

Newsletter of the Mycological Society of America

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President's Corner

Expanding Faculty Positions in Mycology

In my last President's corner I conjectured that the field of mycology is small because it lacks visibility to students at the K-12 and undergraduate levels, and because the taxonomic difficulty of fungi creates a barrier to non-taxonomists that might otherwise study fungi. I suggested that teaching and outreach at all levels are necessary steps toward raising the visibility of our field, and that the web might be a particularly valuable way to expand our teaching and outreach mission. In this issue I want to address the other end of this process: faculty positions.

If we think of the field of mycology as a population, then it's obvious that it grows when on average we each turn out more than one student who successfully gets a job in the field, and conversely the field shrinks when on average we each turn out less than one successful student. Of course we are not all at PhD granting institutions, so those that do have such positions must turn out considerably more than one successful student. However, the rest of the field is not off the hook because training mycology students is a community effort these days. Undergraduate students in USA and Canada usually move to a new school for graduate school, and often move to one or two postdoctoral positions before finding a permanent position. Any of these steps can be rate-limiting. If fewer undergraduates are interesting in pursuing graduate school in mycology then the potentially available graduate slots go unfilled, and if postdocs and permanent positions are not available for the newly minted PhDs, then



**Tom Bruns,
MSA President**

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training more does not increase the size of the field. The emphasis on teaching and outreach in my last column relates to the undergraduate side of this equation; now I want to jump to the issue of permanent mycology positions.

Let's start with the question of how mycology positions are preserved following retirements. This is important because it will be easier to expand the number of positions if we can at least hold on to those that we already have. Here I can only speak for UC Berkeley, but I suspect the process is similar at many other institutions. The days of automatically rehiring someone to fill "Joe's position" are over and probably those days never existed. Instead when someone retires, the department has to put forth a justification to the campus that explains in a persuasive way why they need a "new" position, and this justification is constructed from both research and teaching needs. When positions are discussed at faculty meetings, people are likely to push for hires in fields that are at the cutting edge of a new or expanding field. The fields that people know best are their own, and they often look at an open position as an opportunity to build strength in their field and gain a colleague with whom they can interact and perhaps collaborate. For these reasons if there are no other mycologists on the faculty it may be unlikely that anyone else will push for rehiring a mycologist unless the person that retired filled an indispensable role.

Teaching can certainly be such an indispensable role, but only if the courses taught by the retiring faculty member are critical for a major or are in high demand by students. Plant pathology departments always have need for fungal courses and therefore a mycologist is usually viewed as an indispensable position from both a teaching and a research point of view. But what about other types of biology departments? In these cases, I think it takes concerted effort to justify a mycology position, and I have three examples to illustrate this point. When Terry Henkel was hired at Humboldt State University there were several courses on fungi or forest pathogens that his predecessor David Largent taught and that were in high demand and fulfilled requirements. Similarly Tom Volk, was hired specifically to teach the medical mycology course at University of Wisconsin, La Crosse, when Allen Nelson retired. In the case of University of Hawaii, Hilo, Don Hemmes was able to make a strong argument for rehiring a mycologist because his work in both teaching and research was greatly appreciated by his departmental colleagues, and he made the case that "microbial ecology" was an area they were weak in. The result was Brian Perry

ended up with a job as a mycologist in Hilo! In the emails I received from Don Hemmes and David Largent one other factor certainly was clear, both exercised some political skill in convincing their colleagues that another mycologist was in their department's best interest. But would any of these positions have been successfully preserved if the teaching demand had not been high? I doubt it.

Important herbarium collections can also create an indispensable role for mycologists and they have sometimes tipped the scales toward rehiring. The Thiers Herbarium at San Francisco State University, the Gilbertson Herbarium at the University of Arizona, the University of Michigan Herbarium were certainly part of the justification for hiring Dennis Desjardin, Betsy Arnold, and Tim James, respectively. But these days just maintaining a herbarium is often a hard sell to university administrators, and there are probably many more examples of positions that were lost at herbaria than those that were preserved because of them. So what was the difference in these cases? The visibility of these particular collections, and in the case of Arizona and SF state the research activity of Bob Gilbertson and Harry Thiers, respectively, were certainly major factors. In the case of Michigan, the Lewis E. Wehmeyer endowed chair in mycology, also helped persuade the faculty that hiring a mycologist was a good idea. If only we had more endowed chairs in mycology!

Now let's turn to the question of where new mycology positions come from. My hunch is that most truly new positions that are listed specifically as mycology come from institutions that already have several mycologists in residence. The recent flurry of new mycology positions at the University of Georgiana, Athens comes to mind in this case. Here the legacy effects from a historically strong program in mycology became an argument for rebuilding a new one. I know from serving on a review committee for the Botany Department at Georgia, that the department was proud of their former leadership in the field of Mycology, and that they realized that parts of the field tied in well with current strengths in plant ecology and plant molecular biology. The way they structured these new positions across several departments was a clever way to maximize impact without any single department having to commit all of the resources necessary for the three new hires. But I have no doubts that the current mycologists there helped to influence the decision to recruit.

The most important source of new positions, however, are those that are not listed as mycology positions

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at all, but nevertheless result in hiring of someone who is a mycologist. These are the ones that will expand our field and simultaneously connect it to others. There are probably lots of these, but I will just give a few examples that I assembled after emailing colleagues and former students. A long list could also be assembled from the molecular genetic side of our field, and the absence of those names here just reflects my myopic knowledge of recent hires rather than lack of positions. Here are the examples as they were advertised: David Hibbett (Plant Molecular Systematist, Clark Univ.), Georgiana May (Evolutionary Plant Biologist, Univ. Minn.), Peter Kennedy (Plant-Microbe Interactions, Lewis & Clark College), Lee Taylor (Microbial Diversity and Function, Univ. Alaska), Nicole Hynson (Plant Community Ecology, Univ. Hawaii), Rich Shefferson (Evolutionary Ecology, Univ. Georgia) and Nina Wurzbarger (Below Ground Ecology, Univ. Georgia). Notice that these positions often have plant or microbe in the title. Although the phylogenetic streak in us may bristle at putting fungi back in these categories, when it comes to jobs we should all be happy to call fungi either plants, microbes, or maybe even animals, which is at least phylogenetically closer. Knowing the people listed above, I can say that they all share three things in common: 1) at the time of hiring they had some great publications placed in evolutionary or ecological journals, 2) they all can give great talks, and 3) in addition to mycology meetings they attended other societal meetings (e.g., ESA or SSE).

Is there really anything surprising here? Mycology positions are preserved and refilled when the retiree did a great job, made themselves indispensable to their de-

partment, and probably exhibited some political savvy. Mycologists are hired into other, more broadly advertised positions when they do a great job of connecting with those broader fields, and when people outside the field see their system (i.e., fungi) as being particularly exciting. When I was emailing around to assemble some of this information I received this response from Georgiana May who summarized this point beautifully:

“How to expand mycology positions? I have always thought that this would come from mycologists being excellent scientists first, being able to communicate the value of what they are doing second, and by being mycologists third. This is something I gained from working with John [Taylor]” - Georgiana May

Mycologist is an important term that I have not defined in this essay, and I bring this up at the end because I think that the way we define it can expand the field in another way – through annexation. My definition of a mycologist is simply someone who studies fungi (inclusive of other fungal-like eukaryotes), and who contributes to the body of knowledge about fungi. Some of these people may self-identify as mycologists, and others may self-identify as ecologists, evolutionary biologists, or molecular biologists. I see no reason why people can't wear many hats, and if we succeed in convincing more people that the mycologist hat fits them well, then we have enriched and expanded our field in a wonderful way.

—Tom Bruns
Dept. Plant & Microbial Biology
UC Berkeley

Invitation to a Roundtable on Classification of Environmental Sequences

The 79th annual meeting of the MSA will include a roundtable discussion on strategies and standards for classification of fungal taxa that are discovered solely through environmental DNA sequences (hereafter “environmental species”). A panel of discussants will offer their perspectives and facilitate the conversation, but everyone is welcome to participate and share their views. The goal of this session is to refine the issues and identify areas of agreement and challenge, not to craft a final solution. Results of the discussion will be summarized in a report that we hope will promote further conversation in the broader mycological community. Here, we present five sets of questions that are intended to frame the discussion in Fairbanks and that must be addressed in developing approaches for classification of environmental species. For background on these issues, see Hibbett et al. (2011), Reynolds and Taylor (1991), and the proceedings of the One Fungus-One Name symposium held April 19-21,

2011, at the Royal Netherlands Academy of Arts and Sciences, Amsterdam, which will soon be posted at the International Mycological Association website (<http://www.ima-mycology.org/>). Readers who are unable to attend the MSA meeting are encouraged to e-mail their responses, as well as suggestions for additional questions, to dhibbett@clarku.edu.

1. Form and governance of names of environmental species.

- *Should environmental species be named with Latin binomials (just like specimen-based species), or alphanumeric codes (as in existing special-purpose classifications)? Would a mixed system be useful?*
- *Should the naming of environmental species be governed by the International Code of Botanical Nomenclature? Would*

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a completely separate system be better? Could informal taxon names coexist with Code-compliant names?

- If the naming of environmental species is governed by the Code, is a new type of taxonomic category, such as candidate species, necessary or desirable?
- Can aliquots of DNA from environmental sources, or sub-samples of material from which DNA has been extracted, serve as type material for nomenclatural purposes?
- Are new rules or recommendations needed in the Code? For example, are special rules needed concerning priority of environmental vs. specimen-based names?

2. Character bases and minimal requirements for publication of names of environmental species.

- What loci should be allowed for sequence-based species description? How should the loci be selected for each group of Fungi?
- How many times should a new taxon be detected in independent samples or studies before it can be named?
- Should a search of all relevant sequence databases be required for publication?
- Should a phylogenetic analysis be required to accompany publication? If so, what are the minimum criteria for support?
- How do intragenomic heterogeneity and gene-tree/species-tree conflict affect description of environmental species? Do we know enough about these phenomena to assess their impact on sequence-based taxonomy?
- What kinds of quality-control measures should be required for publication (e.g., chimera-checkers, sequencing quality standards)? How do these differ for Sanger vs. pyrosequencing?
- What are the minimum metadata required? Are there essential metadata beyond date and locality?
- Should registration in a taxonomic database be a requirement for publication of a name of an environmental species?
- Should these criteria be incorporated into the Code as rules or recommendations? Should an independent set of nomenclatural/taxonomic rules be developed for environmental species?

3. Databases, resources, and tools.

- Can the naming and management of environmental species be handled by existing databases and services, including NCBI, MycoBank, Index Fungorum, BOLD, and UNITE? Which of these platforms is prepared to accept names of environmental species now? To what extent does this depend on the form of the names and integration with the Code?
- What new tools and informatics resources are needed to facilitate naming and management of environmental species? Can tools developed for prokaryotes be adapted for use in Fungi?

4. Environmental clade names.

- Can the principles for environmental species names also be applied to clades, or are special protocols required for environmental clades?
- What about environmental taxa based on loci that do not discriminate species (e.g., 18S rRNA, ITS for some groups)? Is it possible to describe clades without designating species? How should the splitting of environmental taxa be handled (when there is no specimen to anchor a species name)?

5. Strategies going forward.

- If changes to the Code are sought, they will need to be submitted for a vote at the next International Botanical Congress, in 2017. What is the timetable for developing such proposals, and what is the contingency plan if they are rejected?
- How can ecologists be enlisted in description of environmental species? Conversely, how can the taxonomic community be mobilized to provide resources for identification of environmental species?
- How can names of environmental species be integrated into higher-level taxonomic databases, such as the Catalogue of Life, Encyclopedia of Life, and GBIF?
- What should be the next steps in this discussion? What groups and organizations should be consulted? How can we ensure that all stakeholders are engaged?
- What financial and human resources are needed to promote classification of environmental species? Where can these resources be found?

Two very basic questions are absent from the list above, including 1) “Does the mycological community need a classification system for environmental sequences?” and, 2) “How can it be done?” We think the answer to the first question is an unambiguous “yes”. We will grapple with the second question on August 2, 2011, in Fairbanks, Alaska. Please join us.

References

Hibbett, D. S., A. Ohman, D. Glotzer, M. Nuhn, P. M. Kirk, and R. H. Nilsson. 2011. Progress in molecular and morphological taxon discovery in Fungi and options for formal classification of environmental sequences. *Fungal Biology Reviews* 25: 38-47.

Reynolds D., J. Taylor, 1991. DNA specimens and the ‘International code of botanical nomenclature’. *Taxon* 40: 311-351.

—David Hibbett
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MSA BUSINESS

Secretary's Report

Greetings everyone! The warm days of summer are upon us. As you plan your talks and design your posters for our annual meeting in Fairbanks, take a little time to get out in the woods and enjoy Nature! Too often we are chained to our desks and computers and see little of the natural world, which is what led us all to mycology in the first place! Enjoy!

Council Business: There were five email polls approved by MSA Council since my last report: three amendments to the bylaws were placed on the ballot for the annual election; Don Natvig was approved as Chair of the Editorial Advisory Committee; and the Honorary Member was approved.

New Members: It is my pleasure to extend a warm welcome to new or returning members. Their membership will be formally approved at the 2011 Annual Business Meeting in Fairbanks, AK.

Australia: Elizabeth Sheedy

Canada: Michelle Hubbard

Germany: Matthias Gube

Mexico: Marisol Sanchez Garcia

Thailand: Chaiwat Boonpeng

United States: Stanley Bartkowiak, Kirk D Broders, Emme Bruns, Jonathan Carver, Anne E Dorrance, Margaret Ellis, Amy T Fox, Zachary T Gossage, Joshua Herr, Kerri Kluting, Stephanie Mcknight, Stephen J Miller, Alija Mujic, Christopher Michael Sthultz, Merje Toome

Emeritus Members: There were no requests for emeritus status since my last report.



Jessie Glaeser,
Secretary
(Photo by Tom Volk)

Reminder: Renewing your MSA membership is easier than ever! Just log in to the MSA website at <http://www.msafungi.org>. There is now an email reminder system available if you have forgotten your MSA user id or password.

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, please contact our Association Manager at Allen Press, the always-helpful Kay

Rose at krose@allenpress.com.

