapment of exogenous spores. Diversity decreased from the green to black layers. In the dry season the growth of indigenous fungi is promoted by the increase in salinity. Many isolates were dematiaceous fungi, C. sphaerospermum and H. werneckii, as well as A. pullulans, Emeriocolopsis, Preussia, Rhodosporidium, Rhizoctonia and fungal endophytes. Fungal molecular signature was detected in microbial mats across layers and seasons suggesting that fungi thrive in this hypersaline consortial. Continued on following page
and Nantucket Island (a Nature Conservancy/Massachusetts preserve). This presentation will review the highlights and challenges of these efforts and identify some of the future needs and opportunities in fungal conservation in the USA in relation to the objectives of the Rio Convention of 1992. Symposium Presentation

Catal, Mursel, Adams, Gerard C.*, Tumbalal, Pavana and Kirk, Willie, Department of Plant Pathology, Michigan State University, East Lansing, MI 48824, USA. gadams@msu.edu. Wildtype isolates of Phytophthora infestans can be heterokaryons with aneuploid, diploid and heterokaryon nuclei which may segregate among zoospores. We are investigating “super-race” strains of P. infestans that produce mitotic zoospores that vary in race, virulence and fungus sensitivity. The goal is to understand the mechanisms of sexual variation which we hypothesize involve rearrangements in chromosomes near the telomeres similar to mechanisms described for Magnaporthe grisea. The experimental approach has been to: 1) determine ploidy, 2) locate avirulence genes near telomeres, 3) separate and isolate telomere fragments, 4) clone and sequence subtelomeric DNA, and 5) correlate rearrangements in subtelomere regions with changes in phenotype. We have used laser flow cytometry for the first time to study nuclear rearrangement in P. infestans. While the majority of our isolates are diploid and none are polyploid, surprisingly, several are heterokaryons of: a) two different diploid nuclei, b) aneuploid and diploid nuclei, and c) aneuploid, diploid, and heterokaryon nuclei. For several heterokaryotic isolates, single zoospore-derived cultures frequently (e.g., 8/32) vary from the parent in nuclear type with some being aneuploid, some diploid, and others heterokaryons of aneuploid and diploid nuclei. This partially explains mitotic variation. Several subtelomeric DNA fragments of about 600 bp are cloned using the Vector system and sequences verify the presence of the telomere repeat at one end of the sequence. Poster

Chalkley, David, Stamenova, Elena and Zhou, Jim.* American Type Culture Collection (ATCC), Mycology Program, 10801 University Blvd, Manassas, VA 20110, USA, jzhou@atcc.org. Enhanced authentication facilitates the determination of the identity of a marine fungus. A fungus isolated from the roots of Rhizophora (black mangrove) in Australia was deposited as Hypoxylon sp. (ATCC® MYA-3540). It grew slowly and produced only pigmented mycelia and a reddish water-soluble pigment on various media. Hypoxylon species generally produce perithecia within stromata when grown on above-ground parts of woody plants, and not in culture. The failure of this fungus to sporulate or produce other structures in several efforts hindered its identification. The genomic ITS sequence of this organism did not change although its mycorrhizal status is generally not recognized in this regard.

Poster

Cifuentes, J.B.* and Vazquez-Estup, R. Area de Biología,Facultad de Ciencias, Universidad Nacional Autónoma de México, México D.F. 04510. jcb@hp.fciencias.unam.mx. New additions to Cystoderma in Central and Southern Mexico. While 50-40 sp. are known worldwide in the genus, in Mexico only five taxa have been recorded: Cystoderma amianthinum, C. cinnabaratum, C. fallax, C. granulatum, C. terrei. Based on the study of more than 150 collections from ENCB, FCME, IBUG and MEXU seven taxa are so far recognized in Mexico. The five previously cited species are confirmed, and two putative new species are added, one of them from temperate forest and one from tropical forest. The putative new species are described and illustrated, notes on related taxa are commented. Poster

Cline, Erica T.*, and Rosmann, Amy Y. 1University of Washington, Tacoma, WA 98402, USA, 2Systematic Botany and Mycology Lab, USDA-ARS Beltsville Agricultural Research Center, Beltsville, MD 20705, USA. ecline@u.washington.edu. Septoria malagutii sp. nov., cause of annular leaf spot of potato. The fungus causing annular leaf spot of potato, reported only from South America, poses a risk as a potentially invasive species due to its ability to flourish in the cooler temperatures typical of potato-producing regions in Europe and North America. Initially described as “Septoria lycopersici var. malagutii”, the variety is not validly published as required by the International Code of Botanical Nomenclature because no type specimen was specifically designated. Specimens of S. lycopersici var. lycopersici and S. lycopersici “var. malagutii” were examined and their rRNA ITS regions and (TEF)-1-alpha genes were sequenced. The “var. malagutii” conidia were significantly longer and narrower with the conidigenous cells significantly shorter and narrower than the “var. lycopersici” cells. Although the sequences were similar — ITS at 99.6% and TEF-1-alpha at 99.2% — the “var. lycopersici” ITS was more similar to several other Septoria species than to its “var. malagutii” counterpart, suggesting that the latter should be recognized as a new species: Septoria malagutii. Poster

Cripps, Cathy L.1* and Horak, Egon. 2Plant Sciences and Plant Pathology Dept., Montana State University, Bozeman, MT 59717, USA. 3Mikrobiologisches Institut, Universität Innsbruck, Technikerstrasse 25, 6. Stockwerk, AT-6020 Innsbruck, Austria. ccripps@montana.edu. Alpine agarics with Dryas octopetala (Rosaceae) in arctic-alpine habitats of the Rocky Mountains (USA). Dryas octopetala is a low woody mat plant common in Ca-rich arctic-alpine habitats. It has a circumpolar distribution and occurs with isolated populations in alpine areas including the middle to southern Rocky Mountains (RM) at latitude 38N. Dryas is anomalous as an ectomycorrhizal genus in the Rosaceae, a family of predominantly AM hosts. During a survey of alpine agarics in the RM, a number of saprobic and mycorrhizal macromycetes were recorded with D. octopetala. A majority of ectomycorrhizal agarics are arctic-alpine species that also associate with alpine willows (Salix spp). During several RM expeditions basidiomata were gathered belonging to seven species of Inocybe, Cortinarius (Telemenia) tenebricus, Entoloma alpicola, E. sericeum, Hebeloma alpinum, Laccaria laccata var. pallidoflora, and Russula aff. delicata. Major portions of Dryas roots host Cerococcum geophilum as well. Most agarics are considered early-colonizers which fits the pioneering status of Dryas and appear to enter opportunistic associations with this host. However, some agarics are recorded exclusively with Dryas over its large range. Examples are the highly specialized, saprobic species Marasmius epidiorys and Clitocybe dryadulica (a first record for the RM). Dryas is of current interest as a model system for global climate change although its mycorrhizal status is generally not recognized in this regard. Contributed Presentation

Crouch, Jo Anne 1*, Johnston, Peter R. 2 and Hillman, Bradley I. 3Rutgers University, New Brunswick, NJ, USA, 2Landcare Research, Auckland, NZ. jcrouch@eden.rutgers.edu. Species concepts in the genus Colletotrichum: are we finally moving towards a consistent and accurate classification after 50 years of von Arxian generalizations? In 1957, Josef von Arx ushered in the modern era of Colletotrichum systematics by decreasing the number of accepted species from >750 to just 11, signifying an end to the hopelessly outdated practice of describing a new species taxon to correspond with every novel host plant association. On the 50th anniversary of von Arx’s landmark treatise and at the genesis of the first Colletotrichum genome sequence (C. graminicola), we present a synthesis of present-day Colletotrichum systematics and the prospects for a long anticipated taxonomic clarification of this economically important genus of plant pathogens. Importantly, the recent formation of the International Subcommission on Colletotrichum and Glomerella Taxonomy, modeled on the successful Penicillium, Aspergillus and Trichoderma groups, will guide the future of this genus, providing a consistent framework for taxonomic treatments and a database of authentic isolates through the Colletotrichum.org website. As a first step towards unraveling the phylogenetic relationships within the major Colletotrichum group species, we present results of our multi-locus phylogenetic analysis of the grass-inhabiting C. graminicola group. Using 4 genes from 3 loci, 11 species Continued on following page
were identified from the C. graminicola circumscription, including 6 novel, morphologically cryptic species largely defined by novel ecological associations. **Contributed Presentation**

Crouch, Jo Anne*, Milgroom, Michael G.; and Hillman, Bradley I. 1 Rutgers University, New Brunswick, NJ, USA; 2 Cornell University, Ithaca, NY, USA. jrcrouch@eden.rutgers.edu. **How have transposable genetic elements transformed the landscape of the Cryptophyta parasitica genome?** The chestnut blight fungus, Cryptophyta parasitica, is well known for harboring a wide array of extrachromosomal genetic elements. Most of these elements are virulence-suppressing cytoplastic viruses, but mitochondrial viruses, plasmids, and transposons have also been identified. Three transposable elements have been identified in the genome of C. parasitica: the DNA transposons Crypt1 and Crypt2, and the retrotransposon Cryret1. These transposons are predicted to be active, are widely distributed in populations of C. parasitica and are also found in the genome of the sympatrically distributed species C. nitschkeri. In addition to intact copies, degenerate transposon sequences have also been identified from C. parasitica; however, no evidence for repeat-induced point (RIP) mutation has been detected, despite the close phylogenetic relationship of C. parasitica to several Sordariomycetes in which RIP has been observed. Here we present an overview of our ongoing studies of transposon distribution and divergence in the genome of C. parasitica. Using a combination of population genetic and phylogenetic tools, we are using these data to explore evolutionary changes over time in this important fungal species, and to test hypotheses derived from nuclear genes and a second class of extrachromosomal element, the hypovirus CHV1. **Contributed Presentation**

Crous, Pedro W. CBS Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, Netherlands. crous@cbs.knaw.nl. **The case for an International Code of Mycological Nomenclature**. Botanists, zoologists and bacteriologists have divergent nomenclatural codes. The International Botanical Congress at Vienna in 1905 adopted the first draft of the present Rules of Botanical Nomenclature, which were revised in 1910, by which time mycologists joined in. In 1930 the International Society for Microbiology, at its first International Congress, recognized that insofar as applicable, the International Codes of Botany and Zoology should be followed for naming microorganisms. Fungi have traditionally been associated with plants; in the botanical code several clauses were inserted that satisfied needs of mycologists. Rules of the ICBN can only be modified at International Botanical Congresses (IBC), which convene every six years. The Committee for Fungi (CF), which is appointed at the IBC, screens mycological proposals, published in Taxon, and its report is then screened by the General Committee and ratified by the IBC. However, Fungi reside in their own kingdom, and require a more flexible and forward looking code than the ICBN. Furthermore, the CF does under the present system not account for its actions to the mycological community in the IMA, nor the IUMS. I argue, therefore, that it is timely to establish a separate Code of Mycological Nomenclature that resides in a mycological association, rather than a botanical one. **Symposium Presentation**

Crous, Pedro W.*, and Groenewald, Johannes Z. CBS Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, Netherlands. crous@cbs.knaw.nl. **Mycosphaerella is polyphyletic.** Mycosphaerella is probably one of the largest genera of Ascomycetes, encompassing several thousand species, with anamorphs residing in more than 30 form genera. Previous phylogenetic studies based on the ITS locus considered the genus to be monophyletic. However, DNA sequence data derived from the 18S and 28S nrDNA genes of an extended set of taxa distinguish several clades and families in what has hitherto been considered to represent the Mycosphaerellaceae. Several important leaf spotting and extremetolerant species need to be disposed to the genus *Teratosphaeria*, for which a new family needs to be introduced. Other distinct clades represent the Schizothryptaceae, a clade consisting of *Di versocontum* spp., and some less well resolved lineages. Within the two major lineages, namely *Teratosphaeria* and *Mycosphaerella*, most anamorph genera are polyphyletic, and new anamorph concepts have to be derived to cope with dual nomenclature within the *Mycosphaerella* complex. **Contributed Presentation**

Cuomo, Christina*, Rokas, Antonis1, Alvarado, Lucia1, Grabherr, Manfred1, Penmetsa, Matthew2, Kodira, Chinnappa1, Galagan, James1, James, Timothy2, Lenox1, Michelle1, Longcore, Joyce4 and Birren, Bruce. 1 Broad Institute of MIT and Harvard, Cambridge, MA, USA, 2 Uppsala University, Uppsala, SWE, 3 Simon Fraser University, Burnaby, BC, CAN, 4 University of Maine, Orono, ME, USA. cuomo@broad.mit.edu. **The genome sequence of the amphibian pathogen *Batrachochytrium dendrobatidis*.** Batrachochytrium is a pathogen of amphibians implicated as a primary causative agent of amphibian declines. *Batrachochytrium dendrobatidis* was identified in 1998 as the cause of amphibian deaths in Australia and Central America, and, more recently, it has been implicated in global frog population declines. We sequenced the genome of strain JEL423, isolated from a sick *Phylomedusa lemur* frog from Panama. We produced a 7X whole genome shotgun assembly, which contains 23.4 Mb of sequence in 348 contigs, linked into 69 scaffolds. The *B. dendrobatidis* genome encodes for a predicted set of 8,794 proteins. We have compared the *B. dendrobatidis* proteome to those of other animal and plant pathogens to identify candidate genes involved in *B. dendrobatidis* pathogenesis. These include several gene families that appear highly expanded in *B. dendrobatidis* compared to other fungi. As no sexual stage has been observed, we have evaluated conservation of genes important for mating and meiosis in other fungi. We have also characterized a set of genes conserved only with nonfungal organisms, some of which play a role in cilia or flagella in those species. As the first representative of the chytridomycete phylum to have its genome sequenced, this genome provides a new vantage point for genomic comparisons across the fungal clade as well as with its sister animal clade. **Symposium Presentation**

Curland, Rebecca* and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. curland.rebe@students.uwlavex.us. **Preliminary mycovdiversity studies of AMF colonization in a southwestern Wisconsin prairie dominated by the invasive exotic plant *Euphorbia esula* (leafy spurge).** *Euphorbia esula* (leafy spurge) is a Eurasian invasive perennial forb that is rapidly colonizing much of North America’s prairies and ranges, typically crowding out native species and destroying rangelands used for livestock grazing. Although *E. esula*’s impact on the plant and wildlife community has been well studied, its impact on the soil microbial community is not currently well understood. Specifically, there is a lack of studies on the dynamic between *E. esula* and native arbuscular mycorrhizal fungi (AMF) populations. Likewise, there is a deficiency of research concerning community feedbacks in terms of native plant species, native AMF community composition, and *E. esula*. We designed a study in southwestern Wisconsin to assess the AMF colonization in field monocultures of *E. esula*, mixed plots of *E. esula* with native prairie plants, and plots of native plants without *E. esula*. Through the combined use of PCR, cloning, RFLP analysis and DNA sequencing, we have identified AMF species that have infected the roots of *E. esula* as well as the roots of some representative native prairie plants at our study site. Our ultimate research goal is to formulate an accurate depiction of the AMF community as it relates to invasion by *E. esula*. **Poster**

Davey, Marie L.*, Tsuenda, Akiko and Currah, Randolph S. Department of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada. mdavey@ualberta.ca. **Morphology and development of *Papulaspora sepedonioides* Preuss.** *Papulaspora* spores are large multicellular conidia with several, thick walled central cells enclosed within a sheath of smaller thin-walled cells. This morphology facilitates survival of adverse environmental conditions. Some aspects of the developmental sequence of these structures have been observed, but the differentiation of the two cell types has not been addressed. An isolate of *Papulaspora sepedonioides*, recovered from spruce cones in Alber-
ta, provided sporulating material that allowed us to revisit development using light, and scanning and transmission electron microscopy. Spiral primordia are formed from short lateral branches on vegetative hyphae. Branching of primordial cells produces ensheathing hyphae, creating a knot-like papulospore initial. Meristematic division of the original primordial cells produces 2-8 central cells. The surrounding ensheathing hyphae become septate and pseudoparenchymatous as the papulospore matures. As mature size is reached, the central cells’ walls become thickened and melanized. Autolysis of the sheathing cells produces a mature papulospore consisting of an outer sheath of thin walled, deflated hyaline cells surrounding a core of thick walled, melanized central cells containing large numbers of lipid globules. We suspect sheath cells both provide additional nutrients to the central cells and provide additional germination potential early in papulospore development. Both central cells and living sheath cells germinated to produce new primordia and germ tubes, suggesting microcytic conidiogenesis occurs in this species. **Contributed Presentation**

Dean, R. A. Center for Integrated Fungal Research, Dept. Plant Pathology, North Carolina State University, Raleigh, NC 27606, USA. Ralph_Dean@ncsu.edu. An “omics” interrogation of fungal pathogenicity. Magnaporthe and rice as well as the genome sequences for several other pathogenic and non-pathogenic filamentous fungi has provided a wealth of new information regarding the raw components of the pathogen’s offensive arsenal and host’s defenses. In my presentation I will discuss some of the novel discoveries that have only come to light as a result of having access to the genome sequences, such as novel classes of secreted proteins, surface receptors and large suites of enzymes involved in secondary metabolism and what role they play a role in the disease process. I will highlight recent results from functional analyses including transcription profiling and high throughput gene knockout experiments. I will close with new strategies, including proteomic and comparative evolutionary approaches we are undertaking. Efforts are currently focused on interrogation of novel non-coding transcripts, transcriptional networks and protein-protein interactions to define the circuitry regulating host-pathogen interactions. In addition, I will discuss new tools and resources we are developing to examine the role of gene duplication in pathogenesis through large-scale comparative analyses of sequenced fungal genomes. **Symposium Presentation**

Degagne, Rebecca S.1, Henkel, Terry W.2* and Steinberg, S.J.11 Department of Environmental and Natural Resources Sciences, Humboldt State University, Arcata, CA 95521, USA. 1-Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA. twhs5@humboldt.edu. Examining the distribution of ectomycorrhizal *Dicymbe* forests in Guyana using satellite imagery and field surveys. Ectomycorrhizal (EM) canopy trees in the genus *Dicymbe* (Caesalpinioideae) form monodominant forests in the Pakaraima Mountains of western Guyana. *Dicymbe* forests, which occur locally in the Upper Potato River Basin as patches within an anectotrophic forest matrix, function as habitat islands for a diverse assemblage of putatively endemic EM fungi. Ground-based studies have not been extensive enough to determine the regional extent of *Dicymbe* forests. Distribution information is critical to allow broader sampling of *Dicymbe* forests and their EM fungal constituents and ultimately inform conservation plans for these unique habitats. The rugged, remote nature of the Upper Potato River Basin study site and the spatially discrete occurrence of *Dicymbe stands suggest that satellite technology may be an ideal tool for examining the extent of these relatively unknown tropical forest systems. The purpose of this project was to examine the distribution of *Dicymbe* forests using remote sensing and GIS technology. Field data and satellite imagery were used to identify and map the location of monodominant *Dicymbe corymbosa* and *Dicymbe altsonii* in the central Pakaraima Mountains. Accuracy assessment on the ground revealed that maps created from the image classification process are accurate at > 70% level. These results suggest that Landsat image classification may be successful on regional and extra-regional scales in identifying tropical forests dominated by EM trees. **Poster**

Dentinger, Bryn T. M.1*, McLaughlin, David J.1 and Henkel, Terry W.2 Dept. of Plant Biology, University of Minnesota, St. Paul, MN 55108, USA. 1Dept. of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA, dem0015@umn.edu. Gaping into gaps: evolution of porcini mushrooms. Phylogenetic studies in the Boletineae, which contains a substantial proportion of the described species of boletes, have suffered from poor backbone resolution resulting in phylogenetic combs that render circumscription of monophyletic groups tenuous. Most of these studies have relied primarily upon rDNA sequences and none have attempted to incorporate length-variation as phylogenetic data. One of the key questions that remains unsolved is: Are porcini mushrooms monophyletic? The answer to this question holds considerable taxonomic bearing because the porcini group contains the type species, *Boletus edulis*, on which the taxonomy of the order Boletales is based. In this study, we compared the phylogenetic utility of length-variable regions of the nuclear LSU DNA and portions of RPBI introns, in combination with the unambiguously aligned regions of these genes, to the unambiguously aligned regions alone. We used a small, broad sampling of taxa in the Boletineae, including representatives of the major groups of porcini. We compared the results of employing alignment-independent methods (implemented in POY) and recoding schemes (INAASE) to those obtained from standard phylogenetic methods. Our results indicate that while the backbone of the Boletineae remains poorly resolved, the hypothesis that porcini are monophyletic cannot be rejected. **Contributed Presentation**

DeSantis, Todd Z., Torok, Tamás, Brodie, Eoin L., Piceno, Yvette M. and Andersen, Gary L.2 Dept. of Ecology, Lawrence Berkeley National Laboratory, Berkeley, California 94720, USA, glanderson@lbl.gov. Characterization of microbial diversity with high-density microarrays. The applicability of biomarkers, such as the ribosomal small subunit (SSU), internal transcribed spacer region (ITS) and the ribosomal large subunit (LSU) for microbial classification are now well accepted. One of the main reasons that the ribosomal operon is the most popular region for molecular phylogeny is that conserved segments can serve as priming sites to create heterogeneous PCR products from environmental samples. Cloning-and-sequencing the PCR products has been the general method of sampling the DNA types but does not scale well for large studies. Instead, hybridizing PCR products to a universal microarray allows a more rapid evaluation. We have developed a high-density microarray system to accurately measure the key prokaryotic components in air, water, and soil environments. Unique regions of DNA within gene sequences of 16S small subunit of bacterial and archael ribosomes are used to identify specific organisms. A minimum of 11 oligonucleotide probes (25-mers) are used in combination to identify, in parallel, any of over 9,000 distinctive species or taxa on a 500,000 probe, high-density microarray. The combinatorial approach of multiple probes has clear advantages over a single probe for the identification of a target sequence. Broad-range bacterial and archael 16S primers that target conserved areas at the 5’ and 3’ ends of the 16S rRNA gene are used to amplify 1400 to 1500-bp fragments for analysis. Building on the success of this phylogenetic microarray, we are developing a prototype high-density microarray to identify eukaryotic microbial community structure. As a first step, a fungal sequence repository was developed, similar to our greengenes site (http://greengenes.lbl.gov) bacterial repository to maintain a comprehensive set of aligned, chimera-screened 18S, ITS and the D1/D2 regions of the 28S rRNA gene sequences. From these alignments, 25-mers potential targets are extracted and filtered based on their physical properties (GC content, Tm, folding potential, self-dimerization potential, synthesis efficiency criteria) and their cross-hybridization potential. Each target gene is progressively clustered into taxa with its nearest neighbors until a set of approved probes are found that target nearly all members of the taxa and do not exhibit cross-hybridization potential. For taxa where the ribosomal operon as a whole is

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distinctive but no probe-level sequence is identified that is not shared with other taxa, a set of probes are designed to a combination of regions on the operon that taken together do not exist in any other taxa. The selected probes will each be paired with a control probe containing a central mismatch to reduce the effects of non-specific hybridization and synthesized on a NimbleGen platform. This microarray could greatly advance our knowledge of the role fungi play in important matters such as bioremediation, carbon sequestration and human diseases in addition to providing a monitoring tool to assess the health of an ecosystem.

**Symposium Presentation**

Dewsbury, Damon R.¹ and Moncalvo, Jean-Marc.² Department of Ecology and Evolutionary Biology, University of Toronto, ON M5S 3B2, Canada. ¹Department of Natural History, Royal Ontario Museum, ON M5S 2C6, Canada. damondewsy@yahoo.com. A molecular phylogeny of Eastern North American morels (genus Morchella) focusing on the “Carolinian” forest zone. Members of the genus Morchella are easily identified in the field but species boundaries are problematic given the limited morpho-characters. DNA sequences of the ITS, LSU, RP2B and EF-1 alpha regions are being obtained from many specimens sampled from four Maryland national parks and southern Ontario. Most of these specimens were collected in the “Carolinian” forest zone, which is characterized by a particular suite of flora dominated by Tuliptrees (Liriodendron tulipifera). The Tuliptree belongs to the Magnoliaceae and thus is quite distinct from other dominant tree species in Eastern North America. It has been noted ancetdally that there is a correlation between these trees and morel fruitings. Sequence data will be used to elucidate a molecular phylogeny to answer several questions. Of the four morphotypes that can be distinguished in the field, do any mask multiple phylogenetic species? Do Southern Ontario morels from the Carolinian zone cluster with Maryland collections, following the tree host/forest ecotype, or with geographically closer taxa from forests with more northern floral elements such as maple (Acer genus) and pine (Pinus genus)? Lastly, this study will begin to address whether there is a need for a taxonomic revision of the genus in eastern North America to provide formal names for morels that are phylogenetically distinct from their European counterparts. 

**Poster**

Dianese, José Carmine* and Pereira-Carvalho, Rita C. Departamento de Fitopatologia, Universidade de Brasília, 70910-900 Brasília, District Federal, Brazil. jcarmine@unb.br. **Fungal conservation with the Rio Convention: the experience of Brazil.** Mycology in Brazil suffered a long period of stagnation mainly after the deaths of Augusto Chaves Batista, Ahmés Pinto Viegas in the 1960s, and more recently the loss of Alcides Teixeira. However, coinciding with the signature of “The Convention on Biodiversity”, a few people woke up for the need of fungal conservation starting with a systematic description of our mycodyversity. Thus major projects involving the study of savanna (cerrado) microfungi, fungi of the “caatinga” (semi-arid Northeast region), survey and description of endomycorrhizal fungi, microfungi of interest to biocontrol of insects and plant diseases, and description of important fractions of the Boletales and other macrofungi, were all initiated after 1992 in Brazil. These efforts, in some instances based upon cooperation with American and European mycologists, although conducted by isolated groups deserve consideration and an effort to present an overview of the mycological progress in our Country in the last 15 years. It must be emphasized that in Brazil the preservation of fungi “ex-situ” in culture collections is clearly left aside with money destined to collections being funneled to collateral activities even in institutions whose primary mission is exactly that of preserving germplasm. With the establishment of the “Centro de Biotecnologia da Amazônia” (Amazonian Biotechnology Center) in Manaus by the Federal Government it is expected that the first step will be the organization of a unique mycological collection, and the same must become real for the cerrado where Embrapa is giving the first steps in the same direction. On the other hand several frustrated experiences led to difficulties in motivating the financing agents to invest in culture collections, treasure still unexplored. Data will be gathered and presented to permit an evaluation of the mycological progress in Brazil post-Rio 92. **Symposium Presentation**

Dianese, J. C.* and Pereira-Carvalho, R.C. Departamento de Fitopatologia, Universidade de Brasília, 70910-900 Brasília, Distrito Federal, Brazil. jcarmine@unb.br. **A new hyphomycete genus based on Alternaria qualearae.** A re-examination suggested by Dr. Emmony Simmons (personal communication) of the type material of Alternaria qualearae Dormeno-Silva & Dianese, deposited in Herbarium UB, led to the conclusion that the specimen does not really belong in an Alternaria species but indeed belongs in a new genus to be published soon. The specimen can not be included in Alternaria because of the presence of a stroma produced by the fungus on the abaxial face of the host leaves, and the fact that a careful examination of the conidial base and the conidigenous cells revealed scars but not the characteristic tretic condition needed to characterize an alternarian species. Finally, a close observation of the conidigenous cells revealed their amelodic condition. The specimen could not be fitted in any of the known genera of dematiaceous hyphomycetes. **Poster**

Didukh, Maryna* and Moncalvo, Jean-Marc. Department of Ecology and Evolutionary Biology, University of Toronto, and Department of Natural History, Royal Ontario Museum, Toronto, Canada. maryna.didukh@gmail.com. **DNA barcoding Pleurotus species (Agaricales, Boletales).** DNA barcoding is an approach designed to increase the efficiency of recovering and documenting species across different kingdoms of life. In numerous groups of animals, a short, ca. 600 bp segment of the cytochrome oxidase 1 gene (CO1) was shown to very be effective for that purpose, and this gene has been proposed as a possible universal marker. However, the utility of CO1 as a species marker in fungi still remains to be tested. Primary disputes over CO1 involve fundamental issues like accuracy (intraspecific variation and interspecific divergence) and the proposed use of single-gene thresholds as an initial step in species discovery. Prior to the barcoding initiative, information on the organization and variation of CO1 in fungi was scarce and restricted mostly to model organisms in the Ascomycota. In this study, over 40 strains of seven species of the genus Pleurotus as well as representatives of other agaricoid taxa were used to assess variation in the target CO1 region and to compare its performance with more widely used nuclear markers: nuclear ribosomal DNA internal transcribed spacer (nrDNA ITS) region and elongation factor-1 alpha (EF-1 alpha). Pleurotus strains were further used to compare cDNA vs. genomic sequences for CO1 and EF-1 alpha in order to retrieve information on nuclear gene organization. **Contributed Presentation**

DiMarco, Michael J. and Silliker, Margaret E.* Department of Biology, DePaul University, 2325 N. Clifton Avenue, Chicago, IL 60614, USA. msillike@depaul.edu. **RNA editing of Didymium iridis atp8 and nad6L mitochondrial genes.** Mitochondrial genomics has provided evolutionary insights, however, in some organisms, the mitochondrial DNA genes appear to be scrambled; functional genes arise after the mRNA undergoes an editing process. In the Myxogastria (plasmodial slime molds) editing is primarily by cytosine-base insertions that alter the transcript to remove stop codons. We characterized editing events in two mitochondrial genes, atp8 and nad6L of Didymium iridis. Total RNA was isolated, reverse transcribed, cloned, sequenced, and aligned with the genomic DNA sequences to reveal the editing sites. Nad6L was edited evenly throughout by C-insertions, while atp8 was predominantly edited at the beginning of the transcript. Editing sites were downstream of a purine-pyrimidine dinucleotide 67% of the time. Given the base composition of the genes, A-T dinucleotides are predicted to occur in 16% of the sequence, however, this dinucleotide pair was found immediately upstream at 57% of all the upstream pur-pyr editing sites. The C-base insertions were preferentially inserted in the 3rd position (wobble position) of the codon to create a correct reading frame. Editing sites were conserved 63% and 85% in atp8 and nad6L, respectively, between D. iridis and Physarum polycephalum, a related Myxogastria. In both organisms a similar mechanism of RNA editing appears to be responsible for maintaining protein function. **Poster**

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Doughan, Greg W.*, Doughan, LeAnn I. and Huryn, Karyn. Department of Plant Pathology and Microbiology, University of California, Riverside, CA 92521, USA. g douhan@ucr.edu.

Species diversity of Hypomyces associated with boletes in California. Mycoparasitic Hypomyces (anamorph = Scedonidium) species are commonly observed parasitizing members of the Boletales. In California, only two species have been recognized; the generalist pathogen H. chrysospermus which infects many genera within the Boletales and the specialist H. microspermus which infects hosts within the Xerocomus chrysenteron complex. We have recently discovered that two pathogenic species occur in both pathogens with two phylogenetic species occurring in each group. However, this was based on a limited sample size and we hypothesized that even more unrecognized diversity occurs in California. Therefore, our objective was to test this by broadening our collections. From Jan 2003 to February 2006, parasitized mushrooms were collected throughout California from Humboldt to Riverside Counties and identified by ITS sequencing. European isolates were also obtained for comparison purposes. Over 120 CA isolates were recovered and we identified two previously unrecognized species occurring in California; H. laevigatum and H. ampulliformis. Contrary to our hypothesis, we only found the four phylogenetic species as were identified in our previous study. All ‘species’ were distributed throughout the sampling range in CA and these same species were also found occurring throughout Europe. However, bolete hosts are not shared between Europe and CA suggesting that the hosts have speciated faster than the parasites. Contributed Presentation

Dourn, Greg W.*, Smith, Matthew E.2, Huryn, Karyn L.1, Westbrook, Andrea3 and Fisher, Alison3. Department of Plant Pathology, University of California, Riverside, CA 92521, USA.