Please do not hesitate to contact me about MSA Business or any questions that you may have about the Society. **Please remember to renew your membership for 2011!** In recent years we have suffered an alarming decline in membership and it would be wonderful to reverse this trend. The first step is for everyone who is currently a member to renew for the upcoming year. And don't forget to recommend MSA to your amateur or professional colleagues who are interested in fungi – be they pathologists, geneticists, ecologists, or people who like to wander around in the woods. There is room in MSA for all!

See you in Fairbanks!

—Jessie A. Glaeser
MSA Secretary

MYCOLOGICAL NEWS

New Collaborative Study Starts with Collecting Trip in Argentina

For three weeks in April, Andrea Romero from CONICET-University of Buenos Aires and her students from several universities in the country, hosted members of the University of Maryland-USDA PEET team studying the Nectriaceae, Hypocreales. Amy Rossman and Catalina Salgado, student of Priscila Chaverri, went in search of hypocrealean fungi in Argentina. With the onset of fall and hoping to miss the cold weather, the first leg of the trip was centered about Bariloche in northern Patagonia amid the southern beech forests (*Nothofagus* spp.). Romina Sanchez from National University of Bahia Blanca, our leader for this portion of the trip, had recently completed her doctoral dissertation on the pyrenomycetes and loculoascomycetes of decaying wood

of *Nothofagus* and knew just where to find these hosts. Beneath the snow-covered mountains we shivered in the unheated biological station but managed to find interesting specimens of *Neonec-tria* that were previously unreported on *Nothofagus*. The highlight of this week was the opportunity to meet Irma Gamundi, expert in Patagonian discomycetes, who provided a very fine high tea to us after a long collecting day (Fig. 1).

The following week we ventured north to the subtropical town of San Miguel de Tucuman. Our hosts, Adrianna Hladki, an expert in the *Xylariaceae* of Tucuman, and Myriam Catania, who completed her dissertation on pyrenomycetes and loculoas-

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comycetes on decaying wood of *Podocarpus parlatorei*, are both at the Fundacion Miguel Lillo and knew the region well. They took us to the Rio Cochuna area that proved to be the motherlode of nectriaceous fungi producing woody substrates with multiple species of *Neonectria* occasionally all on the same stroma. In addition we found such species as *Nectria pseudotrichia*, *Haematonectria haematococca*, *Lanatonectria flocculenta*, *Ophionectria trichospora* and multiple species of *Cosmospora* on various black pyrenomycetes.

The final leg of the trip was based in the Parque Nacional Iguazu near the city of Puerto Iguazu, with permission of the Centro de Investigaciones Ecologicas Subtropicales-CIES and use of their biological station. Mariana Capdet from University of Buenos Aires, studying the pyrenomycetes and loculoascomycetes of palms allowed us to collect in her study areas beneath stands of *Euterpe edulis* and *Syagrus romanzoffiana*. Despite the dry conditions we collected a number of species of *Bionectria* as well as *Ijuhya* and *Protocreopsis* on decaying petioles of palm fronds. The surrounding area has been preserved and in the course of collecting we saw caiman, monkeys, toucans, aguti and coati. True confessions, one day was spent touring the most amazing Iguazu Falls that actually consist of 275 separate falls over a 2.5 km span of the Iguazu River.

With this trip, a study of the hypocrealean fungi of Argentina has been initiated. Andrea Romero and her students and Vi-



Fig. 1. Irme Gumundi, Andrea Romero, Romina Sanchez, Amy Rossman and Catalina Salgado indulging in a few goodies including champagne at Dr. Gamundi home in Bariloche, Argentina.

viana Barrera to work on *Hypocrea* species, will collaborate with Priscila Chaverri and her students including Cesar Herrera studying *Cosmospora*. This project will result in biodiversity studies of these fungi in Argentina as well as a comparison with those species known from Australia and New Zealand.

Amy Rossman and Catalina Salgado greatly appreciate the warm hospitality and bureaucratic breakthroughs provided by Andrea Romero and her outstanding students.

—Amy Rossman
Andrea Romero
Catalina Salgado

6th International Scientific Conference on Bioaerosols

The U.S. Environmental Protection Agency (EPA) has partnered with the Fungal Research Group Foundation to sponsor the 6th International Scientific Conference on Bioaerosols, Fungi, Bacteria, Mycotoxins in Indoor and Outdoor Environments and Human Health. September 6-9,

2011, Saratoga Springs, N.Y. For more information, please visit www.bioaerosol.org.

—Beth Anne Purvis
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EMBO Conference in Spain, October 15–20, 2011

Comparative Genomics of Eukaryotic Microorganisms: Understanding the Complexity of Diversity. 15-20 October, 2011, Sant Feliux, Spain. The conference will address the big evolutionary questions of what makes a eukaryote, how multicellularity arose, evolution of reproduction, and pathogenesis. Lineages of the Eukaryotic Tree of Life (TOL) that until now received only moderate attention, such as the Excavates, Archaeplastids, Amoebozoa and Choanozoa, will be discussed, together with the better studied Chromalveolates and Fungi. Travel reimbursement is available for young researchers. Registration deadline 31 July, 2011.

Information: <http://events.embo.org/11-comparative-genomics/index.html>

MSA Auction Items

The MSA auction is the primary fundraiser for the society and supports major MSA functions including student travel and participation, and symposia. Donations of all kinds are cheerfully and eagerly accepted but please send an e-mail to khughes@utk.edu so we can compile a list.

If you wish to mail your auction item(s) Fairbanks, the mailing address for auction items is:

MSA 2011
c/o Maria Russell
Institute of Arctic Biology
108 Irving I Building
University of Alaska
Fairbanks, AK 99775

Thanks in advance for all you do for the MSA!

MSA ABSTRACTS

MSA Annual Meeting Abstracts 2011

Albu, Sebastian* and Aime, M. Catherine. Louisiana State University Agricultural Center, Department of Plant Pathology and Crop Physiology, Baton Rouge, LA 70803. albuseb@yahoo.com. **Phenology of basidiomycete ballistosporic phylloplane yeasts from seven fern species growing in Baton Rouge, Louisiana.**

A study documenting basidiomycete yeast biodiversity was conducted in Baton Rouge, Louisiana during 2010-2011. The leaf surfaces of seven species of native, introduced and invasive ferns were sampled at biweekly intervals during the course of one year to determine to what degree various temporal and spatial factors as well as hosts influence phylloplane yeast distribution. Qualitative and quantitative analyses of population distribution on abaxial, adaxial, senescent and fresh leaf tissues were conducted and precipitation patterns and fluctuations in temperature preceding collection dates were recorded during this time. Leaf samples from the same fern populations were repeatedly cultured to examine microbial fauna. Preliminary results show a great deal of yeast biodiversity on the fern phylloplane. Results also indicate that species diversity varies between the spatial components of fern phylloplanes. Abaxial leaf surfaces yield greater numbers of total fungi recovered than adaxial surfaces. Additionally, both population numbers and species diversity appear to decrease during periods of colder temperatures on all fern species. Sequencing of the internal transcribed spacer regions within nuclear rDNA repeat has revealed ten to twenty putatively new species or higher taxa within the classes Ustilaginomycetes, Exobasidiomycetes, Microbotryomycetes, and Tremellomycetes.

Albu, Sebastian^{1*}, Blackwell, Meredith², and Aime, M. Catherine¹. ¹Louisiana State University Agricultural Center, Department of Plant Pathology and Crop Physiology, Baton Rouge, LA 70803, ²Louisiana State University, Department of Biological Sciences, Baton Rouge, LA 70803. albuseb@yahoo.com. **Gulf coast tarball-associated yeasts: understudied agents of microbial hydrocarbon degradation and potential human pathogens.**

Several studies aimed at investigating the effects of the Deepwater Horizon oil spill on affected ecosystems seek to characterize the prokaryotic (bacterial) community; none are focused on assessing changes in the eukaryotic microbial (yeasts and related marine fungi) communities despite the enormous importance of these fungi to relevant areas such as healthy ecosystem functioning, hydrocarbon degradation and human disease. In the summer of 2010 we sampled tar balls from a private beach near Perdido, Florida, for yeasts. Our first preliminary experiment, using a single set of standard protocols, resulted in the isolation of four different yeasts from two phyla and three genera-*Rhodotorula*, *Cryptococcus*, and *Candida* – only two of which are unambiguously identifiable to species and two putative new yeast taxa. Furthermore, all of the isolated species belong to phylogenetic clades of known yeasts species that, 1) have been isolated from marine habitats, 2) some have known hydrocarbon degradation abilities, and 3) have also been isolated as the causal agents of human mycoses in compromised individuals. Thus, additional characterization of the yeast flora associated with the Deepwater Horizon oil spill should be essential for recognizing potential health threats to remediation workers, understanding the fate of tar balls especially in regards to microbial degradation, and for the potential to uncover new species with novel metabolic pathways that may provide solutions for future cleanup efforts.

Allameh, Abdolamir and Tahereh, Zigliari*. Faculty of Medical science, Qeghm Azad University, Qeghm Island, 795151393, Iran. allameha@modares.ac.ir. **Comparison of glutathione s-transferase activity and concentration in aflatoxin-producing and their non-toxicogenic counterpart isolates.**

In this study, two techniques were used to compare the specific activity and total concentration of mycelial glutathione s-transferase (GST) in fungal strains isolated from natural sources. The fungi identified as *Aspergillus parasiticus* and *Aspergillus flavus* have been divided into two groups based on their ability to produce aflatoxins. GST specific activity in mycelial preparations were measured spectrophotometrically using 2,1-chloro-2,4 dinitrobenzene as the substrate. The results showed that the mean GST activity in toxigenic isolates was 25.06 micromol/mg protein/min which was 2.8-fold greater than that measured in non-toxicogenic isolates. Moreover the GST concentration was compared in toxigenic and non-toxicogenic isolates using an Enzyme Linked Immunosorbent Assay based on antigen and antibody. The results of ELISA showed that the mean GST level in toxigenic and non-toxicogenic fungi was 1.17 and 0.14 respectively. These results further confirm that aflatoxin production by fungal strains is correlated

with GST expression, and it is possible using ELISA to discriminate aflatoxin-producing fungi from their non-toxicogenic counterparts.

Amend, Anthony S.* , Barshis, Daniel J., and Oliver, Thomas A. Department of Ecology and Evolutionary Biology, University of California, Irvine, CA. aamend@uci.edu. **Coral reefs in hot water: metagenomics and transcriptomics indicate deep branching lineages and novel nutritional roles among fungi associated with heat stressed Pacific corals.**

Scleractinian coral stress tolerance is intricately tied to its association with microbial and fungal symbionts. While much is known about the mutualistic symbiosis between corals and their dinoflagellate photobionts (*Symbiodinium* spp.), little is known about the taxonomy, stability or function of their symbiotic fungal communities. Using targeted gene sequencing and meta-transcriptomics we examine how fungal communities respond to differences in environmental stability and to sub-clade identity of the *Symbiodinium*. Phylogenetic analysis of coral-associated fungi shows a high diversity of Dikarya, including multiple clades separated from known taxa by well-supported and long branches. Our results show that coral-associated fungal communities are highly species rich and phylogenetically diverse, and that eleven taxa within the Agariomycetes, Ustilaginomycetes, Dothideomycetes and Sordariomycetes are found in more than 90% of all coral colonies sampled. Corals in a climatically variable pool contained more phylogenetically diverse fungal communities than a climatically stable pool, and indicator species analysis detected taxa statistically associated with the variable pool and with one of the *Symbiodinium* types. Total fungal community composition varied among coral colonies, but did not correlate with any measured variables, suggesting that obligate symbiotic interactions between fungi and corals, if any, are either restricted to a subset of common taxa or else result from non-specialized traits common within kingdom Fungi. Putative fungal mRNA relating to nitrogen metabolic pathways were abundant in transcript libraries, suggesting a fungal role in mineralization of complex and organic nitrogen sources. Fungus-derived inorganic nitrogen could be advantageous to autotrophic *Symbiodinium* growing in oligotrophic environments.

Anderson, Catherine L.^{3*}, Harris, Steven D.¹, and Moriyama, Etsuko N.² ¹Department of Plant Pathology and Plant Science Innovation, University of Nebraska-Lincoln, NE 68588, ²Department of Biological Sciences and Plant Science Innovation, University of Nebraska-Lincoln, NE 68588, ³Department of Computer Science, University of Nebraska-Lincoln, NE 68588. emoriyama2@unl.edu. **The Fungal Genome Collection: a comparative database for fungal genomes.**

While members of the Kingdom Fungi surround us on a largely microscopic scale, they impact our lives on all levels: health, food and value of property (e.g., mold and wood rot). Currently there are hundreds of complete fungal genomes available from various genome projects (i.e., JGI, Broad Institute, SGD, AspGD, etc.). However, this information is not centralized or easy to use for systematic analysis. To address this situation, we have developed the "Fungal Genome Collection (FGC)". The FGC provides a central repository for fungal genomes of all genera. Comparative genomics information is available for all genomes by way of blast similarity search results against the NCBI nonredundant database, against the UniProt/Swissprot database, and also between all fungal genomes. Blast results are organized in such a way that searching for proteins unique to specific fungal genomes, those unique to the fungal kingdom, or those shared with metazoans or plants, can be done easily. In order to facilitate more efficient functional annotation of diverse fungal genomes, we are adding additional information for each protein sequence. These include: gene ontology information, cellular localization prediction, secondary structure and transmembrane predictions, protein family/domain. A user can navigate through the FGC website using an intuitive and user-friendly graphic interface following the fungal phylogeny. It provides data-search capability through all genomes and comparative analysis. Sequence data and analysis results can be downloaded in various formats. The web interface for FGC is publicly available from: <http://bioinfolab.unl.edu/~canderson/FungalGenomeCollection/>.

Aveling, Theresa Ann^{1*} and Blanco, Reyes². ¹Department of Microbiology and Plant Pathology, University of Pretoria, Pretoria 0002, South Africa. ²Dpto. de Producción Vegetal., EPS Universidad de Almería, Carretera de San Urbano

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4120 Almeria, Spain. terry.aveling@fabi.up.ac.za. **Seed health testing in the International Seed Testing Association.**

Founded in 1924, with the aim to develop and publish standard procedures in the field of seed testing, the International Seed Testing Association (ISTA) is inextricably linked with the history of seed testing. Membership is a collaboration of seed scientists and seed analysts from universities, research centres and governmental, private and company seed testing laboratories around the world. The aim of ISTA is to develop, adopt and publish standard procedures for sampling and testing seeds, and to promote uniform application of these procedures for evaluation of seeds moving in international trade. In many countries import of seed is only permitted if the seed lot is accompanied by an ISTA International Seed Analysis Certificate. One of the ISTA committees is the Seed Health Committee. Healthy seed results in healthy crops thus healthy pathogen-free seed is required for sowing and prevention of disease spread to other countries. International routine validated laboratory tests are required. The Seed Health Committee is responsible for the selection and development of new methods for international seed health testing. How this is achieved is discussed, including the validation procedure through comparative testing and approval of the method. The procedure terminates with the final acceptance by the ISTA membership and publication of the method in the ISTA Rules.

Avis, Peter G. Department of Biology, Indiana University Northwest, Gary, IN. pavis@iun.edu. **Sniffing out the species of foetid *Russula*, important ectomycorrhizal fungi with “nitrophilic” tendencies.**

Despite the well known detrimental impacts of nitrogen addition on ectomycorrhizas, some ectomycorrhizal fungi tolerate or even thrive in nitrogen rich environments. Included in this intriguing group of fungi with “nitrophilic” tendencies are relatively common and frequently dominant fungi often referred to as the foetid *Russula* (including those with names such as *R. amoenolens*, *R. pectinatoides*, *R. pectinata*, etc., and placed into the subgenus *Ingratula* 1 or subsection *Foetentineae*). This group produces notoriously forgettable basidiocarps with odors described by some as “nauseating” and “offensive.” Probably as a result, little attention has been paid to their phylogenetic relationships despite such intriguing ecology (and micromorphology such as exquisitely ornamented ectomycorrhizal mantles). This study addresses this gap and presents results from a phylogenetic analysis of the ITS rDNA region of >80 collections made by the author, colleagues and students and >60 ITS sequences mined from GenBank (including those from sporocarps, ectomycorrhizal roots, hyphae, soil or roots of mycoheterotrophic plants). An alignment of 137 collections examined with parsimony and maximum likelihood approaches indicates that this lineage contains numerous previously undescribed taxa that reflect to some extent geographical distributions but not the use of widely applied names such as *R. amoenolens* or *R. pectinatoides*. There appear to be at least seven well-supported taxa and include those specific to western North America, eastern North America and Europe while morphologically similar collections from tropical regions are quite distinct. “Nitrophilic” tendencies are dispersed across the taxa indicating that this ability is not an isolated trait, but rather a more general feature of these foetid *Russula* overall. The results from this analysis will also be compared to a limited, on-going RPBI analysis and morphological systems of description.

Balint, Miklos^{1*}, Fankhauser, Johnathon D.², Tiffin, Peter², Hallström, Björn¹, O’Hara, Robert B.¹, and Schmitt, Imke¹. ¹Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany, ²University of Minnesota, 250 Biological Sciences Center, 1445 Gortner Ave. St. Paul, MN 55108 USA. mbalint@senckenberg.de. **Assessing diversity of leaf-associated fungal communities on balsam poplar by 454 pyrosequencing.**

Leaf-associated fungi, e.g. foliar endophytes, may have complex effects on the adaptation of host plants, such as conferring tolerance to drought, high salinity, grazing, and to pathogens. We are interested in whether the leaf-associated fungal microbiome plays a role in the adaptation of trees to particular climatic niches. Our model system is balsam poplar (*Populus balsamifera*), a boreal tree species with a broad distribution in northern North America. In the present study we analyzed if there is co-evolution between balsam poplar genotypes and their leaf-associated fungal communities. We used Roche’s 454 pyrosequencing to sequence fungal rDNA-ITS amplicons from the leaves of 28 trees. We found 50-350 molecular taxonomic units in each leaf (sequencing depth: 6000-9000 reads/leaf) based on a 97% similarity threshold. We analyzed these data by 1) comparing molecular taxonomic units against a fungal ITS database by BLAST and ordinating the best hits, and 2) directly clustering aligned molecular taxonomic units. Results from our preliminary data set suggest that there is no effect of host genotype on the composition of leaf associated fungal communities. However, denser sampling of poplar populations and deeper sequencing of fungal communities seem necessary to provide sufficient resolution in the data. Baroni, Timothy J.¹, Kropp, Bradley R.^{2*}, and Evenson, Vera³. ¹SUNY College at Cortland, Dept Biological Sciences, PO Box 2000, Cortland, NY 13045, ²Biology Department, 5305 Old Main Hill, Utah State University, Logan, Utah

84322, ³Curator Sam Mitchel Herbarium of Fungi, Denver Botanic Gardens, 909 York Street, Denver CO 80206. brad.kropp@usu.edu. ***Smithiomyces crocodilinus* sp. nov. prov. an unusual agaric from semi-arid regions in the Rocky Mountains.**

A rather large perplexing agaric has been collected on two occasions in Colorado and Utah in semi-arid habitats and in association with *Cercocarpus* species. The overall macroscopic appearance of this robust white mushroom, including such features as free lamellae and an evanescent collar-like volval ring on top of a napiform stipe base, is somewhat reminiscent of an *Amanita* in the Section *Lepidella*. However, this species clearly differs from all species of *Amanita* by having small, inamyloid, finely punctate basidiospores, a lamella trama of parallel cylindrical hyphae and a stipe that lacks acrophysalidic tissue. The macro- and microscopic characters indicate this is a species of *Smithiomyces*, a genus of rarely encountered agarics currently consisting of only two species, one found occurring naturally in subtropical regions of Florida and Mexico north of the equator (*Smithiomyces mexicanus* (Murr.) Singer) and the other taxon from south of the equator in Brazil (*Smithiomyces lanosofarinus* (Rick) Raitelhuber). The robust basidiomata in association with an ectomycorrhizal host indicate a possible mycorrhizal ecology, but further work is needed to determine the exact ecology of this fungus. The morphological features indicate an affinity with lepiotaceous fungi. We will present detailed illustrations and a phylogenetic analysis of this agaric.

Begerow, Dominik^{*}, Kellner, Ronny, and Hanschke, Christian. Ruhr-Universität Bochum, Geobotanik ND03/174, 44801 Bochum, Germany. dominik.begerow@rub.de. **Intraspecific variation in effector genes of *Ustilago maydis*.**

Specific virulence factors regulate biotrophic key processes like penetration, resource tracking and specific disguise in the interaction of parasitic fungi and plants. To date, the mode of selection of fungal virulence factors and their impact on speciation are poorly understood. The corn smut *Ustilago maydis* lacks a classical gene-for-gene interaction with its host *Zea mays*, but genome data revealed a great number of probably secreted proteins which might be relevant for the pathogenic interaction. In order to find selection patterns in virulence cluster genes within *U. maydis*, we focused on gene clusters encoding secreted effectors that affect different stages of the biotrophic interaction. These included the hypervirulence-associated cluster 2A, partial sequences of cluster 19A associated with markedly reduced virulence and the fungal effector-encoding gene pep1. We estimated the intraspecific variability of 33 and 15 cluster genes encoding secreted and unsecreted proteins, respectively, as well as of internal transcribed spacer sequences, 5.8S rDNA and rpb1. In total, 51 loci from up to 16 strains have been sequenced either completely or partially. The genetic diversity of cluster genes reflected the reported population structure of *U. maydis*, although sequence divergence is low. However, potential virulence genes, encoding for secreted proteins, accumulated significantly more substitutions than genes of unsecreted proteins suggesting their differential selection during evolution.

Bergemann, Sarah E.^{1*}, Baumgartner, Kendra², and Hughes, Karen W.³ ¹Middle Tennessee State Univ., Biology Dept., PO Box 60, Murfreesboro, TN 37132, ²USDA-ARS, Dept. of Plant Pathology, Univ. of California, One Shields Avenue, Davis, CA 95616, ³University of Tennessee, Knoxville, Ecology and Evolutionary Biology, 437 Hesler, Knoxville, TN 37996. sbergema@mtsu.edu. **Evidence for natural hybridization among homothallic members of the basidiomycete *Armillaria mellea*.**

Populations of *Armillaria mellea* (Agaricales, Physalacriaceae) are typically heterothallic; homothallic populations are reported only from Africa (*A. mellea* ssp. *africana*), China [*Armillaria* China Biological Species (CBS) G], and Japan (*A. mellea* ssp. *nipponica*). Monosporous isolates of heterothallic strains are haploid, and their mating behavior is consistent with that of a tetrapolar mating system. In contrast, monosporous isolates of homothallic strains, which are the equivalent of diploid zygotes, bypass the haploid mycelial phase by packaging diploid nuclei into single spores (homoheteromixis). Because *A. mellea* is a virulent pathogen of many crops, the genetic origins of this switch from selfing to outcrossing is of concern with respect to disease spread. In an effort to understand the origins of homothallicism among members of *A. mellea* from different geographic regions, we constructed mutational networks and conducted phylogenetic analyses of multiple, nuclear protein-coding genes. The majority of isolates from the homothallic *Armillaria* CBS G collapsed into a single clade and shared identical haplotypes with heterothallic strains only from China. In homothallic isolates of *A. mellea* from Africa, Japan, and China, haplotypes from diploid isolates segregated into one of two clades with heterothallic populations from China and Europe. This pattern clear of segregation is indicative of hybridization, with putative origins from Europe and China. Whether homoth-

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allism is the ancestral state is unclear, as genealogical discordance is evident among multiple genes and remains the focus of future investigations.

Jerube, Jean A. Laurentian Forestry Centre, Canadian Forest Service, 1055 du PEPS, P.O. Box 10380, Succ Ste-Foy, Quebec city, QC, G1V 4C7, Canada. jberube@forestry.ca. **Fifty new exotic fungal species are introduced annually in Canada on live plant material.**

New exotic and scientifically unknown fungal species with the potential to be pathogenic pests are an important risk to Canadian forests and are often difficult to detect on imported live plant material due to their cryptic nature. We processed 150 asymptomatic live plant samples from 99 exotic host tree species imported in Canada and analyzed them by cloning the PCR amplified fungal nuclear ribosomal ITS RNA present in plant tissues. We obtained 1845 fungal clones representing 267 fungal species, of which 148 fungal species can be considered alien species introduced in Canada in the last three years, with an average of 11.3 fungal species per sample lots. The impact of the introduction of these alien fungal species on the native flora is still unknown.

Bezerra, Andrea Carla C.¹, Cavalcanti, Laise H.¹, and Dianese, José C.^{2*} ¹Depto. de Botânica, Lab. de Mixomicetos, Centro de Ciências, Universidade Federal de Pernambuco, Cidade Universitária, 50.670-901 Recife, PE, Brazil, ²Depto. de Fitopatologia, Universidade de Brasília, Campus Darcy Ribeiro, Asa Norte, 70910-900 Brasília, DF, Brazil. jcarmine@unb.br. **First records of myxomycetes from the Brazilian Pantanal.**

The Cerrado and the Pantanal are two important Brazilian biomes that together represent approximately 30% of our national territory, both highly important to world biodiversity conservation. Pioneering studies on the myxobiota of the Pantanal started in November 2008 and lasted through November 2010, and are expected to continue through 2011. A total of 1122 myxomycete samples were gathered from the Pantanal *stricto sensu* and in the adjacent borders, a transition into the Cerrado in the states of Mato Grosso do Sul and Mato Grosso. The survey led to the identification of 39 species, all of which are first records for the Pantanal. In addition *Cribraria intricata*, *Diachea leucopodia*, *Didymium nigripes*, *Enerthenema papillatum*, *Perichaena corticalis*, *Physarella oblonga*, *Physarum compressum*, and *Tubifera bombardia* are new records for the entire Central-Western region of the country.

Binder, Manfred*, Floudas, Dimitrios, and Hibbett, David S. Clark University, Biology Department, Lasry Biosciences Center, 950 Main Street Worcester, MA 01610-1477. mbinder@clarku.edu. **Reconstructing the evolutionary diversification of wood decay mechanisms in Agaricomycetes using comparative phylogenomics.**

Bioconversion of abundant lignocellulosic substrates is one of the driving forces sustaining the carbon cycle in terrestrial ecosystems. Agaricomycotina play an essential role in wood degradation exploring a variety of saprotrophic life styles in the course of evolutionary history. Shared mechanisms between decay types, which primarily involve the production of white rot and brown rot, are evident but need further scrutiny. White rot fungi are generally capable of effectively degrading all plant cell components. Brown rot fungi on the other hand, modify lignin extensively but don't degrade it to access cellulose and hemicellulose. The incomplete ligninolysis caused by brown rot fungi leaves recalcitrant lignin polymers that cannot be converted easily by other decayers, contributing to carbon sequestration. Here, we report novel insights into the evolution of wood decay mechanisms inferred from twelve new whole-genome sequencing projects in collaboration with numerous other laboratories and the Joint Genome Institute (JGI-DOE). The species were selected to provide a good representation of saprotrophic nutritional modes across the Agaricomycotina and include *Auricularia delicata*, *Coniophora puteana*, *Dacryopinax sp.*, *Dichomitus squalens*, *Fomitiporia mediterranea*, *Fomitopsis pinicola*, *Gloeophyllum trabeum*, *Punctularia strigosozonata*, *Stereum hirsutum*, *Trametes versicolor*, *Tremella mesenterica*, and *Wolfiporia cocos*. Monitoring expansions and contractions of decay-related enzyme families reveals that white rot producing species in the Agaricomycetes are enriched in carbohydrate-active enzymes (CAZYS) and oxidoreductases. In contrast, brown rot fungi have retained some oxidoreductases but have lost their class II peroxidases, the main enzymes responsible for lignin breakdown. Fossil calibrated molecular clock analyses suggest that multiple isoforms of class II peroxidases were present in Agaricomycetes at the late Carboniferous or the early Permian time.