Our objective was to test this by broadening our collections. From Jan 2003 to February 2006, parasitized mushrooms were collected throughout California from Humboldt to Riverside Counties and identified by ITS sequencing. European isolates were also obtained for comparison purposes. Over 120 CA isolates were recovered and we identified two previously unrecognized species occurring in California; H. laevigatum and H. ampulliformis. Contrary to our hypothesis, we only found the four phylogenetic species as were identified in our previous study. All ‘species’ were distributed throughout the sampling range in CA and these same species were also found occurring throughout Europe. However, bolete hosts are not shared between Europe and CA suggesting that the hosts have speciated faster than the parasites. Contributed Presentation

Dunek, Craig* and Volk, Tom. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. dunek.cra@students.uwlax.edu, volk.thom@uwlax.edu, TomVolk-Fungi.net. The incidence of antifungal drugs from fungi. The clinical significance of fungal pathogens has increased dramatically in the past 30 years. Conditions such as aspergillosis, sporotrichosis, blastomycosis, candidiasis, and cryptococcosis are occurring more often and with greater virulence, especially in those who are immunocompromised. Treatment of fungal pathogens with antifungal drugs is normally lengthy and is associated with a plethora of side effects, such as headaches, vomiting, as well as more serious complications such as hepatitis and renal failure. These side effects are not only devastating to the patient but also have a huge economic impact, costing millions every year for increased hospital stays. Once discovered, new antifungal drug classes could reduce side effects as well as lower overall costs in antifungal treatments. However, discovery of antifungal drugs is very difficult, because both humans and fungi have eukaryotic cells. Humans and fungi are so similar that antifungal drugs tend to also be generally anti-eukaryotic, killing both fungal and human cells, thus causing side effects. “Perfect” antibiotics are selective for the infectious agent and at the same time are innocuous to the host. This research looks for new antifungal compounds from fungal fruiting bodies. Extractions from fungal fruiting bodies were tested against six strains of pathogenic fungi: Aspergillus fumigatus, Candida albicans, Cryptococcus neoformans, Ennomia crescents, Sporothrix schenckii, and Tri- chophytus species. The comprehensive screenings of more than two-hundred species of fungi have lead to some possible candidates for new antifungal drugs. These agents once characterized may benefit patients and have a significant economic impact. Contributed Presentation

Edward, Sally M.8 and Spiegel, Frederick W. Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. smedwar@uark.edu. Impacts of land use changes on corticolous slime molds. The development of forest, pastoral and riparian ecosystems has the potential to significantly affect the biodiversity of a given area. Previous research has shown the effects of land use shifts on macro-organism diversity. However, such work has not fully addressed the possible impacts on soil microorganisms. This study will examine the effects of different land uses on the dictyostelid cellular slime molds. Currently recognized as a group within the taxon Eumycetozoa, the dictyostelids are a cosmopolitan group of eukaryotic microorganisms. These soil and humus-dwelling protists spend much of their life cycle as bacteriotrophic amoebae. Upon depletion of their microhabitat, the amoebae aggregate into a multicellular slug, which can then develop into a fruiting body. Collections of soil and dead vegetation were made from 10 sets of paired sites (with one site per pair disturbed by construction) throughout Arkansas. Five samples were collected from each site. The soil samples were diluted according to the Cavender method and grown on WMY agar with E. coli at 20-26 C. Plates were examined for dictyostelid growth, using a Nikon SMZ1500 dissecting microscope, each day on days 3-14. Species richness and diversity were compared for disturbed versus undisturbed sites. The potential of soil microorganisms as indicators of environmental change is also discussed. Poster

Everhart, Sydney E.*, Keller, Harold W. and Ely, Joseph S. Department of Biology, University of Central Missouri, Warrensburg, MO 64093, USA. everhart@ucmo.edu. Corticulous myxomycetes (true slime molds): species assemblages and distribution in the tree canopy of selected forests of Kentucky and Tennessee. Corticulous myxomycetes complete their life cycle on the bark of living trees and vines. Trees with grapevines (Vitaceae) were selected to compare the occurrence and distribution of species in the tree canopy. The double- rope climbing technique was used to access the canopy and sample bark at 3, 6, 9, 12, and 15 meters. Tree species sampled were Acer saccharum, Fraxinus americana, Liquidambar styraciflua, Liriodendron tulipifera, Platanus occidentalis, and Tsuga canadensis. Bark from five trees of each species and their corresponding grapevines, Vitis aestivalis or V. vulpina, was used to prepare moist chamber cultures and induce fruiting of myxomycetes. A total of 580 moist chamber cultures yielded 44 myxomycete species, representing 19 genera, with an additional 2 taxa identified only to genus. Common species found were Echinostelium minutum, Arcyria cinerea, and Perichaena chrysosperma. Variety in occurrence and assemblages of myxomycete species is associated with tree species and bark pH, indicating a few species are restricted to bark of a certain pH, while many species occur over a wide range. Financially supported by Willard North Graduate Research Award, NSF Award DEB-0343447, National Geographic Research and Exploration Award-7272-02, and Discover Life in America Awards 2001-26 and 2002-17. Contributed Presentation

Continued on following page
Everhart, Sydney E.*, Keller, Harold W. and Ely, Joseph S. Department of Biology, University of Central Missouri, Warrensburg, MO 64093, USA. everhart@ucmo.edu. Quantitative analysis of bark characteristics and epiphyte cover on distribution patterns of corticolous myxomycetes (true slime molds) in the tree canopy. Corticolous myxomycetes form plasmodia and fruiting bodies on the bark of living trees and vines. Bark was sampled from 30 trees and 30 grapevines along a vertical transect up to 15 m, to examine the relationship between bark characteristics (pH, water absorption, and thickness), epiphyte cover, geographic location, and myxomycete species. Moist chamber culture technique was used to induce myxomycete fruiting and bark pH was measured after 24 hours using an Orion 610 pH flat probe. Plates were scanned for presence of myxomycetes after 4, 16, and 32 days, and percent cover data was collected in a stratified random design on day 32. Different species of trees and grapevines had significantly different bark characteristics, however, the only tree which had a significant difference in the vertical variation of any bark characteristic was P. occidentalis. Accordingly, P. occidentalis also had a significant decrease in richness of myxomycete species with increasing height in the canopy. Non-metric multi-dimensional scaling and multi-response permutation procedure were performed; distinct species assemblages correspond to each tree and grapevine species and were differentiated by pH, DBH, and elevation. Financially supported by NSF Award DEB-0343447, National Geographic Research and Exploration Award-7272-02, and Discover Life in America Awards 2001-26 and 2002-17. Poster

Exeter, Ronald L.1 and Norvell, Lorelei L.2,3 USDI Bureau of Land Management, 1717 Fabry Road SE, Salem, OR 97306-1720, USA, 2Pacific Northwest Mycology Service, Portland, OR 97229-1309. USA. IiNorvell@pww-ms.com. Ramarias of Pacific Northwest. The colorful coral fungi are among the loveliest denizens of the vast temperate rainforests of western North America. The US government’s Northwest Forest Plan targeted 28 rare or uncommon taxa of Ramaria (Basidiomycota, Gomphales) as worthy of survey and management within the range of the endangered northern spotted owl. Examination of both type and recent collections and reference to classic papers by Marr & Stuntz, Petersen, and others led to the development of a single key identifying all species in the region and the discovery of a new species, Ramaria rasulisporoides. A recent 157-page USDI-BLM publication, Ramaria of the Pacific Northwestern United States (Exeter, Norvell & Cazares, 2006), treats all four subgenera: Lentoramaria, Echinoramaria, Ramaria, and Laeticolora. The lavishly illustrated monograph contains 193 color photos and covers all 90 of the region’s known species and varieties. Each one- to two-page taxonomic treat- ment presents synonyms, field descriptions, summary technical de- scriptions from hard-to-find publications, ecological and distributional data, diagnostic characters, additional comments, and references. Known phylogenetic relationships, taxonomic characters, tables, a new glossary, complete bibliography, and previously published microscop- ic keys are also provided. Poster

Fedorova, Natalie1, McDonagh, Andrew2, Yu, Yan1, Armstrong-James, Darius2, Haynes, Ken2, Bignell, Elaine2 and Nierman, William C.1,3 1J Craig Venter Institute, Rockville, MD, USA, 2Department of Molecular Microbiology and Infection, Imperial College London, London SW7 2AZ, UK. wnierman@jci.org. Transcriptome analysis of Aspergillus fumigatus during early stage mammalian lung infection. Aspergillus fumigatus is a particularly virulent fungus whose spores infect human hosts having compromised immunity. Its success as a pathogen is unique among close phylogenetic relatives and thought to depend upon concerted control over multiple functions including nu- trient acquisition, metabolic plasticity and immunotoxin production. A. fumigatus virulence, and that of other opportunistic fungal pathogens, has escaped definition at the molecular level promoting scepticism re- garding the existence of ‘true’ virulence factors in such species. Newly published genomes for several fungal pathogens and emerging evi- dence for epigenetic control of fungal virulence mechanisms support the view that hierarchical co-ordination of multiple processes may un- derpin fungal pathogenicity. Comparative genomics analysis has raised suspicions that niche adaptation genes may reside in lineage-specific regions of the Aspergillus genomes. To assess transcriptional co-ordi- nation during host niche-adaptation we have characterised A. fumigatus gene expression during initiation of mammalian infection, using labo- ratory cultured germings as a comparator. We show that during the early phase of infection A. fumigatus co-ordinately regulates expression of gene clusters encoding biosynthesis of gliotoxin, iron siderophore, and five other putative secondary metabolites. In addition our analyses identify multiple clusters of physically linked, co-regulated genes, which are likely to share a concerted function, which cannot be pre- dicted from genomic analyses alone. The analysis demonstrated a genome-wide transcriptional reprogramming favoring subtelomeric and lineage-specific genes. Taken together these observations reveal a pattern of co-ordinated gene regulation thus far undiscoversed from in vitro analyses, and provides the first transcriptional snapshot of a fun- gal genome during initiation of mammalian infection. Symposium Presentation

Ferreira, Renato B.1, Inácio, Carlos A.2 and Dianese, José C.2 Centro Universitário de Brasília, UNICEUB, Asa Norte, Brasília, DF, Brazil, 2Departamento de Fitopatologia, Universidade de Brasília, Brasília, DF, Brazil. jcarmine@unb.br. New Ascomycota on petioles of Mauritia flexuosa (Palmae) from Central Brazil. Mauritia flexuosa (Bu- rití) is a palm tree found endemically on swampy areas (“veredas”) of the cerrado. In 2006 leaf samples were collected from the State of Goiás in Central Brazil. Two new Ascomycota were detected on leaf petioles and are now described, as follows: 1. a new xylariaceous as- comycete, forming lesions that are darkened and irregular; ascomata 50 – 213 × 105 - 300 µm, black, partially erumpent, irregular in shape with a convoluted internal lining, and 26 – 13 µm thick black outer wall; par- raphyses: 1 µm diam., hyaline, septate, branched; ascoss: 30 - 50 × 7 - 15 µm, cylindrical, uniseriate, 7–8 ascospores, J+; ascospores: 11 – 17 × 5 - 10 µm, ellipsoid, guttulate when young becoming light-brown to brown, uniseriate, asceptate, with mucilaginous sheath and a clear germ slit. 2. a new Saccariaceae (Doidheomyctecetae) forming colonies 8- 21 mm diam., dark, circular, confluent; greyish, containing dark asco- mata; ascomata 75 – 103 × 225 - 475 µm, superficial, black, circular, discoid, non-ostiolate; upper wall 13 – 24 mm; paraphyses: 40 – 60 × 1 – 2 µm diam., hyaline, filiform, simple; ascos: 20 – 45 × 16 - 34 µm, glo- boso to ovoid, bitunicate; ascospores: 17 – 30 × 8 - 14 µm, hyaline, el- lipsidial, 6 - 8 transversal septa and rarely longitudinal septa, covered by a mucilaginous sheath. Poster

Ferrer, A.1,a, Sarmiento, C.2 and Shearer, C.A.1 1Plant Biology, University of Illinois, 505 S. Goodwin Ave., Urbana, IL 61801, USA, 2Universidad de Los Andes, Bogota, Colombia. aferrer@life.uiuc.edu. Distribution of ascomycete diversity in Costa Rican freshwater habitats. Diversity patterns of freshwater ascomycetes in the tropics are undescribed. As part of an ongoing study of the distribution of freshwater ascomycetes along latitudinal gradients, we undertook a comparative survey of three lowland sites and one lower montane site in Costa Rica. Submerged wood was collected from streams at La Selva, Barra del Colorado and Las Cruces National Park and from lentic habitats in Caño Negro. At each site, 30 samples of submerged, partially decomposed woody debris were collected. Wood samples were incubated in moist chambers and examined periodically for fruit- ing body production. Species richness was higher than that reported from temperate areas and included new species discovered at each site. No one genus or family dominated any site. We recorded very few species that were shared between sites indicating high alpha and beta diversity in this fungal community. Numerous species collected from Costa Rica also have been reported from similar habitats in the pale- otopics, suggesting a global distribution for some tropical freshwater species. Our results highlight the importance of sampling multiple sites to capture freshwater fungal diversity, and indicate that many freshwater taxa remain to be discovered. Poster

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Fungal diversity measured across two decay classes of spruce wood in disturbed boreal forest sites. Woody debris is a key component for maintaining biological diversity in forest ecosystems. Fungi play essential roles in these systems by releasing nutrients from dead wood, directly providing food and indirectly providing shelter for many organisms. Knowledge of fungi associated with woody debris is therefore an important step for management and conservation of forest resources. To investigate fungal diversity in decaying wood, samples were collected from 60 spruce logs in 3 logged and 3 unlogged sites in a boreal forest in northern Ontario. Half of these logs were in an early stage of decay (decay class 1) and half in a late stage of decay (decay class 4). Three wood cores were collected from each log and pooled together. Fungal DNA was extracted from these samples, and the nLSU-rDNA gene was PCR amplified, cloned, and sequenced. These sequences were used to measure fungal diversity in two ways: (1) sequence or operational taxonomic unit (OTU) diversity and (2) phylogenetic diversity. Fungal fruiting bodies were collected from the same logs as a third measure of fungal diversity. We compare fungal diversity among the different sites and logs by using phylogenetic, fruiting body and OTU methods with the hypothesis that each of these measures will yield different results. Preliminary results suggest that fungal diversity measured by phylogenetic diversity differs from fruiting body and OTU diversity measurements. Poster

Fitzsimons, Michael S.¹, Miller, R. Michael² and Jastrow, Julie D.²
¹University of Chicago, Department of Ecology & Evolution, Chicago, IL 60637, USA, ²Argonne National Laboratory, Argonne, IL 60439, USA. Niche axes and scale of study in arbuscular mycorrhizal fungi. Research into microbial niches has only recently begun receiving the attention that such an important topic and diverse group of organisms deserve. In this study, we investigate the niche of a group of mutualistic fungi, the Arbuscular Mycorrhizal Fungi (AMF). Our goal was to determine the relative importance of host plants, soil chemical parameters, and time since disturbance in determining AMF community composition. We found that all three were important, but that the appropriate scale of inquiry is required to identify all three interactions. Time since disturbance was significant at both the point and plot level scales, but soil characters were only significant at the point scale and plant community change only significant at the plot scale. When plants and soil changes are looked at in greater detail (i.e. at the species and individual soil parameter) we found that individual plants do not alter the community enough to produce a signal, but that pH and nitrate levels were clear indicators of AMF community change. The significance of this study lies in identifying time since disturbance as a determinant of AMF community change, pH and nitrate as soil drivers of the community, and that to uncover interactions between groups of organisms, especially those with radically different dispersal abilities, point level comparisons may not be an appropriate scale of study. Poster

Fulgenzi, T.D.¹, Henkel, T.W.¹ and Halling, R.E.² ¹Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA, ²Institute of Systematic Botany, The New York Botanical Garden, Bronx, NY 10024, USA. Boletaceae of Guyana. In the Pakaraima Mountains of Guyana, large expanses of primary mixed rainforest of arbuscular mycorrhizal (AM) tree species are juxtaposed with extensive ectomycorrhizal (EM) monodominant Dicymbe corymbosa (Caesalpinioideae) forests. One component of current research on the Dicymbe system in Guyana is a multi-year investigation of macrofungal diversity in the D. corymbosa stands, and the surrounding mixed forest and comparison of EM and saprotrophic fungal guilds and their ecological significance in these highly contrasting forest types. This work has uncovered >150 species or morphospecies of EM fungi associated with Dicymbe, nearly doubling the number of EM fungi known from the lowland Neotropics. Ongoing systematic work on the EM fungi indicates that >70 % are new taxa at the specific or generic level. Boletaceae are especially rich at the Guyana site, numbering at least 20 morphospecies in numerous genera (Tylopilus, Xerocomus, Austroboletus, Pulveroboletus, Boletellus, Fistulinella, and Phylloporus) from a single collecting area in the Upper Potaro River Basin. Taxonomic novelties and their impact on generic concepts in several bolete genera will be discussed, as well as novel ecological roles and biogeographical implications. Contributed Presentation

Garcia-Sandoval, Ricardo¹ and Hibbett, David S. Clark University, Biology Department, Lasry Biosciences Center, 950 Main Street, Worcester, Massachusetts 01610-1477, USA. rggciasandoval@clarku.edu. Molecular phylogenetics of the Gloeophyllales, insights from ribosomal and protein-coding genes. The Gloeophyllales is a monophyletic group that includes representatives of the genera Gloeophyllum, Neolentinus, Veluticeps, and Helicoeye. Species from Donkioporia and Boreostereum have also been included based on analysis of the nuc-ssu rDNA region alone. In spite of its small size, this clade exhibits a wide diversity of morphological and physiological characters, including species with pileate-sessile, pileate-stipitate and resupinate basidiomata, lamellate or poroid hymenophores, brown or white rot wood-decay capabilities, and bipolar or tetrapolar mating systems. Previous studies using mitochondrial and nuclear rDNA genes suggest that this group is closely related to the Thelephorales, but without strong support. Our current research seeks to assess the phylogenetic placement and composition of the Gloeophyllales. For this purpose, we are extending the taxonomic sampling relative to prior studies, and we are gathering data from nuclear rDNA (ssu and lsu) and protein-coding genes (rpb2 and tef1). Results will be discussed with particular regard to evolution of morphological and physiological characters. Poster

Gayà, Ester¹, Llimona, Xavier², Navarro-Rosines, Pere² and Lutzoni, François.¹ ¹Department of Biology, Duke University, Durham, NC 27708-0338, USA, ²Departamento de Biologia Vegetal (Unitat de Botànica), Facultat de Biologia, Universitat de Barcelona, Av. Diagonal 645, 08028 Barcelona, Spain. eb6@duke.edu. The lobate Caloplaca: phylogeny and taxonomy of a problematic species complex within the Teloschistaceae (Ascomycota). Caloplaca is a widespread and common lichen-forming genus, found mostly in mesic and xeric habitats. Despite its conspicuous habit, it is among the least known taxonomically and the poor understanding of its species has often led to its being overlooked. The delimitation of this genus has always been problematic due mostly to the strong similarity between lobate species of Caloplaca and species of other genera within the Teloschistaceae. Among all lobate Caloplaca species, the C. saxicola group has been the most controversial taxonomically. To provide a comprehensive and more natural classification of this group of lobate Caloplaca, we first tested the hypothesis that these species form a monophyletic group within a broad taxon sampling of the Teloschistaceae, including taxa representing all species groups of Caloplaca. The results from phylogenetic analyses carried out on sequences of the nuclear rDNA internal transcribed spacer region (ITS) are reported. These analyses supported the polyphyly of Caloplaca and allied genera Fulgensia, Teloschistes and Xanthoria. Based also on an ITS phylogeny, together with morphological and anatomical characters, some species in the C. saxicola group thus far accepted were associated with high support values. The same was true for potentially new cryptic species. Contributed Presentation

Gibson, Cara M. Dept. of Entomology, University of Arizona, 410 Forbes Building, PO Box 210036, Tucson, AZ 85721-0036, USA. cgibson@ag.arizona.edu. Microbial community in a wasp parasitoid and its cockroach host. Currently, there is tremendous interest in understanding both the diversity of insect-associated microbes and the effects that they exert on their hosts. Despite frequent and intimate associations with insects, fungi have received comparatively little attention. Often, insects may be infected with multiple symbionts, including simultaneous infection with both fungal and bacterial symbionts. The vertically transmitted fungal and bacterial symbiont...
communities of a particular parasitoid wasp, Comperia mercerti (Hymenoptera: Encyrtidae), and the cockroach it parasitizes, Supella longipalpa (Blattaria: Blattellidae), are examined using both molecular- and culture-based methods. From LSU cloning data there is evidence of two fungi in the wasps (basidiomycete relatives), and three fungi in the cockroaches. Two of the cockroach fungal symbionts are identical to the basidiomycete relatives recovered from wasps and there is an additional lecanoromycete relative. Using general 16S primers, Blattabacterium and Wolbachia are also recovered from the cockroaches. Culturing efforts reveal that only one of the basidiomycete-like fungi from the wasps is cultivable and an additional (possibly nitrogen fixing) bacterium is cultivable from the cockroaches. The characterization of the microbial associates in this system lays the foundation for understanding symbiont contributions to these wasps and cockroaches. This research reveals cryptic fungal diversity in an understudied niche, insect hosts, as well as demonstrates the role that fungi could have in shaping the evolution of host-parasitoid interactions. Poster

Gillevet, Patrick, M., Sikaroodi, M. and Torzilli, Albert, P. Department of Environmental Science and Policy, George Mason University, Fairfax, VA 22030, USA. atorzill@gmu.edu. Analysing salt-marsh fungal community diversity: community ARISA fingerprinting vs. community clone sequencing. Fungi are important decomposers in the detrital-based food webs of temperate salt-marsh ecosystems. Knowing the composition of salt-marsh fungal communities is essential for understanding how detritus processing is affected by changes in community dynamics. Previous results from our laboratory have shown that different salt-marsh plants harbor distinct fungal communities as judged by automated ribosomal intergenic spacer analysis (ARISA) of fungal DNA amplified from the different plant hosts. ARISA fingerprinting data provide non-taxon-specific snapshots of community structure where each peak in a community profile represents an operational taxonomic unit (OTU) of a given amplicon size. In order to associate specific taxa with community OTUs we cloned, fingerprinted, and sequenced the fungal community DNA from each plant in order to match the size and sequence of specific clones with the community OTU sizes. BLAST results indicated that a given OTU amplicon may represent more than one species, confirming earlier observations. Also, the ability to assign a specific taxon to a community amplicon by matching amplicon sizes was limited by the extent of species coverage in the BLAST database. Furthermore, differences in the relative abundances between community fingerprint amplicons and comparable clone abundances suggested significant biases during the cloning process. Nonetheless, the cloning and sequencing data did confirm the conclusion from fingerprinting that plant (substrate) type is an important factor in determining fungal community composition. Poster

Goldmann, Lauren and Weir, Alex. Department of Environmental & Forest Biology, SUNY College of Environmental Science & Forestry, 241 Illick Hall, 1 Forestry Drive, Syracuse, NY 13210, USA. lmgold01@syr.edu. Laboulbeniales from western Russia. As a part of the SUNY-ESF Moscow State University Exchange Program we had the opportunity in summer 2006 to collect Laboulbeniales fungi at the Zvenigorod Biological Station, some 50km west of Moscow, and at the White Sea Biological Station near Poikaonda. The most recent literature of the Laboulbeniales of the western portion of Russia is that by Hulden (1983), who records 41 species. Our collections have added an additional 10 species, including 3 new genera for the region; Aphanan- dromycetes, Euzodiomycetes, and Rhadinomycetes. Of particular interest was our observation of very high levels of infection at both these sites with 15% of collected beetles infected at Zvenigorod, and 14% at the White Sea. These figures are much higher than those recorded by Hulden (1%) and may be related to the range of microhabitats sampled. Poster

Gonzalez, Maria C. and Enriquez, Diana. Departamento de Botánica AP 70-233, Instituto de Biología, Universidad Nacional Autónoma de Mexico, Ciudad de Mexico DF 04510, Mexico, 2Instituto de Oceanología, Agencia del Medio Ambiente, Ministerio de Ciencia, Tecnología y Medio Ambiente de Cuba (CITMA), La Habana, Cuba. mcgy@ibiologia.unam.mx. Microfungi diversity in the coastal sand beach environment of Mexico and Cuba. The marine interstitial microfungi living in sandy sediments between the tide lines of the beaches are important ecologically because they are major decomposers of the vegetable organic matter that enter this marine ecosystem. In this particular environment, named endopsammic, the microbial production is dominated by eumycetes, mainly ascomycetes. Arenomic microfungi have a distinctive physiology, morphology, and adaptation to the endopsammophilous medium. The characteristics that the arenicolous species exhibit are: carbonaceous ascocarps attached to sand grains with a subiculo, papilla with an ostiole opening close to the subiculum, a pseudoparenchyma of thin walled cells with pit-like thickenings, delique- nescent asc of an apical structure, and appendaged ascospores. The genus Corollosporium is considered as one of the most diverse genera adapted to arenicolous habitats and is distributed widely from tropical to temperate regions. During the past decade, a surge has taken place in the investigation of the Mexican and Cuban arenicolous microfungi biodiversity. At present, these countries have an active interest in describing, preserving, and using the biodiversity of marine fungi. The advances in recording the distribution of species from several beaches of Mexico and Cuba are presented. Symposium Presentation

Gross, Stephanie, Suh, Sung-Oui and Blackwell, Meredith. Department of Biological Sciences, Louisiana State University, Baton Rouge, Louisiana 70803, USA. sgross2@lsu.edu. Diet and its effect on the abundance of endosymbiotic gut yeast found in a wood-boring beetle Odontotaenius disjunctus: Passalidae. Pichia stipitis, a xylose fermenting and assimilating yeast, has consistently been isolated from the gut of over 400 adult, wood-boring beetles (Odontotaenius disjunctus: Passalidae). We examined the effect of beetle diet on gut yeasts by varying nutrients provided for the host beetles. Beetles were provided only autoclaved water and starved for 6 da and then were fed different diets, (e.g., decayed wood, sterilized decayed wood, and artificial diet containing polysaccharides and other nutritional resources). Beetles were dissected periodically and yeast colony counts were made on selective agar media. Colonies on each plate were identified based on morphological and some were confirmed as P. stipitis by use of specific primers. After 6 da starvation, the abundance of P. stipitis in the gut decreased substantially when compared to pre-starvation numbers. However, 5 da after reintroduction of food, yeast numbers in the gut increased to approximately pre-starvation levels. We observed no significant difference in colony numbers between beetles fed unsterilized and sterilized wood, but beetles fed certain diets sometimes had low levels of yeasts compared to those fed wood. From this study, we concluded that within the O. disjunctus gut environment P. stipitis is dependent on nutrients provided by the insect diet. Contributed Presentation

Guardia Valle, Vaia1 and Caffaro, Matias J.2 1Unidad Botánica Dep. BABVE F. Ciencias, Universitat Autónoma de Barcelona, 08193 Bellaterra, Spain. 2Department of Biology, University of Puerto Rico – Mayaguez, PR 00681. matcau@gmail.com. First observation of zygosporas in Ascellariales (Trichomycetes). The ecological group of gut endosymbionts trichomycetes (sensu lato) includes two fungal orders, Harpellales and Ascellariales, and two protistan orders, Amoeboidea and Ecrinidea. Ascellariales inhabit the digestive tract of aquatic, terrestrial and marine isopods as well as springtails (Collembola). They have branched and septated thalli and reproduce asexually by arthrospore-like cells. No sexual reproduction has been reported until now. Recently a survey of islands in the Caribbean, a new unnamed species of Ascellaria has been found in terrestrial isopods in Puerto Rico and Dominican Republic. Conjugating tubes and zygospores were observed in this Ascellaria sp. Zygospores are spherical and hyaline in contrast to the ones in Harpellales, which are conical or biconical. Ascellariales zygospores share characteristics with those of Dimargaritales and Kickxellales as well as their septal pore structure, which is present in all three orders plus the Harpellales, thus giving morphological support to this monophyletic group, recently established through DNA analyses. The spherical shape of Ascellaria zygospores reveals a possible ter-
retrial origin of the group in comparison to the conical shape of Harpellales zygospores, which is regarded as an adaptation to aquatic environments. **Poster**

Gueidan, C.¹, Ruibal, C.², de Hoog, G.S.², Untereiner, W.A.³, Gorbushina, A.⁴ and Latzoni, F.¹. Duke University, Biology Department, Box 90338, Durham NC 27708, USA. ¹Centraalbureau voor Schim- melcultures, Uppsalaalan 8, 3584 CT, Utrecht, The Netherlands, ²De- partment of Zoology, Brandon University, 270-18th Street, Brandon, MB Canada. ³Geomicrobiology, ICBM, Carl-von-Ossietzky str 9-11, 26111 Oldenburg, Germany, cg19@duke.edu. **Phylogenetic affilia- tions of non-lichenized rock-inhabiting fungi and their role in the evolution of the Chaetothyriomycetidae.** Rock surfaces harbor ubiqu- itous communities of highly adapted fungi with peculiar lifestyles. Some of these rock-inhabiting fungi are found in semiarid and even desert habitats, and have been shown to be well adapted to extreme environ- mental conditions. Previous studies revealed that these specialized rock-inhabiting strains could tolerate surprisingly wide ranges of tem- peratures, irradiations and osmotic stresses, and are able to grow in con- ditions with low availability of water and nutrients. Particular character- istics of rock-inhabiting fungi include slow meristematic growth and the presence of melanin (as well as carotenoids and mycosporines) in their mycelia. These extremotolerant fungi were previously shown, using ITS similarity, to mostly belong to two classes of ascomycetes, the Eurotiomycetes (mostly in the order Chaetothyriales) and the Doth- ideomycetes. Three ribosomal RNA genes (nucSSU, nucLSU, and mtSSU) were used to estimate their phylogenetic affiliations within the ascomycetes. The order Chaetothyriales includes saprophytes as well as animal or human parasites, and is most closely related to two main- lychenized orders, the Verrucariales and the Pyrenulales. Together, these three orders are recognized as forming the subclass Chaetothyri- omycetidae, which is characterized by a large diversity in lifestyles and habitats. Preliminary results showed that the most recent common ances- tor of this subclass was probably a lichenized rock- inhabiting fungus which is yet to be understood due to the evolution of lifestyles and substrate transitions in the Chaetothyriomycetidae. **Contributed Presentation**

Hallen, Heather E.⁴, Guenther, John C. and Trail, Frances. Department of Plant Biology, Michigan State University, East Lansing, MI 48824, USA, hallneh@msu.edu. **Analysis of gene expression and lipid ac- cumulation during sexual development in Gibberella zeae (anamorph Fusarium graminearum).** Lipid accumulation and storage is vital to survival of all organisms. Stored lipids are then used for develop- ment. In fungi, lipids are stored in vegetative hyphae and spores as lipid bodies. The wheat pathogen, Gibberella zeae, stores lipids mainly as triacylglycerides (TAG) in anticipation of sexual develop- ment. We have characterized the process of lipid accumulation and uti- lization in association with perithecia development in culture and leading up to perithecia development in planta. We examined gene expression patterns for genes associated with lipid biosynthesis and degradation using data collected from Affymetrix GeneChips. Information gathered from these studies indicates an essential role for lipids in the formation of perithecia. **Contributed Presentation**

Halling, Roy E. Institute of Systematic Botany, The New York Botan- ical Garden, Bronx, NY 10458-5126, USA. rhalling@nybg.org. **Queensland boletes: a biogeographic and generic enigma.** A targeted inventory of Boletaceae (s.l.) occurring in NE Australia and else- where in SE Asia has provided exquisite material for revisionary studies on well-known genera and iconic species. As with most early surveys of understudied regions, the application of northern hemi- sphere names to poorly documented specimens has contributed to the perception of globally distributed taxa. However, knowledgeable indi- viduals engaged in a concerted effort with a broader bias are beginning to document localized endemics at one extreme as well as entities that appear to portray little morphological change. Because of an obligate symbiotic lifestyle, coupled with geographic and tectonic constraints on genetic exchange, localized evolutionary pressures appear to have contributed to a heretofore undocumented assemblage of taxa. Examples of such “taxa” have been discovered and documented which show features that would indicate classic undescribed genera and species, possible generic hybrids, distinct but related and widely distributed sib- lings, as well as intercontinental clinal disjuncts with no apparent dis- tinction but for differences in ribosomal coding genes; this latter proba- bly attributed to random drift. **Contributed Presentation**

Hawksworth, David L., Universidade Complutense de Madrid, Calle Manuel Bartolomé Cossío S/N, 28040 Madrid, Spain; and The Natural History Museum, Cromwell Road, London, SW7 5BD, UK. d.hawksworth@nhm.ac.uk. **Index Fungorum to Species Fungorum and the BioCode.** Index Fungorum aims to be a nomenclator of all scientific names proposed for fungi, which is intended to progress towards a Species Fungorum which will provide a reference work giving the currently accepted names of species. The Index Fungorum is now a working tool for all systematic mycologists, and a marvellously imperfect work needed by all. Progress to a Species Fungorum is being made, but depends on the inputs of the international mycological community. The Draft BioCode (1997) was prepared by representatives of all cur- rent five internationally mandated codes to cover all groups of organ- isms, but has as a prerequisite finite lists of nomenclaturally honed names to be considered in the nomenclature of the future. The history and prospects for these three initiatives are discussed. **Symposium Presentation.**

Henk, Daniel A.² and Aime M. Catherine, Systematic Botany and Mycology Laboratory, 10300 Baltimore Ave, Beltsville, MD 20705, USA. dan@st.ars-grin.gov. **Evolution of mating pheromone and recep- tor genes in Pucciniomycotina.** Mating pheromones and their recep- tors act as a switch controlling phototropic changes required for suc- cessful mating in fungi. Although basidiomycete mating pheromones and their processing were first described in Rhodosporidium toruloides, a “red yeast” in the Sporidiobolales, the receptor gene was never described, and much of the mating process remains unexplored in any species of Pucciniomycotina. We used published data from whole- genome-sequencing projects to detect putative mating pheromones and their receptor genes in several Pucciniomycotina. Primers were de- signed for direct amplification and sequencing of a putative receptor gene similar to Sterile 3 (ste3) and a closely linked gene similar to a put- tative nuclear localization protein from other red yeasts. Results sug- gest that pheromones and their receptors, as well as synteny around the pheromone receptor locus, are relatively conserved in the Sporidiobolo- lales. Although only a single ste3 locus could be detected in Sporid- iobolales genomes, three separate loci similar to ste3 were detected in the Puccinia graminis (Pucciniales) genome. In phylogenetic analyses the Puccinia STE3 sequences formed a well-supported clade at the base of the basidiomycetes while the Sporidiobolales sequences formed a well-supported clade nested within the basidiomycetes. **Contributed Presentation**
Henkel, Terry W. Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA. thw5@humboldt.edu. The importance of primary tropical forests for fungal biodiversity. Guyana is fast becoming unique among tropical countries in having the majority of its primary forest estate intact, including biodiversity at all trophic levels. Mycological inventories have historically been wanting in Guyana. Recent explorations have revealed a diverse macromycota in Guyana’s Pakaraima Mountains. Forests dominated by ectomycorrhizal (EM) trees, a relative rarity in lowland Neotropical regions, exist in a patch mosaic in the Pakaraima Mountains and appear to be regionally exclusive habitats for a large assemblage of endemic EM fungi. While ecological threats to Guyana’s ectrophic forests are currently minimal due to the remoteness of the region, the majority of the landscape known to house these systems has no formally protected status. The likelihood of these Gondwanan relicual ectrophic forests and their apparently unique fungal constituents persisting into the future will be discussed. Symposium Presentation

Herrera, Jose. 100 E. Normal, Division of Science, Truman State University, Kirksville, MO 63501, USA. jherrera@truman.edu. Biodiversity of trichomycetes associated with marine arthropods in Puerto Rico. Three being associated to marine crustaceans in the isopod Amoebidium, Genistellospora, Parataeniella, Harpella, Leidyomyces, Paramycobolus, Stachylinia, Smittium, Aselaria, Enterobryus and Taeniellopsis are reported, the last three being associated to marine crustaceans in the isopod Ligia sp., the crab Uca sp., and the amphipod Orchestia sp., respectively. More recently, we have discovered Enterobryus halophilus in the mole crab Emerita portoricensis, which is a new record for this trichomycete for both its host species and distribution. Currently, we are conducting prevalence and abundance studies in beach populations of this organism in Puerto Rico. In this report, we present data of trichomycetes distributions for the Caribbean, which broadens their geographic distribution, adding new information about host range and specificity as well as their ecological preferences reflecting the potential of trichomycetes in terms of their biodiversity. Symposium Presentation

Hernandez Roa, Jonatan and Cafaro, Matias J. Department of Biology, University of Puerto Rico, Mayaguez Campus, Mayaguez, PR 00681, jonatan.her@gmail.com. Biodiversity of trichomycetes associated with marine arthropods in Puerto Rico. The increasing interest in indoor biodiversity has raised an effort to define it, to characterize it and to understand how it is lost. There are few studies about trichomycete diversity in coastal ecosystems in general and even less in tropical coasts. Puerto Rico is an ideal place to conduct the current research on such diversity due to the variety of habitats and ecological zones available for trichomycete hosts, especially marine crustaceans. Only three surveys for trichomycetes in Puerto Rico exist in which Ameobiidium, Genistellospora, Parataeniella, Harpella, Leidyomyces, Paramycobolus, Stachylinia, Smittium, Aselaria, Enterobryus and Taeniellopsis are reported, the last three being associated to marine crustaceans in the isopod Ligia sp., the crab Uca sp., and the amphipod Orchestia sp., respectively. More recently, we have discovered Enterobryus halophilus in the mole crab Emerita portoricensis, which is a new record for this trichomycete for both its host species and distribution. Currently, we are conducting prevalence and abundance studies in beach populations of this organism in Puerto Rico. In this report, we present data of trichomycetes distributions for the Caribbean, which broadens their geographic distribution, adding new information about host range and specificity as well as their ecological preferences reflecting the potential of trichomycetes in terms of their biodiversity. Symposium Presentation

Horn, Bruce W.1 and Peterson, Stephen W.2 1National Peanut Research Laboratory, Agricultural Research Service, U.S. Department of Agriculture, Dawson, GA 39842, USA, 2National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL 61604, USA. bhorn@nprl.usda.gov. Host specificity of Eupenicillium ochrosalmoneum, E. cinnamopurpureum, and two new Penicillium species associated with the conidial heads of Aspergillus. The genus Penicillium comprises species that mostly colonize plant matter. However, early reports suggest that several species are capable of parasitizing Aspergillus. More recently Eupenicillium ochrosalmoneum and E. cinnamopurpureum, both with Penicillium anamorphs, have been observed sporulating on the heads of Aspergillus while resembling to section Flavi during the colonisation of peanut seeds. Little is known about the host specificity underlying these Aspergillus–Penicillium associations. In this study, Aspergillus species representing nine taxonomic sections were paired in
culture with *E. ochrosalmonenum*, *E. cinnamonpurpureum*, and two new species described here based on morphological and molecular characters, *P. exiguum* and *P. georgiense*. Phylogenetic analysis using three loci shows that *P. exiguum* is a sister species of *E. cinnamonpurpureum* and that *P. georgiense* is not closely related to *P. exiguum* or either *Eupenicillium* species, though its precise phylogenetic placement within the genus *Penicillium* is unresolved. *Eupenicillium ochrosalmonenum*, *E. cinnamonpurpureum*, and *P. exiguum* sporulated predominantly on the heads of section *Flavii* species. In contrast, *P. georgiense* was restricted to the heads of section *Nigerii* species. Additional studies are required to clarify whether the *Eupenicillium* and *Penicillium* species are parasitic or simply epibiotic on their hosts. **Poster**