Birkebak, Joshua M.^{1*}, Mayor, Jordan R.², Ryberg, K Martin¹, and Matheny, P Brandon¹. ¹Department of Ecology and Evolutionary Biology, University of Tennessee, 569 Dabney Hall, Knoxville, TN 37996-1610, USA, ²Smithsonian Tropical Research Institute & National Science Foundation International Postdoctoral Fellow, Apartado 0843-03092, Balboa, Ancón, República de Panamá. jbirkeba@utk.edu. **An overview of the ecology, evolution, and systematics of the family Clavariaceae (Agaricales).**

A phylogenetic-based classification of the Clavariaceae has not been produced in depth using molecular phylogenetic analysis. Previous studies have omitted some generic and subgeneric taxa, and intrafamilial relationships have been poorly assessed. The trophic status of the family is unsettled since a saprotrophic strategy has been ascribed to many taxa, but a biotrophic status to a few. A phylogeny of the Clavariaceae based on nLSU data is presented here representing all known generic and subgeneric taxa to elucidate intrafamilial relationships in the family. 180 environmental sequences from GenBank belonging to the Clavariaceae were included in the analysis to provide insights into the ecology of the family. Stable isotope signatures of carbon and nitrogen were analyzed to predict trophic strategies. Most traditional generic concepts are well supported with the exception of poorly supported relationships between the pileate-stipitate genus *Camarophyllopsis*, the monotypic genus *Clavicornona sensu stricto*, and the type genus *Clavaria*. Two different classification schemes for the genera *Ramariopsis* and *Clavulinopsis* are compared against the nLSU phylogeny, but neither is found to be satisfactory. *Clavicornona* is recovered as a member of the Clavariaceae with robust support, while *Scytinopogon* is found to belong to the Trechisporales. Environmental sequence analysis and stable isotope signatures support a biotrophic status for terrestrial samples of Clavariaceae apart from the lignicolous genus *Mucronella*, which is sister to all remaining Clavariaceae.

Bittleston, Leonora S.^{1,2*}, Brockmann, Franz², Weislo, William², and Van Bael, Sunshine A.² ¹Harvard University, 16 Divinity Avenue Cambridge, MA 02138, ²Smithsonian Tropical Research Institute, Apartado, 0843-03092 Panamá, Republic of Panamá. lbittles@fas.harvard.edu. **Endophytic fungi reduce leaf-cutting ant damage to seedlings.**

We examined how the mutualism between *Atta colombica* leaf-cutting ants and their cultivated fungus is influenced by the presence of diverse foliar endophytic fungi (endophytes) at high densities in tropical leaf tissues. We conducted laboratory choice trials in which ant colonies chose between *Cordia alliodora* seedlings with high (E_{high}) or low (E_{low}) densities of endophytes. The E_{high} seedlings contained 5.5 times higher endophyte content and a greater diversity of fungal morphospecies than the E_{low} treatment, and endophyte content was not correlated with leaf toughness or thickness. Leaf-cutting ants cut over 2.5 times the leaf area from E_{low} relative to E_{high} seedlings and had a tendency to recruit more ants to E_{low} plants. Our findings suggest that leaf-cutting ants may incur costs from cutting and processing leaves with high endophyte loads, which could impact Neotropical forests by causing variable damage rates within plant communities. Future directions for this work will also be discussed.

Blanchette, Robert A. Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108. robertb@umn.edu. **Ethnobotany: historic uses of forest fungi by the Indigenous People of Northwestern North America.**

The Indigenous Peoples of North America used many types of forest fungi and they were important resources for tinder, paint, medicine and other cultural uses. Museum collections of natural history materials have become valuable assets to learn more about the early uses of these fungi. Many collections, made over 100 years ago, contain sporophores as well as collection notes on how the objects were used by Native Americans. This presentation reviews the historic use of fungi such as *Echinodontium*, *Phellinus* and *Chlorociboria* and provides new examples of carved *Fomitopsis officinalis* sporophores made by Indigenous Peoples of the Northwest Coast of the United States and Canada (first reported in Mycologia 84: 119-124). *Echinodontium tinctorium*, commonly called the Indian paint fungus, is often believed to have been used as a red pigment since the sporophore context is dark red. However, collection notes from many specimens obtained in the 19th century indicated it was charred and ground to a fine black powder, mixed with spruce gum or tallow and used as a brown/black pigment to protect the face from sunburn and insects, prevent snow blindness and used as a sign of mourning. *Chlorociboria* was used for making a green pigment to paint wood. The use of *Phellinus igniarius* by the native people of Alaska had widespread historic use and the ash from burned sporophores was mixed with tobacco and chewed. The tradition of using *P. igniarius* with tobacco continues today in Alaska and the mixture is called 'Iqmik'. When *P. igniarius* is burned, it produces a fine white ash that when mixed with tobacco and chewed, elevates pH and facilitates delivery of nicotine into the mouth and blood stream.

Bonito, Gregory^{1*}, Reynolds, Hannah¹, Schadt, Christopher², Labbe, Jessy², Tuskan, Jerry², and Vilgalys, Rytas¹. ¹Biology Department, Duke University, Durham NC 27708, ²Oak Ridge National Laboratory, Department of Energy, Oak Ridge TN 37831. gmb2@duke.edu. **Are rhizospheric fungal associates of *Populus deltoides* limited more by edaphic factors or host genotype?**

Populus deltoides is a widespread riparian tree species in areas of southeastern North America where flooding occurs. This species is reported to form both arbuscular and ecto- mycorrhizas and to harbor root endophytes. However,

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the influence of edaphic and genotypic factors in structuring fungal rhizospheric assemblages is not well understood. We address this experimentally by using roots of living plants as bait for bacteria and fungi. Cuttings from various *P. deltooides* genotypes and seedlings of oak and pine were used as "trap-plants". These were grown in sets of soils collected from our field research sites (composed of natural populations of *P. deltooides*). Preliminary assessments of the fungal and bacterial communities grown under the same experimental conditions was made through microscopy, culturing, clone library construction and sequencing. The fungal specific primers ITS1f & ITS4 and LROR & LR3 were used for detecting ectomycorrhizal and endophytic fungi. Arbuscular mycorrhizal communities were targeted by amplifying with a primer set selective towards this group, while bacterial 16S rDNA primers that discriminate against plastid DNA were used to compare bacterial communities. We used 454 amplicon pyrosequencing of these loci for a more comprehensive characterization of microbial communities. After five months, high ectomycorrhizal colonization (>80%) of pine and oak seedlings was observed while most genotypes of *P. deltooides* had low ectomycorrhizal colonization (<10%). Arbuscular mycorrhiza in the genera *Paraglomus* and *Glomus* were sequenced from clone libraries. *Proteobacteria*, *Actinobacteria*, and *Bacteroides* accounted for a large proportion of the bacteria phyla detected. Some fungal species were shared between hosts. For instance, species in the genus *Tuber*, *Hebeloma*, and *Laccaria*, were detected on both oak and *Populus*. The influence of host genotype and soil source on these associations as determined through 454 pyrosequencing will be further discussed.

Booth, Austin G. Department of Philosophy, Harvard University, Cambridge, MA 02138. ostngb@gmail.com. **Fungal populations and individuals: a multilevel selection perspective.**

There has been significant controversy as to just how mycologists ought to conceptualize evolving fungal populations and the individuals that comprise them. This is so not only because many fungal structures and processes are difficult to identify and account for due to practical considerations. Instead, there has been continuing disagreement as to which fungal structures constitute relevant selectional units. One historically important approach to this issue, exemplified by Pontecorvo, emphasizes within-mycelium population dynamics. Another, more recent, approach has emphasized the complex fitness interactions that mycelia themselves engage in, including heterokaryotic mycelia. These two approaches to fungal population biology are typically viewed as rivals. I argue that considerations can be brought to bear in favor of each of these alternatives, and that therefore fungal populations are most accurately described from the perspective of multilevel selection theory. There are population dynamics at the level of submycelial elements (nuclei and mitochondria), particularly in the basidiomycota and the glomeromycota. Various mechanisms are responsible for the maintenance of these sub-mycelial population structures. However, clear population level phenomena can also be found at the level of the mycelium itself. Self/non-self recognition systems are well-understood mechanisms that regulate mycelial fitness interactions, and are thus important in maintaining intergenerational mycelial population dynamics. The multilevel selection perspective on fungal populations no doubt raises many questions, particularly regarding the evolutionary significance of the interplay between mycelial and sub-mycelial populations. However, I suggest that the adoption of a multilevel selection perspective on fungal populations provides a useful framework in which various research questions relevant to fungal population biology can be articulated and assessed.

Borovicka, Jan^{1,2*}, Kotrba, Pavel³, and Gryndler, Milan⁴. ¹Nuclear Physics Institute, v.v.i., Academy of Sciences of the Czech Republic, Rez 130, CZ-250 68 Rez near Prague, Czech Republic, ²Institute of Geology, v.v.i., Academy of Sciences of the Czech Republic, Rozvojova 269, CZ-165 00 Prague 6, Czech Republic, ³Department of Biochemistry and Microbiology, Institute of Chemical Technology, Prague, Technická 5, CZ-166 28, Prague 6, Czech Republic, ⁴Institute of Microbiology, v.v.i., Academy of Sciences of the Czech Republic, Videnska 1083, CZ-142 20 Prague 4, Czech Republic. borovicka@ujf.cas.cz. **Hyperaccumulation of metals in macrofungi.**

In recent years, interest in the biogeochemical roles of fungi in the environment has increased rapidly. The subject area of a new research discipline termed "geomycology" considers fungi as biogeochemical agents and interactions between fungi and geological substrates are studied. Macrofungi (macromycetes) are able to absorb trace elements into mycelium, transport them and deposit them in fruit-bodies. This ability is species-specific and certain macrofungal species are effective accumulators of elements like cadmium, zinc, mercury, silver, gold, vanadium, iron, manganese, arsenic, antimony, rubidium, cesium, chlorine, and bromine. Some macrofungal species are able to accumulate extremely high concentrations of elements and are called "hyperaccumulators". It should be stressed that the ability of macrofungi to hyperaccumulate metals is apparently higher than that of most vascular plants. Metal-hyperaccumulating plants typically grow on substrates with high levels of

accumulated elements such as mine tailings or serpentine soils whereas hyperaccumulating macrofungi are found in non-metalliferous unpolluted areas. At least 3 elements have been found to be hyperaccumulated in macrofungi: vanadium in *Amanita muscaria* (and related species), arsenic in *Sarcosphaera coronaria*, and silver in *Amanita strobiliformis* (and related species). The biological importance of this process is unknown but possible role of defense against natural enemies should be considered. Investigations on the chemical forms of the accumulated elements have revealed that vanadium is present as an organometallic compound (amavadine) with unclear biological function, arsenic is present in methylated forms (mainly methylarsonic acid) and intracellular silver in wild-grown fruit-bodies and cultured extraradical mycelia of *Amanita strobiliformis* were found to be sequestered by cysteine-rich peptides (metallothioneins). Understanding of the biological role of metal hyperaccumulation and the uptake, transport and sequestration mechanisms might bring not only the knowledge of roles of fungi in biogenic transformations of elements, but possibly also interesting applications, e.g. in bioremediation techniques.

Branco, Sara. Centro Investigação Montanha, Escola Superior Agrária de Bragança, Portugal. sara.mayer.branco@gmail.com. **Serpentine soils promote ectomycorrhizal fungal diversity.**

Serpentine soils impose physiological stresses that limit plant establishment and diversity. The degree to which serpentine soils entail constraints on other organisms is, however, poorly understood. Here I investigate the effect of serpentine soils on ectomycorrhizal (ECM) fungi by conducting a reciprocal transplant experiment, where serpentine and non-serpentine ECM fungal communities were cultured in both their native and non-native soils. Contrary to expectation, serpentine soils hosted higher fungal richness compared to non-serpentine, and most species were recovered from serpentine soil, suggesting ECM fungi are not specialized or strongly affected by serpentine edaphic conditions.

Brown, Shawn P.^{1*}, Jumpponen, Ari¹, Cázares, Efrén², Strömmer, Rauni³, and Trappe, James M.² ¹Division of Biology, Kansas State University, Manhattan, KS 66506, ²College of Forestry, Oregon State University, Corvallis, OR 97331, ³Department of Environmental Ecology, University of Helsinki, Lahti, Finland. ari@ksu.edu. **Community assembly of fungi on a glacier forefront - lessons learned and questions yet unanswered.**

Life on a glacier forefront consists of a constant struggle against dispersal limitations and environmental and biotic stressors. Extreme daily and seasonal temperature fluctuations, erratic weather patterns with late-season snow packs, and high UV radiations are all common themes at glacier forefront systems. Recently deglaciated substrate affords the unique opportunity to address questions of fungal primary succession and community assembly. Here, we synthesize twenty years of research on fungal community dynamics at Lyman glacier forefront in the Glacier Peak Wilderness Area in the North Cascade Mountains in Washington State. Successional theory suggests that early colonization may be driven primarily through stochastic processes leading to community divergence whereas deterministic processes and converging patterns may drive later community establishment. We focus on this very idea: is possible to detect deterministic converging dynamics that drive fungal community assembly? If so, what are the primary controls of these patterns? Alternatively, are early fungal communities stochastically assembled from a broad local/regional propagule pool? Our studies indicate that soil microbial biomass accumulates over time in this system but that many fungal distribution patterns appear inextricably linked to plant establishment. Our recent data show that soil fungal communities are compositionally distinct between the rhizosphere soils and those sampled from non-vegetated areas as determined by PLFA. Next generation sequencing show that fungal communities are clustered temporally. Additionally, fungal communities converge phylogenetically in soils under plant canopies compared to non-vegetated soils indicating that plant establishment leads to selection of specific community components from available resident propagule pool. Although our studies over the past twenty years have provided insight into some fundamental dynamics of fungal community assembly, much remains to be learned about fungal successional dynamics.