Horton, Thomas R.*, Ashkannejhad, Sara M. and Galante, Tera E. 1 SUNY, College of Environmental Science and Forestry, 246 Illick Hall, Syracuse, NY 13210, USA, 1USDA Forest Service, Plumas National Forest, 875 Mitchell Ave, Oroville, CA 95996, USA. throrton@esf.edu. **Symposium Presentation**

Ectomycorrhizal fungi on coastal sand dunes in Oregon. We investigated the ecology of ectomycorrhizal fungi on coastal sand dunes in Oregon. Over 100 species were collected during the fall fruiting season for two consecutive years, with *Cortinarius*, *Inocybe*, *Laccaria*, *Lactarius*, *Rhizopogon*, *Russula*, *Tricholoma*, and *Tricholomopsis* being particularly species rich and productive. Pine seedlings were colonized by many of these fungi when in close proximity to mature trees stands, but almost exclusively by *Suillus* and *Rhzopogon* species in the middle of the dunes where mycelial networks were absent. Although many of the fungi produce biunculate spores, it was concluded that these spores were homokaryotic, so the establishment of new dikaryons in the middle of the dunes still requires two spores of opposite mating type. Deer feces contained tens of millions of suilloid spores per deposit, providing ample opportunity for spores of opposite mating type to be deposited together. Laboratory bioassays with deer feces yielded abundant mycorrhizae of *Suillus* and *Rhizopogon* species. We are now investigating why other disturbance species such as *Laccaria*, *Hebeloma*, *Inocybe* and *Thelephora* are not observed on seedlings in the middle of the dunes by investigating wind dispersal and survival of outplanted seedlings inoculated with these fungi. **Symposium Presentation**

Huang, Bo1, Humber, Richard A.2 and Hodge, Kathie T.3* 1Anhui Provincial Key Laboratory for Microbial Pest Control, Anhui Agricultural University, Hefei 230036, China, 2Dept of Plant Pathology, Cornell University, Ithaca, NY 14853, USA, 3USDA-ARS Plant Protection Research Unit, Plant, Soil & Nutrition Laboratory, Tower Road, Ithaca, NY 14853, USA. kh11@cornell.edu. Basidiobolus: infrageneric relationships and biology. The genus *Basidiobolus* is a pivotal one. Its species include opportunistic agents of human disease, cryptic inhabitants of leaf litter, and coprophilous fungi of frog dung. Its large primary mitospores are forcibly discharged by a unique mechanism involving explosive rupture of the sporogenous cell. Various molecular-based studies have assigned *Basidiobolus* to its traditional home in the order *Entomophthorales*; others have placed it among flagellate fungi. We undertook a study of infrageneric relationships in *Basidiobolus*, using isolates from culture collections plus our own collections isolated from decaying litter. Our results based on phylogenetic analysis of multiple genetic loci clarify species concepts, and unexpectedly reveal two major clades supported by both molecular and phenotypic evidence. Our sampling of *Basidiobolus* and its allies will ultimately help resolve taxon sampling issues among early-evolving fungal lineages. **Poster**

Hughes, Karen W.*, Petersen, Ronald H. and Hick, Edgar B. Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA. khughes@utk.edu. The agamic taxa biodiversity inventory in the Great Smoky Mountains National Park. The Great Smoky Mountains National Park Agamic ATBI is in the third year of collection and documentation. As part of the documentation, genetic identifiers based on the ribosomal ITS region have been obtained wherever possible. Using an arbitrary criteria that 98% or greater sequence homology as indicating conspecficity, we calculated the proportion of collections which are represented in GenBank. Of 533 collections, 23 matched a sequence deposited as an environmental sample. These were predominantly collections from Duke Forest generated by O’Brien et al. (2005) and thus may logically represent the same taxon as found in the GSMPN. An additional 159 collections matched named species in GenBank. No genetic match was found for 159 collections indicating that in spite of the large numbers of fungal sequences in GenBank, species coverage is still poor. Many of the collections were heterozgous for multiple indels which may be a function of populations from different glacial refugia rehybridizing in the southern Appalachians. Several lines of evidence suggest that one glacial refugium was in Central America. The proportion of heterozygotes for indels varied among genera. At this time, the discovery curve does not seem to have leveled off and it is clear that much more needs to be done in the Great Smoky Mountains. **Poster**

Hustad, Kevin P.1*, Vernier, Kimberly L.1, Methven, Andrew S.1 and Miller, Andrew N.2 1Eastern Illinois University, Charleston, IL 61920, USA, 2Illinois Natural History Survey, Champaign, IL 61820, USA. vphustad@eiu.edu. Terrestrial macrofungal species composition and richness in old growth prairie groves. This study is investigating species composition and richness of terrestrial macrofungi in Brownfield (26.1 ha) and Trelease Woods (24.5 ha), Champaign Co., Illinois. These woods are remnants of a larger, pre-settlement prairie grove now encircled by houses, fragmented forests, prairie and agricultural land. Although initially a virgin, deciduous upland forest dominated by oak, ash and maple with a high, closed canopy and fairly open (Brownfield Woods) to moderately dense (Trelease Woods) understory, sugar maple is rapidly becoming the dominant tree species. Beginning with a windstorm in November 1994 that damaged canopy trees in Trelease Woods, fallen trees in both woods have been tagged with an ID number, date of windfall, dbh and location relative to a network of marked grids. Terrestrial and wood-inhabiting macrofungi on the forest floor are being surveyed along twenty, 100 m long transects. Among the questions to be answered are: i) How does macrofungal species composition and richness change in relation to adjacent vegetation? ii) How does macrofungal production vary within and between years? iii) How does macrofungal species composition and species richness change within and between years? iv) How do tree windfalls perturb macrofungi species composition and richness patterns?; and, v) Are other parameters influencing macrofungal species composition spatially auto-correlated? **Poster**

Hyde, Kevin D.1*, Zhang, Y.1, Jeewon, R.1 and Fournier, J.2 1 Centre for Research in Fungal Diversity, School of Biological Sciences, The University of Hong Kong, Pokfulam Road, Hong Kong SAR, P.R. China, 2Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA. hydeKD@hku.hk. FESIN, introduction to a new fungal/ecological research coordination network. The National Science Foundation has funded a research coordination network designed to bring together mycologists and ecologists (FESIN: Fungal Environmental Sampling and Informatics Network). The focus of FESIN is threefold: to coordinate the development of rapid identification methods for fungi from environmental samples, to create cyberinfrastructure for the retrieval of multiple layers of biologically relevant information on fungal taxa, and to stimulate educational and outreach opportunities in fungal ecology. This network is open to all interested people and will meet alternately at MSA and ESA annual meetings. Proposed topics include: 1) Nucleic acid-based identification of fungi in ecological settings: current limitations and future directions; 2) Building a microarray for identification of fungi in the environment, a joint effort between European and North American Scientists; 3) Connecting sequence data with the ecology of taxa; 4) Ecological genetics in the ornate era; genomes, proteomes, and fungal ecology; and 5) Fungal ecology: cultivating a new generation of fungal ecologists. **Symposium Presentation**
that higher ligninolytic and cellulolytic enzyme activities resulted in lanase, 1,4-α-xylosidase. The two manganese-independent peroxidases were detected in fungi isolates test-Portus squamosus, Cochliobolus heterostrophus, Grifola frondosa, Grifola umbellata, straw by forty, Greensboro, NC 27411, USA. omon@ncat.edu. cannot be ruled out. of the remaining 8 T-toxingenes from race T. The data obtained so far is unique and found just one. We are currently investigating the origins for T-toxin production and the sporadic phylogenetic distribution of the 9 known T-toxin genes, unraveling the evolutionary history of the genes is not straightforward. T-toxin genes are distributed at two loci associated with the breakpoints of a reciprocal translocation and encompass ca. 1.2 Mb of A+T rich, highly repetitive DNA present in race T, but missing in non-T-toxin producing race O, and from all other species of Cochliobolus. Furthermore, the T-toxin genes are not clustered, unlike genes required for biosynthesis of most fungal polyketides e.g. lovastatin and aflatoxin. Together, these data suggest that the T-toxin genes may have been acquired by race T from an unknown source and that, upon integration of this DNA, a reciprocal translocation occurred, distributing the genes at two loci. To further investigate evolution of the T-toxin locus, we sequenced 117 close and distant relatives for the presence of new ChPKS1 orthologs and found just one. We are currently investigating the origins of the remaining 8 T-toxin genes from race T. The data obtained so far do not contradict the horizontal transfer hypothesis, but a vertical origin cannot be ruled out. Contributed Presentation

Inderbitzin, Patrik1,2, Schoch, Conrad2 and Turgeon, B. Gillian.1 Cornell University, Plant Pathology, Ithaca, NY, USA, 2Oregon State University, Dep. of Botany and Plant Pathology, Corvallis, OR, USA, prin@uckac.edu. Exploring the evolutionary origins of T-toxin, the Cochliobolus heterostrophus polyketide virulence factor implicated in the Southern Corn Leaf Blight epidemic. The polyketide virulence factor, T-toxin, is produced by race T of the ascomycete Cochliobolus heterostrophus, the cause of Southern Corn Leaf Blight. Due to complex structural features of the locus, Tox1, required for T-toxin production and the sporadic phylogenetic distribution of the 9 known T-toxin genes, unraveling the evolutionary history of the genes is not straightforward. T-toxin genes are distributed at two loci associated with the breakpoints of a reciprocal translocation and encompass ca. 1.2 Mb of A+T rich, highly repetitive DNA present in race T, but missing in non-T-toxin producing race O, and from all other species of Cochliobolus. Furthermore, the T-toxin genes are not clustered, unlike genes required for biosynthesis of most fungal polyketides e.g. lovastatin and aflatoxin. Together, these data suggest that the T-toxin genes may have been acquired by race T from an unknown source and that, upon integration of this DNA, a reciprocal translocation occurred, distributing the genes at two loci. To further investigate evolution of the T-toxin locus, we sequenced 117 close and distant relatives for the presence of new ChPKS1 orthologs and found just one. We are currently investigating the origins of the remaining 8 T-toxin genes from race T. The data obtained so far do not contradict the horizontal transfer hypothesis, but a vertical origin cannot be ruled out. Contributed Presentation

Isikhuemhen, O.S.1,2 and Mikiaishvili, N. Mushroom Biology & Fungal Biotechnology Laboratory, SAES, North Carolina A&T State University, Greensboro, NC 27411, USA. omon@ncat.edu. Lignin, cellulose, and hemicellulose degrading enzyme production by selected polypores. Lignocellulose degrading enzymes and biodegradation of wheat straw by Grifola frondosa, Grifola umbellata and two strains of Poryporus squamosus (1165 and 456) were investigated. Lignin, cellulose and hemicellulose degrading enzymes, as well as loss of organic matter (LOM) were assayed at 16, 30, 44 and 60 days from start of experiment. Lignin modifying enzymes, laccase, manganese dependent and manganese independent peroxidase were detected in fungi isolates tested. Cellulose degrading enzymes detected were carboxymethyl cellulase and cellobiohydrolase and hemicellulose degrading enzymes were xyylanase, 1,4-α-xyllosidase. The two Polyporus strains tested produced more lignocellulose degrading enzymes than G. frondosa and G. um- bellata. In hemicellulose degradation, Grifola strains produced more xylosidase than the P. squamosus strains. However, the reverse was the case with xyylanase, for which P. squamosus strains showed activities in the order of 36% (456) and 10% (1165) higher than G. umbellata. The highest LOM (36%) was in P. squamosus (1165), followed by 456 (34%), G. frondosa (20%) and G. umbellata (7%). Our results indicate that higher ligninolytic and cellulolytic enzyme activities resulted in higher levels of degradation (LOM) in wheat straw substrate. Optimization of wheat straw degradation under solid-state fermentation is under investigation. Poster

Isikhuemhen, O.S.1,2, Sisson, J.2, Liedl, B.E.2 and Chatfield, J.M.2 Mushroom Biology and Fungal Biotechnology Laboratory, School of Agriculture & Environmental Sciences, North Carolina A&T State University, Greensboro, NC 27411, USA. 2Agricultural and Environmental Research Station, Gus R. Douglass Land-Grant Institute, West Virginia State University, Institute, WV 25112, USA. omon@ncat.edu. Cultivation of Agrocybe aegerita on solid waste from thermophilic anaerobic digestion of poultry litter. Solid waste (SW) effluent from thermophilic anaerobic digestion of poultry litter was tested as substrate for the cultivation of Agrocybe aegerita (black poplar mush-room). Substrate combinations tested contained 0, 10, 25, 50 75 and 100% SW. Ten replicates of each substrate combination, after sterilization at 121 °C for 3 h, was inoculated with spawn from the test fungus, incubated at 25 °C and transferred to the fruiting house upon pinning. Significant differences existed between substrate combinations evaluated by fresh and dry weight yields. Substrate combinations with 100% and 75% SW appeared to be the best, producing mean fresh weight yields of 321.75 g and 308.94 g and mean dry weights of 31.79 g and 28.26 g, respectively. They out performed the positive control, which had mean fresh and dry weights of 278.23 g and 22.65 g. In general, any substrate combination that had 50% or more SW out performed the positive control. Results indicate that solid waste effluent can be used for A. aegerita cultivation. A pilot study for commercial application of SW in the cultivation of A. aegerita is ongoing in our laboratories. Poster

Iturriaga, Teresa1,3, Hawksworth, David L.2 and Crane, J. Leland.3 1Departamento de Biología de Organismos, Universidad Simón Bolívar, Apartado 89000 Sartenejas, Baruta, Edo. Miranda, Venezuela, 2Departamento de Biología Vegetal II, Facultad de Farmacia, Universidad Complutense, Plaza Ramón y Cajal, Ciudad Universitaria, Madrid 28040, Spain, 3607 E Peabody Natural Resources Building, Illinois Natural History Survey, Champaign, IL 61829, USA. titurri@usb.ve. A new lichenicolous fungus on Leptogium from Venezuela. A new species of Sporidesmium is described from the decaying thallus of an unidentified Leptogium species growing on unidentified tree bark from the Guaramacal National Park in Bocoró, Táchira State, in western Venezuela. This is only the second lichenicolous species to be described under this generic name, and differences from that species and similar species in Sporidesmium s. lat are discussed. A more precise generic placement will have to await a molecularly based taxonomy of the genus. The original material comes from a mycologically little-explored region of the country, and brief information on previous mycological (including lichenological) studies in the area is provided for the first time in English. A new combination of another species under the same genus Sporidesmium is also made. Poster

Izzo, Antonio D.1 and Mazzaola, M. USDA Agricultural Research Service Tree Fruit Laboratory,1104 N. Western Ave., Wenatchee, WA 98801, USA. Izzo@trf.ars.usda.gov. Assessing the utility of a taxonomic macroarray for monitoring fungal community development in soils exhibiting suppression of root disease. A broad range of fungi can impact plant health either directly or indirectly, and the interactions that lead to the development of a healthy or diseased plant are very complex. We tested the viability of a membrane-based PCR product taxonomic macroarray as a means to monitor the transformation of soil fungal communities following the incorporation of Brassica seed meals (BSM) known to have differential impact on members of the pathogen complex that incites replant disease (ARD). Tests with probes of known composition demonstrated that the approach is capable of distinguishing DNA sequences differing by amounts that generally translate into sub-generic lineages. Tests using mixed-community probes constructed from soils amended with either of two BSMs indicated that Trichoderma species were initially preferentially dominant in amended

Continued on following page
soils known to suppress the *Pythium* spp. component of ARD whereas the fungal community was more evenly distributed in the soils conducive to *Pythium* spp. growth. This pattern supported both visual observation of sporulation patterns and other molecular analyses (cloning and T-RFLP) of the fungal community resident to these soils. Membrane-based macroarrays coupled with environmental probes represent a very accessible and powerful tool for studying fungal communities and their dynamics. **Poster**

Jackson, Jason\(^1\)\(^2\)\(^3\), Richter, Daniel D. Jr.\(^2\)\(^4\) and Vilgalys, Ryta\(^5\), Department of Biology and \(^2\)Nicholas School of the Environment and Earth Sciences, Duke University, Durham, NC, USA. jaj2@duke.edu.

**Quantitative PCR assessment of fungal community change.** Here we describe a quantitative assay to measure the relative abundance of basidiomycete fungi in forest soils using real-time PCR. We developed and tested a set of novel, taxon-specific primers. The primers are nested hierarchically within the basidiomycota and ascomycota and target several known ectomycorrhizal and saprophytic groups. We use this assay to estimate shifts in the relative abundance of these taxa during old field succession in a series of grassland, pine, and mixed forest plots in the South Carolina Piedmont. Previous studies using clone libraries have found extremely high basidiomycete diversity in both pine and hardwood stands from this system, and that the diversity in both forests is dominated by ectomycorrhizal fungi. Clone libraries are a powerful estimate of species richness but are not quantitative. This assay allows for an estimate of the relative abundance of the dominant fungal taxa in forest soils and, combined with measures of total fungal biomass, provides the ability to characterize community responses to land use change. **Contributed Presentation**

Jarvis, Elisabeth\(^6\) and Volk, Thomas J. 3024 Cowley Hall, University of Wisconsin-La Crosse, La Crosse, WI, 54601, USA. jarvis.elis@uwlax.edu.

**Preliminary studies of mycодiversity from differently aged prairies.** Over the past 30 years the Midwest has seen a dramatic proliferation in acres of prairie restoration. Over time the quality of these restorations has improved drastically as restorationists have come to a better understanding of prairie plant communities. However, most of these restorations never achieve the complex structure or diversity of prairie remnants. While the proper proportions of plant species may be replicated today, little information exists on the microbe community of pre-settlement prairie soil. This is especially true with arbuscular mycorrhizal fungi (AMF). Although the role of plant AMF interactions in prairie structure and diversity have been documented, the species of AMF have not. Past studies have used spores to identify species of prairie AMF, but recent research have shown that spores do not accurately reflect the whole population. In our research, we compared *Andropogon gerardii* (Big Bluestem) root samples from differently aged prairie restorations and prairie remnants. AMF species were identified using nested PCR with AMF specific primers. Our working hypothesis is that we expect to find much higher diversity of fungi in the older and remnant prairies. With further research, we hope that our mycodiversity lists can help facilitate the restoration of native fungi along with native plants. **Poster**

Jenkinson, Thomas S.\(^*\), Celio, Gail J., Padmanee, Mahajabeen, Dentinger, Bryn T. M., Meyer, Michelle E. and McLaughlin, David J. Dept. of Plant Biology, University of Minnesota, St. Paul, MN 55108, USA. tsjenkinson@riseup.net. Wha choo talkin bout, *Suillus*? ultrastructure of cystidia in sliny boletes. Cystidia of *Suillus americanus* and *S. graminatus* (Boletales) were examined cytochemically and ultrastructurally using cells prepared by freeze substitution. We present the first study showing ultrastructural details of the cystidium to be conserved in two closely related species. The results are presented for inclusion in the AFTOL Structural and Biochemical Database (http://aftol.umn.edu). The cystidia of these *Suillus* species appear to be united by a series of conserved characters, including secretion mechanisms, smooth tubular endoplasmic reticulum, and abundant free ribosomes. The remarkable conservation of these subcellular traits suggests that ultrastructural details of cystidia may provide a wealth of characters for phylogenetic analysis. Inclusion of such characters in phylogenetic analyses may have the power to resolve or provide support for monophyletic groups at the level of family or genus. **Poster**

Johnson, James E.\(^*\), Belmont, Susan F. and Wagner, R. Steven, Central Washington University, 1000 E. University Way, Ellensburg, WA 98926, USA. jjohnson@cwu.edu. **Chytridiomycosis and declines of Pacific Northwest amphibian populations.** The chytrid fungus *Batrachochytrium dendrobatidis* (Bd) has been implicated in mass mortalities and declines of amphibian species worldwide. The fungus has been detected on a variety of amphibians in the Pacific Northwest, but there has been little evidence presented of mass mortality events or population declines. Using PCR and microscopy the presence of Bd was associated with a mass mortality event at Swamp Lake (Kittitas Co., WA) involving several amphibian species. The fungus has also been associated with mortality of the endangered Northern leopard frog (*Rana pipiens*) in the Potholes Reservoir (Grant Co., WA). In a third population at Engelhorn Pond (Kittitas Co., WA), demographic changes in abundance have been estimated in a population of *Hyla regilla* since 2002 using mark-recapture methods. During the spring of 2006, Bd was detected in the population using PCR analyses. Consequently, we implemented a swabbing/PCR procedure for all captured/recaptured individuals to measure pathogen prevalence. Initial prevalence of the disease was approximately 43% and mark-recapture results suggest a decline in the number of recaptured individuals compared to previous mark-recapture years. In addition, no individuals testing positive for Bd were recaptured. The results of this study suggest that Bd is responsible for a significant decline in abundance at this site. These data suggest that Bd is responsible for significant amphibian mortality, and may have widespread implications for persistence of other Northwest amphibians. **Contributed Presentation**

Joneson, Suzanne\(^*\), Dietrich, Fred\(^2\), Lutzoni, François\(^3\) and Armaleo, Daniele.\(^2\). Department of Biology, Duke University, Durham, NC 27708, USA. \(^2\)Department of Molecular Genetics and Microbiology, Duke University, Durham, NC 27710, USA. sjl2@duke.edu. **Differentially regulated genes and lichen symbiosis.** Lichens are the symbiotic association of fungi (mycobionts) with green algae and/or cyanobacteria (photobionts). Although one fifth of all known fungi form obligatory lichens with photobionts, we know nothing of the genetic or molecular mechanisms underlying this nutritional mode. Here we present the first investigations into differentially expressed genes in early lichen development including pre-contact, and initial contact of the symbionts. We used Suppression Subtractive Hybridization to find up-regulated genes between the fungus *Cladonia grayi* and the green alga *Asterocloris sp*. in *in vitro* resynthesis. We sequenced over 2000 fungal and algal clones, and used BLAST and FASTA algorithmic searches of protein and conserved protein domain databases to characterize our sequences. This dataset represents the first global survey of fungal and algal gene sequences involved in lichen symbiosis, and a summary of these genes and their putative functions will be presented. The results of this study allow us to identify candidate genes of early lichen development for future research. **Symposium Presentation**

Jumpponen, A.\(^*\), Jones, K.L. and Blair, J.M. Division of Biology, Kansas State University, Manhattan, KS, USA. arri@ksu.edu. **Use of a massively parallel sequencing (MPS) to assess soil eukaryote responses to altered precipitation and warming.** To test eukaryote responses to rainfall and warming in a tallgrass prairie, we used MPS of the ITS1. The acquired 100bp reads were screened for quality, those with intact primers, without ambiguous bases, and meeting length thresholds were binned at ≥98% similarity. Across 24 plots, the sampling intensity (~1,500 reads/plot) sufficiently covered diversity and species-effort curves reached a plateau. A quarter of a complete MPS run generated 41,512 sequences across 5,066 Operational Taxonomic Units (OTUs) and included 1,802 non-singletons (92% of the reads) and 3,264 singletons. The non-singletons represented Fungi (82.1%), unknown eukaryotes (13.6%), Viridiplantae (1.9%), and Metazoan
Kasuga, Takao1*, Mibey, Richard K.2 and Mutitu, Eunice W.3
1NARL, Kenya Agricultural Research Institute, P.O. Box 14733 Nairobi, Kenya, 2Department of Botany, University of Nairobi, P.O. Box 30197 Nairobi, Kenya, 3Department of Crop Protection, University of Nairobi, P.O. Box 30197 Nairobi, Kenya. gmkarkiuki@yahoo.com.

Some potential mycoherbicides candidates for the biocontrol of water hyacinth in Kenya. A survey of plant pathogenic fungi associated with naturally infected water hyacinth Eichhornia crassipes was conducted at different sites in Kenya. Twenty fungal isolates belonging to different genera were isolated. Two Alternaria spp. isolates designated WI3B1 and WI3B2 were found to be pathogenic to the water hyacinth both under green house and field conditions. On the basis of conidial measurements, growth characteristics and pigmentation in cultures, the two Alternaria spp. were identified as A. alternata and A. eichhorniae respectively. A. eichhorniae caused severe leaf blight. Symptoms started to appear between fifth and the seventh day after inoculation and were manifested in the form of leaf spots and leaf blotsches usually on the older leaves. For A. alternata, symptoms appeared 3 days after inoculation as small yellowish, chlorotic lesions with necrotic brown centers. Later these lesions enlarged gradually and centers turned dark brown with pale yellow margins. Contributed Presentation

Kariuki, George M.1*, Mibey, Richard K.2 and Mutitu, Eunice W.3
1NARL, Kenya Agricultural Research Institute, P.O. Box 14733 Nairobi, Kenya, 2Department of Botany, University of Nairobi, P.O. Box 30197 Nairobi, Kenya, 3Department of Crop Protection, University of Nairobi, P.O. Box 30197 Nairobi, Kenya. gmkarkiuki@yahoo.com.

Fungal Population Diversity and Fluorescent Myxomycetes in Chickpea fields in India. Population diversity of Fusarium oxysporum and fluorescent pseudomonas was studied in rhizosphere and rhizoplane of healthy, partially and completely wilted chickpea plants. A total of 117 isolates of F. oxysporum were collected from different commercial grower’s field in Ludhiana District of Punjab State. Results of pathogenicity test revealed that the isolates of F. oxysporum included both pathogenic and nonpathogenic strains. Amongst all the isolates of F. oxysporum studied, 58 were pathogenic and 59 nonpathogenic isolates. The maximum number of pathogenic isolates was present in soils of completely wilted plants whereas its minimum number enumerated in soil samples of healthy plants. In contrast, maximum number of nonpathogenic isolates was obtained from rhizosphere and rhizoplane of healthy plants. On the basis of wilt development the pathogenic isolates of F. oxysporum were further categorized as highly, moderately, least pathogenic. Diversified populations of fluorescent pseudomonas differed in their antagonistic potential. Out of 90 isolates of fluorescent pseudomonas maximum antagonistic isolates were obtained from rhizosphere and rhizoplane of healthy chickpea plants, while maximum no. of least antagonistic (23) and non-antagonistic (5) were obtained from soil collected from completely wilted plants.

Poster

Kaur, Ramandeep1* and Singh, Rama S. 2
1Entomology and Nematology Department, University of Florida, Gainesville, Florida 32611, USA, 2Department of Plant Pathology, Punjab Agricultural University, Ludhiana-141001, Punjab, India. ramanz15@yahoo.com.

Population diversity of Fusarium oxysporum and fluorescent pseudomonas in chickpea fields in India. Population diversity of Fusarium oxysporum and fluorescent pseudomonas was studied in rhizosphere and rhizoplane of healthy, partially and completely wilted chickpea plants. A total of 117 isolates of F. oxysporum were collected from different commercial grower’s field in Ludhiana District of Punjab State. Results of pathogenicity test revealed that the isolates of F. oxysporum included both pathogenic and nonpathogenic strains. Amongst all the isolates of F. oxysporum studied, 58 were pathogenic and 59 nonpathogenic isolates. The maximum number of pathogenic isolates was present in soils of completely wilted plants whereas its minimum number enumerated in soil samples of healthy plants. In contrast, maximum number of nonpathogenic isolates was obtained from rhizosphere and rhizoplane of healthy plants. On the basis of wilt development the pathogenic isolates of F. oxysporum were further categorized as highly, moderately, least pathogenic. Diversified populations of fluorescent pseudomonas differed in their antagonistic potential. Out of 90 isolates of fluorescent pseudomonas maximum antagonistic isolates were obtained from rhizosphere and rhizoplane of healthy chickpea plants, while maximum no. of least antagonistic (23) and non-antagonistic (5) were obtained from soil collected from completely wilted plants.

Poster
Kennedy, Allison* and Campbell, Jinx. University of Southern Mississippi Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39564, USA. allison.kennedy@usm.edu. Fungal diversity of Gulf Coast saltmarshes: how community profiles can aid coastal restoration. Saprophytic fungi are the dominant decomposers of standing saltmarsh plants such as Spartina alterniflora and Juncus roemeriatus and thus perform vital roles in coastal ecosystem nutrient cycling. Saltmarshes are critical habitats but are declining worldwide primarily due to human-induced disturbances. In an attempt to counter these losses in the northern Gulf of Mexico, marsh restoration efforts have increased; however, it is currently estimated that half of these restoration projects fail. This study assessed the role of saprophytic marine fungi as indicators of coastal saltmarsh ecosystem function and the length of time needed for establishment of the marine fungal saprophyte community in created marshes. Created saltmarshes of differing ages were compared with two natural reference saltmarshes using maritime fungal saprophyte diversity and abundance, and belowground fungal biomass. Morphological and molecular methods (ITS T-RFLP analysis) were used to generate fungal community fingerprints. Belowground living fungal biomass was measured using the index biochemistry ergosterol. The resulting community profiles revealed similar fungal communities in natural saltmarshes and created saltmarshes aged three years and older, with a 1.5 year-old created marsh showing lower levels of fungal colonization. Fungal saprophyte communities can serve as indicators of restoration success and must be considered when planning coastal restoration activities. Symposium Presentation

Kim, Hyo Jin*, Kim, Kyung Mo², Hong, Soon Gyu¹, Lim, Young Woon¹ and Jung, Hack Sung¹.¹ Department of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea, ²Department of Agricultural Biotechnology, College of Agricultural Life Sciences, Seoul National University, Seoul 151-921, Korea, ³Polar Bio Center, Korea Polar Research Institute, KORDI, Incheon 406-840, Korea. minervas@snu.ac.kr. IGS polymorphisms of Trametes versicolor. Sequence polymorphisms were observed in the IGS I region of 19 Trametes versicolor strains. In aligned IGS I sequences of T. versicolor, T. pubescens, and T. velutina, three polymorphic regions consisting of six types (Types 1 and 1-1, Types 2 and 2-1, and Types 3 and 3-1) were discovered. Based on IGS I sequences, polymorphism-specific PCRs, and maximum-likelihood trees, it was inferred that Types 1-1 and 3-1 were diverged from Types 1 and 3 respectively that exist in the common ancestral state of T. versicolor and T. velutina. It is probable that the speciation of T. versicolor was followed by the occurrence of Type 2-1 from Type 2 of the most recent common ancestor. It is suggested that Type 2-1 occurred through the expansion of Type 2 with the microsatellite (TAG)2 caused by the common ancestor. It is suggested that Type 2-1 occurred through the expansion of Type 2 with the microsatellite (TAG)2 caused by the common ancestor. It is suggested that Type 2-1 occurred through the expansion of Type 2 with the microsatellite (TAG)2 caused by the common ancestor. It is suggested that Type 2-1 occurred through the expansion of Type 2 with the microsatellite (TAG)2 caused by the common ancestor. It is suggested that Type 2-1 occurred through the expansion of Type 2 with the microsatellite (TAG)2 caused by the common ancestor.

Inocybe splendens complex. Species concepts for Inocybe splendens differ among mycologists. The most widely accepted concept for this species now encompasses a fairly wide range of morphological variation and includes two varieties, var. splendens and var. phaeoleuca. Inocybe splendens is ectomycorrhizal with both angiosperms and gymnosperms and is characterized by having smooth spores, pleurocystidia, and metuloid caulocystidia distributed over the stipe. A preliminary phylogenetic analysis of Inocybe splendens variants from Europe and the western United States indicates that Inocybe splendens is polyphyletic, falls into several clades, and that most of the specimens going by this name from Europe and the western United States are not conspecific. Spring-fruited specimens from the Olympic Peninsula appear to represent an undescribed taxon. This study was supported in part by NFSAT (grant ARB-1-3230-YE-04).

Kropp, Bradley R.*, Sirunyan, A.*, Matheny, P. B. and Nanagulayan, S.G.¹ Utah State University, Logan, UT 84322, USA.¹ Department of Botany, A. Manoogian St. 1, 0025, Yerevan State University, Armenia; Faculty of Biology, ² Biology Department, Clark University, 950 Main St., Worcester, MA 01610, USA. bkrkop@biology.usu.edu. Preliminary phylogenetic analysis of the Inocybe splendens complex. The most reliable method for yeast identification is from DNA analysis. RAPDs can give accurate identification, especially when species are from narrowly defined groups and the profiles are scanned and compared by pattern-matching software. More widely used is comparison of sequences from the ca. 450-600-nucleotide domains 1 and 2 (D1/D2) variable region at the 5' end of the large subunit rRNA gene. D1/D2 sequences for all known ascomycetes (1) and basidiomycetes (2) were published nearly a decade ago. The widespread use and expansion of these datasets has resulted in a near doubling of known yeasts and these datasets, which are accessible in GenBank, are widely used in clinical diagnostics, ecology and biotechnology. How well does the D1/D2 region compare with other gene sequences for rapid species identification, and are species relationships determined from D1/D2 congruent with analyses from other gene sequences? Examples of multi-gene analyses will be presented and the usefulness of D1/D2 and other single gene sequences for phylogenetics and for barcoding species will be discussed. J. Kurtzman, C. P. and C. J. Robnett. 1998. Antoiné van Leeuwenhoek 73:331-371. 2, Fell, J. W., T. Boekhout, A. Fonseca, G. Scorza and A. Statzell-Tallman. 2000. Int. J. Syst. Evol. Microbiol 50:1351-1371. Symposium Presentation

Continued on following page
Lau, Carrie K. and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. lauer.carr@students.uwlax.edu. 

Ornamental plants as potential reservoirs for Scedosporium apiospermum, an emerging fungal pathogen of humans. Scedosporium apiospermum (teleomorph Pseudallescheria boydii) is an emerging, opportunistic fungal pathogen. It can cause a degree of infections, ranging from minor allergic reactions to fatal systemic infections. Research suggests that many such infections have been misdiagnosed as more common aggressively growing fungi, such as Penicillium and Aspergillus species. The implications of misdiagnosis are significant due to the inherent resistance of S. apiospermum to many antifungal therapies, especially Amphotericin B (AmB). S. apiospermum is even able to use AmB as primary carbon and nitrogen sources. In general, little is known about the ecology, physiology, and transmission of this fungus. The objective of our research is to formulate a selective medium to aid in rapid and appropriate diagnosis. The media was supplemented with chemicals that S. apiospermum has a tolerance to, such as cycloheximide and AmB. Our second objective was to isolate S. apiospermum from common ornamental plants in houses, hospitals and offices. Identification was carried out using PCR and morphological characteristics. The purpose of this research is to provide insight into the ecological niche of S. apiospermum and to delineate possible reservoirs for its transmission to humans, both of which may aid in the proper diagnosis, treatment, and prevention of infections caused by S. apiospermum. 

Lee, Keunsub* and May, Georgiana. Plant Biological Sciences and Ornamental Plants, Ornamental Plants. 

Competitive interactions between endophytic Fusarium verticilloides and Ustilago maydis reduce smut disease severity. An ascomycete fungus Fusarium verticilloides is widespread throughout the world and often causes symptomless infections. We have investigated the effects of endophytic F. verticilloides on the fitness of maize and a fungal pathogen, Ustilago maydis using in planta experiments. In planta interaction experiments were conducted in a greenhouse with multifactorial design: 2 F. verticilloides isolates X 2 U. maydis genotypes X 3 timing of F. verticilloides inoculation. The mixture of two mating compatible sporidia of U. maydis was inoculated onto the whorl of 9-day-old maize seedlings and the spore suspension of F. verticilloides was pipetted onto the 7, 9, and 11-day-old maize seedlings. Maize height and smut disease symptoms were measured at 17 and 19 days after planting, respectively. Our data suggested that the endophytic isolates of F. verticilloides do not directly enhance maize growth but can reduce smut disease incidence when the two fungi were simultaneously inoculated to maize seedlings in the greenhouse conditions. 

Lee, Maria*, Volk, Thomas J., Cooper, Chester R. and Chandler, Julie M. Department of Microbiology, University of Wisconsin, La Crosse, WI 54601, USA, Department of Biology, University of Wisconsin, La Crosse, WI 54601, USA, Department of Biological Sciences, Youngstown State University, Youngstown, OH 44555, USA, Proteomics Research Group, Youngstown State University, Youngstown, OH 44555, USA. lee.mari@students.uwlax.edu. 