Bruns, Emme L.^{1*}, Carson, Martin L.², and May, Georgiana¹. ¹University of Minnesota, Dept. Ecology, Evolution, and Behavior, 1987 Upper Buford Circle, Saint Paul, MN, 55108, ²United States Department of Agriculture - Agriculture Research Service, Cereal Disease Laboratory, University of Minnesota, Saint Paul, MN, 55108. bruns094@umn.edu. **Pathogen traits involved in local adaptation vary with host genetic diversity.**

Pathogens with dispersal ranges greater than their host are predicted to be locally adapted, but which aspects of host population structure drive local adaptation, and which pathogen traits are involved? We investigated the effect of host genetic diversity on two pathogen fitness traits, infectivity and spore production, using eight naturally occurring populations of oat crown rust (*Puccinia coronata*

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t. f.sp. avenae) collected from both monocultures and genetically diverse mixtures of oats. We sampled 28 *P. coronata* isolates from each population and measured infectivity against a set of eight oat cultivars present in the mixture. Next we inoculated each pathogen population onto four different host treatments (3 different monocultures and 1 mixture) and measured total spore production. We found that *P. coronata* populations from mixed host populations were able to infect a broader range of host genotypes than *P. coronata* populations from monocultures. However, the broader host genotype range observed in the populations from mixtures did not translate into improved spore production on the mixture treatment. Instead, spore production on the mixture treatment was strikingly similar among pathogen populations, suggesting that there may be a cost associated with broader infectivity. In contrast, we found significant differences in spore production among pathogen populations on the monoculture treatment. Pathogen populations from monocultures produced significantly more spores on their 'home' monoculture cultivar than on any other host treatment, and they produced significantly more spores than pathogen populations from mixtures. We conclude that host genotype mixtures select for the ability to infect a broad range of hosts while monocultures select for increased reproduction on the abundant host. Thus, different pathogen traits may be involved in pathogen local adaptation to a heterogeneous host population than are involved in adaptation to a genetically uniform host population.

Buaruang, Kawinnat^{1,2*}, Nirongbutr, Pimpa¹, Mongkolsuk, Pachara¹, Boonpragob, Kansri¹, and Manoch, Leka². ¹Department of Biology, Faculty of Science, Ramkhamhaeng University, Bangkok 10240, Thailand, ²Department of Plant Pathology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand. agrlkm@ku.ac.th. **Biodiversity of foliose Parmeliaceae (lichenized Ascomycota) in Thailand.**

Thailand is an ecologically diverse country rich in biodiversity, there are over a hundred national parks, wildlife sanctuaries and non-hunting areas to preserve and protect the country's vast natural resources. The lichen family Parmeliaceae in Thailand has been studied for about 102 years. Twenty-three genera and 154 species were reported from 20 provinces in Thailand. Taxonomic identification was based on morphological and anatomical characters. This family is characterized by development of the foliose growth form. The symbiotic relationship between the algae and the fungi forms in stratified layers. The main thallus contains 4 layers: upper cortex, algal layer, medulla and lower cortex. Unlike the upper cortex, the colors of lower cortex have different pigment and have some appendages to attach to the substratum. Vegetative propagules (isidia, soredia, phyllidia, and pustules) and other structures (rhizines and cilia) are important characters used to identify the Parmeliaceae. In some cases, lichen substances are also important for identification of Parmeliaceae at the species level.

Burchardt, Kathleen M.* and Cubeta, Marc A. Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695. kmpitche@ncsu.edu. **High-throughput pyrosequencing for identifying microsatellite markers to examine the population genetics and disease ecology of the blueberry pathogen *Monilinia vaccinii-corymbosi*.**

Monilinia vaccinii-corymbosi (Mvc) is an economically important fungal pathogen that can reduce the health and fruit yield of blueberry (*Vaccinium* spp.). The fungus causes mummy berry disease, which is characterized by blighting of shoots followed by desiccation and premature drop-off of infected fruit. The life history of Mvc is complex and involves wind disseminated ascospores that cause the blight phase and bee dispersal of conidia from infected shoots to flowers that infect the developing fruit. Currently there is no information on the genetic diversity and structure of field populations of Mvc. However, this information is critical for understanding disease ecology and developing more effective strategies to manage mummy berry disease. The primary objective of this study was to develop informative microsatellite markers for Mvc for use in subsequent population genetic analyses. To address this objective, a geographically diverse collection of 228 Mvc isolates was generated by sampling conidia on infected blueberry shoots from eight fields; one field in Oregon, Washington, and Michigan, and five fields in North Carolina. Microsatellite loci were identified using 454 pyrosequencing from an isolate of Mvc to generate 135,661 reads with an average length of ~355 bp. Sequence reads were screened for microsatellite repeats for primer design with the program MSAT-COMMANDER. Marker development and screening of a geographically diverse subsample of Mvc isolates is currently in progress and will be reported. Future research will focus on using genetic-based markers identified from polymorphic microsatellite and sequence loci to examine the population genetics and disease ecology of Mvc.

Burdsall, Harold H., Jr.^{1*} and Miller, Andrew N.² ¹CFMR, USDA-FS, Madison, WI and Fungal & Decay Diagnostics, Black Earth, WI, ²University of Illinois, Illinois Natural History Survey, Champaign, IL. burdsall@fungalddecay.com. **Lignicolous Basidiomycota of the Great Smoky Mountains National Park.**

The Great Smoky Mountains National Park (GSMNP) is an International Biosphere Reserve that spans more than half a million acres (2200 km²) along the mountainous border between eastern Tennessee and western North Carolina. It is the site of an on-going All Taxa Biodiversity Inventory. A week's collecting of resupinate basidiomycota on wood in the GSMNP yielded 110 specimens. These specimens represented 22 currently accepted families, 46 genera, and 69 species. One potentially new genus and two probable new species were collected and will be described later. Because only two hours were spent collecting in the conifer zone, the vast majority of the specimens and species collected are associated with deciduous tree species. A list of the species collected is provided and several species are discussed because of their unique distributions or unusual characteristics.

Burdsall, Harold H., Jr.^{1*}, Nakasone, Karen K.¹, Glaeser, Jessie A.¹, and Petersen, Ronald H.² ¹USDA Forest Service, Northern Research Station, One Gifford Pinchot Dr., Madison, WI 53726, ²Dept. of Botany, University of Tennessee, Knoxville, TN 37996. burdsall@fungalddecay.com. **A synopsis of the 1968 L.R. Hesler Symposium.**

Our understanding of the evolution and phylogeny of the higher Basidiomycota has advanced greatly in the past 15 years. Forty years ago, a major volume on evolution in this group of fungi was published following an international symposium in honor of Dr. L.R. Hesler, mycologist at the University of Tennessee, Knoxville. Highlights of the symposium and rediscovered pictures of the participants are presented. Learn about some of the great mycologists upon whose shoulders we stand.

Busby, Posy E.^{1*}, Aime, M Catherine², and Newcombe, George³. ¹Department of Biology, Stanford University, 371 Serra Mall, Stanford CA 94305, ²Department of Plant Pathology and Crop Physiology, Louisiana State University, 455 Life Sciences Bldg. Baton Rouge, LA 70803, ³College of Natural Resources, University of Idaho, Room 203D 975 W. Sixth Street Moscow, ID 83844-1133. busby@post.harvard.edu. **The fungal pathogen community of *Populus angustifolia*.**

Populus angustifolia, the narrowleaf cottonwood, is a dominant species in riparian ecosystems of the Rocky Mountains in western North America. The fungal parasites of *P. angustifolia* are poorly studied relative to those of *P. trichocarpa*, the other western North American species of *Populus* in section *Tacamahaca*. We sampled fungal leaf pathogens of *P. angustifolia* throughout its range to determine their distributions, host preferences, and in some cases, closest phylogenetic relatives. *Phyllactinia populi*, two species of *Mycosphaerella* (*M. angustifoliorum*, and a previously undescribed species, hereafter, *M. wasatchii* sp. nov.), and *Drepanopeziza populi* were found in multiple sites, but only a single population of *Melampsora* rust (*M. x columbiana*) was found. *Phyllactinia populi* is a powdery mildew fungus that is common on *Populus* in Asia but uncommon on *Populus* in NA, apart from *P. angustifolia*. Phylogenetic analyses revealed that *Mycosphaerella angustifoliorum* evolved from a diversification of *Mycosphaerella* on *Populus* distinct from that of *M. populorum* (NA), *M. populiicola* (NA), and *M. populi* (European). *Mycosphaerella wasatchii* sp. nov. evolved from a western diversification of *M. populorum*. *Melampsora occidentalis*, *Mycosphaerella populiicola*, and species of *Venturia* and *Taphrina*, all common pathogens of *P. trichocarpa* in western NA, were not found on *P. angustifolia*. Overall, the leaf pathogen communities of *P. angustifolia* and *P. trichocarpa* had little in common. One possible explanation is suggested by phylogenetic analyses of *Populus*: a Beringian migration into NA from Asia by the ancestor of *P. angustifolia*.

Bödeker, Inga TM^{1*}, Clemmensen, Karina E.¹, de Boer, Wietse², Olson, Åke¹, and Lindahl, Björn D.¹ ¹Swedish University of Agricultural Sciences, Department of Forest Mycology and Pathology, Box 7026, SE-75007 Uppsala, ²NIOO-KNAW, PO Box 50, NL-6708 PB Wageningen, Netherlands. inga.bodeker@slu.se. **Fungal peroxidases and soil organic matter decomposition: Are ectomycorrhizal *Cortinarius* species the key players?**

Boreal forests act as a global sink of carbon due to a large accumulation of recalcitrant organic matter. Nitrogen is immobilized in recalcitrant organic compounds, leading to low plant nutrient availability in these ecosystems. Fungal peroxidases (ClassII) are likely to play a key role in degrading recalcitrant polyphenolic compounds of leaf litter and humus in boreal forest soils. These enzymes have mainly been studied in model "white rot" wood decomposers, but peroxidase activity is also commonly measured in humus and soils. In soils, typical "white-rotters" are absent but, instead, ectomycorrhizal fungi predominate. It has often been reported that peroxidase activity increases under low nitrogen availability, suggesting a key role of these enzymes for fungal nitrogen mobilization. When fungi forage for nitrogen, carbon could be released as a side effect. By using degenerate PCR primers, we found that peroxidase-encoding genes are widely spread among ectomycorrhizal genomes. In particular, a group

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of *Cortinarius* species contained several peroxidase genes each. In order to investigate whether mycorrhizal peroxidase genes are actively expressed and if their regulation responds to nitrogen, we sampled fertilized and non-fertilized plots in a subarctic birch forest and a boreal pine forest. Enzyme assays showed that Mn-peroxidase activity was more than twice as high on control plots compared to fertilized ones. Furthermore, in unfertilized plots, we detected co-localization of high peroxidase activity and several different ectomycorrhizal *Cortinarius* species and one *Piloderma* species. Thus, we hypothesize, that this particular genus is an ecologically important key player in decomposition of recalcitrant carbon in boreal forest ecosystems.

Cantrell, Sharon A.^{1*}, Lodge, D Jean², and Pérez-Jiménez, José R.¹ ¹Department of Biology, School of Science and Technology, Universidad del Turabo, PO Box 3030, Gurabo, PR 00778, ²Center for Forest Mycology Research, USDA-Forest Service, Northern Research Station, Luquillo, PR 00773-1377. scantrel@suagm.edu. **Climate, vegetation and soil fungi – a story from a subtropical elevation gradient.**

Soil fungal communities respond to multiple abiotic and biotic factors that change along elevation gradients. The limited information available on fungi and microbial processes along elevation gradients is primarily from temperate areas and very little from tropical regions. This study documents changes in fungal and bacterial diversity, and abundance and composition of microbial functional groups along a subtropical elevation gradient. The elevation gradient is located in eastern Puerto Rico and comprises five forest types, each with characteristic vegetation. Soil samples were collected every three months from March 2003 thru December 2004. Soil fungal and bacterial communities were analyzed using fatty acid methyl esters (FAME) and TRFLP profiles. Our results produced humped distributions for Shannon diversity of FAME and fungal to bacteria (F:B) ratios. Microbial communities differed significantly among forest types. TRFLP were more frequently unique to forest types in fungi than bacteria. In multiple linear regression (MLR) models, soil moisture was predictive for all but Actinomycete FA abundance, and forest type contributed significantly to these same models for F:B ratios and all FA except for Gram negative 10Me18:0 and Gram positive 15:0. Diversity in this elevation gradient is higher at mid-elevations. Most Gram negative and Gram positive bacterial FAME were positively related to soil pH in MLR models, lower pH in mid-elevation forest soil may suppress bacteria favoring fungi. These data can be used as a benchmark for monitoring changes in microbial communities along elevation gradients caused by natural and anthropogenic disturbances, as well as global and regional climate changes.

Carbone, Ignazio^{1*}, Horn, Bruce W.², Moore, Geromy G.¹, Olarte, Rodrigo A.¹, Worthington, Carolyn J.¹, Monacell, James T.^{1,3}, Singh, Rakhi¹, Stone, Eric A.³, Elliott, Jacalyn L.¹, Hell, Kerstin⁴, Chulze, Sofia N.⁵, Barros, German⁵, Wright, Graeme⁶, and Naik, Manjunath K.⁷ ¹Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695, USA, ²National Peanut Research Laboratory, Agricultural Research Service, USDA, Dawson, GA 39842, USA, ³Bioinformatics Research Center, North Carolina State University, Raleigh, NC 27695, USA, ⁴International Institute of Tropical Agriculture, Cotonou, Republic of Benin, ⁵Departamento de Microbiología e Inmunología, Universidad Nacional de Río Cuarto, Córdoba, Argentina, ⁶Department of Primary Industries, Queensland, Kingaroy, Australia, ⁷Department of Plant Pathology, College of Agriculture, Karnataka, India. ignazio_carbone@ncsu.edu. **Evolutionary mechanisms within a single cell, populations and species that influence aflatoxin contamination of crop plants.**

Mycotoxins, and especially the aflatoxins, are an enormous problem in agriculture, with aflatoxin B₁ being the most carcinogenic known natural compound. The worldwide costs associated with aflatoxin monitoring and crop losses are in the hundreds of millions of dollars. *Aspergillus flavus* and *A. parasiticus* are the most common agents of aflatoxin contamination of oil-rich seed and grain crops. Sexually compatible strains vary greatly in their degree of fertility. Differences in fertility may be the result of female sterility, changes in DNA methylation, epistatic interactions between genetically different nuclei or other epigenetic modifications. We are currently exploring these possibilities using sexual crosses. The extent to which sexual and asexual reproduction restricts genetic exchange and recombination in these species is largely unknown, but is critical to understand for both fundamental and practical applications, such as biological control. To study this we examined natural genetic variation in *A. flavus* and *A. parasiticus* sampled from single peanut fields in the United States, Africa, Argentina, Australia and India. We found that differences in the proportions of *MATI-1* and *MATI-2* were correlated with the amount of asexual and sexual reproduction in populations. For both *A. flavus* and *A. parasiticus*, when the number of *MATI-1* and *MATI-2* was significantly different, there was extensive linkage disequilibrium in the aflatoxin cluster and isolates grouped into specific toxin classes, either the non-aflatoxigenic class in *A. flavus* or the B₁-dominant and G₁-dominant classes in *A. parasiticus*. We compared these results to variation in ex-

perimental populations. Crossovers in the aflatoxin cluster of F1 progeny coincided with recombination hotspots observed in natural populations, indicating that a single generation of sex can generate contemporary patterns of recombination and toxin diversity. Our work shows that a combination of ecological factors, asexual/sexual reproduction and balancing selection may influence aflatoxin diversity in these agriculturally important fungi.