Proteomics profiling of dimorphism in Penicillium marneffei, an opportunistic fungal pathogen of humans. Penicillium marneffei is a unique thermal dimorphic fungus. It causes disease among immunocompromised patients and is endemic in parts of Southeast Asia. Although the exact mode of transmission is unknown, inhalation of the spores is thought to cause initial pulmonary infection, which then disseminates to other organs. It can be fatal if diagnosis is not done early and no treatment administered promptly. The main objective of this proteomics research is to characterize some of the proteins produced by P. marneffei that effect dimorphism. P. marneffei was cultured at 25 degree Celcius and 37 degree Celcius for the mold and yeast phase, respectively. The cells of each phase were processed for two-dimensional gel electrophoresis. Protein profiles from each phase were compared for unique protein spots. These spots were excised and the proteins separated via mass spectrometry. From these data, specific proteins can be correlated with genes known to be associated with dimorphism. From these profiles, one protein or more can be selected and studied as possible diagnostic marker(s) or antifungal target(s) for the disease. A comprehensive molecular-based understanding of dimorphism as developed in P. marneffei may be useful in understanding more about other dimorphic fungal pathogens such as Blastomyces, Histoplasma, Coccidioides, Paracoccidioides, and Sporothrix. 

Letcher, Peter M.*; Velev, Carlos G.; Powell, Martha J. and Churchill, Perry F. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, Alabama, USA, Dept. of Biodiversity y Biologia Experimental, Universidad de Buenos Aires, Buenos Aires, Argentina. lethch006@bama.ua.edu. 

Waking a sleeping giant: diversity in the Rhizophydiales. The genus Rhizophydatum (Chytridiomycetes, Chytridiomycota) has long been a taxonomically challenging entity, with over 229 described taxa. Members of the genus occur in both soils and aquatic habitats as saprophytes and parasites. Traditionally, species were artificially characterized based on substrate or host. Thallus characters were similarly problematic, often intergrading with those of other genera. Our recent studies of the monophyletic Rhizophydatum clade using ultrastructural and molecular analyses have revealed remarkable diversity and highlight the need for taxonomic revision of this group. A new order, Rhizophydiales, was excised from the Chytridiidae and erected based on a unique suite of zoospore ultrastructural character states and molecular-based phylogeny. Kappamyces was the first chytrid genus established based on molecular phylogenetics. Most recently, ultrastructural and molecular analyses of 140 isolates in Rhizophydiales from diverse habitats have resulted in delineation of ten new families and twelve new genera. Within the new order Rhizophydiales there are more than twenty distinct zoospore morphologies represented, a variety in form that suggests we have only begun to discover the diversity that resides in these classically considered “little round chytrids”. 

Contributed Presentation

Lewis, David P.* and Ovrebo, Clark L. Gulf States Mycological Society, RR 2, Box 194-L, Newton, TX 75966, USA, Department of Biology, University of Central Oklahoma, Edmond, OK 73034, USA. plewis@ius.net. New species described and bibliography of Agaricae fungus from East Texas. East Texas is an area of great biodiversity, is a transition zone from the mesophytic gulf coast into the more xeric southwest, and with abundant moisture and tree diversity provides excellent habitats for the appearance of fleshly higher fungi. While plants have been documented in eastern Texas for over 150 years, little work has been accomplished on the higher fungi. Forty-nine taxa of agarics and boletes have been described from east Texas.

Continued on following page
Harry Thiers initiated the first survey of the agaric and bolete mycota of East Texas in the mid 1950s. He described 30 new taxa and reported over 200 species of agarics and boletes. Starting in the 1970s, David Lewis and Bill Cibula began surveys of the Big Thicket National Preserve and surrounding areas and reported their findings in various publications and reports and helped document several new taxa. O.K. Miller, E. Both, R. Singer, S.L. Miller, B. Buycx, H.V. Smith, A.H. Smith and N.S. Weber are other mycologists who have documented or described new species from this region. Despite these initial inventories, eastern Texas remains an area in need of critical analysis of its agaric and bolete mycota where it is estimated that over 3000 species of higher fungi exist. An All Taxa Biotic Inventory project was initiated in the Big Thicket National Preserve in 2006 to further document the fungal diversity.

**Poster**

Lewis, David P.1,2, Overbo, Clark L.3 and Mata, Juan L.3 1Gulf States Mycological Society, RR 2, Box 194-L, Newton, TX 75966, USA, 2Department of Biology, University of Central Oklahoma, Edmond, OK 73034, USA, 3Department of Biology, University of Southern Alabama, Mobile, AL 36688, USA. plewis@jas.net. New species described and bibliography of Agaricalean fungi from Louisiana, Mississippi and Alabama. The United States Gulf Coast is an area of great biodiversity, is a transition zone from the mesophytic gulf coastal plain into the more humid tropics, and with abundant moisture and tree diversity provides excellent habitats for the appearance of fleshy fungi. Early research on the agars and boletes of the three Gulf States, Louisiana, Mississippi and Alabama was prevalent from the 1890s to the 1920s. W.A. Murrill, F.S. Earle, L.M. Underwood and C.H. Peck described many species. Centers of collecting activity include New Orleans, Biloxi and Ocean Springs, (Mississippi) and Auburn, Alabama. Many of these new taxa were reported in North American Flora and Mycologia by W.A. Murrill, although F.S. Earle and L.M. Underwood made many of the collections. Many of the taxa described over a century ago have not been collected since their original description. Recently, from the 1970s to the 1990s, new taxa of agarics and boletes were described by W. G. Cibula, G. M. Mueller, T. Feibelman, R. Singer, A. Bessette, E. Both, T. Baroni, D. Jenkins, N. Weber, A. H. Smith and L. Hesler. It is estimated that from 3000 to 5000 species of fleshy fungi occur along the Gulf Coast, but no extensive treatment is available.

**Poster**

Lindley, L.A.*, Brown, M.W., Lawrence, A., Silberman, J.D. and Spiegel, F.W. Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville, Arkansas 72701, USA. llindner@uark.edu. Schizoplasmodium: a genus reconstituted. When the Protostelid slime mold genus Schizoplasmodium was described in 1966 it included a single species, S. cavostieloides. Two new species were described that same year, S. ovatum and S. gracile. In 1970, Olive moved the long-stalked species S. ovatum and S. gracile to a new genus Nematostelium. The discovery of an amoeboflagellate stage in the life cycle of an organism that otherwise looked like Nematostelium “Schizoplasmodium” gracile led to the description of a third genus Ceratiomyxella. In 1976, Olive added two rare ballistosporous species to the genus Schizoplasmodium, S. obovatum, and S. seychellatarum. We performed detailed morphologic reassessment and molecular analyses of these taxa to assess their phylogenetic relationships. Gene sequences from the small subunit of the ribosome (SSU rDNA) place these organisms into a well supported clade. Additionally, the characters which separate the organisms as individual species: stalk-length, spore dispersal method, and presence/absence of an amoeboflagellate stage in the life-cycle are overwhelmed by the majority of life-cycle, morphological, ultrastructural, and molecular characters that hold these organisms together as a morphotypic group. Here we present morphological and molecular evidence that shows that these organisms are all closely related. Both morphology and molecular data support the synonymy of Nematostelium gracile and Ceratiomyxella tahitiensis thery casting doubt on the validity of genus Ceratiomyxella. On this basis we propose to move the species Nematostelium ovatum, Nematostelium gracile, and Ceratiomyxella tahitiensis into the genus Schizoplasmodi-um and to rename them as Schizoplasmodium ovatum, Schizoplasmodium gracile, and Schizoplasmodium tahitiensis respectively. Poster

Lindner, Daniel L.*, and Banik, Mark T. Center for Forest Mycology Research, Madison Field Office of the Northern Research Station, USDA-Forest Service, One Gifford Pinchot Drive, Madison, Wisconsin 53726, USA. dlindner@biotec.or.th. A comparison of direct sequencing versus cloning and sequencing for studying fungal associates of spruce roots. To better understand DNA sequencing as a tool to assess fungal root associates, 40 root tips were collected from a single Picea glauca root system. Genomic DNA was isolated from 20 small root tips (SRT, 1.0 - 2.0 mm long) and 20 large root tips (LRT, 5.0 - 6.0 mm long). All 20 of the SRT and 17 of the LRT yielded visible PCR bands with primers ITS1F/ITS4. The resultant PCR products were sequenced directly using primer ITS4 and also cloned using the Promega pGEM-T Vector System II. The 20 SRT all yielded DNA that was identified with direct sequencing as one of four commonly associated root fungi. Thirteen of the LRT also yielded DNA whose sequences matched one of these same four fungi while the other 7 yielded no useful sequence from direct sequencing. Cloning of the PCR products followed by sequencing resulted in the detection of additional fungi beyond those found via direct sequencing in 7 SRT and 2 LRT. In addition all 7 of the LRT that yielded no usable sequences with direct sequencing produced identifications when cloned. Overall, direct sequencing indicated the presence of 4 fungal taxa on both SRT and LRT, while cloning indicated the presence of 8 taxa on the SRT and 14 on the LRT. Furthermore cloning resulted in the recovery of usable sequences from 100% of the root tips sampled compared to 83% for direct sequencing.

**Poster**

Lombard, Lorenzo1, Bogale, Mesfin2, Montenegro, Fernando2, Wingfield, Brenda D.1 and Wingfield, Michael J.1 1Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa, 2Fundacion Forestal Juan Manuel Durini, Ecuador. lorenzo.lombard@fabi.up.ac.za. A bark canker disease of the tropical hardwood tree, Cedrelina catenaeformis in Ecuador. Cedrelina catenaeformis is an indigenous leguminous tree that occurs naturally in the Amazonian regions of Ecuador, Peru and Colombia. This tree is an economically valuable component of local forestry industries and it is also culturally important to rural communities in these countries. A canker disease has recently emerged on C. catenaeformis in Ecuadorian plantations of this tree. The disease is characterized by severe cracks in the bark, from which gum exudes, wood discoloration associated with these cracks as well as die-back and stunted growth. Isolations from cankers consistently yielded species of Fusarium. These species were identified as F. solani, F. oxysporum and F. decemcellare based on morphology as well as on comparisons of their partial translation elongation factor-1 alpha gene sequences. In inoculations, all three Fusarium species gave rise to cankers similar to those found on trees under natural conditions and they were consistently re-isolated from the lesions. The canker disease on C. catenaeformis appears to be caused by three species of Fusarium, all of which are equally pathogenic.

**Poster**

Luangsa-ard, Janet Jennifer*, Tasanathai, Kanoksri, Ridkaew, Rungpet and Hywel-Jones, Nigel. National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand Science Park, 113 Paholyothin Rd., Khlong 1, Khlong Luang, Pathum Thani 12120, Thailand. jujen@biotec.or.th. Phylogenetic distribution and relationships of Ophiocordycps producing Hymenositile and Hirsutella anamorphs in Thailand. Hymenositile has its known teleomorph in the genus Ophiocordycps and is closely related to the Hirsutella anamorphs producing the same teleomorph. There are about 13 species of Hymenositile known worldwide, all are pathogens of arthropods and several of these are found in Thailand. These are Hy. dipertigena (O. dipertigena), Hy. nutans (O. nutans), H. aurantiaca (O. myrmecophila/O. irangiensis), Hymenositile spp. linked to O. phaeococphala and O. pseudolydii. There are ca. 80 known species of Hirsutella worldwide with teleomorphs in three genera: Ophiocordycps, Torrubiaella

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and Cordycepioideus. This suggests of a polyphyletic nature of the genus. In Thailand Ophiocordycipes species linked with Hirsutella anamorphs are O. unilateralis, O. brunneapunctata, O. communis, O. humbertii, O. cf. aciculatus and O. rhioides. Of these six teleomorphs, only two were formally linked to Hirsutella anamorphs (O. unilateralis – H. formicarum and O. humbertii – H. saussurei) although on the host Hirsutella anamorphs have been identified. Molecular work has shown the close relationship of Hymenosithe and Hirsutella and there are species sharing features of these two genera in their morphology. Our results show that the genus Hymenosithe is derived from Hirsutella, occupying more the upper branches in the tree infecting dipteran flies to wasps and ants. \textit{Contributed Presentation.}

Manoch, L.*, Jeamjitt, O., Dethoup, T., Eamvijarn, A. and Pikulklin, S. Department of Plant Pathology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand. agrflm@ku.ac.th.

\textit{Some notewothy ascomycetes from soil and plants in Thailand.} During the course of an ecological survey on the ascomycetes of Thailand, soil samples and diseased plants were collected from various locations. Alcohol and heat treatments, soil plate, dilution plate methods and Gochnauer’s glucose ammonium nitrate agar were used to isolate soil fungi. The supplementation of actidine (cyclohexemide) to agar media was employed to isolate keratinolytic fungi. The tissue transplating technique and half strength potato dextrose agar (PDA) were employed for isolation of plant parasitic fungi from diseased tissues. Morphological characteristics of the ascomycetes were determined, such as growth rate, color, texture on different agar medium. Microscopic characters were examined under stereo, light and scanning electron microscopes. The results revealed that a number of Pyrenomycetes were found from soil including Echinopodospora spinosa, Gelasinospora dictyophora, G. hip-hopotomata, Nectria viridescense popotomata, and N. dodgei. Species of Eurotiales (Trichocomaceae) from soil included Emericella rugulosa, E. variecolor, E. penicilium spp., Eurotium spp., Hamygera avellanea, and Talaromyces spp. Several species of keratinolytic fungi were found including Arachniotus sp. and related genera. Pyrenomycetes from diseased plants were Nectria hematococca with Fusarium solani anamorphic state (blight of orchid leaf), Gnomonia sp. on cinnamon leaf, Leptothesphaerulina sp. with Phoma sp. anamorphic state (blight of cabbage), and one unidentified species of Pyrenomycetes on decaying Ficus twig. Pure cultures of all fungal isolates are being maintained at the Fungal Culture Collection at the Department of Plant Pathology, Kasetsart University for further investigations. \textit{Poster}

Mata, Juan L.¹  and Ovrebo, Clark L.² ¹Dept. of Biological Sciences, University of South Alabama, Mobile, AL 36695, USA, ²Dept. of Biology, University of Central Oklahoma, Edmond, OK 73034, USA. jmata@usouthal.edu.

\textit{New reports of Gymnopus for Costa Rica and Panama.} Field trips to the Caribbean lowlands of Costa Rica and Panama in the last two decades have yielded several dozen collybioid collections. Morphological examination of those collections has resulted in the discovery of species not previously reported for this region of Central America. The distribution range for Gymnopus luxurians, initially described from southern United States and recently reported in Dominican Republic, is extended into the Caribbean lowlands of Costa Rica and Panama. Similarly, G. subprunosa, known from the Greater Antilles, is reported for Panama. Other new reports for Panama, but previously recorded from Costa Rica, are G. neotropicus, G. omphalodes, G. subcylathiformis, and G. luxariar var. copeyi. \textit{Poster}

Matheny, P. Brandon¹ ², Aime, M. Catherine³, Buyck, Bart¹, Desjardin, Dennis E.¹ ², Horak, Egon⁴ and Lodge, D. Jean⁴ ² Biology Department, Clark University, 950 Main St., Worcester, Massachusetts 01610, USA, ³USDA-ARS, Systematic Botany and Mycology Laboratory, Room 304, Building 011A, 10300 Baltimore Ave, Beltsville, Maryland 20705-2350, USA, ⁴Museum National D’histoire Naturelle, Département Systématique et Evolution, Bâtiment de Cryptogame, Herbarie de Mycologie, Case postale 39 – 57, rue Cuvier, 75231 Paris Cedex 05, France, ²Department of Biology, San Francisco State University, San Francisco, California 94132, USA, ⁵Ex-Curator Cryptogamic Herbarium ZT, Federal Institute of Technology, ETH, CH-8092 Zurich, Switzerland, ⁶International Institute of Tropical Forestry, USDA Forest Service-FPL, PO Box 1377 Luquillo, Puerto Rico 00773-1377. pmatheny@clarku.edu.

\textit{The evolution of tropical species of Inocybaceae (Agaricales).} Neotropical and paleotropical species of the ectomycorrhizal (EM) mushroom family Inocybaceae currently comprise 18 percent of the species-level diversity in the family from tropical latitudes, including lowland and montane habitats. This poor representation of tropical taxa, combined with the assumption that morphological traits of tropical species are advanced, suggests that tropical taxa may be recently derived, and that the family as a whole had a temperate Northern or Southern hemisphere ancestral area (center of origin). As a consequence, species of Inocybaceae are thought to have migrated or dispersed relatively recently into tropical areas. A corollary of these hypotheses would suggest the EM symbiosis has switched repeatedly to tropical angiosperm partners of Casuarinaceae, Fabaceae, Fagaceae, Dipterocarpaceae, Myrtaceae, Polygonaceae, Uapacaceae, and perhaps other partners from temperate gymnosperm and angiosperm partners. Our recent research has uncovered multiple novel lineages of Inocybaceae, almost all of which likely contain endemic undescribed species from tropical latitudes. In particular, the diversity of the family has been undersampled in Miombo woodlands of Zambia, mixed dipterocarp/Fagaceae forests of Thailand and India, and in the neotropics. We test these hypotheses in a phylogenetic context using a molecular dataset of multiple nuclear genes. We report that tropical taxa of Inocybaceae tend to be diffuse (polyphyletic) throughout the family phylogeny, and that tropical clades represent both early diverging and recently derived lineages. \textit{Poster}

McDonald, Tami R.¹, Armaleo, Daniele and Lutzoni, François. Department of Biology, Duke University, Durham, North Carolina, USA, tm3@duke.edu.

\textit{Epigenetics of the lichen symbiosis.} DNA methylation is a key regulator of development in higher eukaryotes. Although present at negligible levels in many fungi, DNA methylation is considerably higher in lichen-forming fungi. In the lichen Cladonia grayi, the DNA of the apysymbiotically grown fungus is relatively unmethylated, while the DNA of the fungus in symbiotic association with its algal partner is highly methylated. As DNA methylation is one hallmark of epigenetic gene silencing, this observation suggests that gene silencing may be a critical step in the formation or maintenance of the lichen symbiosis. To determine which sequences are subject to methylation, we made a library of methylated DNA from the fungal component of the lichen. Analysis of clones from the library suggests that most targets of DNA methylation are protein-coding sequences rather than intergenic regions, transposable elements or repeated DNA. The implication is that these regions are downregulated or silenced in the symbiotic state. The correlation between DNA methylation on these candidate regions and the presence of related marks of epigenetic silencing, including transcriptionally repressive histone H3 methylation, presence of linker histone H1 and heterochromatin binding protein are being investigated. \textit{Poster}

McKenzie-Porter, Teresita¹, Skillman, Jane E.¹ and Moncalvo, Jean Marc.¹ ²Department of Ecology and Evolutionary Biology, University of Toronto, 25 Willcocks Street, Toronto, ON M5S 3B2, ²Department of Natural History, Royal Ontario Museum, 100 Queens Park, Toronto, ON M5S 2C6. terri.mclenon@utoronto.ca. \textit{Application of phylogenetic methods to assess fungal diversity and community structure from DNA sequences.} Advances in molecular biology techniques, expansion of nucleotide sequence databases, and development of novel bioinformatic tools are collectively making large DNA-based environmental microbial surveys more common. These methods routinely detect hundreds of divergent sequences from even small halfgram samples of soil that are often difficult to identify because they poorly match sequences of known taxa in public databases. Phylogenetic methods can be used to classify unknown sequences, detect new

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taxa, and assess the functional diversity of taxa in a sample by comparison with known references. However, easy-to-use methods to cluster sequences and determine significant taxonomic and functional differences among samples are still in their infancy. Our objective is to compare four methods that are currently available: 1. Phylogenetic diversity measure (Faith 1992 Biol Cons 61:1); 2. Phylogenetic test (Martin 2002 AEM 68: 3673); 3. Libshuff analysis (Schloss et al. 2004 AEM 70: 5485); and 4. Unifrac analysis (Lopezun & Knight 2005 AEM 71: 8228). For this comparison we use LSU-rDNA sequence data obtained along a single core of forest soil to test whether or not fungal community structure changes significantly in relation to depth. The significance of our findings is discussed in the more general context of estimating fungal biological diversity from environmental samples. Contributed Presentation

Mena Portales, J. Instituto de Ecología y Sistematica, Carretera de Varona Km 3.5. Catedal. Boyeros. A.P. 8029. Ciudad de la Habana 10800. Cuba. julio.mena@infomed.sld.cu. Preparing a national conservation strategy for fungi: the Cuban experience. Cuba, as a signatory to the 1992 Rio Convention on Biological Diversity, developed the National Study on Biological Diversity in the Republic of Cuba, finished in 1995 and published by Vales et al. (1998), and the National Strategy of Biological Diversity and Action Plan in the Republic of Cuba (Vilamajo et al., 2002). These diagnoses of Cubas fungal biodiversity status were no more than a start which left many holes because of the unique characteristics of these organisms and the dispersed nature of mycological information. A national conservation strategy explicitly for fungi was therefore developed, based on information in the computerised databases of the UK Darwin Initiative project, Fungi of the Caribbean (1997-2000) and Cuban mycological literature. The document is probably the first in Latin America specifically to address conservation of fungal diversity and is one of only very few in the world. The strategy has two parts: in the first, the current state of knowledge of Cuban fungi is reviewed and analysed in respect of taxonomic and ecological groups, while legislative aspects, environmental education and resources available for study and conservation of Cuban fungi are also covered; in the second, the strategy itself and an action plan are set out in respect of the holes identified in the first part. The document has the same goals as those of the Cuban National Strategy of Biodiversity, but it focuses more fully on the issues which must be addressed before this unique and key group of organisms can be conserved and at the same time used sustainably and rationally. Symposium Presentation

Miller, Bradley W.* and Fox, Thomas R. Forest Nutrition Cooperative, Virginia Polytechnic Institute and State University, Department of Forestry, Chatham Hall, Blacksburg, Virginia 24061, USA. bmwillergk@hotmail.com. Ectomycorrhizal rhizosphere affects on long-term inorganic and organic P pools in forest soils. Phosphorus is one of the most limiting nutrients in the soil due to strong sorption to amorphous Fe and Al oxides. Ectomycorrhizal fungi secrete a variety of organic acids, such as oxalate, to solubilize P from amorphous surfaces. A loblolly pine plantation established in 1980 was fertilized once with 250 lbs. per acre of diammonium phosphate. Twenty years later pine trees responded with a height increase greater than six feet. Soil samples analyzed suggest that the majority of P applied is now sorbed to Fe- and Al-oxides with a small but significant increase in organic P in fertilized plots. We will present results of the effects of the ectomycorrhizal rhizosphere (ER) on organic and inorganic P pools in fertilized and control plots of a loblolly pine stand 27 years after fertilization. Ectomycorrhizal short roots in fertilized and control plots will be compared to the bulk soil using NMR. Total P content of amorphous Fe- and Al-oxides will be also be compared. We will also report the results comparing P released by single and sequential oxalate additions to soil fractions in an attempt to measure the long-term affects of the ER and P fertilization on organic and inorganic P pools. Results will advance our understanding of the ER on P pools in forest soils. Contributed Presentation

Mims, Charles W.1,4, Richardson, Elizabeth A.2 and Taylor, Josephine.3 1Department of Plant Pathology, University of Georgia, Athens, GA 30602, USA, 2Department of Plant Biology, University of Georgia, Athens, GA 30602, USA, 3Department of Biology, S. F. Austin State University, Nacogdoches, TX 75962, USA. cw.mims@uga.edu. Orange rust of Rubus: a fascinating challenge for mycologists. Orange rust is a common disease of blackberry (Rubus spp.) in the U. S. and has been studied at the light microscopic level by numerous early workers. The disease is very important in the northeastern but also is widespread in southern states. From a mycological standpoint, orange rust is particularly interesting because of the fact that it is caused by two different pathogens that produce virtually identical symptoms. One is Gymnoconia peckiana which is demicytic while the other is a microcyclic species known as Gymnoconia nitens. Both are autotoxic rusts that cause permanent systemic infections involving roots. Crowns on infected roots give rise to weak spindly shoots with pale green stunted leaves whose undersides become bright orange as the result of the development of sorus filled with bright orange spores. In the case of G. peckiana these spores are aeciospores but in G. nitens they are actually teliospores. The study of orange rust disease becomes even more complicated because of the fact that G. nitens has been shown to exist in two forms that likely were confused with one another prior to 1924. One of these forms possesses spermatogonia and produces four-celled basidia while the other typically lacks spermatogonia and produces two-celled basidia. In this study we used a combination of light and electron microscopy to examine nuclear behavior during both teliospore formation/germination and basidium/basidiospore formation in both forms of G. nitens. At this time it is unclear if karyogamy and meiosis occur in either of these two forms. Contributed Presentation

Minter, D.W. CABI, Bakeham Lane, Egham, Surrey, TW20 9TY, UK. d.minter@cabi.org. Microfungi - orphans of the conservation movement. Despite evidence of decline in many populations, fungi are almost completely unprotected worldwide. Most conservation law covers only animals and plants. Most protected areas lack policies to manage fungi in their care. The need for fungal conservation is rarely vocalized, so most policymakers are unaware of the issue. The few existing resources are directed only to Basidiomycetes and perhaps lichen-forming fungi. For the non-lichen-forming microfungi, the conservation gap is total. This symposium presentation will describe a new initiative which aims to address the problem. Three specialist groups are being established for conservation of microfungi at a global level. These groups will aim to work in collaboration with the two existing IUCN Species Survival Commission Specialist Groups (one for fungi in general, the other for lichens) and with conservation-minded mycologists worldwide. The groups will prepare global conservation plans for the organisms they represent and seek to stimulate awareness of threats, including climate change. A draft and preliminary website for each group has been constructed (www.cybertruffle.org.uk/ascos for non-lichen-forming ascomycetes & conidial fungi, www.cybertruffle.org.uk/rustsmut for rusts & smuts, and www.cybertruffle.org.uk/moulds for chromists, chytrids, myxomycetes and zygomycetes). Those websites will make available each plan and, it is hoped, will evolve to become a focus for conservation of microfungi, providing information and advice. Symposium Presentation

Mongkolsamrit, Suchada, Luangsara-ard, Janet Jennifer* and Hywel-Jones, Nigel. National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency, 113 Paholyothin Rd., Khlong 1, Khlong Luang Pathum Thani 12120, Thailand. jajen@biotec.or.th. Phylogenetic relationships of Hypocreella species producing orange stromata in Thailand. Hypocreella discoides is a fungal pathogen of white flies producing an Aschersonia samoensis as the anamorph. It was described by Petch (1921) and a complete re-description was made by Hywel-Jones & Evans (1993). Field material provisionally labeled as Hypocreella cf dis-
coidea were compared with *H. discoidea* strains because they were morphologically similar, having orange color and producing perihetica and pycnidia embedded in the stromata. These were all *Hypocrella* telemorphs with orange stroma and producing whole ascospores. For the molecular study a phylogeny based on sequences of the 5.8S rDNA and flanking internal transcribed spacers regions clearly showed that *Hypocrella cl discoidea* is distinct from a clade of *H. discoidea*. This indicates that there is more than one species based on orange stromata. A review of all *Hypocrella* specimens stored at Kew Gardens (UK) showed that this material (mostly on bamboo but also on dicotyledo- nous plants) has not been previously collected and named. Work is un- derway to describe this as a new species in the genus *Hypocrella* from Thailand. The name *Hypocrella calendulina* is proposed to highlight the orange color of the stromata. **Poster**

Morgenstern, Ingo* and Hibbett, David S. Department of Biology, Clark University, Worcester, MA 01610, USA. imorgensten@clarku.edu. **Characterization of a manganese peroxidase gene in Fomitiporia mediterranea (Hymenochaetales).** White-rotting fungi in the basidiomycetes are capable of degrading lignin, hereby performing an ecologically important role in the global terrestrial carbon cycle. Lignin degradation is achieved by the secretion of extracel- lular peroxidases, namely manganese peroxidase (MnP), lignin perox- idase (LiP) and versatile peroxidase (VP). Although white rot taxa occur widespread over the phylogenic tree in almost all major clades, the presence of genes encoding for lignin degrading peroxidases based on sequence data has only been established in a few lineages. These in- clude the polyporoid, euagarics, and russuloid clades. Recently, we re- ported the presence of a MnP encoding gene based on a partial se- quence in *Fomitiporia mediterranea*, which is a member of the hymenochaetid clade. In a phylogenetic analysis this sequence takes a basal position in a well defined clade of “classical” MnPs. Our current research is aimed at obtaining a full-length sequence for this gene and to compare it with characterized full-length MnP sequences found in polyporoid and euagarics species. Results from this analysis may not only help us to better understand the evolution of lignin degrading en- zymes in the basidiomycetes, but may also be of interest in an applied field. *F. mediterranea* is associated with a plant disease (Esca) affect- ing grape vines in Europe and other parts of the world. Symptoms of the disease include an extended white rot in the trunks of affected vines. **Poster**

Mueller, Gregory M. * and Hosaka, Kentaro. Department of Botany, Field Museum of Natural History, 1400 S. Lake Shore Drive, Chicago, IL 60605-2496, USA. gmueller@fieldmuseum.org. **Using the Laccaria-Hydnumgium clade as a model to study diversity, biogeographic, and host specificity patterns of macrofungi.** Due to its cos- mopolitan distribution, frequency of collection, manageable size (75-100 species worldwide), and utility in studies on ectomycorrhizas, the Laccaria - Hydnumgium clade is an appropriate model system to study diversity, biogeographic, and host specificity patterns of macro- fungus. Multigene phylogenetic analyses were undertaken with material covering the distribution and much of the morphological range of the clade. *Hydnumgium* is nested within Laccaria, consistent with our pre- liminary data. A number of previously undescribed species were un- covered. All taxa from temperate South America and Australasia, in- cluding 3 of 4 taxa from Papua New Guinea, form a basal paraphyly. Taxa from Northern Hemisphere, including tropical America and Asia form a well-supported clade nested within the austral grade. While we detect a strong vicariance signal, dispersal and subsequent radiations are responsible for the current distribution patterns. Historical host specificity may not strongly supported in our phylogeny. Some New Zealand Nothofagus-associated taxa form a monophyletic group, while others are intermixed within the austral grade that is represented mostly by Myrtaeae-associated taxa. Our data suggest Nothofagus-associ- ated taxa dispersed into New Zealand after the reestablishment of Nothofagus on the islands. **Presidential Address**

Murrin, F.* and LeCointre, C. Department of Biology, Memorial Uni- versity of Newfoundland, St. Johns, Newfoundland, A1B X9, Canada. fmurrin@mun.ca. **Mycorrhizal mushroom communities in the boreal forest of Newfoundland: the impact of introduced moose.** Within the boreal forest of Terra Nova National Park on the island of Newfoundland, disturbances due to insect activity and browsing by moose (*Alces alces andersoni*) are resulting in the replacement of Bal- sam Fir (*Abies balsamea*) with species such as Black Spruce (*Picea mariana*), thereby changing the landscape and reducing biodiversity within this park. The purpose of this research is to determine the im- pact of these disturbances on the ectomycorrhizal communities in Bel- sam Fir/Feather Moss stands and we report here preliminary results of two seasons of study. Fruiting bodies were collected in control and moose enclosure plots within five previously-established study sites with different levels of past insect disturbance. Species identifications and fruiting body numbers were recorded to determine species rich- ness, frequency and similarity among plots and sites. At selected sites, fruiting bodies of non-mycorrhizal species were also processed. While preliminary data support the hypothesis that lack of moose browsing has a positive effect on ectomycorrhizal community structure, we found no evidence that the ectomycorrhizal community varies with level of past insect disturbance. While moose are native to much of Canada, they were introduced to the island of Newfoundland in 1878 and again in 1904. The insular, and thus isolated, nature of Newfoundland may increase the effect of this invasive herbivore on forest community structure and mycorrhizal diversity. **Poster**

Ndiritu, George, G.* and Spiegel, Fredrick, W. 1 Department of Bio- logical Science, University of Arkansas, Fayetteville, AR 72701, USA, 2Centre for Biodiversity, National Museums of Kenya, 40568 00100, Nairobi, Kenya. gndirir@uark.edu. **Assessment of protostelid diversi- ty from natural and anthropogenic impacted tropical habitats in Kenya.** Protostelids are unicellular eukaryotic microorganisms which have amoebal trophic cells and fruiting bodies in their life cycles. They tend to show a ubiquitous distribution and are primarily microbivorous of bacteria, fungi, algae and often abundant, on or in decaying plant ma- terial. In spite of their omnipresence in most habitats where they are sus- pected to play an important ecological role, protostelids are still some of the most understudied organisms world wide. In order to contribute more information, a rapid assessment survey was carried out in August 2005 to determine protostelid occurrence in Aberdare region, in central Kenya. Samples were collected from 45 sites (20 by 20 m each) along an elevation gradient (1785 to 3396 m) in habitats under different land use regimes and different vegetation types. Seventeen species were re- covered from all substrates. Species richness was highest in ground litter (16), followed by aerial litter (13), aerial bark (10) and ground bark (7). The most frequent species on the ground litter were Protostelium mycophaga, Solfiformum, irregularis, Schizoplasmodiopsis pseudoen- dospora and S. ameboidea whereas P. mycophaga and S. irregularis were most abundant in aerial litter. Species richness, composition and microhabitat preferences in Aberdare region correlated more strongly to those reported in temperate countries than to those recorded from relat- ively similar tropical habitats in Costa Rica and Puerto Rico. However some of the shared species showed significant morphological variation. Species richness and abundance decrease with increase in elevation whilst land use regimes seemed to influence protostelid assemblages but in an unclear way. **Poster**

Ndiritu, George, G.*, Spiegel, Fredrick, W. and Stephenson, Steven L. Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. gndirir@uark.edu. **Distribution and ecology of the assemblages of myxomycetes associated with major vegetation types in Big Bend National Park, USA.** A study was carried out to obtain data on the distribution and ecology of the assemblages of myxomycetes associated with aerial litter and ground litter in Big Bend National Park in Texas. Twelve plots (each 30 by 30 m) were estab- lished along an elevation gradient (564 to 1807 m) during March 2005. Samples of bark from living trees and litter were obtained from these

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plots, which encompassed all of the major vegetation types in the Park. For the 447 moist chambers prepared, 95.8% (428) produced some evidence (either fruiting bodies or plasmodia) of myxomycetes. Overall, 68 species were recorded (57 from aerial litter and 54 from ground litter, respectively). The most abundant species were *Perichaena depressa* (13% of 975 records), *Arcyria cinerea* (9%), *P. chrysosperma* (8%), *Badhamia gracilis* (8%), *Didymium squamulosum* (5%), *Physarum pusillum* (5%) and *D. anellus* (5%). Species composition of the assemblages of myxomycetes present varied between aerial litter and ground litter as well as among the major vegetation types. Environmental factors such as site moisture conditions changed spatially in the Park while values of pH differed for the various substrates sampled. Presumably, these factors are largely responsible for the observed differences in species assemblages and distribution patterns in the Park. **Poster**

**Nevell, Lorelei L.** Pacific Northwest Mycology Service, Portland, OR. *Further analyses. Important ectomycorrhizal genus, and establishes the groundwork for hypotheses for species distribution and morphological evolution in this* logical Nomenclature.