Carlsen, Tor^{1*}, Seierstad, Kristian S.^{1,2}, Fossdal, Renate M.¹, Skrede, Inger¹, Engh, Ingeborg B.¹, Miettinen, Otto³, Larsson, Karl-Henrik², and Kausserud, Håvard¹. ¹Microbial Evolution Research Group (MERG), Department of Biology, University of Oslo, Norway, ²National Centre for Biosystematics, Natural History Museum, University of Oslo, PO Box 1172 Blindern, NO-0318 Oslo, Norway, ³Botanical Museum, Finnish Museum of Natural History, Helsinki, Finland. tor.carlsen@bio.uio.no. **Phylogeography and speciation of boreal wood-inhabiting fungi.**

Biogeographic studies show that fungi, like plants and animals, have complex histories of vicariance and dispersal. Fungal distributions are shaped by continental drift and climatic fluctuations such as ice ages. Reproductively isolated sub-populations accumulate genetic differences through genetic drift or natural selection. This phenomenon is observed in many fungal taxa even at intracontinental geographic scales. In fungi, morphological phenotypes seem to evolve more slowly than intrinsic reproductive barriers, creating problems, as nomenclature and species descriptions are mainly based on morphological characters. It is not surprising that there are many examples of fungal morphospecies in which partially or totally reproductively isolated sub-groups have been identified. Terms used for such sub-groups include cryptic species, sibling species, breeding units or intersterility groups. Multi-locus sequence data from species of boreal wood inhabiting fungi (in the genera *Trichaptum*, *Gloeoporus* and *Serpula*) has revealed diverse, complex evolutionary histories among these fungi where reproductive and geographical barriers have shaped the genetic substructure of the morphospecies. There is evidence of allopatric divergence within a morphospecies, followed by range expansion and secondary contact leading to interbreeding and recombination. Morphospecies also exhibit the formation of varying levels of reproductive barriers between sympatric genetic lineages, which may be linked to ecological factors such as host and substrate specificity.

Carroll, Emily T.^{1*}, Alexander, Ian J.², and Taylor, Andy FS¹. ¹The James Hutton Institute, Soils group, Macaulay Drive, Aberdeen, AB15 8QH, UK, ²University of Aberdeen, Biological Interactions in the Soil, Cruickshank Buildings, St Machar Drive, Aberdeen, AB24 3UU, UK. emily.carroll@hutton.ac.uk. **Alpine ectomycorrhizal fungi in Scotland: exploring the biogeography of undiscovered fungal communities.**

In the Scottish alpine environment there is a suite of dominant plant species that supports an ecologically significant community of ectomycorrhizal (ECM) fungi. These habitats are experiencing rapid change under the influences of elevated nitrogen (N) deposition, climate change and changing land use, to which ECM fungal communities can be particularly susceptible. However, assessment of the potential impact of these drivers is hampered by scarce species recording within these habitats, and a near complete lack of understanding of community composition with relation to habitat, climate or host species. This study therefore employs a broad biogeographical survey, aiming to provide data on species presence, whilst allowing comparisons to be made between communities experiencing different levels of N deposition across climatic gradients. Ten sites were selected to cover the highest range of N deposition present in the Scottish landscape (5 to 18.2 kg N/ha/y), including the furthest North-South, East-West locations possible. The roots of three hosts *Arctostaphylos uva-ursi*, *Arctostaphylos alpinus* and *Betula nana* were sampled giving 6800 (mean) mycorrhizal root tips per plant per site. These were analysed using titanium 454 sequencing to assess species presence and approximate relative abundance. Fungal fruit bodies were also collected, photographed, described and ITS DNA sequences were analysed. Preliminary findings indicate that: whilst many parallels can be drawn with Scandinavia/Europe, there appears to be a somewhat unique alpine ECM community in Scotland, with fruit body collections highlighting a number of unrecognised species. *A. uva-ursi* acts as a reservoir of fungal species, including many previously described as Pine-specific associates. This study has provided new UK habitat and altitude records for ECM fungi, including several accounts of extremely rare species, indicating the alpine zone may be their primary habitat within the UK. Analyses of the communities in relation to climate and N deposition are to be presented.

Carter, Keith A., Serpe, Marcelo, and White, Merlin M.^{*}. Department of Biological Sciences, Boise State University, 1910 University Drive, Boise, ID 83725-1515. keithcarter@u.boisestate.edu. **Identification of mycorrhizal species associated with *Artemisia tridentata* ssp. *wyomingensis* in Southwestern Idaho.**

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Reintroduction of *Artemisia tridentata* ssp. *wyomingensis* (Wyoming big sagebrush) in burned areas has proven difficult due to high seedling mortality. A factor that could improve seedling survival is the establishment of symbiotic associations with arbuscular mycorrhizal fungi (AMF). As a first step to investigate this notion, we have begun to identify and multiply native AMF species that colonize Wyoming big sagebrush. Identification of species is based on molecular methods, which involve DNA extraction from soil samples and sagebrush roots, and the use of nested PCR with primers specific for AMF. Extraction, amplification, and sequencing of mycorrhizal DNA from both soil and sagebrush roots has been conducted successfully from seven sites in southwest Idaho. The sequences analyzed thus far show that two genera, *Glomus* and *Entrophospora*, were present. Furthermore, in both the soil and the roots of sagebrush seedlings the most common species were *Glomus intraradices* and *G. microaggregatum*. Data gathered from soil samples show additional species, including *G. claroideum* and *E. infrequens*. DNA has also been amplified from greenhouse pot cultures which were grown with soil from the seven field sites. The amplified DNA will be used to increase sequence data resolution and the pot cultures to isolate mycorrhizal spores and initiate monospecific cultures.

Carver, Jonathan P.* and Volk, Thomas. Dept. Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601. carver.jona@uwlax.edu. **Survival of the mutualist: an educational poster on mycorrhizal and other root fungi.**

Mycorrhizal associations between terrestrial plants and soil fungi are ubiquitous in nature with over 90% of land plants forming some sort of symbiotic relationship with fungi in their root systems. These symbioses are generally considered mutualistic with the plant supplying sugars to the fungus in exchange for soil nutrients and water. The fossil record shows that these plant-fungal associations have existed for at least 400 million years. In fact the ability of plants to form mutualistic relationships with soil fungi may have been instrumental in allowing plants to adapt to life on land. Even to this day mycorrhizae are very important to terrestrial plant growth with their ability to alter plant nutrient uptake, plant water relations, and plant resistance to pathogens. The importance of mycorrhizae to plants and their abundance in terrestrial ecosystems makes it of paramount importance that we understand these plant-fungal associations. It is important to understand not only the ecology of these associations but also the types of mycorrhizae that exist and the plants and fungi that form these mutualisms. The most commonly recognized types of mycorrhizal fungi are arbuscular mycorrhizae, ectomycorrhizae, ericoid mycorrhizae, and orchid mycorrhizae. However, there are also other plant-fungal associations, such as monotropoid mycorrhizae and dark septate endophytes, which do not fit neatly into the above mentioned categories yet need to be included in a thorough overview of the mycorrhizal symbiosis. This poster on mycorrhizal fungi would be appropriate as educational material for such classes as mycology, botany or ecology. Both the well known mycorrhizal fungi and the more obscure mycorrhizae like associations are covered. The generalized ecology of mycorrhizal symbioses is discussed along with the specific similarities and differences between the types of mycorrhizae.

Castro-Longoria, Ernestina^{1*}, Lichius, Alexander^{1,2}, Yáñez-Gutiérrez, Mario E.¹, and Read, Nick D.². ¹Department of Microbiology, Center for Scientific Research and Higher Education of Ensenada (CICESE), Ensenada, Baja California, Mexico, ²Fungal Cell Biology Group, Institute of Cellular and Molecular Biology, Rutherford Building, The University of Edinburgh, Edinburgh, UK. ecastro@cicese.mx. **BUD-6 and BNI-1 have complementary functions in the filamentous fungus *Neurospora crassa* and are required to maintain Spitzenkörper integrity.**

Polarized growth is a central process in the function and morphogenesis of many cell types in eukaryotes. A key multiprotein complex involved in assembling the cytoskeleton and secretory machinery required for polarized growth, is the polarisome. Proteins constituting this complex in yeasts are Spa2, Pea2, Aip3/Bud6, Bni1, and probably Msb3 and Msb4. In this study we investigated the role of the putative polarisome components BUD-6 and BNI-1 in the filamentous fungus *Neurospora crassa*. Both proteins showed distinct localization during the establishment and maintenance of polarized tip growth, and overlapping localization patterns during septum formation, macroconidiogenesis and cell fusion. Results from phenotypic analyses of *bud-6* and *bni-1* gene deletion strains were consistent with their suggested roles derived from the localization data. Lack of either protein induced hyperbranching, and defects in polarized growth, septation and conidiation. A remarkable finding was the absence of the Spitzenkörper (Spk) in mature hyphae of both mutants, indicating essential roles in maintaining Spk integrity, and the functional organization of the apical tip growth apparatus. Considered together, our findings suggest that BUD-6 and BNI-1 perform multiple and to some extent complementary functions during polarized tip growth, septation and cell fusion, which are dependent on the developmental stage. The concerted yet spatially separated action of BUD-6 and BNI-1 within the apical

dome of mature hyphae might represent a novel and unique aspect of the filamentous fungal polarisome.

Cavinder, Brad and Trail, Frances*. Department of Plant Biology, Michigan State University, East Lansing, MI 48824-1312. trail@msu.edu. **Regulation of ascospore discharge show divergence among Sordariomycetes.**

Ascospores are forcibly discharged from many ascomycetous fungi, yet the mechanism of this process remains poorly understood. We have investigated several aspects of active discharge in *Fusarium graminearum*. Calcium signaling is essential to the process through the functions of Mid1, and Cch1, two calcium ion channels. A third putative calcium channel, Fig1, also has an important, but broader role in development in *F. graminearum*. Interestingly, these regulatory mechanisms are not shared by *Neurospora crassa*, indicating a divergence in at least the regulatory portion of the mechanism.

Charlton, Nikki D.*, Trammell, Mike, Hopkins, Andrew A., and Young, Carolyn A. The Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401. ndcharlton@noble.org. **Characterization and population structure of Canada wildrye endophytes.**

Canada wildrye (CWR, *Elymus canadensis* L.) is a cool season grass known to harbor sexual *Epichloë* sp. (*E. elymi*). More recently, asexual hybrid *Neotyphodium* sp. (*E. elymi* x *E. amarillans*) have been found in several populations of CWR. To further examine the endophyte populations of CWR, a collection of wild CWR populations from west Texas and Mexico (98CWR8, 04CWR6, and 04CWR2 Mx) were characterized for endophyte status, phylogeny and alkaloid potential, and both endophyte-infected and endophyte-free lines were evaluated for field persistence. Pure cultures of endophytes from these CWR lines were isolated and characterized based on morphological characteristics. Further analyses of specific alkaloid genes via PCR were performed to determine alkaloid potential, and *in planta* chemotypes were confirmed. The evidence indicated that there was chemotypic diversity within both the ergot alkaloid and loline pathways in the 04CWR2 Mx lines. To evaluate other CWR populations collected from Kansas to Texas, we are developing a system to identify the frequency of hybrids using High Resolution Melting (HRM) analysis, which provides a high throughput rapid screen to identify genotype variation within small amplicons. Target sequences have been identified for variations, such as single nucleotide polymorphisms (SNPs) and indels within introns of the housekeeping genes *tefA* and *tubB*. Variation of an individual is identified by changes in the shape of the melting curve profile when compared to reference samples. We have used HRM to look for variation within endophytes found in *Elymus* sp. to distinguish hybrid and non-hybrid endophytes within our represented group. These collections will be evaluated to determine the prevalence of hybrid and non-hybrid species and whether there is a correlation with variation in chemotypic diversity.

Choi, Young-Joon* and Pfister, Donald H. Farlow Herbarium, Department of Organic and Evolutionary Biology, Harvard University, 22 Divinity Ave., Cambridge, MA 02138, USA. dpfister@oeb.harvard.edu. **Revisiting the genus and species concepts of the genus *Scutellinia* based on morphology and phylogenetic analysis.**

The cosmopolitan genus *Scutellinia* forms a well-defined group within the family Pyrenomataceae (Pezizales). The approximately 60 species recognized are characterized mainly by wall ornamentation and size of ascospores, morphological characters of hairs, and substrate and geographic origins, but molecular phylogenetic analyses include only a scattering of species. For a comprehensive taxonomic study of *Scutellinia*, about 150 specimens covering Asia, Europe, and North and South America were analyzed using LSU and ITS rDNA sequences. It revealed more than 50 phylogenetic lineages, from which 30 species were identified using combined data on morphology, substrates, and geographic origins. In addition, the phylogenetic analysis discovered a dozen cryptic species, suggesting that this genus exhibits a species diversity higher than expected. The present work also pointed to a few taxonomic confusions at the species level; many specimens of *S. crinita*, *S. scutellata*, and *S. erinaceus* were inter-mixed; *S. kerguelensis* specimens formed a well-supported group, but revealed a high level of sequence divergence; and those that seems to be like *S. subhirtella* were divided into two groups. Our studies revealed that the broad species concept applied for these species needs to be re-evaluated, and therefore a further extensive study is required to confirm whether they are species complexes or several distinct species. Interestingly, two phylogenetic groups distant from other *Scutellinia* species were found. *S. setosa*, with smooth ascospores, is clearly differentiated from other species with ornamented spores, and four species of the section *Minutae* formed a distinct group with some species of *Cheilymenia* and *Kotlabaea*. Infra-generic concepts within *Scutellinia* suggested by several taxonomists are not supported by the present results. Shape of hairs and wall ornamentation of ascospores are useful characters for delimita-

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tion of species in *Scutellinia*, but are not suitable criteria at the level of subgenus or section.

Corcoran, Padraic*, Sun, Yu, and Johansson, Hanna. Dept. of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, Sweden. padraic.corcoran@ebc.uu.se. **Genomic insights into the divergence and introgression between *Neurospora tetrasperma* and other heterothallic species of *Neurospora*.**

The evolutionary genetic analysis of diverged populations and species allows us to gain insights into the evolutionary processes that play an important role in speciation. The development of Next Generation Sequencing (NGS) methods has allowed the study of these processes at the level of whole genomes. Here we present the study of whole genome sequence data from 3 lineages of the pseudohomothallic *Neurospora tetrasperma* that have been compared with the closely related *N. crassa* genome to reconstruct the history of divergence and introgression among the *Neurospora* species. We find a reduced level of nucleotide divergence between the Mat a chromosome of all *N. tetrasperma* strains and *N. crassa* as compared to the analysis of Mat A. Together with phylogenetic analysis of genes from along the mating type chromosome, these results indicate the action of post-divergence gene flow between *N. tetrasperma* and other heterothallic species of *Neurospora* along the Mat a chromosome. We also find evidence for reduced genetic degeneration on the mat a chromosome as compared to the Mat A chromosome in *N. tetrasperma*. These results indicate that introgression may have acted to impede the degeneration of the Mat a chromosome in *N. tetrasperma*. *N. tetrasperma* possesses a unique mating system when compared with the other heterothallic species of *Neurospora*. This has inspired a number of previous studies of natural strains of *N. tetrasperma*. However, there is still much that is unknown about this mating system, and in particular, the levels of outcrossing in natural populations. We have initiated a population genomic study of 3 *N. tetrasperma* populations. As part of this study we have isolated 96 homokaryons from 48 heterokaryotic strains. These 96 strains shall be sequenced with NGS to generate a genome-wide polymorphism data set allowing for analysis of the population genetic consequences of pseudohomothallism.

Corradi, Nicolas. Canadian Institute for Advanced Research, Department of Biology, University of Ottawa, Ottawa, Canada. ncorradi@uottawa.ca. **Acquisition of an animal gene by two microsporidia.**

Intracellular parasites are widely recognized for having evolved a number of molecular tools to fully benefit from their hosts. The microsporidia, for example, have acquired a number of ATP transporters from co-infecting bacteria through lateral gene transfer (LGT), that they now use to literally steal energy from the cells they invade. These fungal-like organisms are known to infect virtually all animals, yet no members of the group have ever been found to have received genetic material from their hosts by LGT. This is rather surprising, given the abundance of these parasites in many animals. Here we report the identification of a microsporidian gene from the genome of a recently sequenced species isolated from an arthropod. The gene is absent from any other members of the group with publicly available genome data, and encodes for a protein involved in the de-novo synthesis of purines. Surprisingly, all phylogenetic analyses using those genes and homologues from other eukaryotes significantly grouped both microsporidian sequences in a clade exclusively composed of homologues from Arthropods. This phylogenetic incongruence strongly indicates that these genes are of Arthropod origin. This suggests that the microsporidia has acquired the gene through LGT directly from its host. The present report represents the first report of an LGT between an animal host and its intracellular parasites, with obvious beneficial effects for the recipient of this transfer.

Corradi, Nicolas. Canadian Institute for Advanced Research, University of Ottawa, Ottawa, Canada. ncorradi@uottawa.ca. **Clues of sexual reproduction in the genome of arbuscular mycorrhizal fungi.**

Arbuscular mycorrhizal fungi (AMF) represent an ecologically relevant and evolutionarily intriguing group of symbionts of land plants, producing multinucleate spores and hyphae that are currently thought to have propagated clonally for over 500 My. This long-term absence of sex in AMF is a puzzling evolutionary feature that has sparked scientific interest for some time. A provoking alternative for their successful and long evolutionary history in the absence of an obvious sexual cycle is that these organisms may have cryptic sex, allowing them to recombine alleles and compensate for deleterious mutations. We explored this hypothesis by searching the genomes of two AMF for the primary molecular tools required for a sustainable sexual cycle in other fungi, and by studying the physical and molecular interactions of genetically different strains of one species under laboratory conditions. Our investigations resulted in the identification of many AMF genes notoriously involved in the process of sexual reproduction in many fungi. These genes include the vast majority of genes involved in the process of meiosis, and many that typically compose the mating-type locus (or that are directly related to mating) in other fungal lineages. Our

study suggests that these putatively asexual fungi may very well undergo a cryptic form of sexual reproduction, and indicates that these ecologically critical fungi may not be the evolutionary scandals that they have been long held to be.

Craig, Anjel J.* and Hoeksema, Jason D.² ¹Biology building 324, Northern Arizona University, PO Box 5640, Flagstaff, AZ, 86011-5640, ²University of Mississippi, PO Box 1848 University, Lafayette, MS 38677. ajc352@nau.edu. **Fine scale spatial analysis of ectomycorrhizal fungal community composition in a forest restoration site in Northern Mississippi.**

Models predicting the occurrence of ectomycorrhizal fungi (EMF) on the fine roots of plants have only recently begun to be employed by ecologists seeking to discern patterns of local occurrence and biogeography of these cryptic belowground symbionts. Restoration strategies such as burning and thinning may have strong impacts on EMF, and knowledge of EMF response and predictive occurrence models are needed. Using molecular methods, we identified the EMF community on woody plant root tips in a restoration project in northern Mississippi, comparing the EMF community between replicated control and treatment (burned and thinned mechanically or via tornado disturbance) plots at three different sites in mixed upland forest. We also quantified abiotic factors that may affect the EMF community, including litter depth, canopy openness, burn history, and soil compaction. These measured environmental variables were used in a logistic regression to predict occurrence of the two most abundant species, *Russula cf. flavisscans* and *Craterellus cornucopioides*. Results from molecular analysis indicate a high level of diversity in the ectomycorrhizal community, with 68 EMF operational taxonomic units (OTUs) detected 2 or more times, and nearly 100 OTUs found only once. Treatment plots were dominated either by species in the family Russulaceae with relatively high representation by species in the families Sebacinaceae, Thelephoraceae, and Cantharellaceae; or were dominated by Thelephoraceae. Spatial analysis revealed spatial autocorrelation (SAC) in the most disturbed plot at scales of approximately 10 meters, a greater spatial scale of SAC than reported in other EMF studies. Further spatial analyses explored if environmental variables with SAC corrections explain a significant portion of EMF community structure. Further, we will construct models to predict occurrences of these most abundant species with these environmental variables. These results represent the first assessment of EMF diversity in Mississippi and may provide guidance for future adaptive management strategies.

Crawford, David R. Departments of Philosophy and Biology, Duke University, Durham, NC 27708. david.crawford@duke.edu. **The role of cellularization in the evolutionary development of hierarchy in the Fungi.**

In this paper I argue that the developmental idiosyncrasies of the filamentous fungi challenge the traditional conceptual frameworks for multilevel selection based on plant and animal evolution. The filamentous fungi show a diversity of coenocytic and septate forms, both throughout development and between clades. The separation of cytokinesis and karyokinesis in the filamentous fungi provides the possibility of a coenocytic state in mycelia containing multiple partially independent nuclei. This has enabled the fungi to benefit from ecological opportunities unavailable to multicellular plants and animals - substrate exploration and colonization favors the flexibility of nuclear and/or organellar transport offered by the coenocytic state. This separation has also enabled the filamentous fungi to benefit from a number of selective advantages typically associated with multicellularity in plants and animals. Most important is compartmentalization, which the filamentous fungi achieve through septum-formation and/or septum-plugging. This approach allows for the development of complex structures and close nuclear control in heterodikaryotic states while not imposing these constraints on the entire life cycle. I argue that levels-of-selection processes within the filamentous fungi demonstrate that in evolutionary theory the transition from unicellularity to multicellularity needs to be understood not only in terms of the intergenerational unicellular/multicellular dynamics described in plant and animal lineages, but also in terms of the intragenerational process of cellularization. Importantly, the filamentous fungi offer not just a case study of an exception to current models but an exception which involves an evolutionarily significant and ecologically ubiquitous group with implications for the study of the evolution of development. I offer brief comparisons to work on levels of selection in Volvicine algae, Dictyostelids, and Myxogastriids.

Cripps, Cathy L.^{1*} and Horak, Egon.² ¹Plant Sciences & Plant Pathology Department, Montana State University, Bozeman, MT 59717-3150, USA, ²Nikodemweg 5, AT-6020 Innsbruck, Austria. ccripps@montana.edu. **Synopsis of Rocky Mountain arctic-alpine macro-fungi: central and southern floristic zones.**

Arctic-alpine (AA) habitats cover 8% of the Earth's land. While much is known of fungi in other AA habitats, little was known of macrofungi in the Rocky Mountain alpine zone before this on-going NSF survey. Here we sum-

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marize results for the central and southern Rocky Mountain alpine zone. True alpine fungi occur above tree-line and away from conifers within this strictly-defined physiographic region. This survey covers the Beartooth Plateau in MT/WY for the Central Floristic Region (lat 45°N) and the Front Range, San Juan Mountains, Sawatch Range for Southern Floristic Region in CO (lat 36°-38°N) and reports over 165 species in 46 genera and 11 families (ca 1 500 collections). It is estimated that over 75% are known as AA macrofungi. Of these, we estimate 2-5% are new to science, 75% are new records for this Rocky Mountain alpine zone and half are new to CO, MT and/or WY. Over half (56%) are ectomycorrhizal with *Salix reticulata*, *S. arctica*, *S. planifolia*, *S. glauca*, *Betula glandulosa*, *Dryas octopetala* or *Polygonum viviparum*. The most diverse ECM families are Cortinariaceae and Inocybaceae with over 74 species. Saprobic genera occur with bryophytes or are terrestrial primarily in grassland; macrofungi on woody debris are rare. A greater diversity is reported in southern mountain ranges which are more diverse in geology and habitat. The southern extent of the Rockies at 36-38°N likely includes the southernmost extent of some AA fungi in the Northern hemisphere. Fruiting can be sparse due to a continental climate, drying winds, low relative humidity, periodic droughts, fire, strong diurnal temperature fluctuations and high elevations of 3 000-4 000 m. In 2008 the International Arctic-Alpine Mycology Symposium was held on the Beartooth Plateau which also increased our knowledge of fungi in this region and results are online in *North American Fungi*.

Cripps, Cathy L.¹, Larsson, Ellen², and Horak, Egon³. ¹Plant Sciences & Plant Pathology Department, Montana State University, Bozeman, MT 59717, ²Department of Plant & Environmental Sciences, University of Gothenburg, Göteborg, Sweden, ³Nikodermweg 5, AT-6020 Innsbruck, Austria. ccripps@montana.edu. **Subgenus *Mallocybe* (*Inocybe*) in the Rocky Mountain alpine zone with molecular reference to European arctic-alpine material 7,000 km across the globe.**

The genus *Inocybe* (including subgenus *Mallocybe*) is a significant component of the ectomycorrhizal community in arctic and alpine habitats in terms of both diversity and distribution. Species are associated primarily with low woody shrubs of *Salix*, *Betula* and *Dryas*. There is evidence that shrubs are expanding in arctic-alpine habitats making the ectomycorrhizal fungi that support them of high interest. *Mallocybe* appears to be a dominant subgroup of *Inocybe* in Arctic-alpine habitats. Here we provide the first detailed report for six *Mallocybe* taxa with willows from the Rocky Mountain alpine zone (WY, MT, CO) including: *Inocybe arthrocytis*, *I. dulcamara*, *I. leucoloma*, *I. leucoblema* and in the *I. fulvipes* group, *I. substraminipes* and other taxa. Phylogenetic analysis matched Rocky Mountain specimens to arctic-alpine specimens from Scandinavia. ITS sequences of Kühner and Favre type specimens were used as references for several clades. Type drawings were matched to taxa as well and results show the importance of using both type DNA and type morphology as references to prevent identification errors of a difficult group. A Blast Search for root tip sequences, revealed close molecular matches for a specimen in the *Fulvipes* group to samples from Svalbard, Norway, British Columbia, China and Mongolia. Data suggest that these species have a broad intercontinental range in arctic-alpine habitats; some are known from subalpine habitats.

Croll, Daniel¹*, Stukenbrock, Eva², and McDonald, Bruce¹. ¹Plant Pathology, Institute of Integrative Biology, ETH Zürich, Switzerland, ²Department of Organismic Interactions, Max Planck Institute for Terrestrial Microbiology, Marburg, Germany. daniel.croll@agrl.ethz.ch. **Population genomics of dispensable chromosomes in *Mycosphaerella graminicola*.**

Fungal genomes are known to be highly plastic, including contributions from horizontal gene transfer and hybridizations and with extensive copy-number polymorphism. Some fungal species harbour one or more chromosomes that are not found in all isolates of the same species. Such chromosomes were termed supernumerary or dispensable, as their presence was not required to complete parts of the life cycle. In fungal pathogens, dispensable chromosomes were shown to harbour genes involved in virulence on hosts. *Mycosphaerella graminicola*, a major leaf pathogen of wheat, harbours the highest known number of dispensable chromosomes. We performed whole-genome resequencing of a *M. graminicola* population to identify polymorphisms among the eight known dispensable chromosomes. All dispensable chromosomes showed significant length variation due to large segmental deletions, including complete absence of certain chromosomes. In order to understand population genetic processes acting on the dispensable chromosome polymorphisms, we performed PCR assays at <100kb intervals along the chromosomes to assess presence-absence of chromosomal segments. Among 96 isolates of a global collection, we found population-specific patterns in segmental deletions and differences in frequencies of dispensable chromosomes among populations. We extended the PCR assays to 48 progeny from two controlled crosses from one Swiss population. We show that a substantial portion of the variation observed in dispensable chromosomes among isolates in a population may be generated through meio-

sis. Our data showed that dispensable chromosomes of *M. graminicola* are extremely plastic. Frequent mating among isolates carrying different sets of dispensable chromosomes contributes to the extreme length polymorphism found among chromosomes. Highly polymorphic regions of fungal genomes may be an important contributor to the rapid evolution of pathogenicity.