**Full-fledged partner of the International Code of Botanical and Mycological Nomenclature.**

"We are currently conducting physiological studies on various species of the genera *Coprinus*, *Coprinellus*, and *Coprinopsis*, to elucidate mechanisms of wood decay and to screen for bioremediation and bioconversion. We are interested in the role of biodegradation in the decay of wood, and the potential for the use of wood decay fungi in the bioremediation of contaminated sites. Our studies have shown that certain fungi, such as *Phylloporus*, have the potential to degrade a variety of organic materials, including lignin and cellulose. These fungi are of particular interest because they are capable of growing and reproducing on a wide range of substrates, including wood, paper, and plastics. This makes them ideal candidates for use in bioremediation applications.**

**Phylogeny of the widely distributed ectomycorrhizal bolete* Tylopilus ballouii.** Dispersal over historical and contemporary time scales influences numerous processes including speciation, metapopulation dynamics, and responses to environmental change. To date, the biogeographic studies of hymenomycetes have focused on saprobic species; however, ascomycetous (EM) taxa are likely to exhibit different patterns due to their obligately symbiotic life cycles. As a widely-distributed, easily recognized morphospecies, *Tylopilus ballouii* is a promising model for biogeographic and population genetics studies for EM fungi over multiple spatial and temporal scales. Here, we present a phylogeographic analysis of *T. ballouii* from both Old and New World populations using RPB1 sequence data. The recognition of several well-supported clades and significant sequence divergence in both protein coding and non-coding regions suggests that *T. ballouii* is a species complex rather than a single species. While the analysis does reveal some evidence for geographic structuring, it also yields some unexpected results; while these results cannot discount the possibility of infrequent long-distance dispersal, the degree of observed sequence divergence indicates that populations have been isolated for a significant time. We are currently sampling additional loci for an expanded dataset with improved geographical representation and additional samples from within geographical areas. **Contributed Presentation**

**Ovrebo, Clark L.**, Hughes, Karen W. and Halling, Roy E. **1Department of Biology, University of Central Oklahoma, Edmond, OK 73034, USA. 2Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA.** Institute of Systematic Botany, The New York Botanical Garden, Bronx, NY 10458, USA. *Coverage*
A new species of Tricholoma from Costa Rica. Collections of an undescribed species of Tricholoma sect. Genuina were made in the oak forests of Costa Rica. The fungus is characterized by the light yellowish brown, viscid pileus, very pale yellow lamellae and stipe, and by crowded lamellae. DNA was extracted using a modified CTAB buffer followed by alcohol precipitation. Primers ITS1F and ITS4 were used for PCR of the ribosomal RNA ITS region. Dideoxy sequencing was primed with ITS5 in the forward direction and ITS4 in the reverse direction with alignment and trimming done manually. Parsimony analysis was performed in PAUP using 1000 bootstrap replicates. A monophyletic clade of nine Tricholoma collections resulted. A second clade appeared as a sister to the first clade, the latter containing two collections deposited in GenBank as Tricholoma ustale and T. ustaloides respectively, but with poor bootstrap support. Two additional collections comprise a third clade which is basal to the putative T. ustale/T. ustaloides clade. Collections in the first clade represent a hitherto unnamed species of Tricholoma apparently related to the second white-gilled clade from California. Collections in the third clade differ in ITS sequence from the first clade by only 1.52%. The third clade may represent a sibling species or all three clades may represent a single large species complex which has diverged over distance and time.

Poster

Padmasree, Mahajabeen1, Matheny, P. Brandon1 and McLaughlin, David J. 1Dept. of Plant Biology, University of Minnesota, St. Paul, MN 55108, USA, 2Biology Department, Clark University, Worcester, MA 01610. USA. padma0003@umn.edu. Rocking the coprinoid boat: a phylogenetic study of the little brown mushroom genus Psathyrella. The first broad phylogenetic study of the mushroom genus Psathyrella was based on 132 sequences from the nuclear ribosomal large subunit gene and parsimony and Bayesian analyses. For this study Psathyrella sequences were generated and analyzed to represent approximately one tenth of the known species worldwide, and most sub-generic subdivisions. Representatives of the coprinoid genera (Parasola, Coprinopsis, and Coprinellus) were included to evaluate relationships in Psathyrellaceae with Coprinus in the outgroup. Psathyrella was found to be polyphyletic, with representatives in seven clades. Most species of Psathyrella, including its type species P. gracilis, formed a large clade with Coprinellus. Generic limits of Parasola, Lacrymaria, and Coprinopsis are affected. Morphological character traditionally used to subdivide Psathyrella and the two major taxonomic systems are evaluated based on phylogenetic analyses. Contributed Presentation

Palencia, Edwin R.1*, Klich, Maren2 and Bacon, Charles W.3 1University of Georgia, Plant Pathology Department, Athens, GA 30604, USA, 2USDA, ARS, SRRC, New Orleans, LA 70124, USA, 3USDA, ARS, Russell Research Center, Athens, GA 30604, USA, edwin.palensa@ars.usda.gov. Molecular differentiation of species within the Aspergillus section Nigri by using an automated repetitive-PCR method. Some species in the Aspergillus section Nigri are known for their production of mycotoxins, including ochratoxin A, a chlorinated cyclic polyketide compound. Ochratoxin A has been classified as possible carcinogenic to humans by the International Agency for Research on Cancer, and the evidence suggests nephrotoxic, teratogenic and carcinogenic activities in laboratory animals. The accurate classification and identification of ochratoxigenic species within the A. niger aggregate has been elusive since the morphology of most of the members is very similar. Molecular biology techniques have been developed in order to differentiate species within this aggregate, however most of them are impractical for routine identification and they required too much time. In this work, we report the use of an automated repetitive-sequence-based DNA fingerprinting method which reduces the time and labor required by other molecular methods. We used 27 Aspergillus section Nigri species and strains that were previously identified by microscopy and our results indicated a high concordance between the automated DNA fingerprinting system and morphology. Poster

Pérez-Martínez, José M.1* and Pfeipenbring, Meike.2 1 Tropical Research and Education Center, University of Florida, 18905 SW 280th Street, Homestead, FL 33031, USA, 2 Botanisches Institut, J. W. Goethe-Universität Frankfurt am Main, D-60054 Frankfurt am Main, Germany. jgerzem@ufl.edu. New records and new hosts of smut fungi (Ustilaginomycetes) from Cuba. Field work yielded new data on smut fungi in Cuba. Ustilago chrysogoponis is recorded for the first time for Cuba and the Neotropics on the new host plant Schizachyrium hirtiforum. Sporisorium bicornis known from Brazil and Colombia is found for the first time in Cuba. Sporisorium ellisi known only from USA and Mexico is now reported on the new host Andropogon glomeratus from five localities for this country. The presence of Sporisorium andropogonis is confirmed. Descriptions, illustrations, and notes on distribution and ecology of the new records are provided. Poster

Perry, Brian A.1*, Desjardin, Dennis E.1 and Moncalvo, Jean-Marc.2 1Department of Biology, San Francisco State University, San Francisco, CA 94132, USA, 2Center for Diversity and Conservation Biology, Royal Ontario Museum and Department of Botany, University of Toronto, Toronto, ON M5S 2C6, Canada. brian_perry@post.harvard.edu. Molecular systematics of the mycenoid fungi (Mykena and allied genera). Our research focuses on phylogenetic systematics in the mushroom genus Mycena s.l. and allied mycenoid fungi (Tricholomataceae, Euagaries). With over 1880 species epithets published in Mycena alone, the mycenoid fungi represent one of the most diverse groups of saprotophic mushrooms. Mycena tax play major roles in litter decomposition, nutrient recy-
cling and retention, soil genesis, litter binding, and as a food source for innumerable animals. Within the group, morphological diversity is remarkably high. Body forms range from stipitate-lanellate or pleurotoid forms to reduced-cyphelloid forms with smooth hymenophores and tiny cupulate basidiomes, and even poroid forms. To date no comprehensive classification system exists for the mycenoid fungi, and very little is known about the natural relationships and phylogenetic placement of the over 60 described genera within the Euagarics. To determine the phylogenetic relationships of these fungi and infer patterns of character evolution and biogeography, we are generating multi-locus sequence datasets from three nuclear and two mitochondrial loci for both tropical and temperate mycenoid taxa. Preliminary results suggest *Mycena s.l.* is a non-monophyletic assemblage, and the mycenoid fungi appear to represent several independent lineages within the Euagarics. **Contributed Presentation**

Picard, Kathryn T., Powell, Martha J. and Letcher, Peter M. The University of Alabama, Tuscaloosa, AL 35486, USA. kathryn.picard@gmail.com. **Chytrid fungi diversity of the Scottish mainland and northern isles.** The Scottish mainland is divided into two distinct geographical areas, the Highlands and the Lowlands. The Highlands are characterized by thin, rocky soils and acidic peat bogs, while the Lowlands possess richer soils resulting from glacial till deposition. We investigated the diversity of chytrid fungi in both Highland and Lowland soils. A third sampling from the Orkney Islands, whose topography is similar to that of the Lowlands, was also included in this study. Soil samples were prepared in aquaculture with four bait representatives of refractory materials found in soil detritus. Observed taxa were recorded and, when possible, isolated and brought into culture. Preliminary data indicate that the predominant chytrids in both Highland and Lowland soils are members of the family Terramycetaceae and genus *Kappanymes*, which exhibit cosmopolitan global distribution. However, these taxa were more common in Lowland soils, which also exhibited higher frequencies of two other cosmopolitan species, *Rhizophyctis rosea* and *Chytrionyces hyalinus*. The Orkney samples, despite geographical similarities to the Lowlands, had a low overall frequency of taxa. The absence of chytrids in Orcadian soils may be due to alkaline soils or heavy concentrations of bacteria resulting from agriculture. In future studies, the chytrids isolated from these soils will be analyzed molecularly to determine their evolutionary proximity to other global populations. **Poster**

Podila, G.K.1,*, Martin, F.2, Kohler, A.1, Duplessis, S.2, Grigoriev, I.V.1, Rouze, P.1, Detter, C.J.1, Richardson, P.1 and Muratet, M.1 1Dept. of Biological Sciences, The University of Alabama in Huntsville, Huntsville, AL 35899, USA, 2INRA-Nancy, 54280 Champenoux, France, 'US DOE Joint Genome Institute, Walnut Creek, CA 94598, USA, 4Flanders Interuniversity Institute for Biotechnology (VIB), B-9052 Ghent, Belgium, podilag@uah.edu. **Genomics and transcriptomics of ectomycorrhizal symbiont *Laccaria bicolor*. **Laccaria bicolor** is a ubiquitous ectomycorrhizal symbiont of tree roots. The mycorrhal basidioocytes have a beneficial impact on plant growth and nutrient cycling in forest ecosystems, yet our understanding of this ectomycorrhizal symbiosis is highly limited. To elucidate the genetic basis of this ecologically and biologically important behavior, the *L. bicolor* genome sequence has been determined. The genome assembly contains about 20,355 predicted protein-encoding genes. A complete transcription profile of the *L. bicolor* genome was analyzed using oligonucleotide microarrays representing the predicted gene models, then queried with messenger RNA from multiple tissues and life stages. 74% of the predicted genes were expressed in either free-living mycelium, mycorrhal symbiotic tissues or fruit body. These results also provide independent support and validation for predicted gene models. Genomic and transcriptomic analysis of this first symbiotic fungal sequence yielded insights into unexpected aspects of the symbiont biology. This fungus also possesses expanded protein families associated with plant interactions, such as signaling proteins and mycorrhiza-regulated small-secreted proteins. WD40- and TPR-repeat containing proteins – key integrators of stress and nutrient availability signals – are very abundant and mainly expressed in symbiotic tissues. The *L. bicolor* genome illuminates the dual ecological behaviors of ectomycorrhizal fungi with their hyphal networks permeating the soil and their symbiotic tissues interacting with plant root cells. **Symposium Presentation**

Porras-Alfaro, Andrea1,*, Herrera, Jose2, Sinsabaugh, Robert L.1 and Navig, Donald O.1 1Department of Biology MSC03 2020, 1 University of New Mexico, Albuquerque, NM 87131-0001, USA, 2Division of Science, Truman State University, Kirksville, MO 63501, USA. aporas@umm.edu. **Effect of nitrogen fertilization on fungal communities in a semiarid grassland.** Although drylands constitute one-third of the Earth’s terrestrial surface, our knowledge about fungal communities and the impact the nitrogen deposition has on these communities is very limited. We studied the effect of long-term nitrogen (N) fertilization on the diversity and composition of soil, endophytic, and arbucular mycorrhizal fungi (AMF) in a semiarid grassland. Soil and *Bouteloua gracilis* root samples were collected at the Sevilleta National Wildlife Refuge (New Mexico, USA) from control and N-amended plots. Small subunit and internal transcribed spacer rDNA were amplified using AMF and fungal specific primers. Soil and root fungal communities were dominated by Ascomycetes and *B. gracilis* roots were mainly colonized by dark septate fungi. Differences in fungal diversity were found among samples (roots, cyanobacteria-crust and rhizosphere soil) and between treatments (nitrogen vs. control plots). Soil samples have higher fungal diversity than roots. Roots collected in nitrogen plots have higher fungal diversity than control roots. In contrast to roots, fungal diversity in the rhizosphere declined with nitrogen amendment while diversity in crusts appeared unaffected. Our data suggest that the heterogeneous micro-topography, characteristic of semiarid grasslands, may be influencing a differential response of fungal communities to N enrichment. **Contributed Presentation**

Prompputtha, Ithayakorn1,*, Hyde, Kevin D.2, Peberdy, John F.3 and Lumyong, Saisomnon.4 1Section for Biodiversity, Illinois Natural History Survey, 1816 S. Oak St., Champaign, IL 61820, USA, 2Centre for Research in Fungal Diversity, Department of Ecology and Biodiversity, The University of Hong Kong, Pokfulam Road, Hong Kong SAR, China, 3University of Nottingham, Institute for Enterprise and Innovation, Nottingham University Business School, Jubilee Campus, Nottingham NG8 1BB, UK, 4Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai, Thailand, 50200. ppm118@yahoo.com. **How can endophytes survive as saprobes after host senescence?** Endophytic fungi live in healthy plants and can change their mode of lifestyle to become saprobes when leaves decay. To illustrate the way in which endophytes can acquire nutrients after host senescence and survive as saprobes, the succession of fungi during leaf decay of *Magnolia liliflora* and the expression of enzymes in individual 9 species that were found as both an endophyte and a saprobe were determined. Freshly fallen senescent leaves of *M. liliflora* were incubated in trays covered with gauze. The trays were placed outdoors and sprayed with sterile water once a day. The leaves were collected over a period of 88 days and assays were conducted for cellulase, laccase, mannansase, polygalacturonase and xylanase using sterilized leaves as the control. A succession in enzyme production starting with xylanase, followed by beta-mannansase and cellulase, and finally polygalacturonase and laccase was observed. An isoform of beta-mannanase was also compared using native polyacrylamide gel electrophoresis and activity staining techniques and was found to be similar among endophytes and their saprobic counterparts. These results suggest that endophytes possess the necessary enzymes required to change lifestyle and directly become saprobes after host senescence. **Poster**

Pruet, Grechen*, Bruhn, Johann and Mihail, Jeanne. Division of Plant Sciences, University of Missouri - Columbia, 110 Waters Hall, Columbia, MO 65211, USA. gbebc07@mizzou.edu. **Native fungal community composition on roots of truffle infected oak seedlings.** Ectomycorrhizal fungi play integral roles in many forest ecosystems. Anthropogenic factors have caused precipitous declines in fruiting by
some ectomycorrhizal mushroom species. Truffles, the hypogeous ascomycetes of the ectomycorrhizal genus *Tuber*, are currently cultivated in orchards to offset declining wild production. Truffle cultivation begins by germinating host seeds, inoculating the host seedlings with truffle spores, growing the seedlings in greenhouses until the mycorrhizal relationship is well established, and then transplanting the seedlings. Little is known in the USA about the effect of native ectomycorrhizal species on colonization of host trees by the European Burgundy truffle fungus (*Tuber aestivum*). Here we identify the fungal community composition in the greenhouse in three types of potting media, and then track fungal community composition for two years after transplanting. We found that the infection rates of fungal species commonly present in the greenhouse decline to low levels in the field. We also found that after two years of field growth, both *Tuber aestivum* colonization levels and native ectomycorrhizal species richness and abundance increased, indicating that native species, in the short term, do not displace the introduced *Tuber* spp. 

Continued Presentation

Raja, H.A.1*, Miller, A.N. 2 and Shearer, C.A. 1 1Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA. raja@uiuc.edu. The latitudinal, habitat, and substrate distribution of freshwater ascomycetes. Freshwater ascomycetes play an important ecological role in aquatic ecosystems as decomposers of organic matter. Despite evidence of their ecological role, there is a lack of knowledge of freshwater ascomyte identities, phylogenetic relationships, geographical distributions and species richness patterns. To address these issues, we are surveying freshwater ascomycetes using a latitudinal approach by collecting submerged herbaceous and woody debris in freshwater habitats around North and Central America to answer the following questions: 1) Do community composition and species richness differ among latitudinal gradients from the subarctic to tropical areas? 2) Do species richness and composition differ between lentic and lotic habitats? 3) Are species substrate specialists or generalists? Research to date reveals: 1) Species composition is quite different among subarctic, temperate and tropical latitudes, but we found high species overlap at temperate and tropical latitudes between the eastern and western hemisphere; 2) Some geographically broadly distributed species occur in both lentic and lotic habitat types, but more species occur only in one or the other habitat; 3) More species occur on wood, while fewer species are found on herbaceous material; species occurring on wood were also observed on herbaceous substrates, while those colonizing herbaceous substrates were seldom recorded on wood. 

Continued Presentation

Raja, H.A.1*, Miller, A.N. 2 and Shearer, C.A. 1 1Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA. 2Illinois Natural History Survey, Center for Biodiversity, 1816 Oak Street, Champaign, IL 61820, USA. raja@uiuc.edu. *Aquapoterium pinicola* gen. et sp. nov. from freshwater habitats in Florida. During investigations of freshwater ascomycetes along the Florida peninsula, a very small, hyaline discomycete fungus was found on submerged pine needles from lotic and lentic habitats. Based on morphological characteristics and 28S large subunit nuclear ribosomal sequence data, the new genus is placed in the Helotiales (Leotiomycetes). The characteristic features of this new fungus are white to cream colored, minute apothecium, stipitate or sessile, appearing goblet like; cylindrical-clavate, slightly cymbiform asci; hyaline smooth-walled, 1-celled, guttulate, short clavate-cylindric ascospores surrounded by an irregular mucilaginous sheath; subhymenial, ectal excipulum, medullary excipulum of the apothecium simple and composed of textura oblieta type of tissue. The fungus differs from other closely related species in the Helotiales such as *Aquasdiscula* and *Hyphomycopsis* in having a relatively simple excipulum made up of only one type of tissue. *Aquapoterium pinicola*, a new genus and species, will be described and illustrated. 

Poster

Redeker, Dirk1,2, Raab, Philipp1, Oehl, Fritz1, Camacho, Francisco J.2 and Courtecuisse, Regis.3 1Botanical Institute, University of Basel, Switzerland, 2Dept. of Environmental Science, University of Californi-

nia, Riverside, USA, 3Dept. of Botany, University of Lille, France. dirk.redecker@unibas.ch. Phylogeny of a novel clade of sporocarp-forming species of glomeromycotan fungi. Since the early times of taxonomy of arbuscular mycorrhizal fungi (Glomeromycota) the focus has shifted from sporocarpic species to species forming spores singly. For many of the sporocarpic species described in the 1970’s and earlier, no molecular data have been available and their phylogenetic position thus has remained unclear. We obtained nuclear-encoded ribosomal DNA sequences from specimens of glomeromycotan sporocarps from tropical islands that were assigned to the morphospecies *Glomus subverticulatum* and the newly-described species *Glomus megalocarpum*. Molecular phylogenetic analyses placed all species analyzed as a monophyletic sister group to the *Diversispora spurca/Glomus versiforme* clade (*Glomus* group C) within the Diversisporales. The phylogenetic divergence from other known species suggests that this clade may constitute a new genus. The consequences of these findings for taxon definition within the Diversisporales and the possible adaptation of these taxa to islands will be discussed. 

Continued Presentation

Redhead, S. Neatby Bldg., ECORC, CEF, Agriculture & Agri-Food Canada, Ottawa, Ontario, Canada, K1A 0C6. redheads@agr.gc.ca. Naming pleomorphic fungi – the debate on how to deal with Articl e 59 of the International Code of Botanical Nomenclature. Fungi are the only living organisms that are legitimately permitted by any Code of Nomenclature to bear multiple Latin scientific binomial names. This convention is rooted in the historical treatment of fungal names before their life-cycles were fully understood. It has been allowed to continue because it is still extremely difficult to precisely match morphological forms with others expressed by the same holomorph and, at the generic level, to recognize as congeneric taxa that may not resemble each other morphologically. The advent of phylogenetic analyses of fungi using DNA-DNA sequence comparison independent of phenetic morphological comparisons has re-opened the door to the methodology for describing and naming fungi with multiple morphologies. Molecular based phylogenies now allow mycologists to directly compare and confidently place morphologically dissimilar taxa leading to the recognition of or confirming previous suspicions of conspecificity or other close relationships. However, with over 250 years of historical names, agreed upon rules for naming and describing different morphological forms (anamorphs, teleomorphs), and a lack of consensus or alternatives, mycologist face the dilemma of trying to standardize the naming of fungi in line with other sciences, without creating chaos. The issue is so divisive amongst mycologists that it served as the lightning rod for debate at the 8th International Mycological Congress (IMC8) on whether to abandon completely the International Code of Botanical Nomenclature (ICBN). Previous discussions at IMC7 resulted in proposals to change ICBN Art. 59, which deals with names for pleomorphic fungi, published by David Hawksworth. Changes were made to ICBN Art. 59 at the 17th International Botanical Congress, based upon these suggestions, and epitypification of anamorph names by teleomorphs is now permitted. However, this action has not yet been tested and several published recommendations were sent to a Special Committee assigned to draw up recommendations for the next IBC. This Committee is now examining all of Art. 59 as well as the outstanding previously published proposals. 

Symposium Presentation

Rehner, Stephen A.1,2 and Meleying, Nicolai.2 1Insect Biocontrol Laboratory, USDA-ARS, Beltsville, MD 20705, USA, 2Department of Ecology, The Royal Veterinary and Agricultural University, Frederiksborg, Denmark. Stephen.Rehner@ars.usda.gov. Local phylogenetic and population genetic diversity of the entomopathogen *Beauveria* in adjacent agricultural and non-agricultural habitats. The hierarchical genetic diversity of *Beauveria* in a tilled agricultural field and an adjacent naturally vegetated hedgerow in Denmark was determined. *Beauveria* isolates originated from soil, phylloplanes and latent-infected in-

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sects. Molecular phylogenetic analysis revealed the presence of three distinct lineages: 1) B. bassiana s.l., for which five phylogenetic species were observed, 2) B. pseudobassiana nom. prov., a lineage that is unrelated but morphologically similar to B. bassiana s.l., and 3) B. brongniartii. All species detected were present in hedgerow soil samples but only one species of B. bassiana s.l. was recovered from the agricultural soils. Mating type determination and multilocus microsatellite genotyping results suggest a local clonal genetic structure for four of the five B. bassiana s.l. phylogenetic species. The study results suggest that hedgerows may be important reservoirs of entomopathogenic fungi in agricultural landscapes. **Contributed Presentation**

Reynolds, Hannah T. and Vilgalys, Rytas. Department of Biology, Duke University, Durham, NC 27708, USA. htr@duke.edu. **Competitive ability of the sooty mold S. spongiosa.** *Scorias spongiosa,* a sooty mold in the Capnodiales (Dothideomycetes), grows on the honeydew of the bee aphid *Gryllurophilus imbricatus.* In the Duke Forest, the fungus was found growing in large quantities on any surface covered in honeydew: beech leaves and bark, understory plants, rocks, and even rotting leaf litter. *Scorias spongiosa* was isolated from conidia and grew at a relatively slow rate, suggesting it produces antimicrobial compounds in order to thrive in environments generally dominated by communities of fast-growing fungi and bacteria. To test this hypothesis, bioassays were conducted on Potato Dextrose Agar plates. *Scorias spongiosa* was grown with several other microbes, including fungi and bacteria isolated from the beech phylloplane and leaf litter. Zones of inhibition and growth rate of both microorganisms on the plate were then measured. To investigate whether *S. spongiosa* produces diffusible antimicrobials, it was grown in potato dextrose broth (PDB) for one month and the broth tested. The results of these experiments on the competitive ability of *S. spongiosa* against a host of ecologically relevant microorganisms will be presented. **Contributed Presentation**

Rivera, Karol1*, Urb, Mirjam2, Thorn, R. Greg2, Louis-Seize, Gerry3 and Seifert, Keith A.1 *Biodiversity (Mycology & Botany), Agriculture & Agri-Food Canada, Ottawa, ON K1A 0C6, 2Department of Biology, University of Western Ontario, London, ON N6A 5B7. riverak@agr.gc.ca. An **undescribed species of Penicillium from Costa Rican caterpillars.** About 20 strains of a new species of *Penicillium* were isolated from the digestive track of the leaf-eating caterpillar *Rotschildia lebeau* collected from *Spodasis monbin* leaves in the Area de Conservación Guanacaste, Costa Rica. The fungus produces a monoverticillate and slightly vesiculate penicillus that is characteristic of *Penicillium* subgenus *Aspergilloides,* and subglobose, slightly roughened conidia. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to greenish grey, velutinous colonies, and clear, yellow exudates. On CYA the fungus produces turquoise grey to. **Contributed Presentation**

Rizvi, Leena1* and Moncalvo, Jean-Marc. Royal Ontario Museum, 100 Queen’s Park, Toronto, ON M5S 2C6, Canada. leenatorontofo@hotmail.com. **Identifying the host in the lobster mushroom.** The lobster mushroom consists of basidiomycota fruiting body hosting a parasitic ascomycete, *Hypomyces lactifluorum* (Hypocreales). Lobster mushrooms have so far been reported from North and Central America. It is considered to be a prime edible, but questions remain about the taxonomic identity of the host mushroom. The identification is important to ensure that the host is not toxic. The taxonomic identity of the mushroom host, however, is difficult to ascertain because the parasite alters its morphology and renders it sterile. Based on tissue anatomy it has been suggested that the host belongs to the Russulaceae. In this study, we used DNA sequences from the nuclear ribosomal internal transcribed spacer region (ITS) in order to identify the mushroom host of *H. lactifluorum* from a broad geographic sampling in its geographic range. Results have so far shown that the host species of *H. lactifluorum* belong to genera *Russula* and *Lactarius.* Several species so far identified belonging to the genus *Russula* are species of subsection *Lactarioideae* (R. brevipes complex). Preliminary data also suggests that their distribution may follow a geographical pattern. *Lactarius* hosts could not be assigned to species from currently available ITS sequence database. **Poster**

Robbertse, B.*. Reeves, J., Schoch C.L. and Spatafora, J.W. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA. robbertse@science.oregonstate.edu. **Characterization of ascomycotan proteome profiles using phylogenomics.** Conventional phylogenetic analyses with more limited character sampling have more difficulties in resolving deep node relationships. However, using the data from whole genomes holds promise for elucidating deep evolutionary relationships. We have developed a pipeline of perl scripts that connects several stand-alone programs to perform phylogenomic analysis and produce robust phylogenetic trees without excessive user input. Phylogenomically generated phylogenies provided a well-supported framework and are useful for creating phylogenetically informed protein clusters. Protein clusters were identified and the profiles of different ascomycete proteomes compared. This process was also used to compare the profiles of multi-copy proteins and singletons. Overlying phylogenetically informed clusters with GO predictions and SignalP analyses revealed an adaptation in certain protein families which contributed to the success of each fungus in their specific biological niche. **Symposium Presentation**

Robert, Vincent A. Curator of the Yeast Division, Centraalbureau voor Schimmelmicrobiologie, Uppsalalaan 8, 3584 CT Utrecht, Netherlands. robert@cbcb.knaw.nl. **Registration of new fungal names: MycoBank in practice.** The Mycobank initiative was launched in 2004 and was aimed as a repository of all available fungal names and associated data. In 2005, a first Internet portal was proposed and allowed registered users to deposit their new names and associated data to the MycoBank database. In 2006, a new and user-friendly version of the website was released. Very soon, we’ll introduce new features to the system that will allow, among many others, to perform polyphasic identifications, automated curation of sequences associated with Genbank, etc. A short demonstration of the system will be made. **Symposium Presentation**

Robertson, Larry D. and Horner, Hollis. Indoor Environmental Consultants, Inc., 2484 Hwy. 39 North, Jewett, Texas 75846, USA. ldr@iescinc.net. **Post remedial assessment and clearance criteria for mold remediation projects.** Post-remedial collection of 2,193 fungi samples were evaluated as a component of a three (3) tiered clearance criteria for mold remediations projects. Criterion #1 was the visual evaluation of remediated areas for the absence of fungal growth. Criterion #2 was the visual evaluation of surfaces in remediated areas for the absence of visible debris. Criterion #3 involved the evaluation of total fungal bioaerosol samples with a pre-defined post-remedial clearance criterion of < 2,000 particles/m³ of total fungi, with individual sub-categories comprised of <666 particles/m³ *Cladosporium*-like spores, <666 particles/m³ *Aspergillus*/Penicillium*-like spores, <666 particles/m³ mixture of spores from other genera with no individual component comprising > 33% of this sub-category, and < 22 particles/m³ *Stachybotrys*/Mennoniella*-like spores. Ninety-four (94%) of the population achieved clearance on the first assessment. One (1%) percent of the initial failing population was related to fungal growth in the remediated area. Data obtained in this investigation support the modification of clearance criteria of *Stachybotrys*/Mennoniella*-like spores to 88 particles/m³. No specific health concerns were documented after the clearance of these areas; however, these guidelines are not intended to represent any specific medical or health related threshold regarding health. The authors conclude the three (3)-tiered clearance criteria provide a reasonable and obtainable clearance guideline, provided some

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latitude exists with respect to evaluating levels of all categories of fun-
gal spores and the potential impact of an outdoor bias on a case-by-case basis. **Contributed Presentation**

Rojas, Carlos* and Stephenson, Steven L. Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. rojas@uark.edu. **Ecology of myxomycetes from high-elevation areas of the Neotropics.** Results from recent studies of myxomycetes in high-elevation areas of the Neotropics suggest that the assemblages of species present are consistent with a pattern that reflects the occurrence of temperate islands in a tropical landscape. For this reason, the ecology of myxomycete assemblages in selected study sites in Mexico, Guatemala and Costa Rica are being investigated. All three general study areas are reported to have been glaciated in the last 15 thousand years, which means that major recolonization events may have played an important role in determining the taxonomic composition of the assemblages of species associated with these areas. Preliminary results show a correlation between species richness and soil nutrient status and suggest that for some species of myxomycetes there may be specifici-
ty in the myxomycete-plant relationship, which is sometimes reflected at the microhabitat and/or temporal level. Forested and non-forested areas also differ in the species composition of the assemblages of myx-
omyctes present, and differences in composition were also found among different types of forests. These results may favor the idea that for these Neotropical areas, species of myxomycetes are responding more directly to microenvironmental pressures than predicted by the neutral theory, which may be an indication that, after all, some myx-
omyctes are not cosmopolitan. **Contributed Presentation**

Rojas, Carlos1*, Stephenson, Steven L.1 and Biffi, Daniela.2 1Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA, 2Department of Biology, University of Beloit College, Beloit, WI 53511, USA. **Resource partitioning and niche overlap in three species of Ceratiomyxa.** The mycotozoan genus Ceratiomyxa seems to have a cosmopolitan distribution; howev-
ner, two of the three macroscopic species within the genus have been re-
ported only from tropical regions of the world. In theory, these two tropical species might be expected to display more narrow niches than their cosmopolitan counterpart, due to their specialization for tropical environments. However, ecological data documenting this phenom-
one in mycotozoans are largely lacking. As part of an ongoing investiga-
tion of these organisms in the Amazon forests of southeastern Peru, the ecology of the three macroscopic species of Ceratiomyxa was studied. The results from in-situ measurements of environmental factors asso-
ciated with their fructifications show a clear separation of niches be-
tween species, which may be an indication of resource partitioning in the genus. Interestingly, the cosmopolitan species C. fruticulosa shows a broader niche than either C. murchella or C. sphacelarea, a pat-
tern reported for generalist species. The latter species is characterized by the lowest overall niche overlap values, a possible indication of spe-
cialization. Additional data are necessary to more firmly substantiate all the patterns observed. This project was supported by a grant from Ama-
zon Conservation Association. **Poster**

Rellows, Adam W.1*, Landolt, John C.2 and Stephenson, Steven L.1 1Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA, 2Department of Biology, Shepherd Universi-
ty, Shepherdstown, WV 25443, USA. arolloin@uark.edu. **DicysteIDIIId associated with North American grasslands.** DicysteIDIIId (cellular slime molds) are phagotrophic bacteriovores that have been widely studied in forested ecosystems worldwide. These organisms are com-
monly recovered from the soil-litter interface zone that consists of high-
ly decayed leaves and other plant debris. In contrast, the dicysteIDIIId associated with grassland ecosystems have received relatively little at-
tention. Eight grassland study areas were sampled for dicysteIDIIId to further elucidate the assemblages of dicysteIDIIId present and their ecology within grasslands. For the most part, the results obtained rein-
force earlier more limited studies that reported lower species richness and diversity for dicysteIDIIId in grasslands when compared to forested ecosystems. Interestingly, intensive sampling at the Konza LTER study area in Kansas found unique assemblages of species associated with grasslands and gallery forests. In addition, the effects of fire and graz-
ing were evaluated with respect to the assemblages of dicysteIDIIId present. **Poster**

Rollins, Adam W.*, and Stephenson, Steven L. Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. arolloin@uark.edu. **Ecology of grassland myxomycetes.** Myx-
omyctes are phagotrophic eukaryotes that produce fungus-like fruiting bodies. Their occurrence has been documented worldwide in virtually every type of ecosystem from the Polar Regions to the Tropics. How-
ever, with the exception of studies carried out in gallery forests or those that have examined dung as a substrate, grasslands have been largely neglected. Myxomycete surveys conducted across mid-continental United States tall grass, mixed grass, and short grass study areas indi-
cated that myxomycetes are abundant components of grassland ecosys-
tems. Distinct assemblages of myxomycetes were found to be associ-
ated with each grassland type. In addition, the ecological factors associated with various microhabitats were found to influence the dis-
tribution and occurrence of the species of myxomycetes present. The microhabitat represented by dung supported the most distinct assem-
blage of myxomycetes, and the assemblages of myxomycetes associat-
ed with aerial microhabitats in grasslands were found to differ from those occurring on ground microhabitats. This research was supported in part by grants from the Prairie Biotic Research Inc. and the Wyoming Native Plant Society. **Poster**

Rossman, Amy Y. USDA ARS Systematic Botany & Mycology Lab, Beltsville, MD 20705, USA. arossman@nt.ars-grin.gov. **Towards one generic name for monophyletic lineages.** With the integration of asexually reproducing fungi into meaningful phylogenies, the need to use the same generic name for a monophyletic lineage has become ur-
gent. At present Article 59 of the International Code of Botanical Nomenclature (ICBN) requires the use of a sexual state name for sex-
ually reproducing species (teleomorph) while a second generic name must be used for asexually reproducing species (anamorph) in the same lineage. As a result two different generic names must often be used for species in one lineage. This dual nomenclature is confusing to non-my-
cologists as well as many mycologists and needs to be changed. Al-
lowing asexually reproducing fungi to be placed in teleomorph genera would be a major step forward in solving this problem. Various pro-
posals will be presented on how to move in this direction using exam-
iples from both well-studied and under-studied groups of fungi. In ex-
amining this issue care must be taken to separate nomenclatural from taxonomic issues such that nomenclatural guidelines can be developed that apply to unknown situations and unintended consequences of changes to nomenclature rules are anticipated. The goal is to formulate proposed changes to the ICBN that will solve this problem that mycol-
ogists can agree on so that changes can be implemented at the next In-
ternational Botanical Congress in 2011. **Symposium Presentation**

Ryberg, Martin1*, Nilsson, R. Henrik1, Kristiansson, Erik2, Jacobsson, Stig3 and Larsson, Ellen.1 1Department of Plant and Environmental Sciences, Göteborg University, Göteborg, Sweden, 2Department of Math-
ematical Statistics, Chalmers University of Technology, Göteborg, Sweden. martin.ryberg@dpcse.gu.se. **Prospects of using emerencia to fetch sequence metadata from GenBank – a case study of the ecto-
mycorhizal genus Inocybe (Basidiomycota).** The lack of well iden-
tified reference sequences hampers DNA-based species identification. This has lead to a situation where many environmental samples remain unidentified. We used emerencia, a bioinformatics tool for automated downloading and BLAST:ing of fungal ITS sequences, to fetch unidentified sequences of Inocybe from GenBank. The unidentified se-
cquences were divided into species that were identified using a reference dataset of sequences from a phylogenetic study. For species delimita-
tion and identification both phylogenetic methods and sequence simi-
larity based clustering were used. 177 unidentified sequences divided

**Continued on following page**
into 97 species were found. Of these species 33% were identified to species level. The ecology and distribution of the genus and its species were explored using sequence metadata stored in GenBank as well as data from the papers in which the sequences were originally published. We conclude that Inocybe is widely geographically distributed, from snowy and fully humid climate in Northern Europe to equatorial savannah in South East Asia. Many species were reported to form associations with several hosts, including ecto-, arbutoid and orchid mycorrhiza. The methods used here hold a great potential to utilize valuable information available from environmental samples for use in a species and taxonomy oriented framework. Contributed Presentation

Schoch, Conrad L.*, Sung, Gi-Ho and Spatafora, Joseph W. Dept Botany and Plant Pathology, 2082 Cordley Hall, Oregon State University, Corvallis, Oregon 97331, USA. schochc@science.oregonstate.edu. When the forest is a single tree: towards a complete phylogeny of Ascomycota. The Assembling the Fungal Tree of Life project (AFTol) generated large amounts of data that resulted in multiple publications and resolution numerous deep nodes within the Fungi. These results have informed the working phylogenetic classification of Fungi and tested and developed hypotheses regarding the evolution of fungal morphology, ecology, and life histories. As part of this process several large multigene data sets devoted to class level lineages were recently produced in the Deep Hypha edition of Mycologia (vol. 98, No. 6). We mined these datasets and combined all relevant data in a phylum wide analysis with unpublished data from the AFTol project to present the most complete and extensive Ascomycota phylogeny to date. This study includes more than 400 taxa, representing 56 orders and the majority of known Ascomycota diversity, and provides the first opportunity to combine all classes presented in the current classification. We use this phylogenetic hypothesis as a template to test and present hypotheses about character evolution, radiation events, and the existence of novel fungal lineages. The framework will also be used to point towards that will be productive for the next generation of phylogenetics and the emerging field of phylogenomics. Contributed Presentation

Simpson, Nicholas* and Jumpponen, Ari. Division of Biology, Kansas State University, Manhattan, KS 66506-4901, USA. fungi@ksu.edu. Inter- and intraspecific variation in the carbon and nitrogen nutritional preferences of arctic ericoid mycorrhizal fungi. Ericoid mycorrhizal fungi utilize a broad range of organic sources to acquire both nitrogen and carbon. Although capable of using diverse nutritional sources, individual fungi within these communities will show preference to one or more sources. It remains unclear, however, whether this variability in nutritional preference occurs mainly within a species or among species. To address this question, we isolated 540 fungal pure cultures from the surface-sterilized hair roots from twelve individuals of five ericaceous plant species from Toolik Lake LTER in northern Alaska. The cultures were segregated into RFLP phenotypes and the dominant fungi were then identified by sequencing. Four strains from four of the most dominant species groups were then randomly selected and grown for four weeks in liquid culture with a single nitrogen source and ten days in liquid culture with a single carbon source. The six amino acids used as nutritional sources represent resource pools that remain constant throughout the growing season, fluctuate across the growing season, and those that are only available at certain points of the growing season. Using biomass as proxy for successful uptake of a particular nutritional source and pH as a proxy for extra-cellular enzymatic activity we will partition the variance within and among species and determine the relative importance of the inter- and intraspecific variation. Contributed Presentation

Six, Diana L.*, Stone, W. Doug2 and Woolfolk, Sandra W.3 2 Department of Ecosystem and Conservation Sciences, College of Forestry and Conservation, University of Montana, Missoula, MT 59812 ,USA. 3Department of Entomology and Plant Pathology, Mississippi State University, Mississippi State, MS 39762, USA. diana.six@cfc.umn.edu. Ambrosiella and Geosmithia species associated with an exotic ambrosia beetle, Xylosandrus mutilatus (Coleoptera: Curculionidae, Scolytinae), in Mississippi. Xylosandrus mutilatus is an ambrosia beetle of Asian origin that has recently established in the US. Female X. mutilatus transport fungi to plants in highly specific mesonatal mycangia. The mycangial fungi provide a primary nutritional resource for the beetles. Our objective was to identify the fungi associated with X. mutilatus in Mississippi where the beetle is best established. Isolations from mycangia revealed an Ambrosiella species, Geosmithia obscura, G. lavendula, and a yeast, Candida homolentoma. The Ambrosiella species appears to be undescribed but closely related to Ambrosiella hartii. The presence of the two Geosmithia species with this beetle was surprising. Associations between Geosmithia and scolytine beetles have previously only been observed for phloem-colonizing bark beetles in Europe. This is the first record of these fungi in association with a sapwood-colonizing ambrosia beetle. Our results indicate that several fungi are associated with the mycangia of X. mutilatus in the US. It is likely that most, or all, of these fungi are exotic, and have been introduced along with the beetle. Because X. mutilatus is highly polyphagous, our results indicate that its establishment will result in the exposure of many new plants in North America to these fungi. Poster

Smith, Matthew E.* and Jaffe, Bruce A. Department of Nematology, University of California at Davis, mesmith@ucdavis.edu. PCR primers with enhanced specificity for nematode-trapping fungi (Orbiliales). Nematode-trapping fungi are a monophyletic lineage within the Orbiliales that use specialized structures to capture and consume nematodes in soil, litter, wood and other substrates. These fungi have been studied because of their unique predatory life histories and because they are potential control agents of plant- and animal-parasitic nematodes. Ecological studies of nematode-trapping fungi have mostly used culture-based methods, but molecular detection techniques are now available and should be useful. We developed Orbiliales-specific PCR primers for the ITS and 28s rDNA to detect nematode-trapping fungi from soil without culturing and also to screen isolates for phylogenetic placement in the Orbiliales. We used these primers to selectively amplify, clone, and sequence Orbiliales directly from soil, litter, and wood and we compare the results of molecular detection with those obtained using a culture-based method. Of the eight species of nematode-trapping Orbiliales detected with our culture-based assay, only three were detected with PCR. Our molecular sampling, however, detected 18 species of uncultured Orbiliales, many of which are closely related to nematode-trapping fungi and parasites of nematode eggs. Our results suggest that the combined use of Orbiliales-specific PCR primers and culture-based techniques may enhance future studies of nematode-trapping Orbiliales. Poster

Snetselaar, Karen*, Vasta, Lauren, Jennings, Joseph and McCann, Michael. Biology Department, Saint Josephs University, Philadelphia, PA 19131, USA. ksnetsel@sju.edu. Location of Ustilago maydis infection structures on maize silks. The corn smut fungus Ustilago maydis can only complete its life cycle by infecting living epidermal cells of its host plant. Infection begins with formation of appressoria on susceptible plant surfaces. Despite considerable efforts, appressoria have not been induced to form on artificial surfaces. In order to better understand the factors that induce appressorium formation, we examined and characterized numerous infection structures on maize silks. Silks were examined 14 hrs after inoculation with compatible fungal cells. An initial survey indicated that the majority of appressoria were found on silks that were about 180mm in length than on longer or shorter silks, so study focused on silks of this length. While more appressoria were found in the bottom and middle third of the silk compared with the top third, further analysis indicated that the size of the epidermal cell was more important than its location along the silk. Most appressoria formed over epidermal cells that were about 300 micrometers long. In addition, out of more than 200 appressoria examined, more than 90% formed over the long sidewalls of adjacent epidermal cells rather than either the short endwalls or in the middle cells. We speculate that the

Continued on following page
fungus preferentially forms appressoria between epidermal cells that are elongating. *Poster*

Sogonov, M.V.1, Castlebury, L.A.2*, Mejía, L.C.1, Rossman, A.Y.2 and White, J.F.1 1Department of Plant Biology and Pathology, Cook College, Rutgers University, New Brunswick, NJ 08902, USA, 2USDA-ARS Systematic Botany and Mycology Laboratory, Beltsville, MD 20705, USA, Lisa.Castlebury@ars.usda.gov. Revision of genera in the Gnomoniaceae, Diaporthales, Ascomycota. The Gnomoniaceae (Diaporthales) is a common but inconspicuous family of fungi associated with plants. Fungi in the Gnomoniaceae occur mostly as symptomless endophytes of hardwood trees, usually forming ascomata on overwintered leaves or twigs. However some are pathogenic and capable of causing various anthracnose, blight and canker diseases. This family also includes some species associated with herbaceous plants and conifers. Here we present a taxonomic revision of the family based on multigene phylogenetic analyses. Analyses of a dataset consisting of five gene regions (beta-tubulin, EF1A, RPB2, ITS and LSU) for 98 gnomoniaceous strains (ca. 80 species) showed little correlation with classical generic concepts. Revised generic concepts for Gnomonia, Plagiotomonia, Cryptosporiella, Pleurocera, and Ophiognomonia are proposed based on the results of our analyses. One additional as yet unnamed genus is also proposed. Eighty additional species were placed in these genera using the ITS gene region. Morphological and biological tendencies are identified for each clade and compared with previous morphological generic concepts. *Contributed Presentation*

Spiegel, F.W.1*, Shadwick, J.D.1, Brown, M.W.1 and Hermes, D.E.2 1Department of Biological Science, University of Arkansas, Fayetteville, AR 72701, USA, 2Biology Discipline, University of Hawaii, Hilo, HI 96720, USA, fsiegel@uark.edu. Protostelids of the Hawaiian Archipelago. During a series of trips from 1998 to 2007, the major habitats on the islands of Hawaii, Maui, Molokai, Lanai, Oahu, and Kauai have been collected for protostelids, the morphologically simplest members of the slime mold taxon, Eumycetozoa. Though the Hawaiian Islands are the most remote archipelago on Earth, this isolation has not proven to be a barrier to the establishment of protostelids. All 33 described species of microscopic protostelids have been recorded on the island of Hawaii and at least one other island. In addition, over twice that many possible undescribed species have been observed. Some of these are relatively common and are in the process of being isolated and described. The range of habitats in the archipelago is extensive. Altitudes range from sea level to over 4000m, and rainfall ranges from less than 10cm per year to over 1200cm per year. This results in wet, mesic, and dry forests, grasslands, and scrub. In addition, there is both extensive human and natural, volcanic, disturbance. While protostelids are found in all habitats except the highest elevation alpine scrub, they are not abundant in dry to mesic forests. The flora of each island differs in some respects from each of the others, and some possible explanations for this will be suggested. *Contributed Presentation*

Spriggs, Ekaterina1, Schlert, Joseph1, Barnard, Kobus1 and Pryor, Barry M.2* 1Department of Computer Science, University of Arizona, Tucson, AZ 85721, USA, 2Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA, bmpyor@u.arizona.edu. Modeling complex 3-dimensional structure in Alternaria and applications to morphometric analysis. Statistical analysis of complex morphological structures represents one of the most challenging aspects of comparative biology. This task is even more daunting for structural analysis of lower organisms due to the added challenges of time-consuming microscopy, image processing, and subsequent data analysis. This project focuses on diversity in sporulation structures among small-spore catenulate species in the fungal genus Alternaria, which exhibit considerable morphological plasticity in reproductive structures that is dependent upon cultural conditions of substrate, temperature, light and humidity. Further complicating taxonomic structure for this group of fungi is the presence of numerous isolates with intermediate characteristics that do not clearly segregate into recognized species. To develop a high-throughput method for statistically supported morphometric analysis of diversity in fungal reproductive structures, systems are being developed to fit complex fungal morphological data from 2-D microscopy into predictive 3-dimensional models. Initial efforts are focused on computer modeling of spore and hyphal structures using Bayesian inference to fit models to image data. A second effort is toward building a system for fitting data from 3D models to a stochastic Lindemayer system (L-system) for computer generated reconstructions of *Alternaria* morphology, including a web interface for domain specialists to create instantiations of various species under various conditions. A third effort is to build a visualization interface for large scale 3-dimensional (holographic) facilities where domain specialists can optimally see the effects of various choices of structural parameters, optionally overlaid or connected to real data from 3D microscopy. Given model fits, mycologists can then engage in large scale quantitative morphometric and taxonomic studies, which will enable the subsequent linkage to other complex data sets such as gene expression data, metabolite profiles, and measurements of ecological fitness. *Contributed Presentation*

Stajich, Jason E.1*, Rosenblum, Erica B.2, Taylor, John W.1 and Eisen, Michael B.1 1Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720, USA, 2Department of Molecular and Cellular Biology, University of California, Berkeley, CA. 94720 USA, jason_stajich@berkeley.edu. Comparative genomics of fungal kingdoms: a view from the chytrids. The availability of genome sequences from most phyla of fungi provides an opportunity to study shared and unique genes and features of fungi. We have developed computation pipelines to explore evolution of genes and gene families across fungi. Using the recently available genome of the Chytrid *Batrachochytrium dendrobatidis*, Zygomyce, Basidiomycete, and Ascomycete genomes it is possible to infer loss and gain events of genes, genome features such as introns, and biosynthetic pathways. We have found lineage specific expansions and contractions of gene families that may correlate with changes in life history or ecological niche of sampled fungi. In addition, comparisons between fungal and animal genomes allow inference of genes and processes specific to individual clades of fungi and to the fungi themselves. We have focused on interesting patterns of genes involved in cell wall biosynthesis across the fungi, saproporphic lifestyles of Ongylenes fungi, and lignin and cellulose degrading pathways in the Basidiomycetes. *Symposium Presentation*

Stefani, F.O.P.1*, Moncalvo, J-M.2 and Hamelin, R.C.1 1Centre d’étude de la forêt, Université Laval, Sainte-Foy, (QC), Canada, G1K 7P4, 2Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, 100 Queen’s Park, Toronto, Ontario, Canada, M5S 2C6, Natural Resources Canada, Canadian Forest service, 1055 du Peps, Sainte-Foy, QC, G1V 4C7, Canada. frstefani@ciif.forestry.ca. Fine scale analysis of ectomycorrhizal diversity from transgenic poplar root-tips and cloned soil samples to assess impact on non-target organisms. Genetically engineered trees are currently developed to improve fiber quality, growth or tree resistance against insects and pathogens. Addressing the impacts of GMOs before their deployment is an important step during the research and development process as the genetic constructs and the new traits expressed may lead to detrimental effects on non-target organisms. We compared fungal diversity in root-tips and soil in 3 untransformed and 3 GUS-transformed *Populus tremula* x *P. alba* grown in a plantation in Quebec, Canada. Four roots and 4 soil samples were sampled in the proximity of each tree. We amplified and sequenced the internal transcribed spacer (ITS) of 1152 root-tips and of 1152 clones from the organic layer and the mineral layer. We identified 46 ectomycorrhizal OTUs from the root-tips analysis, 23 from the clones in the organic layer and 21 from the clones in the mineral layer. *A Cortinarius* sp represented 41.5% of the root-tips and 71.4% of the clones sequenced from the organic layer whereas the mineral layer was largely dominated by *Acremonium* sp. (77%). Significant differences between the 2 treatments were recorded from the root-tips analyses and from the clones in the organic layer. *Contributed Presentation*
Stephenson, Steven L.1,8, Schnittler, Martin2 and Novozhilov, Yuri K.3  
1Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas 72701, USA, 2Botanical Institute and Botanical Garden, Ernst Moritz Arndt University Greifswald, Grimmer Str. 88, D-17487 Greifswald, Germany, 3V.L. Komarov Botanical Institute of the Russian Academy of Sciences, Prof. Popov St. 2, 197376 St. Petersburg, Russia. ststeph@uark.edu. **Global distribution patterns of myxomycetes.** The myxomycetes (plasmodial slime molds or myxogastrids) are a group of eukaryotic microorganisms usually present and sometimes abundant in terrestrial ecosystems. Evidence from molecular studies suggests that the myxomycetes have a significant evolutionary history. However, due to the fragile nature of the fruiting body, fossil records of the group are exceedingly rare. Although most myxomycetes are thought to have very large distributional ranges and many species appear to be cosmopolitan or nearly so, results from recent studies have provided evidence that spatial distribution patterns of these organisms can be successfully related to (1) differences in climate and/or vegetation on a global scale and (2) the ecological differences that exist for particular habitats on a local scale. A detailed examination of the global distribution of four examples (Barbeyella minitissima, Ceratomyxa morchella, Leocarpos fragilis and Protophysarium philioenum) demonstrates that these species have recognizable distribution patterns in spite of the theoretical ability of their spores to bridge continents. (Funded by grant DEB-0316284 from the National Science Foundation). **Poster**

Stolze-Rbyczynski, Jessica L.3 and Money, Nicholas P. Botany Department, Miami University, 316 Pearson Hall, Oxford, Ohio 45056, USA. stolzej@mhuioho.edu. **Ballistospore discharge in *Tilletia caries*.** *Tilletia* is a genus of smut fungi (Ustilaginomycetes) that includes *T. caries* and *T. foetida*, that cause common bunt and stinking smut. These fungi invade wheat seedlings and sporulate within the mature ovary walls to form the bulb cells. Teliospores are released and can spread when the delicate bulb cells rupture upon harvesting of the wheat. When the teliospores germinate they form primary sporia, and these give rise to ballistospores. A few seconds prior to the launch of the ballistospore, a drop of fluid (called Buller’s drop) develops at its base. The drop enlarges until it approaches the volume of the spore and then spore and drop are catapulted into the air. Until recently, the launch process eluded analysis, but spore motion has now been studied using ultra high speed video microscopy. Images of this mechanism by *T. caries* were obtained at 50,000 frames per second and demonstrate that spore discharge occurs when the expanding Buller’s drop merges with fluid on the spore surface. Although this coalescence may result from the directed collapse of Buller’s drop onto the spore, it may also involve the movement of the spore toward the drop. The release of surface tension at coalescence provides the energy and directional momentum to propel the spore and drop into the air. The estimated velocity of ballistospore discharge is 0.95-1.20 meters per second. Understanding the biomechanics of spore discharge by this pathogenic smut is a vital part of efforts to develop effective control strategies for pathogen management. **Contributed Presentation**

Suh, Sung-Oui1*, Nguyen, Nhu H.2 and Blackwell, Meredith.1 1Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803, USA, 2Department of Plant and Microbiology, University of California, Berkeley, CA 94720, USA. ssuh@lsu.edu. **Yeasts near *Candida albicans* isolated from plant- associated insects.** Ascomyete yeasts were isolated from the digestive tracts of phytophagous beetles in 8 families, and other plant-associated insects including earwigs, crickets, and roaches. Based on a comparison of DNA sequences and other taxonomic characteristics, a total of 41 isolates were identified as *Candida orthopsilosis*, *C. pseudorhagii*, *C. maltosa*, *C. guilliermondii*, *C. tropicalis*, *Lodderomyces elongisporus*, *Candida famata* and four novel *Candida* species. A phylogeny based on SSU and LSU rDNA sequences indicated that most of the new species and other yeasts isolated in this study were closely related to members of the *C. albicans/L. elongisporus* clade which includes many clinically important yeasts, such as *C. albicans* and *C. dubliniensis*. None of ~1000 yeast isolates associated with mycophagous insects that we examined was related to the *C. albicans* clade. The results showed that the habitats and diets of host insects are closely correlated with the gut yeast distribution in insect hosts. Furthermore, certain insects may be vectors of certain clinically important yeasts. **Contributed Presentation**

Taerum, Stephen J.1*, Klepzig, Kier D.2, Six, Diana L.3, Hofstetter, Rich W.4 and Ayres, Matt P.1 1Department of Biological Sciences, Dartmouth College, Hanover, NH 03755, USA, 2Southern Research Station, USDA Forest Service, Pineville, LA 71360, USA, 3Department of Ecosystem and Conservation Sciences, University of Montana, Missoula, MT 59812, USA, 4School of Forestry, Northern Arizona University. Flaggstaff, AZ 86011, USA. Stephen.Taerum@dartmouth.edu. **Abiotic factors that influence the co-occurrence of fast- and slow-growing genotypes of *Ophiostoma* associated with southern pine beetles (*Dendroctonus frontalis*).** A major goal in life history theory is to understand why organisms vary in their growth rates. Growth rate is a major fitness component because of its generally strong effects on survival and reproduction. Despite this, we have a limited understanding of the factors that maintain genetic variation in growth rates in nature. Fungi are of particular interest because they have been surprisingly neglected in life history theory, despite their ubiquity, diversity of ecological roles, and their frequent functions as ecological engineers. Preliminary studies suggest that species within *Ophiostoma* have very high genetic variation in growth rates. We are examining how different abiotic factors affect the growth rates of blue stain fungi (*Ophiostoma* spp.) associated with southern pine beetles (*Dendroctonus frontalis*). Using growth assays, we are testing if *Ophiostoma* strains vary in their growth rates because selection for high fitness in favorable abiotic conditions yields genotypes with relatively low fitness in unfavorable environments. We are testing how the strains grow under the following abiotic conditions: 1) unfavorable temperatures; 2) low nutrient substrates; and 3) unfavorable water potentials. This study will demonstrate if selection maintains variable growth rates in *Ophiostoma* because optimal growth strategies vary among heterogeneous environments. **Contributed Presentation**

Taylor, John W. Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720-3102, USA. jtaylor@nature.berkeley.edu. **Fungal barcoding.** The study of fungi stands to gain a great deal from barcoding, the use of variable DNA regions to identify individuals to species. Barcoding will identify fungi in collections and also in nature where, due to their size, microscopic fungi are routinely overlooked. Barcoding seems likely to allow ecologists to account for the microscopic fungal community as easily as they now account for macrobes. To be useful for microscopic fungi, primers used for PCR amplification associated with barcoding from the environment must amplify fungi from all known clades and have a high likelihood of amplifying fungi from unknown clades. Recent careful work on the main barcoding region, mitochondrial cytochrome oxidase 1 (CO1), shows that the priming regions are too variable to be practical (Seifert et al. 2007 PNAS 104:3901). This work, and that of others, also shows that CO1 harbors many large introns, which complicate barcoding. A molecule different than CO1 is needed for fungi. Recent studies have successfully barcoded fungi from environmental samples and recovered species and clades new to science (e.g., Schadt et al. 2003. Science 301:1359; Suh et al. 2004. Int. J. Syst. Evol. Microbiol. 54:2409). These studies have employed regions of nuclear rDNA. At a recent meeting on fungal barcoding, it was proposed that the internal transcribed spacer (nuc rDNA ITS) be used for fungal barcoding. **Symposium Presentation**

Thiery, Odile* and Redecker, Dirk. Institute of Botany, University of Basel, Hebelerstr.1, CH-4056 Basel, Switzerland. Odile.Thiery@unibas.ch. **Development of mitochondrial genes as molecular markers in the Glomeromycota.** The only molecular markers available covering all families of arbuscular mycorrhizal fungi (AMF, Glomeromycota) are the nuclear-encoded ribosomal genes. **Continued on following page**
However, these genes show numerous variants within a single fungal isolate. The mitochondrial large subunit rDNA (mtLSU) has been shown to be homogeneous within isolates of *Glomus*, but the sequence data were limited to *G. intraradices* and *G. proliferum*. By using previously-designed and new specific primers, we obtained mtLSU sequences from other taxa of the Glomeromycota. Although clearly showing a phylogenetic relationship, partial mtLSU sequences of *Scutellospora verrucosa* differ from *Glomus* in their intron content and are distinct in their exon sequence. Additional mtLSU sequences from the Gigasporaceae and other families are investigated. Using these data, the variable regions might help in distinguishing genotypes and the more conserved regions will be used to elucidate the phylogeny of the Glomeromycota. **Poster**

Thompson, Lisa*, Goldmann, Lauren, Wright, Angela and Weir, Alex. Department of Environmental & Forest Biology, SUNY College of Environmental Science & Forestry, 241 Illicic Hall, 1 Forestry Drive, Syracuse, NY 13210, USA. lithomps@syr.edu. **Laboulbeniales from Costa Rica.** There has been much recent interest in documenting the mycota of Costa Rica, with particular emphasis on the macrofungi, and lichenized and non-lichenized ascomycetes associated with wood. The diversity of fungi associated with insects, however, has received little attention to date. As one of the focal collection areas for our NSF-PEET Grant investigating the phylogeny of Laboulbeniales, we have unveiled a surprising richness of Laboulbeniales taxa within this region. To date only limited sampling has taken place in Puenterales Province and at Montevede, yet, more than 50 species of Laboulbeniales have been recorded. This represents a significant addition to the approximately 20 known species recorded by Thaxter, and more recently by the late R.K. Benjamin. Of the 50 newly recorded taxa approximately half are thought to represent undescribed species. We are continuing to examine our collections and are confident that much more remains to be discovered about the Laboulbeniales of this region. **Poster**

Toledo-Hernandez, Carlos, Zuluaga-Montero, Anabella, Rodriguez, Jose A. and Bayman, Paul.* Departamento de Biologia, Universidad de Puerto Rico - Rio Piedras, PO Box 23360, San Juan PR 00931, pbayman@uprpr.edu. **Variation in fungal communities of sea fans (Gorgonia ventalina).** Diseases are threatening many species of corals in the Caribbean. One of the best-known diseases of corals is aspergillosis of sea fans, caused by *Aspergillus sydowii*. However, the source of inoculum and the mycoflora of healthy sea fans are largely unknown; it is not clear if the presence of the pathogen is sufficient to cause aspergillosis or how the microbial community changes when a colony becomes diseased. We isolated fungi from sea fans (*Gorgonia ventalina*) with aspergillosis, healthy sea fans and sea water in Puerto Rico from 2003-2007. Fungi were identified by sequencing the nuclear ribosomal ITS region. Different methods of isolation of fungi were compared. For *A. sydowii*, one of the most common species, aflatoxin production in vitro was determined by HPLC. We found variation in fungal communities of sea fans at several different levels: differences between healthy and infected tissues, differences between sea fans and seawater, differences between sampling dates, differences in fungi isolated from different sizes of tissue pieces, and differences in aflatoxin production among isolates. In many cases these differences were significant. This variability complicates efforts to understand the disease, and suggests that several opportunistic pathogens may be responsible. **Poster**

Tuggle, Alicia A., Melhart, Christy A., Slay, Michael E. and Stephenson, Steven L.* Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. slsteph@uark.edu. **Cave crickets as vectors for dictyostelids in caves.** A study was carried out to determine if dictyostelid cellular slime molds (dictyostelids), which are known to occur in cave habitats, were associated with a species of cave cricket (*Ceuthophilus gracilipes*) in Pigeon Roost Cave in Benton County, Arkansas. Cave crickets were captured alive and rinsed in a water/wetting agent solution in a small sterile plastic tube. The rinsed, live crickets were then placed in a container to collect any fecal matter they might deposit. The tubes with the water/wetting agent solution as well as the fecal matter left in the container were plated out on hay-infusion agar and these plates examined for colonies of dictyostelids. Four species of dictyostelids were recovered from the rinse wash and/or the fecal matter, which suggests that the cave crickets can serve as vectors to transport dictyostelid spores within the cave habitat. Since the distribution does not prove that the genes corresponding to these probesets are unique to sexual development (some genes may be expressed in vegetative growth conditions not yet studied), it does provide a distinct group of genes associated with development on which to focus further studies. At 72 hours following induction of sexual development, the timepoint at which transcripts for meiotic processes and ascos and ascospore differentiation are likely to be first detected, the highest number of uniquely-expressed genes is present. This is the first whole-genome analysis of expression during sexual development in a filamentous ascomycete. Symposium Presentation

Trail, F., 1, 2, Hallen, H. E. 1 and Cavinder, B. 3 Department of Plant Biology, 1Department of Plant Pathology, and 2Genetics Program, Michigan State University, East Lansing, MI, USA. trail@msu.edu. **Update on the genetics and physiology of the mechanism of forcible ascospore discharge.** With an acceleration of 8,500,000 m s $^{-2}$ within the ascus, the ascospores of *Gibberella zeae* (anamorph *Fusarium graminearum*) hold the biological record (Trail et al., 2005). However, the minute size of the spores compared to most other far-flung propagules goes hand in hand with prodigious acceleration, and there do not appear to be any unusual structures driving the spore release. We have begun structural and genetic dissection of the ascus to determine the components that drive its unusual function. We will present an update of the genetic and physiological components we have identified that contribute directly to spore release. **Poster**

Trusty, Paul* and Cripps, Cathy L. Plant Sciences and Plant Pathology, Montana State University, Bozeman, MT 59717, USA. paultrusty@yahoo.com. **Ectomycorrhizal fungi of whitebark pine seedlings on burned and adjacent unburned forests in regard to restoration strategies.** Whitebark pine (*Pinus albicaulis*) is a keystone species in the Northern Rocky Mountains critical to watersheds and maintenance of wildlife diversity at high elevations. Blister rust, mountain pine beetles, and fire suppression have compounded the decline of whitebark pine forests throughout its range. Serious efforts are underway to restore these forests using natural and prescribed fires as a management tool to eliminate competitors and stimulate whitebark pine seedling regeneration. An important restoration component is post-fire plantings of rust resistant whitebark pine seedlings. This study is evaluating the mycorrhizal colonization of rust resistant nursery seedlings in the Fridley Burn, (Gallatin County, MT) in comparison to those regenerating naturally in the burn and on adjacent unburned forest. Morphotyping and ITS analysis of ectomycorrhizal roots revealed that 1) all seedlings were colonized with fungi, 2) the severe burn reduced diversity and caused a shift in fungi (burned: *Pseudotomentella, Amphinema, Wilcoxina*, Thelephorids: unburned: *Piloderma, Cenococcum, Rhizopogon spp;* both: *Rhizopogon*), and 3) exotic nursery fungi persist after 5 years. This study will help determine if appropriate mycorrhizal fungi are available on severe burns for effective mycorrhizization of whitebark pine seedlings planted after a severe fire for restoration purposes. **Poster**

Continued on following page
crickets can forage outside the cave, it is possible that they also introduce spores to cave habitats from outside sources. Poster

Tunlid, Anders. Department of Microbial Ecology, Lund University, SE 223 62 Lund, Sweden. anders.tunlid@bioecol.lu.se. Evolutionary genomics of the ectomycorrhizal fungus Paxillus involutus. It is well known that ectomycorrhizal (ECM) fungi can differ markedly in their ability to form mycorrhiza and to promote the growth of the host plant. Generally such phenotypic differences could be the result of variations in gene content, quantitative differences in gene expression, and structural differences in gene products. We have used cDNA microarrays to compare the transcriptome and genomes of strains of Paxillus involutus. The analyses included Nau, that is not compatible with birch and poplar, and the two compatible strains Maj and ATCC 200175. The array contained reporters for 1075 putative unique genes in P. involutus, derived from a collection of expressed sequence tags (ESTs). On the genomic level, Nau and Maj were very similar. Only 16 out of 1,075 genes analyzed by microarray-based hybridizations had signals indicating differences in gene copy numbers. In contrast, 66 out of the 1,075 genes were differentially expressed in Maj compared to Nau after contact with birch roots. Thirty-seven of these symbiosis-regulated genes were also differentially expressed in the ATCC strain. Comparative analysis of DNA sequences of the symbiosis-regulated genes showed that two of them have evolved at an enhanced rate in Nau due to relaxed or positive selection. Symposium Presentation

Untoo, Showkat Ahmad, Singh, Rama S., Singh, Narinder and Mann, S.K. Department of Plant Pathology, Punjab Agricultural University, Ludhiana-141004, India. ramassingh@rediffmail.com. Efficacy of single and combined formulations of Trichoderma harzianum and Pseudomonas fluorescens against foliar blight of wheat. Trichoderma harzianum (TH38) and Pseudomonas fluorescens (P12) have been reported as potential biocontrol agents against various soil born plant pathogens. These antagonists are present in the Biocontrol Lab, Department of Plant Pathology, Punjab Agricultural University, Ludhiana (India). Both the isolates were compatible to each other. The tale based formulations were developed singly and in combinations of the 2 bioagents and evaluated against foliar blight of wheat (Drechslera / Alternaria spp.) on two varieties i.e. HD 2329 and PBW 343 in field experiment. The Treatments were given as seed treatment @ 6.0g formulation / Kg seeds (ST), and combination of ST + one / two foliar spray (FS) @ 6g / litre. The seed germination and disease intensity were recorded. The seed germination was significantly higher due to treatments of bioagents as compared to control and fungicide treatment. Seed germination was 66.3 – 77.5; 66.9 – 73.4 and 70.9 – 73.0% due to seed treatments of TH38, P12 and TH38+P12, respectively, whereas 68.8 and 56.2% seed germination was observed with treatment of Raxil and control, respectively. The incidence of foliar blight was also decreased significantly due to treatments of bioagents. On HD 2329, the disease intensity was 29.6; 28.3 and 27.1% due to ST; ST +1 spray and ST + 2 sprays of T. harzianum, respectively. Similar treatments of P. fluorescens gave 29.4; 25.4 and 25.2% foliar blight intensity. However, the ST; ST + 1 spray and ST + 2 sprays with combined formulation of T. harzianum + P. fluorescens gave 27.9; 25.2 and 27.1% foliar blight intensity. Disease intensity of 30.6 and 41.5% was observed due to treatment of Raxil and control, respectively. The similar trend of data was recorded on PBW 343. The ST; ST + 1 spray and ST + 2 sprays gave disease intensity of 36.9; 34.4 and 33.7% due to T. harzianum; 34.2; 32.3 and 27.5% due to P. fluorescens and 35.0, 32.7 and 29.4 % with combined formulation of T. harzianum + P. fluorescens, respectively, as compared to 33.3 and 43.8% due to treatment of Raxil and control, respectively. Overall, the treatments of combined formulation of T. harzianum + P. fluorescens were the best with maximum plant stands as well as minimum foliar blight intensity. Poster

URen, Jana M.1,*, Gallery, Rachel2, Dalling, James W.2 and Arnold, A. Elizabeth.1 Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA, 2Department of Plant Biology, University of Illinois Urbana-Champaign, Urbana, IL 61801, USA. juren@email.arizona.edu. Diversity and origins of seed-associated fungi in tropical forests. In intact tropical forests, pioneer trees establish by seed germination in canopy gaps, but gap formation is spatially and temporally unpredictable. Some pioneers increase recruitment success through soil seed banks, but soil-borne microbes can severely limit seed survival over time. Recent studies examining seeds of the neotropical pioneer Cecropia in Panama and Costa Rica recovered diverse assemblages of ascomycota similar to endophyte communities in the same forests. We examined soil-incubated seeds of C. insignis in Panama to address the hypothesis that seeds harbor vertically transmitted symbionts (endophytes) that enhance survival in soil. In contrast to expectations based on vertical transmission, diversity of seed-associated fungi was high. Dominant fungi differed among and within seed lots. When incubated together, seeds from different origins (Panama, Costa Rica) had highly similar fungal communities. Little genotypic overlap was observed between seed-associated and foliar endophytic fungi; however, phylogenetic analyses indicated a close evolutionary relationship between these guilds. Our data suggest a shared evolutionary history for endophytes and seed-associated fungi, and indicate that if fungal symbionts enhance the survival of Cecropia seeds in soil, they are likely acquired – like foliar endophytes – by horizontal transmission from the surrounding environment. Poster

Vernier, Kimberly1,1, Hustad, Vincent1, Methven, Andrew1, Meiners, Scott1 and Miller, Andrew2. 1Department of Biological Sciences, Eastern Illinois University, Charleston, IL 61920, USA, 2Illinois Natural History Survey, University of Illinois, Champaign, IL 61820-6970, USA. fungusfairy@hotmail.com. Communities of wood decay in old growth prairie groves. This study is investigating communities of wood-decaying macrofungi associated with Quercus rubra and Acer saccharum tree windfall in Brownfield (26.1 ha) and Trelease Woods (24.5 ha), Champaign Co., Illinois. These woods are remnants of a larger, pre-settlement prairie grove and are now encircled by houses, fragmented forests, prairie and agricultural land. Although initially a virgin, deciduous upland forest dominated by oak, ash and maple with a high, closed canopy, sugar maple is rapidly becoming the dominant tree species. Beginning in November 1994, fallen trees in both woods have been tagged with an ID number, date of windfall, dbh and location relative to a network of marked grids. Data is being collected on 40 Quercus rubra and Acer saccharum logs in decay stage II and decay stage III. The following objectives are being addressed: I) Do species diversity and richness on decay stage II and decay stage III logs differ between study sites? II) Do fungal communities differ between tree species? III) Will species diversity be lost from the stand as oak is replaced by sugar maple? IV) Which environmental and abiotic variables can best explain the species composition and richness of wood-decaying fungi on logs in decay stage II and III? and V) Compare the distribution of fungal species within and on the logs. Contributed Presentation

Virella Perez, Carlos R.* and Cafaro, Matias J. Department of Biological, University of Puerto Rico, Mayaguez Campus, Mayaguez, PR 00681. cr.virella@gmail.com. Mycellial fungi associated with the guts of millipedes found in Puerto Rico. Millipedes are an ecologically important group of arthropods. They are responsible for 5-10% of leaf litter degradation annually. However, in the tropics they may commute up to 25% of the litter, making it available for other organisms for further processing. The intestinal microflora of the millipede may play an important role in this process. We identified the fungal components of the intestinal microflora of three widespread millipede species of southwestern Puerto Rico; Trigonialis lombiardii, Spiropreptus soronis and Anadenobolus monticorinus. Digestive tracts were obtained by dissection using fine scissors and forceps. Midguts and hindguts were dissected separately and their contents inoculated in Potato Dextrose Agar and Yeast Malt Agar. Colonies were counted and identified. Aspergillus niger and other Aspergillus species were the most abundant organisms comprising 30% and 14% of all isolated colonies, respectively. Trichoderma hamatum, Paecilomyces lilacinus, Neosartorya fischeri and Mortierella alpina were also present. The guts of millipede species contained a high diversity of fungal species, with the most abundant species being Aspergillus niger and Aspergillus terreus. In addition, we identified several rare species that are not commonly found in other ecosystems. Continued on following page
centrate on the core Spizellomyces lost from ing proteins that act in the same meiotic pathway) were independently combined sequences of ribosomal genes. Phylogenetically informative methods of phylogenetic inferences are used to analyze separate and group in the Spizellomycetales. Maximumparsimony and Bayesian revision of the order Spizellomycetales, we used over 70 cultures in from soils representing a broad geographic range. As a beginning to the revision of the order Spizellomycetales, we used over 70 cultures in molecular and ultrastructural analyses to evaluate backbone support for groups in the Spizellomycetales. Maximum parsimony and Bayesian methods of phylogenetic inferences are used to analyze separate and combined sequences of ribosomal genes. Phylogenetically informative zoospore ultrastructural characters are also explored. Results support the monophyly of genera analyzed thus far, except for the genus Spizellomyces. Establishing well-supported sub-clades of spizellomycetean chytrids allows the University of Maine to concentrate on Powellomyces sub-clade cultures and the University of Alabama to concentrate on the core Spizellomyces and Rhizophlyctis sub-clades. The high degree of genetic divergence in this group demonstrates that new genera and new orders will have to be erected. It is clear that broad geographic sampling is needed to fully reveal the genetic diversity found within the Spizellomycetales. Poster

Wakefield, William S.*, Powell, Martha J., Letcher, Peter M. and Brooks. Micheal C. University of Alabama, Dept. of Biological Sciences, 411 Hackberry Ln., Tuscaloosa, AL 35487, USA. wswakefield@gmail.com. Phylogenetic and morphological research on spizellomycetean chytrids (Chytridiomycota). The Phylum Chytridiomycota is commonly considered aquatic fungi because they reproduce with zoospores. However, despite their adaptations to dispersal in water, chytrids are common in soil. The University of Alabama and University of Maine are training three graduate students and are working together to collect and culture spizellomycetean chytrids from soils representing a broad geographic range. As a beginning to the revision of the order Spizellomycetales, we used over 70 cultures in molecular and ultrastructural analyses to evaluate backbone support for groups in the Spizellomycetales. Maximum parsimony and Bayesian methods of phylogenetic inferences are used to analyze separate and combined sequences of ribosomal genes. Phylogenetically informative zoospore ultrastructural characters are also explored. Results support the monophyly of genera analyzed thus far, except for the genus Spizellomyces. Establishing well-supported sub-clades of spizellomycetean chytrids allows the University of Maine to concentrate on Powellomyces sub-clade cultures and the University of Alabama to concentrate on the core Spizellomyces and Rhizophlyctis sub-clades. The high degree of genetic divergence in this group demonstrates that new genera and new orders will have to be erected. It is clear that broad geographic sampling is needed to fully reveal the genetic diversity found within the Spizellomycetales. Poster

Poster

Wakefield, William S.*, Powell, Martha J., Letcher, Peter M. and Brooks. Micheal C. University of Alabama, Dept. of Biological Sciences, 411 Hackberry Ln., Tuscaloosa, AL 35487, USA. wswakefield@gmail.com. Phylogenetic and morphological research on spizellomycetean chytrids (Chytridiomycota). The Phylum Chytridiomycota is commonly considered aquatic fungi because they reproduce with zoospores. However, despite their adaptations to dispersal in water, chytrids are common in soil. The University of Alabama and University of Maine are training three graduate students and are working together to collect and culture spizellomycetean chytrids from soils representing a broad geographic range. As a beginning to the revision of the order Spizellomycetales, we used over 70 cultures in molecular and ultrastructural analyses to evaluate backbone support for groups in the Spizellomycetales. Maximum parsimony and Bayesian methods of phylogenetic inferences are used to analyze separate and combined sequences of ribosomal genes. Phylogenetically informative zoospore ultrastructural characters are also explored. Results support the monophyly of genera analyzed thus far, except for the genus Spizellomyces. Establishing well-supported sub-clades of spizellomycetean chytrids allows the University of Maine to concentrate on Powellomyces sub-clade cultures and the University of Alabama to concentrate on the core Spizellomyces and Rhizophlyctis sub-clades. The high degree of genetic divergence in this group demonstrates that new genera and new orders will have to be erected. It is clear that broad geographic sampling is needed to fully reveal the genetic diversity found within the Spizellomycetales. Poster

Wang, Zheng*, Savelkoul, Elizabeth and Logsdon, John M. Jr. Department of Biology & Roy J. Carver Center for Comparative Genomics, University of Iowa, Iowa City, IA 52242, USA. zhengwang@uiowa.edu. Using a meiotic gene inventory to study the evolution of sex in fungi. The diversity of reproductive modes is a central theme in the evolutionary history of fungi. However, a comprehensive study of the evolution of sex in fungi is difficult given the lack of physical evidence of sexual life cycles in many fungal lineages, including some serious pathogens. Since meiosis is a cellular process crucial for sexual reproduction, an investigation of the presence and evolutionary histories of meiotic genes will illuminate the evolution of sex in fungi. Available data from more than 40 fungal genome projects and a robust framework phylogeny of fungi from the AFTOL project allow the study of meiotic gene evolution from a wide diversity of fungi. Those fungi from which completed genomes are available represent comparatively well-studied systems and comprise various life-styles, including some putatively asexuals. An investigation of fungal meiosis, a process requiring numerous genes and gene families, may also be helpful in resolving some phylogenetic puzzles and assisting genetic studies of meiosis in fungi other than yeasts. We have conducted a phyloinformatic analysis of key meiosis genes across 30 fungal genomes representing major fungal lineages. Our initial results show that homologs of the meiosis specific genes Msd1, Hop2 and Dmc1 (encoding proteins that act in the same meiotic pathway) were independently lost from Ustilago maydis, Candida guilliermondii and Neurospora-related fungi. In contrast, the microsporidian Encephalitozoon cuniculi has homologs of Hop2 and Msd1 but not Dmc1. To extend our survey beyond the completed fungal genomes, we have designed degenerate PCR primers for ten meiosis specific genes: Rad51, Dmc1, Spo11, Hop2, Msd1, Msd4, Msh5, Rad21, Rad54 and Rdi54. We are investigating the presence of these genes among twenty ascomycetes; these selected taxa include pathogens, endophytes, some lichen-forming fungi, and species not known to have a sexual life cycle. Results from these ongoing analyses will be presented. Contributed presentation

Poster

Intraspecific variation is common in cosmopolitan species of myxomycetes. However, there is little information on the limits of this variation, and no study of a cosmopolitan myxomycete has included a consideration of the growth of each specimen under standard conditions. It is hypothesized that the variation among specimens may be the result of phenotypic plasticity, but few previous studies have attempted to provide data to answer this question. In order to understand the intraspecific variation of Didymium squamosum, a cosmopolitan species, molecular analysis of a mitochondrial marker for individuals representing specimens from world-wide collecting sites was carried out. A morphological analysis revealed appreciable variation in micro and macro characters and developmental features. Characters used in the analysis were measured or
determined from both herbarium specimens and agar cultures of those same specimens. Characteristics measured from culture including time to germination, color of plasmodium and time until fruiting varied among specimens. Also, a preliminary comparison of features showed variation between the herbarium specimen collected in the field or from moist chamber culture and the fruiting bodies from agar culture of the same isolate. Contributed Presentation

CANCELED Winsett, Katherine E.1*, Stephenson, Steven L.1, Cavender, James2 and Cavender, Nicole.3 1Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville, AR 72701, USA, 2Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA, 3Restoration Ecology, The Wilds, Cambridge, OH 43732, USA. kwinset@uark.edu. Eumycetozoa of South Africa. The first survey for myxomycetes in South Africa since the first decades of the twentieth century was undertaken during October and November of 2006. The major ecosystems of the country including indigenous forest, savanna or bushveld, grassland, and fynbos were sampled. The survey was the first to involve collecting material for moist chamber cultures, which should, based on the results obtained in surveys elsewhere, result in significant additions to the list of species known for the country. Notably, collections from the fynbos represent material unique to a region in South Africa, since this biome is not found anywhere else in the world. The data generated from this survey are a part of the NSF-funded Planetary Biodiversity Inventory (PBI) effort for eumycetozoans and represent one of only a few extensive sets of data available for the African continent. Poster

Witiak, Sarah Melissa1*, Samson, R.A.2, Varga, J.3, Rokas, A.3 and Geiser, D.M.1 1Department of Plant Pathology, Penn State University, University Park, PA 16802, USA, 2Centraalbureau voor Schimmelcultures, Utrecht 3588, The Netherlands, 3Broad Institute, 7 Cambridge Center, Cambridge, MA 02142, USA. dggeiser@psu.edu. A many-locus phylogeny of the genus Aspergillus. The extensive biological diversity of the genus Aspergillus is reflected in its high degree of DNA sequence diversity. Inferring a comprehensive phylogeny for the genus is important for many reasons, particularly for taxonomy, comparative genomics, and for species discovery. Phylogenetic analyses using one or a few loci generally resolve relationships at the sectional level, but fail to provide strong inferences in backbone nodes, due in part to the high degree of sequence variation between subgenera and sections. Here we utilized the available complete genome sequences to design primers that amplify across most of the genus, providing new loci useful for phylogenetics in the genus. Phylogenetic analyses using eight of these new loci in combination with others already available produced the same tree topology as inferred by complete genome comparisons. Initial results indicate that the application of this many-locus approach to a broad set of taxa will lead to strong phylogenetic inferences useful for the study of the genus. Contributed Presentation

Woolfolk, Sandra W.1* and Baird, Richard E. Department of Entomology and Plant Pathology, Mississippi State University, MS 39762, USA, sww3@entomology.msstate.edu. Fungal associations with red imported fire ants Solenopsis invicta Buren and mounds in Mississippi. A study is being conducted in Mississippi to determine fungi associated with red imported fire ants (RIFA) and their mounds. Active mounds containing RIFA, mound soils and plant debris were collected from Hinds, Madison, and Leake Counties along Natchez Trace Parkway, Mississippi in March, July, and November 2004. The three counties were selected because they have been confirmed to be occupied by RIFA. Five mounds were collected per time per sampling location. Once transported to the laboratory, samples were processed and isolated onto Sabouraud's dextrose agar plus yeast (SDAY) amended with streptomycin sulfate and chlorotetracycline. Approximately 1500 isolates of fungi were obtained. Isolated fungi were initially grouped based on morphological features. Two representative isolates from each group were selected and molecular identification is currently being performed using molecular technique. The initial molecular procedures (DNA extraction, polymerase chain reactions, and DNA purification) have been completed. The DNA sequencing procedure is in progress to obtain all fungal sequence data. Fungal taxa that have been shown as potential entomopathogens in other insects will be tested as potential microbial control agents against RIFA. Poster

Wu, Wenyong1,2*, Hutton, Carol L.3 and Labandeira, Conrad C. 1Spezielle Botanik und Mykologie, Fachbereich Biologie, Philipps-Universität, Marburg, D-35032, Germany, 2National Museum of Natural History, Smithsonian Institution, PO Box 37012, MRC121, Washington DC 20013, USA. chwenyingwu@gmail.com. Fungal fossils and plant-fungi interactions from a 300 million-year-old coal-ball deposit. We present our study on fungal fossils and their associated plants from a 300 million-year-old Late Pennsylvanian coal-ball deposit collected in the Calhoun Coal of Berryville, Illinois. The dominant plants are species of the extinct tree-fern Psaroniopsis. Both symbiotic and parasitic fungal structures have been found endophytically in the root and rhachis, respectively. Spires and vesicular and arbuscular mycorrhizae with intracellular and intercellular hyphal structures frequently appear in root tissues. The fungus in the rhachis cells features entire reproductive and vegetative life stages, including spore germination, formation of coiled hyphae, and hyphal terminal at a vesicle. This condition resembles the structure of extant mycorrhizal fungi. In one endophytic association between an insect galler and its Psaroniopsis plant host, there was fungal colonization in the area among the insect coprolites (fossilized fecal pellets) and galled tissue, indicating a diffuse tritrophic relationship. We tentatively identify species of fossil fungi, using morphological characters from light microscopy and SEM. We also utilized X-ray SEM with an energy dispersive spectroscopy system to elucidate the nature of fossil preservation. This investigation is an effort to further understand the currently poorly known paleomycological world. Poster

Yafetto, Levi1*, Davis, Diana J.2 and Money, Nicholas P. 1Department of Botany, Miami University, Oxford, OH 45056, USA, 2Department of Chemistry and Physical Science, College of Mount St. Joseph, Cincinnati, OH 45233, USA. yafetti@muohio.edu. Mechanisms of rhizomorph development in Armillaria mellea. The extraordinary destructive abilities of some wood decay fungi and pathogens lies in their ability to form root-like organs called rhizomorphs. Rhizomorphs are complex structures that conduct water, nutrients, and oxygen over long distances, allowing fungi to spread through hard-packed soils between food sources. The pathogen Armillaria mellea forms rhizomorphs in culture and serves as an excellent model for developmental studies. This poster presents information on (i) the stimulation of rhizomorph extension in A. mellea by increasing medium gel strength; (ii) features...
of rhizomorph anatomy that support their invasive behavior; (iii) data on osmolyte accumulation, and (iv) novel measurements of the forces exerted by rhizomorph tips. These experiments reveal similarities and differences between the development of rhizomorphs and their constituent hyphae that begin to explain the effectiveness of rhizomorphs as exploratory organs. *Poster*

Yeo, Sumin, Kim, Yunjung, Song, Hong-Gyu and Choi, Hyoung T. ¹ Division of Life Science and Research Institute of Life Sciences, Kangwon National University, chunchon 200-701, S. Korea. htchoi@kangwon.ac.kr. *Degradation of hormone mimicking chemicals by genetically transformed *Irpex lacteus*. As disposable plastic waste uses increase, so does the risk posed by human exposure to hormone mimicking chemicals (HMCs) which are generated during the treatment of the plastic waste. White-rot basidiomycetes have the enzymes including laccase, lignin peroxidase and manganese peroxidase for the degradation of lignin. They also degrade many recalcitrant compounds such as dyes, explosives and many pesticides. We have isolated a white-rot fungus *Irpex lacteus* from Korea, and examined its degrading activity against several HMCs. It showed very good degrading activity against bisphenol A and phthalates even though it showed a very low laccase activity. We have cloned laccase cDNAs from *Phlebia tremellosa* and *Trametes versicolor*, and introduced the cDNA to *I. lacteus* through genetic transformation. The insertion of the laccase cDNA has been confirmed by Southern hybridization, and laccase activity was also confirmed using a chromogenic substrate. The degradation of HMCs by the transformants has been compared with the wild type, and the removal of estrogenic activity of the HMCs has also been analyzed using the yeast (two hybrid) reporter system. *Contributed Presentation*

Zanzot, James W.¹, de Beer, Z. Wilhelm², Eckhardt, Lori G.¹ and Wingfield, Michael J.² ¹School of Forestry and Wildlife Sciences, Auburn University, AL, USA, ²Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa. zanzojw@auburn.edu. *A new Ophiostoma species in the *O. pluriannulatum* complex from lobolly pine roots*. Various Ophiostomatoid fungi have been implicated as contributing factors to the decline of pines in the southeastern US. During a survey for these fungi in lobolly pine (*Pinus taeda*) roots at Fort Benning, GA, we encountered a species of *Ophiostoma* with a *Sporothrix* anamorph, morphologically similar to *O. pluriannulatum*. This species has not been reported from pine roots in this region. Moreover, a closely related congener, *O. subanulatum*, is reported to infect conifer roots, and we sought to identify this fungus based on morphology, as well as ITS and beta-tubulin sequence comparisons. Isolates observed were grossly similar to those of *O. pluriannulatum*, with unusually long perithecial necks, but different in culture morphology. Sequences of the ITS rDNA were identical to those of *O. pluriannulatum*, and similar to *O. multiannulatum* and *O. subanulatum*. Sequence data from the beta-tubulin gene region revealed the absence of intron 4 and presence of intron 5, similar to the latter two species, but distinct from *O. pluriannulatum*, which has intron 4 and not intron 5. Phylogenetic analyses of beta-tubulin sequences showed that all of our isolates group together in a clade distinct from *O. multiannulatum* and *O. subanulatum*. Given the arrangement of introns, we believe that our isolates represent a novel species. This new fungus is currently being described, and its pathogenicity, biology and ecology are also being studied. *Poster*

Zhou, Fang⁴ and Weir, Alex. Environmental and Forest Biology, State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13210, USA. Zhhou01@syr.edu. *Light- and transmission electron microscope studies on the penetration of *Hesperomyces virescens* (Ascomycota, Laboulbeniales) parasitic on *Hormania axyridis* (Coleoptera, Coccinellidae).* The interaction between *Hesperomyces virescens* (Laboulbeniales) and the lady beetle *Hormania axyridis* (Coleoptera, Coccinellidae) was studied using light (LM) and transmission electron microscopy (TEM). Thin sections through developing spore stages revealed the presence of a very narrow penetration peg originating at the foot of the *Hesperomyces* thallus and extending through the outer layers of the cuticle of the insect. Beneath this, in the hemocoel of the host, a small bulb-like haustorium was formed from which rhizoid-like fungal hyphae developed. In some sections presence of those rhizoids was observed throughout a large area of the hemocoel. Here we compare the penetration apparatus observed to those known in a range of entomopathogenic and plant parasitic fungi. *Poster*
Northern Thailand and the Mushroom Research Centre

During the period of January 5 to 19, 2008, three individuals (Steve Stephenson and two of his graduate students, Adam Rollins and Carlos Rojas) from the Laboratory for the Study of Eumycetozoans at the University of Arkansas made a planning visit (funded by a grant from NSF) to northern Thailand. The primary objective of the visit was for Stephenson to discuss the possibility of future collaborative research projects involving the University of Arkansas and researchers and students at Chiang Mai University, Mae Fah Luang University and the Mushroom Research Centre.

Our trip began at the Mushroom Research Centre (MRC), which is located in a mountainous area 64 km northwest of the city of Chiang Mai. MRC promotes the study of fungal biodiversity by providing a place where graduate students can live, work and conduct their research, ultimately leading to an advanced degree. MRC is equipped with a lecture hall, a lab, and a well-stocked mycology library as well as various chalets and a cozy pond-side restaurant with an inviting crackling fireplace to warm oneself during the cool mountain evenings in the winter months. Our primary host during the visit to MRC was Thida Win Ko Ko, a graduate student who is currently studying the myxomycetes of northern Thailand.

During our visit to MRC, we presented a three day training session on myxomycetes, which began with a general introduction to the group and progressed to the biology, taxonomy and ultimately the ecology and the global distribution of these organisms. Participants in the training session consisted of students and scientists from seven countries (China, Indonesia, Laos, Myanmar, the Philippines, Thailand and Vietnam) throughout Southeast Asia (Fig. 1). As part of the training session, participants had the opportunity to collect and study specimens in the field, and they now have the knowledge to pursue further research relating to the myxomycetes (Fig. 2). As part of this activity, Adam and Carlos also gave presentations on their PhD research projects, which involve developing a better understanding of biogeographical patterns in myxomycetes. This experience provided a great opportunity for us to interact with the various

Continued on following page
students and researchers. We were able to gain insights and an understanding of the educational process as it exists in Southeast Asia and to establish research linkages with other students and researchers across the region. This part of the trip proved a valuable experience for us.

After the conclusion of the training session, we visited the Doi Inthanon (the “roof of Thailand”). The summit of this mountain, with an elevation of 2565 m, is the highest point in Thailand and represents the last substantial peak of the Himalayan system. The high elevation of this mountain nestled in a region of surrounding lowlands creates a unique situation. Here there are many co-occurring vegetation types, which result in the mingling of tropical species and some species more commonly associated with higher latitudes (Fig. 3). Given these factors, Doi Inthanon is one of the most biodiverse areas in Thailand, and we obtained samples from various microhabitats for the isolation of fungi and all three groups of eumycetozoans. In addition, Carlos established two study plots that will be used to provide the data necessary to compare and contrast the results obtained from his ongoing work, which involves examining the myxomycetes associated with high elevation mountaintops in the Neotropics.

We then traveled north to visit with students and researchers working at Mae Fah Luang University (Fig. 4), which is located in the city of Chiang Rai. Here we met with Kevin Hyde, Director of the Mushroom Research Centre and a professor of mycology at Mae Fah Luang University. Stephenson presented a seminar on his ongoing studies of myxomycete biodiversity, and we met with faculty members and graduate students to discuss possible future collaborative research projects involving researchers at this institution and the University of Arkansas. In addition, we traveled to two forest study sites, one located near the Nanglai-nai Waterfall and the other in Lamnamkok National Park, to collect specimens of myxomycetes and samples for laboratory isolation. During this portion of our trip, we visited a picturesque rural village where the road ended and the people existed by growing crops and planting teak.

The trip concluded with a visit to Chiang Mai University (CMU) in the city of Chiang Mai. We met with Professor Saisamorn Lumyong and discussed the possibilities of future collaborations between our two universities. While at CMU, Adam and Carlos interacted with graduate students and gave presentations on their respective research projects. In turn, Professor Lumyong’s graduate students gave short presentations about their own research projects, which ranged from mycorrhizal relationships to the production of biofuels. While in Chiang Mai, we visited the Chiang Mai night bazaar and climbed the “stairway to enlightenment” to visit the famous Wat Phrathat Doi Suthep Rajvoravihara temple.

The trip, which was an extraordinary educational experience, was both productive and enjoyable. We learned valuable scientific lessons with respect to international interactions, collaborations and research linkages, while becoming fully immersed in a cultural experience that taught us about such things as ghost houses and elephant souls. At present, Southeast Asia is a relatively understudied region with respect to fungi and particularly the myxomycetes. However, the prospect of research collaborations is strong, since people we met are willing and eager to establish such collaborations. We would encourage our fellow mycologists to consider working in this region of the world.

—Adam W. Rollins
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—Carlos Rojas
crojas@uark.edu

Fig. 3. General aspect of the mountains from Doi Inthanon.

Fig. 4. Campus of Mae Fah Luang University in Chiang Rai.
In the past two winters, thousands of bats were found dead in caves near Albany, New York and a cave in Vermont, where about 200,000 local bats hibernate each year. Dubbed as “White Nose Syndrome”, a remarkable “symptom” is that white *Fusarium* mycelia surround the noses of some of the bats (Figure 1), both dead and living. *Cladosporium* and *Candida* also were observed occasionally. New York State wildlife pathologist Dr. Ward Stone believed that *Fusarium* was not the cause of the bat deaths because it only presented in the “outermost part of the skin” and “no tissue reaction was found” except for a couple of cases. Stone said that bats were seen flying in daylight over wide areas of eastern New York in the past a few winters. Apparently, the unusual weather woke the hibernating bats up and had resulted in widespread malnutrition and stress for bats to find food when little or none was available. However, another New York State wildlife biologist Alan Hicks said that a new pathogen may have been introduced to the Albany-area caves and spread from there. Further investigation is underway.

**Fig. 1. A cluster of bats with “White Nose Syndrome” in a New York cave. The arrows point to their noses surrounded by *Fusarium* hyphae. Photo by Nancy Heaslip.**

**Smoky Mountains Treetop Exploration Airs on **Wild Chronicles**

A University of Central Missouri research team from the Department of Biology was featured on the PBS program “Wild Chronicles,” broadcast in February as Episode #318 on PBS television stations nationwide. Entitled “Smoky Mountains Treetop Exploration,” the 5-7 minute segment was taken from footage filmed by National Geographic Society television producer Jason Orfanon during July 2008 in the Great Smoky Mountains National Park. Boyd Matson served as the host and narrator.

The storyline documents the exploration of the tree canopy using the double rope climbing technique by the UCM research team. Two graduate student climbers, Sydney E. Everhart and Courtney M. Kilgore, demonstrate how to access, climb, and gather samples (myxomycetes, macrofungi, lichens, mosses, liverworts, and ferns) from the tree canopy. Dr. Harold W. Keller, visiting professor of biology at UCM, coordinates the ground crew and serves as the principal investigator for the research project titled “RUI: Biodiversity and Ecology of Tree Canopy Biota in the Great Smoky Mountains National Park.” This project was financially supported in part by the National Geographic Committee for Research and Exploration Grant, National Science Foundation, Biodiversity Surveys and Inventories Award, Division of Environmental Biology, and Discover Life in America Award.

**Wild Chronicles** looks at the human relationship with nature, highlighting breakthrough science that offers real hope for the future. This television series airs on public television stations supported by National Geographic Society Mission Programs—the arm of the Society that supports pioneering research and field expeditions through programs such as the Committee for Research and Exploration, the Expeditions Council, the Conservation Trust, and the Explorers-in-Residence Program. “Season three of Wild Chronicles continues to build on the strong success of reporting directly from the field, as the story happens,” said Boyd Matson, host of Wild Chronicles. “Visiting the field sites of the scientists and adventurers that we work with every day and becoming part of the story helps this series transport viewers into an otherwise unseen world of exploration.”

Boyd Matson also conducted a 20-minute interview with Kilgore and Keller about their adventures, which aired on National Geographic Weekend. This is a new radio program hosted by Boyd Matson that highlights stories of “exploration to the far corners of the planet and the hidden corners of your own backyard.” It airs on radio stations on Saturdays and Sundays.

Attribution: Quotations from “Wild Chronicles” web site.

—Harold W. Keller and Courtney M. Kilgore

haroldkeller@hotmail.com
Announcing the 2008 Annual

Mycological Society of America Meeting

10 – 13 August, 2008
State College, Pennsylvania

MSA FORAY: Sunday, 10 August
THREE FULL SESSION DAYS: Monday – Wednesday, 11-13 August
SOCIAL AND AUCTION: Wednesday, 13 August

For information on all aspects of the upcoming meeting please go to the MSA Website and follow the links:

http://www.msafungi.org/

IMPORTANT DATES:

Registration: Early deadline for registration is April 15, 2008.

Abstract submission: The deadline for abstract submission is April 15, 2008, for contributed presentations and posters.

We look forward to seeing you at Penn State. Please check the MSA website for continually updated meeting and foray information and for links to our meeting registration, housing, and abstract submission sites.
Christopher D. Crabtree from the University of Central Missouri received the MNRC 2008 Award for best student poster. The Missouri Natural Resources Conference (MNRC) was held at Tan-Tar-A Resort, Osage Beach, at Lake of the Ozarks, in central Missouri, January 30 to February 1, 2008. Graduate student Christopher D. Crabtree from the University of Central Missouri (UCM) was honored with the award for best student poster by the Society for Conservation Biology (SCB) Missouri Chapter. This award is given annually for the best student poster and is based upon biological/ecological significance and importance, experimental design, and poster aesthetics. This award carries with it a one year membership to SCB and a one year subscription to Conservation or Conservation Biology, SCB’s publications. Christopher also won the honor of best graduate student poster at the Central Scholars Symposium at UCM in April of 2007 for preliminary results of his research. His research and MNRC poster are entitled “Macrofungi and myxomycetes associated with specific community types of Ha Ha Tonka State Park, Missouri”.

—Harold W. Keller
haroldkeller@hotmail.com

On behalf of the University of Toronto, I am pleased to invite you to attend the relaunched Great Lakes-St. Lawrence Spring Workshop in Mycology, to be held on April 26 and 27, 2008 at the University of Toronto, Chestnut Street Conference Centre in Toronto.

The format we are planning for this meeting will follow that of its predecessors, with registration beginning Saturday morning at 8-10 AM followed by a program of 15 min oral presentations, lunch, and more oral presentations, concluding at 4 pm. We are planning an optional group dinner and keynote address on Saturday evening. The workshop will conclude with a final session of oral presentations from 9 am ending at noon on Sunday. Details including a preliminary program, registration information, accommodation options will follow shortly.

This is an excellent opportunity for you and your students to showcase new and interesting research within our local mycology community. In other words, please send us a couple of talk titles - we need you on our program!

I recognize that April is not far off, but do hope that you will be able participate. I would greatly appreciate it if you could provide Agatha Blancas with confirmation of your planned attendance, and we will include you on the workshop mailing list (agatha.blancas@utoronto.ca, 416-978-5883). Thank you very much.

—James Scott
james.scott@utoronto.ca

John W. Rippon is among the foremost medical mycologists of our time, having written seven books and more than 80 scientific publications on medical mycology. John was among the first mycologists to see the importance in fungi that infected people, and he also is an excellent field mycologist—a very rare combination of qualities. He was honored by the Mycological Society of America as a Distinguished Mycologist in 1996.

John grew up in Toledo, Ohio and showed scientific promise at an early age, winning a Westinghouse Scholarship for Science. John received his Ph.D. from the University of Illinois in 1959. After teaching at Loyola University of Chicago for a few years, he became a professor at the University of Chicago Department of Medicine, where he researched from 1963-1989. Besides overseeing the mycology diagnostic lab there, he taught courses in medical mycology, medical microbiology, and dermatology. During that time, he was also a guest Professor at Hines VA Hospital in Chicago, where he was an Infectious Disease faculty consultant. Dr. Rippon was much sought after throughout the world for his expertise, lecturing in a “couple dozen” countries on every inhabited continent, including almost every country in South America. Dr. Rippon’s recognition of the value in studying medically important fungi became very important in the early 1980’s because of the combination of several immunosuppressive issues: the AIDS epidemic became apparent, and various clinical therapies such as corticosteroid therapy and chemotherapy became available—thus the incidence of human fungal infection skyrocketed. During that time Dr. Rippon wrote the first major textbook on medically important fungi. By the time the third edition of “Medical Mycology: the pathogenic fungi and the pathogenic actinomycetes” was published in 1988, it had become the gold standard for medical mycology throughout the world, translated into Spanish and Polish (and
pirated into Chinese). Because of Dr. Rippon’s polished writing style and meticulous attention to detail, his textbook, long out of print, is still coveted by medical professionals and mycologists.

Since his retirement in 1989 John now spends half his time at his retirement home in Michigan and half the year in Florida (can you guess which half where?). John has been a lifelong birdwatcher and has seen more than 3000 species of birds in his world travels. He spends his free time leading birding expeditions, flower walks, mushroom walks and lecturing about natural history. He has recently begun writing online book reviews on vertebrate paleontology and DVD reviews of opera performances. He is a dedicated oenophile and continues to identify molds as a consultant for various companies. John is truly a renaissance man, and we are honored to have this fellowship in his name.

—Tom Volk
volk.thom@uwlax.edu

Middle Atlantic States Mycology Conference (MASMC 2008)

The annual Middle Atlantic States Mycology Conference has taken place every spring since 1979. MASMC meetings also coincide with the appearance of many spring fungi including Morchella spp. This small meeting provides new students and postdocs an opportunity to present their research findings in a less formal venue than larger national and international meetings. This year’s MASMC and morel foray will be hosted April 18-20 by your friends at Duke University, Durham NC. Registration forms are now available on the MASMC web site (www.biology.duke.edu/masmc/). Registration is due by March 31. Both oral and poster presentations are welcome. For additional information, please contact: Dr. R. Vilgalys (email: fungi@duke.edu), Biology Department, Duke University, Durham, NC 27708

We look forward to seeing you in Durham this spring!

—Rytas Vilgalys
fungi@duke.edu

Introduction to Food- and Air-Borne Fungi

Introduction to Food- and Air-Borne Fungi. 9-13 June 2008, Ottawa, Canada. More than 100 mould and yeast species common in indoor air and on food will be examined, including important species of Penicillium, Aspergillus, Fusarium, Trichoderma, Stachybotrys, Cladosporium, Mucor, Rhizopus, Alternaria and Scopulariopsis. This five day course is appropriate for those interested in food spoilage, indoor air quality, industrial hygiene, mycotoxins, pharmaceuticals, biodeterioration, etc. Instructors: Robert A. Samson and Jos Houbraken, Centraalbureau voor Schimmelcultures. Keith A. Seifert and John Bissett, Agriculture and Agri-Food Canada.

For more information, please contact Keith A. Seifert, Biodiversity Theme (Mycology & Botany), Eastern Cereal and Oilseed Research Centre, 960 Carling Ave., Agriculture and Agri-Food Canada, Ottawa, Ontario K1A 0C6 CANADA. Phone: 613-759-1378. Fax: 613-759-1701. Email: seifertk@agr.gc.ca or visit the course web site at http://www.indoormold.org.

—Keith Seifert
seifertk@agr.gc.ca

Fleshy Fungi of the Highlands Plateau

Fleshy Fungi of the Highlands Plateau, Highlands Biological Station, Highlands, North Carolina. July 14-26, 2008. An introduction to the fleshy ascomycetes and basidiomycetes that occur in the Southern Appalachian Mountains. Emphasis will be placed on analysis of macro- and micromorphological features to aid in species identification. The daily routine will consist of a morning lecture on identification, ecology, and phylogeny of fleshy fungi followed by a field trip until early afternoon. Collections will be examined and identified after returning from the field, providing an opportunity to assemble an impressive collection of fleshy fungi.

Housing is available at the station for $60-100 per week (with linen). The station does not serve meals but a fully equipped kitchen is available, with grocery stores and restaurants available in town. Three semester hours of credit is available from Western Carolina University or UNC-Chapel Hill. Comprehensive course fee is $400. For additional information contact Dr Andrew S. Methven, Department of Biological Sciences, Eastern Illinois University, Charleston, IL 61920; phone (217) 581-6241; Email: asmethven@eiu.edu or Dr James Costa, Director, Highlands Biological Station, PO Box 580, Highlands, NC 28741; phone (828) 526-2602; Email: hbs@email.wcu.edu; Website: www.wcu.edu/hbs

—Andrew Methven
asmethven@eiu.edu
Greetings, MSA members! As the American Phytopathological Society’s affiliate representative to MSA, I invite you to join plant pathologists in the APS Centennial Celebration. The Centennial meeting in Minneapolis, Minnesota, July 26-30, 2008, will celebrate a “History of Excellence and a Future of Promise.” The meeting will feature extended special plenary sessions with internationally-renowned speakers, covering the topics of “Agriculture, Food Security and Public Health: Global Issues – Global Solutions” and “Tomorrow’s Agriculture – Six Trends You Can’t Afford to Miss.” More details, including a list of speakers and topics, are available at: http://www.apsnet.org/

The Mycology Committee of the American Phytopathological Society is sponsoring and organizing a special session entitled: “Assembling the Fungal Tree of Life: From Linnaeus to Deep Hypha and Beyond.” Speakers will include mycological systematists from the Deep Hypha Research Coordination Network and the Assembling the Fungal Tree of Life (AFTOL) project. Scheduled speakers are Meredith Blackwell, David McLaughlin, Conrad Schoch, Cathie Aime and André Levesque, and the session will end with a panel discussion of the importance of phylogenetic studies.

MSA members may also enjoy reading the February 2008 feature article on www.apsnet.org which is an excerpt, “Poisonous Fungi and Mycotoxins,” from the new book by Frank Dugan entitled Fungi in the Ancient World (APS Press, 2008).

See you in Minneapolis!

—Carol Stiles
APS Affiliate Representative to MSA
cstiles@ufl.edu
China-Japan Pan-Asia Pacific Mycology Forum 2008

The organizing committee warmly invites you to attend the China-Japan Pan Asia Pacific Mycology Forum, Changchun, China, 28 July – 5 August, 2008. The forum will provide an opportunity for sharing information on all aspects of mycology and foster constructive interaction between participants from all over the world. The working language of this conference will be English.

Main Topics
I. Symposia
(1) Mycotoxins
(2) Edible and medicinal mushrooms
(3) Phylogeny and taxonomy of fungi
(4) Ecology of fungi
(5) Molecular biology and genetics
(6) Medical mycology
II. Workshops
(1) Identification of clinically important micro-fungi (Aspergillus, Penicillium, yeasts etc.)
(2) Identification of powdery mildew and rusts and other plant pathogens
(3) Identification of slime molds
(4) Biology of entomogenous fungi
(5) Methods for molecular phylogeny

For more details, please visit: http://www.junwusuo.com
Conference Contact details
Email: yuli996@126.com, puliu1982@yahoo.com.
Tel: 0431-84510966, 0431-84532989, 13500812634 / Fax: 0431-84510966
For more information about this conference, please visit: http://www.junwusuo.com

International Congress on Systematics and Ecology of Myxomycetes

The Sixth International Congress on the Systematics and Ecology of Myxomycetes will be held from 4-10 October 2008 in Nikita Botanic Garden, Yalta, Crimea, Ukraine. Participation is essential for those interested in myxomycetes, and the Congress provides the further opportunity to enjoy the wonderful scenery and historical treasures of the Crimean coast. The Organizing Committee looks forward to welcoming you! Full information about this event can be obtained from the Congress website: www.icesm6.org.

—David Minter
d.minter@cabi.org

Saccardo’s Sylloge Fungorum Now Available Online

The Cyberliber website (www.cybertruffle.org.uk/cyberliber) and the LibriFungorum website (http://194.203.77.76/LibriFungorum/) now have the whole of Saccardo’s Sylloge Fungorum freely available on-line. Although individual volumes are stored on different servers, a co-operative arrangement means that all of them are equally available from both sites. At this juncture, it is appropriate to recognize the terrific achievement of Dr P.N. Chowdhry whose far-sighted efforts lay behind most of the monumental work of digitizing these volumes. Completion of the Saccardo volumes on-line means that Cyberliber and LibriFungorum now provide open access to all the main historical catalogues of the fungi and of mycological literature - something which probably no other biological kingdom has yet managed. These websites now provide free access to more than 131,000 scanned images of pages of mycological literature. Cyberliber, in particular, hosts more than 30 volumes of Mycologia, 66 volumes of Mycotaxon, 8 volumes of Acta Mycologica, 10 volumes of Sydowia, 8 volumes of Catathelasma, all of Grevillea, all of Michelia, all of the sanctioning works of Fries and Persoon, and much much more.

—David Minter
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Seeking Air-Dried Collections of Red Nectaria-Like Fungi

Priscila Chaverri, Howard University, with Amy Rossman and Gary Samuels, SMML, USDA-ARS, received funding from NSF to study the systematics of three genera of red nectaria-like fungi including true Nectria species. If anyone collects these fungi and is willing to share them, please send air-dried specimens to Amy Rossman, SMML, Rm. 304, B011A, 10300 Baltimore Ave., Beltsville, MD 20705. Thank you so much.

—Amy Rossman
Amy.Rossman@ars.usda.gov

Fungal Conservation in Canada and the USA

There has been a lot of superb work on fungal conservation carried out in North America but, as yet, there seems to be no continental-level or national groups dedicated to this topic. MSA Members involved in fungal conservation in Canada and/or the USA, with views on this topic, or with an interest in establishing such a group are invited to contact Dave Minter who is trying to collect information on this topic.

—David Minter
d.minter@cabi.org
Mycology, Vols. 1 and 2, DVD-ROM


This two-volume DVD set includes line drawings of fungal structures, still photographs, and videos arranged in life cycle format. The contents are interactive through a menu system and are arranged in taxonomic categories. Much to the delight of many teachers, the videos are converted from the earlier highly praised videos and film clips prepared by John Webster in collaboration with IWF. The images are of the highest quality. The line drawings and life cycles parallel those used in Webster and Weber’s 3rd edition of Introduction to Fungi published by Cambridge University Press in 2007; the contents of the DVDs follow that classification. This classification offers a practical approach for teaching about fungi in all their ecological and taxonomic diversity. Volume 1 contains Chytridiomycota and Zygomycota as well as “slime mold groups” and Oomycota; volume 2 contains Ascomycota and Basidiomycota.

Students are drawn to the video material showing hyphal growth, development of structures and events leading to spore discharge and dispersal. One can, for example, show students zoospores in action, one can watch clamp connection formation, and see the life cycle of an ascomycete in ways that inform lecture and laboratory work. The time-lapse photographs bring students to an understanding of what they may previously only have conjectured from observations in the laboratory or in the field. I worry a bit that these wonder time lapse videos make laboratory work with real specimens more challenging to present particularly if a student is impatient for the fast pace these images provide.

In practical terms one should know that these are PC products. MAC users are out of luck. The DVD contents are rightly and justifiably protected and the proprietary software that operates the programs allows one to enter the system via a series of menus or optionally to scan barcodes in order to by-pass the menus. Barcodes are printed from a PDF that is contained on the disc and using it allows the presentation to be interspersed and integrated with others lecture materials. For those accustomed to presentations with embedded graphics there is no option but to switch to the DVD to show the images.

The DVDs offer an effective backbone around which to structure laboratory tutorials. They allow students to explore in parallel the images and living material. In this way the navigational awkwardness is alleviated to some extent because of the more directed observations and the slower pace of study. It is also possible to purchase a local area network (LAN) license that might be practical for large laboratories with multiple workstations.

In whatever way teachers use these discs, the videos in particular will draw students into a more serious study of the fungi and will engender puzzlement and surprise, stimulate questions, and generally bring students to a deeper understanding of the fungus world.

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Exploitation of Fungi: Symposium of the British Mycological Society held at the University Manchester September 2005.


This volume arises from the BMS Symposium on Exploitation of Fungi held at the University of Manchester in September 2005, the purpose of which was twofold: to highlight current and future fungal exploitation, and to serve as an interface between current research and future commercialization. It does the mycological community a great service by stressing the importance of fungi in biotechnology, including the latest developments in biological, biochemical, and molecular research methods. Cambridge University Press states that this volume “will have broad appeal, not only to mycologists and microbiologists, but also to biomedical scientists, biotechnologists, environmental and molecular scientists, plant pathologists and geneticists” and I wholeheartedly agree.

Recent advances in molecular genetics and the release of whole genome sequences are catapulting fungal exploitation forward. This volume outlines how the fungal ability to secrete large quantities of proteins, in combination with complex secondary metabolic pathways, produces a diverse range of bioactive compounds now highly sought-after by the pharmaceutical industry. In addition, fungal products are increasingly being developed as alternatives to conventional pest control strategies, while certain fungal species can serve as bioremediation agents capable of transforming environmental pollutants into less-harmful compounds. Seventeen wide-ranging chapters present fungal exploitation from a modern perspective, and are authored by a selection of leading researchers from thirteen countries.

A section on “Comparative and Functional Fungal Genomics” begins this volume. The application of these powerful tools to the creation of biorefineries is discussed, noting that nine of the U.S. Department of Energy’s top 12 chemical building blocks can be produced by fungal fermentation processes. The Aspergillus niger and Trichoderma reesei genome projects and their industrial implications are examined in light of the challenges of making use of genomics information now available. Lessons learned from rice blast disease (Magnaporthe grisea) genomics are then presented, followed by a section on bioactive molecules. This includes a molecular and genetic analysis of symbiosis-expressed secondary metabolite genes from two mutualistic fungal endophytes of grasses, and the potential of fungal metabolites to serve as lead compounds for the synthesis of agricultural fungicides.

The largest section of this well-written volume is devoted to fungal bioremediation, covering such intriguing subjects as “Metal stress and the single yeast cell” and “Bioluminescence-based fungal biosensors”. The latter details an exciting monitoring tool for biologically assessing remediation sites prior to and during clean-up. In Chapter 12, “White rot fungi and xenobiotics”, Harvey and Scheer present this highly oxidizing, non-specific biological system and its potential to solve a broad suite of contamination problems via bioaugmentation. Clear explanations and illustrations of several metabolic pathways associated with xenobiotic metabolism are given and the types of wastes treatable are outlined. Challenges facing white rot fungi in bioremediation are discussed: competition from native fungi, interactions with pre-existing soil conditions, and the issue of “scaling up” when inoculating large areas. The importance of microcosm studies is stressed, concluding that the whole fungus, rather than individual enzymes, may be best suited to in situ bioremediation. This thread continues in Chapter 13, “Metal and mineral transformations: a mycoremediation perspective”. Other topics well-covered in this diverse volume include protein folding and secretion, and fungal biocontrol of subterranean pests, perennial weeds, fungal plant pathogens and fungal invertebrate parasites.

The fungi comprise a highly diverse kingdom of eukaryotic organisms, and this book thoroughly conveys the biotechnological implications of this diversity. It benefits from the inclusion of commercialization success stories, such as Trichoderma-based biofungicides, and proteome and genome analyses that illustrate the potent role of functional studies in future research. Finally, a comprehensive index increases the value of this volume for readers.

—Allison Walker
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Compendium of Brassica Diseases


This guidebook of Brassica diseases is one of the most anticipated compendia awaited by those who work in plant pathology, students, farmers and others. This book cannot be missing in any mycology collection.

Fifty-nine international researchers could be considered authors of this compendium. Separated into three parts, this book has over a hundred pages in which one can obtain a complete review of these crop plants from their taxonomy and genetic relationships among Brassica species, considering their production management, through different diseases that affect them: fungi and oomycetes, bacteria, mollicutes, viruses and nematodes. The last part of the book is dedicated to noninfectious diseases, those caused by pollution and environmental effects as well as genetic abnormalities, herbicide injuries, nutritional deficiencies and postharvest disorders. Furthermore, the book has a detailed glossary in which one can find all the terminology used in the book as well as a species index.

Every one of the chapters dedicated to diseases is supported by pictures showing symptomology and disease signs in the case of fungi as well as diagrams of disease cycles and charts. Pictures are found in every chapter of the book. This characteristic helps to understand the subjects in a practical and didactic way. For this reason this book can be used as a reference for everybody who needs to diagnose and solve problems related to diseases of these crops destined for the vegetable market, seeds, oil and spices, and livestock feed.

—Carolina Martinez
Unidad de Fitopatología.
Servicio Agrícola y Ganadero.
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Compendium of Rose Diseases and Pests


Who has a rose at home and would like to know what disease is affecting it? Well, in this guidebook, you will find over eighty pages and twenty-nine international authors answering all those questions related to phytosanitary conditions and management of your roses, because it is a practical guide to the diagnosis of diseases of these plants.

Larger than the former edition, this book is divided into three parts with chapters covering general subjects about rose parentage/hybrids, cultivar classification, general maintenance/production practices to more specific and varied topics such as rose diseases, infectious and noninfectious diseases/disorders, and disease and pest management.

The chapters related to infectious diseases include those caused by fungi, bacteria, viruses and associated organisms, and nematodes. Similar to other editions, each specific subject is supported by pictures showing symptomology and disease signs in the case of fungi as well as diagrams of disease cycles. This feature helps to understand each topic in which one can compare symptoms and pathogen agents as you read the book. This situation is repeated in the other chapters. For example, the chapter of noninfectious symptoms, such as those caused by pollution and toxicities, is discussed and illustrated with color photographs that help distinguish them from bacterial, fungal, nematode, and viral symptoms. Also a new section with color illustrations of pests and the symptoms they cause helps to identify the insects and mites that attack roses.

At the end of the compendium, an appendix is included with the scientific and common names of all the pathogen agents mentioned, plus a complete glossary with all the terminology used in this review and finally an index to look for the different subjects.

—Carolina Martinez
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In the pursuit of truffles, a basic understanding of the ecology of the fungi and the need for a sharp eye is required. As the authors explain, truffle fungi are mycorrhizal, so “the first step to finding truffles is to find habitats with appropriate host trees.” The reader is briefed on truffling tools and techniques, microhabitatstosearch,e.g.lowspotsorareasadjacenttorottinglogs, and is reminded to push the duff back over the areas that have been disturbed. The experienced truffer is also aware of activity by the “local experts, the small animals” and where they have been creating little digs in the earth recently.

The second section of the *Field Guide to North American Truffles* profiles ninety species of truffles, arranged alphabetically by genera. The inclusion of a short identification key in this front section would have been a beneficial addition. Each profile provides a concise description of the species and its fruiting season, distribution, morphological features, and also includes general comments and a gastronomic desirability rating (delicious, tasty, palatable, insipid, or inedible). One key feature adds tremendous utility to this book. Each species profiled contains color photographs of both the fruiting body and the spores.

A glossary of terminology and a section on “the Meaning of Scientific Names” covers common truffle terms, Latin and Greek nomenclatural roots, and truffle names that honor esteemed mycologists. An index follows. Lastly, information is provided about the thirty-year old North American Truffling Society to which readers may join or contact regarding questions about truffles or the identification of specimens.

There is no book comparable to the *Field Guide to North American Truffles*. This book could only happen thanks to a group of people so passionate and knowledgeable about these fungi. Whether you are just piqued by truffles, or are already well acquainted with these underground fungal jewels, the *Field Guide to North American Truffles* will be a valuable field companion. Amateur and professional mycologists alike will find great value in this book and it will be a welcomed addition to any mycology classroom and lab.

—Gregory Bonito  
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Annotated list of polypores for the Iberian Peninsula and Balearic Islands


This commendable effort is a top quality presentation for a part of the planet for which many of us have little knowledge. More than a list, the book provides the following: a map of the provinces, a list of the fungal herbaria that hold voucher specimens including private collections, a bibliography of Spanish literature (852 references), of course, the list of specimens arranged alphabetically according to genus, bibliographic references cited in the catalogue, and finally an index to genera, species and infraspecific taxa. In the list of species, one finds a full citation for each genus and species, synonymy, type location and other data, chorology, substrate, herbaria and occasionally notes that reflect the specific knowledge of the authors. This is a valuable little book for polypore specialists, regional conservation biologists, libraries and those interested in global distributions of fungi as a measure of the changing world. The book may also serve as a model presentation for other regions.

—Ed Setliff  
Professor Emeritus  
Cazenova, New York  
esetliff@hotmail.com
These stories provide insights into our beginnings as partners in our own rights. Some of these women married and raised families in addition to pursuing their passion for science, whereas others devoted their lives to the work. These women slowly became recognized in their fields, often with the help of male colleagues.

I loved reading this book. I now have a good reference for the details of lives about which I’ve read a little, but which I have occasionally referred to in lectures (for example, Flora Patterson, in 1905, was the first person to identify as a fungus the pathogen responsible for chestnut blight disease). As a graduate student in the 1960’s, I heard stories about the exploits of women who commanded attention at meetings and proved their hypotheses with clearly stated facts. These stories gave me the courage to report my work and this book will be an inspiration to women and men who continue the search for scientific knowledge.

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Recently Received Books


Previously Listed Books


**REMINDER: MSA Directory Update**

Is your information up-to-date in the MSA directory? The Society is relying more and more on email to bring you the latest MSA news, awards announcements and other timely information, and our newsletter. To ensure that you receive Society blast emails and the Inoculum as soon as it comes out, and so that your colleagues can keep in touch, please check the accuracy of your email address and contact information in the online directory. This can be accessed via our web site at www.msafungi.org. If you need assistance with updating your membership information, or help with your membership log-in ID and password, please contact Kay Rose, Association Manager at Allen Press, at krose@allenpress.com.
MycoLotus 1 Crossword

All words are 5 letters in length. For example, Clockwise clue #1 and Counter-Clockwise clue #1 both start from the same letter/square marked #1, then curve in to the center. Except for personal use, this puzzle may not be reproduced without permission.

—Juliet Pendray
aloe@netrover.com
Vancouver Mycological Society

COUNTER-CLOCKWISE
1. Ovens used to dry wood to prevent fungal decay
2. Spanish for fungus
3. Fungus in Ultima Online role playing game
4. Hard shelving polypores
5. 5th or 7th day in Roman calendar
6. Hardened in pottery ovens
7. Son of Orgon in Moliere's Tartuffe
8. Voudun pantheon Papa
9. Fifth Kingdom
10. Larch Needle Cast genus
11. Plant tissue for moving water, also used as a highway for hyphae
12. Binding agreements
13. Ustilago scitaminea smut makes sugar _____ grow black whips
14. Uredinales members
15. Friend of fungi like Chaga, Piptoporus and Leccinium scabrum
16. Amsterdam term for (now outlawed) shroom
17. Tove before it gimbals
18. Typical substrata for lichens like Verrucaria, Rhi- zocarpon, Caloplaca

CLOCKWISE
1. Pejorative term for eccentrics
2. Sharpened
3. e.g. Growth, absorption, storage and senescence, in hyphal tips
4. (Latin) Leathers or skin layers
5. Dark rain-filled clouds
6. Kuwaiti term for desert truffles
7. Wash this in Trichoderma cellu-lase enzymes for a hip 1990's look
8. e.g. Zoophagus "lethal lol-lipops," or cheese in a mousetrap
9. Makes matted material
10. (suffix) Fungi
11. (abbr. prefix) Yellow
12. (Latin) To graze or forage
13. These form when bacteria culture or vinegar is combined with milk
14. Amusement park attractions
15. Hits shins against coffee table
16. (prefix) Spore produced in a pycnidium
17. This apparatus is a dictyosome
18. Some Agaricus species have two of these
**Stir-fried Oyster Dish**

*Pleurotus ostreatus* (Jacq.) P. Kumm.

6 (1 ½ cups) Oyster mushrooms
2 ½ tablespoons cooking oil
1 (1 ¼ cups) broccoli
1 stalk green onion
1 oz ginger sliced
2 pieces ground garlic
¼ cup cooking wine
¼ teaspoon salt (to taste)
1 tablespoon soy sauce
1 teaspoon sugar
1 teaspoon cornstarch mixed with 1 tablespoon water

1. Wash mushrooms then cut and slant into oyster style. Wash broccoli and cut into bite-size pieces. Cut green onion into 3-cm lengths. Slice and ground the garlic and ginger; set aside.

2. Heat wok: add 1 tablespoon oil; and stir-fry oyster mushrooms with ¼ cup cooking wine and ¼ teaspoon salt. Stir, add green onion segments and ginger slices, continue to stir fry for a few seconds.

3. Simmer: add in 1 tablespoon soy sauce and 1 teaspoon sugar. Simmer until juice is absorbed by oyster mushrooms and liquid is reduced to approximately ½ cup.

4. Last steps: add broccoli and continue to stir for five seconds. Add garlic and thicken with cornstarch. Drizzle with ½ tablespoon hot oil (heated separately) and serve.

—Mo Mei Chen

mmchen@nature.berkeley.edu

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**Mycolotus 1 Answers**

|------|---------|-----------|---------|---------|-------------|---------|---------|---------|---------|
MYCOLOGICAL JOBS

Faculty Position in Molecular Plant Pathology at Ohio State

A 9-month tenure-track position at the Assistant Professor level is available in the Department of Plant Pathology, The Ohio State University, Ohio Agricultural Research and Development Center (OARDC), located in Wooster, OH. The position is 90% research and 10% teaching.

The successful candidate will conduct basic research on plant pathogens and their interactions with host plants. Candidates should have documented experience with modern techniques of cell biology, biochemistry, molecular biology, genomics and/or proteomics. The individual selected for this position will be expected to develop a strong interdisciplinary and extramurally-funded research program in pathogen biology. Potential research topics may include but are not limited to: the molecular basis of pathogen interactions with their hosts, comparative and functional genomics of plant pathogens, molecular ecology of plant pathogens in managed or natural ecosystems, and/or the evolution of pathogenicity in oomycetes, fungi, bacteria or nematodes that infect plants. The assigned laboratory is housed in the same building as the Molecular Cellular Imaging Center, a premier core facility housing the latest instrumentation for conducting molecular research. Collaborations with other faculty in the Department and OSU’s Plant Molecular Biology and Biotechnology (PMBB) Program will be encouraged.

The incumbent should have a strong commitment to graduate education, teach an advanced course in molecular plant pathology, and participate in team-taught courses in support of the Department’s core curriculum. A Ph.D. in plant pathology or related biological sciences is required. Research experience in molecular-plant microbe interactions, a strong publication record in pathogen biology, grant writing experience, and postdoctoral experience are preferred.

The application deadline is March 21, or until a suitable applicant is found. Applicants must submit a curriculum vita, a copy of academic transcripts, a concise statement of research plans and teaching goals, a copy of two relevant manuscripts, and the names and complete addresses of four references to be contacted. Applications materials should be sent to Dr. Brian McSpadden Gardner, MPP Search Committee Chair, Department of Plant Pathology, The Ohio State University-OARDC, 1680 Madison Avenue, Wooster, OH 44691 or via e-mail as a single pdf document to mcspadden-gardner.1@osu.edu. For additional information or questions please contact the Department Chair, Dr. Mike Boehm, at 614-292-1375 or boehm.1@osu.edu.

The Ohio State University is an Equal Opportunity, Affirmative Action Employer. Women, minorities, Vietnam-era veterans, disabled veterans and individuals with disabilities are encouraged to apply.

Ph.D. or Postdoctoral Fellow in Food and Bioproduct Sciences

The Opportunity: A Ph.D. graduate student or Postdoctoral Fellow is sought to carry out a research project with financial support from a Saskatchewan Agriculture and Food - Agriculture Development Fund (ADF) grant. The funded project will investigate the topic “Development of Novel Microbial Biopesticides for Efficient Plant Pathogens Biocontrol.”

Qualifications: The applicant should have a strong academic background in molecular biology, microbiology, biochemistry or one of the natural sciences. A strong commitment to pursue a research career, good communication and writing skills, and the ability to work in a team environment are essential qualities. For Ph.D. studies, the candidate should have a minimum overall weighted average (University of Saskatchewan grade system equivalent) of 72% before considering submission of an application. A successful application to the College of Graduate Studies at the University of Saskatchewan will be required. Information on College admission requirements and application forms can be obtained at http://www.usask.ca/cgsr/.

Stipend: For the successful Ph.D. candidate, the standard rate for a University graduate stipend will be awarded.

Deadline: April 1, 2008

Contact Information: PRIOR TO MAKING AN APPLICATION, please send your CV to Dr. Vladimir Vujanovic at vladimir.vujanovic@usask.ca; Fax (306) 966-8898.

How to Apply: For Ph.D. studies, send a complete application package which includes: an application form (GSR101), curriculum vitae, academic transcripts, English-equivalency test results, three letters of recommendation forms (GSR100) (each in individually sealed envelopes), an application fee, and a covering letter stating how your background and qualifications match the position. Please quote position #vv2008.02 and mail package to: Graduate Secretary, Department of Food and Bioproduc foregoing, 51 Campus Drive, University of Saskatchewan, Saskatoon, SK, Canada, S7N 5A8.
M.S. or Ph.D. Graduate Assistantship in Marine Mycology Research

The Department of Coastal Sciences (http://www.usm.edu/gcrl/coastal_sciences/) at the University of Southern Mississippi (http://www.usm.edu) is requesting applications from highly qualified students for its MS or PhD program in coastal sciences with a focus in marine mycology. The Department of Coastal Sciences is located at the Gulf Coast Research Laboratory (http://www.usm.edu/gcrl) in Ocean Springs, MS (http://www.oceanspringschamber.com/) on the Gulf of Mexico.

Current research in marine mycology at GCRL includes the diversity of saprophytic marine fungi in natural and created saltmarshes; marine fungi as indicators of human impact on coastal environments; improving salt-marsh restoration using symbiotic fungal associations; fungal infections of captive and wild-stranded bottlenose dolphins; and colonization and species succession on artificial reefs.

Successful applicants will be provided a 12-month Research Assistantship with a tuition waiver. Candidates should possess a relevant BS degree (GPA >= 3.0), and MS (GPA >= 3.5) if applying for the PhD program. The position is available starting summer 2008 and will be open until filled. Interested individuals should contact: Dr Jinx Campbell, Asst Professor Marine Mycology, Department of Coastal Sciences, University of Southern Mississippi, Gulf Coast Research Lab, 703 East Beach Drive, Ocean Springs, MS, 39564; (228) 818-8878; e-mail: jinx.campbell@usm.edu.

Mushrooms in Their Natural Habitats (Vols. I and II), 1949

info@michaelsbooks.com

Mold Testing and Identification Services

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*If this membership is given after June 1, please add $10 to cover postage for past issues.
Below is an alphabetical list of websites featured in *Inoculum* during the past 12 months. Those wishing to add sites to this directory or to edit addresses should email <jinx.campbell@usm.edu>. Unless otherwise notified, listings will be automatically deleted after one year (at the editors discretion).

A New Web Page About Tropical Fungi, Hongos Del Parque “El Haya” (58-5) hongosdelhaya.blogspot.com/

Ascomycota of Sweden www.umu.se/myconet/asco/indexASCO.html

Australasian Mycological Society Website (53-4) bugs.bio.usyd.edu.au/AustMycolSoc/Home/ams.html

Authors of Fungal Names (54-2) www.indexfungorum.org/AuthorsOfFungalNames.htm

Bibliography of Systematic Mycology www.speciesfungorum.org/BSM/bsm.htm

British Mycological Society (54-1) www.britmycolsoc.org.uk/

Cold Spring Harbor Laboratory; Meetings & Courses Programs (58-2) meetings.cshl.edu

Collection of 800 Pictures of Macro- and Micro-fungi www.mycolog.com

Cordyceps Website www.mushtech.org

Cornell Mushroom Blog (58-1) hosts.cce.cornell.edu/mushroom_blog/

Cortbase (58-2) andromeda.botany.gu.se/cortbase.html

Corticoid Nomenclatural Database (56-2) www.phyloinformatics.org/

Coverage in Ukraine of Higher Fungal Ranks (56-2) www.cybertruffle.org.uk/lists/index.htm

Cyberliber Mycological Publications (57-4) www.cybertruffle.org.uk/cyberliber/index.htm

Cyberliber (58-3) www.cybertruffle.org.uk/cyberliber/

Cytobase Imaging of the Fungi (58-6) www.fpl.fs.fed.us/rwu4501/index.html

Cybertruffle’s Fungal Valhalla (56-2) www.mycologia.org

Entomopathogenic Fungal Culture Collection (EFCC) www.mushtech.org

Fun Facts About Fungi (55-1) www.herbarium.usu.edu/fungi/funfacts/factindx.htm

Fun From Veracruz (53-6) www.uv.mx/institutos/forest/hongos/fungavera/index.html

Fungal Environmental Sampling and Informatics Network (58-2) www.bio.utk.edu/fesin/

HighWire Press (58-3) mycologia.org

Index of Fungi www.indexfungorum.org/names/names.asp

ING (Index Nominum Genericomum) Database (52-5) ravenel.si.edu/botany/ing/

Interactive Key, Descriptions & Illustrations for Hypomyces (52-6) nt.ars-grin.gov/sbmlweb/fungi/keydata.cfm

Interactive Key to Hypocreales of Southeastern United States (57-2) nt.ars-grin.gov/sbmlweb/fungi/keydata.cfm


JSTOR (58-3) jstor.org

Libri Fungorum Mycological Publications (58-3) 194.203.77.76/LibriFungorum/

Mold Testing and Identification Services (58-2) www.pioneer.net/~microbe/abbelab.html

Mountain Justice Summer (58-3) www.MountainJusticeSummer.org

Mycologia On-Line (53-3) www.mycologia.org

Mycological Progress (52-3) www.mycological-progress.de

The Myconet Classification of the Ascomycota www.fieldmuseum.org/myconet

Mycosearch web directory/search engine (51-5) www.mycosearch.com

Mushroom World [new Korean/English site in 2001] (51-6) www.mushworld.com

NAMA Poison Case Registry (51-4) www.sph.umich.edu/~kwcee/mpcr

Northeast Mycological Federation (NEMF) foray database (58-2) www.nemfd.org


Pleurotus spp. www.oystermushrooms.net

Rare, Endangered or Under-recorded Fungi in Ukraine (56-2) www.cybertruffle.org.uk/redlists/index.htm

Registry of Mushrooms in Art members.cox.net/mushroomsinart/

Searchable database of culture collection of wood decay fungi (56-6) www.fpl.fs.fed.us/rwu4501/index.html

Small Things Considered. A microbe blog on microbes in general, but carries occasional pieces specifically on fungi. schaechter.asmblog.org/schaechter/

Species of Glomeromycota Website (55-3) www.amf-phylgenomy.com

Systematics of the Saprolegnieae (53-4) www.iillumina-dlib.org

Tree canopy biodiversity project University of Central Missouri (58-4) faculty.cmsu.edu/myco/

Tripartite Similarity Calculator (55-1) www.amanitabear.com/similarity

The TRTC Fungarium (58-1) bbc.botany.utoronto.ca/ROM/TRTCFungarium/home.php

U.S. National Fungus Collections (BPI) Complete Mushroom Specimen Database (57-1) www.ars.usda.gov/ba/psi/sbml

Website for the mycological journal Mycena (56-2) www.mycena.org/index.htm

Wild Mushrooms From Tokyo www.ne.jp/asahi/mushroom/tokyo/
NOTE TO MEMBERS:
Those wishing to list upcoming mycological courses, workshops, conventions, symposia, and forays in the Calendar of Events should include complete postal/electronic addresses and submit to Inoculum editor Jinx Campbell at jinx.campbell@usm.edu.

April 5–8, 2008

9th European Conference on Fungal Genetics (ECFG9)
Edinburgh, Scotland
www.ecfg.info

April 18–20, 2008

Middle Atlantic States Mycology Conference (MASMC 2008)
Duke University, Durham, NC
www.biology.duke.edu/masmc/

April 26–27, 2008

Great Lakes-St Lawrence Spring Workshop in Mycology
University of Toronto, Canada

June 9–13, 2008

Introduction to Food- and Air-Borne Fungi
Ottawa, Canada
www indoormold.org

June–October, 2008

Seminars at the Humboldt Institute
Humboldt Institute, Maine
www.eaglehill.us/mssemdes.html

July 14–26, 2008

Fleshy Fungi of the Highlands Plateau
Highlands Biological Station
Highlands, NC
www.wcu.edu/hbs

July 26–30, 2008

APS Centennial Celebration
Minneapolis, Minnesota
www.apsnet.org

July 27–August 2, 2008

Myxomycete Seminar
Humboldt Field Research Institute, Maine
www.eaglehill.us

July 28–August 5, 2008

China-Japan Asia Pacific Mycology Forum 2008
Changchun, China
www.junwusuo.com

August 5–10, 2008

IUMS (International Union of Microbiological Societies)
Congress 2008

XII Bacteriology and Applied Microbiology
XII International Congress of Mycology
XIV Congress of Virology
Istanbul, Turkey
Abstract deadline: 31 January 2008
www.iums2008.org/

August 9–14, 2008

MSA Meeting
State College, Pennsylvania,
United States
www.outreach.psu.edu/programs/mycology

September 4–7, 2008

North American Mycological Association (NAMA) Annual Foray
In memory of Dr. Orson K. Miller
Hosted by: Southwest Idaho Mycological Association (SIMA)
McCall, Idaho

October 4–10, 2008

Sixth International Congress on the Systematics and Ecology of Myxomycetes
Nikita Botanic Garden, Yalta, Ukraine
www.icsem6.org

July 25–30, 2009

BSA/MSA meeting
Snowbird, Utah
Inoculum is published six times a year and mailed with Mycologia, the Society’s journal. Submit copy to the Editor as email (in the body, MS Word or WordPerfect attachment in 10pt Times font), on disk (MS Word 6.0, WordPerfect, *.tif, *.jpg), or hard copy. Line drawings and sharp glossy photos are welcome. The Editor reserves the right to edit copy submitted in accordance with the policies of Inoculum and the Council of the Mycological Society of America.

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MSA Homepage: msafungi.org

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____ A.H. & H.V. Smith Award
____ Clark T. Rogerson Award

Other Funds

____ Alexopoulos Prize
____ Karling Lecture Fund
____ Uncommitted Endowment
____ Other (specify)

I wish to pledge $__________ a year for__________ years

____ to the following fund(s) _________________________

____ to some other specified purpose _________________________

____ to the uncommitted endowment

Name: _____________________________________________

Address: ___________________________________________

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____ Check ____ Credit Card (Visa, MC, etc): __________________

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Signature: _________________________________________

Please send this completed form and your contribution to:

A. Elizabeth Arnold, Chair

MSA Endowment Committee
Division of Plant Pathology and Microbiology
Dept. of Plant Sciences
University of Arizona
Tucson, AZ 85721
arnold@ag.arizona.edu
(520) 621-7212

Please make checks payable to the
Mycological Society of America
The Mycological Society of America
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You are encouraged to inform the Sustaining Membership Committee of firms or foundations that might be approached about Sustaining Membership in the MSA. Sustaining members have all the rights and privileges of individual members in the MSA and are listed as Sustaining Members in all issues of *Mycologia* and *Inoculum*.
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AREAS OF INTEREST

Mark most appropriate area(s)

____ Cell Biology – Physiology (including cytological, ultrastructural, metabolic regulatory and developmental aspects of cells)

____ Ecology – Pathology (including phytopathology, medical mycology, symbiotic associations, saprobic relationships and community structure/dynamics)

____ Genetics – Molecular Biology (including transmission, population and molecular genetics and molecular mechanisms of gene expression)

____ Systematics – Evolution (including taxonomy, comparative morphology molecular systematics, phylogenetic inference, and population biology)

PAYMENT

____ CHECK  [Payable to Mycological Society of America and drawn in US dollars on a US bank]

____ CREDIT CARD:   _____ VISA   _____ MASTERCARD

Expiration Date: ____________________________

Account No: __________________________________

Name as it appears on the card: ________________________________

Mail membership form and payment to:

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Attn: Kay Rose
P.O. Box 1897, Lawrence, KS 66044-8897
Phone: (800) 627-0629 or (785) 843-1221
Fax: (785) 843-1274
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