Cummings, Griffin A.¹*, Largent, David L.², Abell-Davis, Sandra E.³, and Bergemann, Sarah E.¹ ¹Middle Tennessee State University, Biology Dept., PO Box 60, Murfreesboro TN 37132 USA, ²Humboldt State University, Biological Sciences, 1 Harpst St, Arcata CA 95521 USA, ³James Cook University School of Marine and Tropical Biology, PO Box 6811, Cairns Queensland 4870 Australia. griffin.cummings@gmail.com. **Surveys of entolomatoid fungi from New South Wales and northern Queensland uncover several new species of *Pouzarella* (Basidiomycota, Entolomataceae).**

Recent efforts to document and describe the diversity of fungi of the *Entolomataceae* Kotl. & Pouzar from northern Queensland and central New South Wales Australia have yielded several collections of the species within the genus, *Pouzarella* Mazzer. Using morphological methods in conjunction with molecular sequence data obtained from three gene regions [mitochondrial small subunit (mtSSU), 25-28S nuclear large subunit rDNA (LSU), and a gene encoding the second largest ribosomal subunit (RPB2)], ten species of *Pouzarella* are described. Eight of the ten species (*P. albostrigosa*, *P. farinosa*, *P. fusca*, *P. pilocystidiata*, *P. lageniformis*, *P. pamii*, *P. parvula* and *P. setiformis*) are described as new to science. In addition, two species (*P. debilis* and *P. lasia*) originally described from Papua New Guinea, the Solomon Islands and Ceylon are reported for the first time in Australia. Phylogenetic analyses support the separation of ten *Pouzarella* species into three clades. Morphological characters common to these clades, as well as taxonomic novelties uncovered in these surveys, will be discussed.

Curjel Yuste, Jorge. CREAM (Centre de Recerca Ecològica i Aplicacions Forestals), Edifici C, Universitat Autònoma de Barcelona; 08193 Bellaterra, Spain. j.curjel@creaf.uab.cat. **Fungi and soil organic matter decomposition in the Mediterranean basin: what will be the role of fungi in a drier and warmer world?**

Few studies have been conducted on how climate change may affect soil microbial communities and, furthermore, on how possible climate-change induced alterations in the ecology of microbial communities may affect soil CO₂ emissions. Ongoing climatic changes in the Mediterranean basin, with longer summer droughts and higher temperatures are submitting the microbial community to an important adaptive force. The adaptive force is even more pronounced for fungi, especially symbiotic fungi, because drought-induced tree mortality and forest decline in this region is triggering ecological succession and hence new plant-fungal distributions and relations. Here we present the results of two different studies designed to investigate climate-change driven changes in soil microbial communities and its implication on soil CO₂ emissions from Mediterranean ecosystems. Firstly, we studied the climatic effect over soil microbial (bacterial and fungal) community structure and diversity in experimental areas of precipitation/throughfall exclusion using Terminal Restriction Fragment Length Polymorphisms (TRFLP). Secondly, we studied the effect of climate-change driven plant succession on microbial community composition and diversity (pyrosequencing technique; Genome Sequencer Titanium FLX system (454) Life Sciences). We further studied how climate-change induced changes in microbial communities may affect decomposition of soil organic matter, soil respiration and the response of those fluxes to climatic fluctuations. Our results show that fungal community might be more resistant to drought, and hence less sensitive to ongoing climate change scenarios, than bacteria. Moreover, both SOM decomposition and its response to temperature showed a strong dependence on fungal biomass and diversity, suggesting that future microbial-derived soil CO₂ emissions in this region will be strongly dependent on fungi. On the other hand, climate change-driven changes in plant distribution will also be associated to substantial changes in the microbial community diversity and composition which should be taken into account to understand future trends in soil CO₂ emissions.

Dalman, Kerstin, Olson, Åke, Durling-Brandström, Mikael, Himmelstrand, Kajsa, Lind, Märten, and Stenlid, Jan*. Dept of Forest Mycology and Pathology, Box 7026, 75007 Uppsala, Sweden. Jan.Stenlid@slu.se. **Population genomics and association mapping in *Heterobasidion annosum*.**

Fungi are ideal eukaryotes for population genomics work since they are haploid and have relatively small genome sizes. *Heterobasidion annosum* (Fr.) Bref. *sensu lato* (*s.l.*) is a necrotrophic pathogen causing severe damages to coniferous forests in the northern hemisphere. In this study a genome-wide association mapping was performed for 23 *H. annosum sensu stricto* (*s.s.*) homokaryotic haploid isolates and four virulence traits. A reference sequence

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was constructed by a *de novo* assembly of two of the isolates and reads from the other isolates were aligned to the contigs. The number of Single Nucleotide Polymorphism (SNP) markers present in at least two individuals generated from the sequencing was 33018. The virulence traits were measured as lesion length in the phloem and fungal growth within the sapwood in both pine and spruce following artificial inoculations on the stem of 2-year-old seedlings. Twelve SNP markers distributed on seven contigs were found to be significantly associated with fungal virulence ($p < 0.0001$). Out of these, two with the lowest p and six markers all located to one contig were found to be placed into LD-blocks ranging between 1.2 and 31.2 kb. Following annotation, genes were identified as candidates for pathogenicity, including calcineurin, acetylglutamate kinase/synthase, cytochrome P450 monooxygenase, serine carboxypeptidase (ToxD), quinone oxidoreductase and two flavin-containing monooxygenases.

Davey, Marie L.^{1,2*}, Kausserud, Håvard², and Ohlson, Mikael¹. ¹Department of Ecology and Natural Resource Management, Norwegian University of Life Sciences, N-1432 Ås, Norway, ²Molecular Evolution Research Group, Department of Biology, University of Oslo, N-0316 Oslo, Norway. marie.davey@umb.no. **Seasonal fluctuations in size and composition of fungal communities associated with boreal bryophytes as detected by amplicon pyrosequencing and biochemical assays.**

Bryophytes are a dominant vegetation component of the boreal forest and are thought to host a high diversity of fungi that play important ecological roles in nutrient cycling. However, relatively little is known about the size and composition of fungal communities associated with these hosts. The bryophytes *Hylacomium splendens*, *Pleurozium schreberi*, and *Polytrichum commune* were repeatedly collected throughout the year from two locations in boreal spruce forests in southern Norway. 454 amplicon pyrosequencing of the ITS2 region of rDNA was used to characterize the fungal communities associated with these mosses and to investigate seasonal fluctuations in community composition and diversity. The biochemical marker compound ergosterol was quantified and used as a proxy for fungal biomass to allow for estimations of the size of these fungal communities. Our preliminary results indicate the fungal communities associated with mosses are dominated by ascomycetous species, and that the fungal species richness associated with a single moss shoot remains relatively constant throughout both the growing season and the winter. Community composition varied between host species but a clear seasonal pattern was not observed. The bryophilous fungal communities were all very diverse and exhibited a high degree of patchiness, heterogeneity, and variability. The overall fungal biomass associated with the moss communities remained stable throughout the seasons, but varied between both the host species and the photosynthetic and senescent tissues of the moss.

Davis, William J.^{*}, Powell, Martha J., and Letcher, Peter M. Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487. mpowell@biology.as.ua.edu. **Culture-based inventory demonstrates regional diversity among Chytridiomycetes.**

The purpose of this investigation is to determine diversity of Chytridiomycetes (=chytrid fungi) within a limited geographical region through intensive collecting, culturing, and phylogenetic analyses. Our previous culture-based sampling for chytrids has emphasized a global perspective to ascertain genetic diversity of chytrids at a broad-scale range. As might be expected from this approach, these inventories identified some chytrid phylotypes that were geographically limited or rarely cultured. However other chytrid phylotypes were cosmopolitan and abundant, indicative of a global distribution. The state of Alabama is considered a biodiversity hotspot, in part because of its varied geography and geology, and provides us access to a wealth of habitats. Surveys of chytrid diversity in Alabama, however, have been limited. A recent molecular inventory of environmental samples from two lakes in Alabama revealed phylotypes with high nucleotide homology with known chytrids; but several phylotypes were unique, harkening local untapped diversity. We have used an “in-your-own-backyard” approach involving a number of students to assist in sampling and detection of chytrids. Preliminary results show genetic divergence in genera and species within a limited geographical range. Establishing a species concept for chytrids is an ongoing process. These results contribute to the assessment of the genetic range of phylotypes within a lineage, a necessary consideration for species delimitation. This study also demonstrates the importance of intensive sampling to portray biodiversity of chytrids adequately and is foundational for future molecular environmental and systematic studies of chytrids in this region.

Dee, Jaclyn M.^{1*}, Lowry, David S.², Mollicone, Marilyn RN³, Berbee, Mary L.⁴, and Roberson, Robert W.⁵ ¹Department of Botany, University of British Columbia, Vancouver, BC, V6T-1Z4, Canada, ²School of Life Sciences, Arizona State University, Tempe, AZ, 85287, USA, ³School of Biology and Ecology,

University of Maine, Orono, ME, 04469, USA, ⁴Department of Botany, University of British Columbia, Vancouver, BC, V6T-1Z4, Canada, ⁵School of Life Sciences, Arizona State University, Tempe, AZ, 85287, USA. deej@interchange.ubc.ca. **It happens all the time: cytological and phylogenetic evidence for gain and loss of hyphae in the class Monoblepharidomycetes (Chytridiomycota) highlights a common transition in fungal evolution.**

Thanks to hyphae, Fungi can achieve immense sizes and thrive in varied ecosystems. However, environmental conditions repeatedly forced these branched and elongate filaments to adapt resulting in the convergent rise of yeasts in most of the fungal phyla. To learn more about the evolutionary transitions between hyphae and their related unicellular forms, we compared the cellular organization of Chytridiomycota to well-characterized terrestrial Fungi. We focused on the hyphal tip and cytoskeletal organization of mycelial members of the Monoblepharidomycetes, a group of very early diverging zoospore fungi that possesses a variety of body plans from sprawling mycelia to simple crescent or rod-shaped, unicellular thalli. Using light (LM) and transmission electron microscopy (TEM), we observed the subcellular organization of two mycelial species, *Monoblepharis macrandra* and *Gonapodya prolifera*. Though we did not observe an organized Spitzenkörper (Spk) in LM or TEM images, we noted an array of vesicle types at hyphal apices, some of which were similar to those found in other Fungi. Moreover, in mycelial species studied previously, a robust microtubular “highway” transports materials throughout the fungal body. Curiously, in these organisms, immunofluorescence imaging revealed sparse microtubules distributed in astral-like arrays emanating from the surfaces of nuclei. Elaborate networks of actin microfilaments stained with rhodamine-phalloidin pervaded the mycelium and actin plaques were concentrated in the cortex of growing hyphal tips. This may reflect a method of organellar and vesicular transport predominated by the actin cytoskeleton. Finally, our analysis of 40 new ribosomal DNA sequences suggests that some unicellular members of the group are derived from hyphal ancestors. Taken together, these data provide evidence for the ancient rise and consequent loss of hyphae in aquatic Fungi that mirrors a similar evolutionary pattern found in terrestrial lineages.

Dianese, José C., Souza, Erica S.C., Inácio, C.A., Vales, H.M.M., Boiteux, L.S. Depto. de Fitopatologia, Universidade de Brasília, Campus Darcy Ribeiro, Asa Norte, 70910-900 Brasília, DF, Brazil. jcarmin@unb.br. **Interaction between a non-gloeosporioid endophytic *Colletotrichum* species and *Uromyces euphorbiae* on leaves of *Chamaesyce hirta*.**

Chamaesyce hirta (Euphorbiaceae) grows widely in most warm regions of the world including in several states in USA. In Brasília, plants infected with *Uromyces euphorbiae* characteristically show rust pustules (485-220 mm diam.) delimited by a light yellow band. Both urediniospores and teliospores of the fungus are formed. However, only inside those yellow areas around the rust pustules, *Colletotrichum* acervuli were produced. Thus, surveying several leaves 74% of the yellow bands showed infection by a *Colletotrichum* species with typically allantoid conidia (31 (27) 23 x 3-4) in acervuli measuring 86-44 mm, bordered by a palisade of long black setae (up to 140 x 5 mm). Thus, *Colletotrichum* acervuli were not shown in 26% of the pustules, and were never formed in areas of the leaf where *U. euphorbiae* was not present. Isolation from healthy areas of the leaves and from leaves showing no rust infection, revealed that the associated fungus was indeed an endophyte. Sequencing rDNA fragments amplified using ITS-4 and ITS-5 primers revealed that the endophyte and the pustule-infecting fungus belonged in the same species. Further research is needed to clarify the physiological aspect of the interaction between the plant parasitic Pucciniaceae and the endophytic coelomycete involved. Finally, the *Colletotrichum* specimen studied apparently belong in a new species of this genus.

Dickie, Ian A.^{1*}, Fukami, Tadashi², Wilkie, Paula¹, Allen, Robert B.¹, and Buchannan, Peter K.¹ ¹Landcare Research, Box 40, Lincoln 7640, New Zealand, ²Department of Biology, Stanford University, Stanford CA 94035-5020, USA. dickie@landcareresearch.co.nz. **Using wood-decay fungi to test the ecological significance of assembly history for species, communities, and ecosystem outcomes.**

Assembly history, or the order of species immigration into communities, has the potential to exert wide-ranging effects across multiple levels of ecological organization, influencing species, communities and ecosystems. The potential importance of assembly history is shown from laboratory microcosm experiments. Nonetheless, it remains unclear whether assembly history effects on individual species attenuate at the level of communities and ecosystems and the degree to which these effects are ecologically significant. Here we address this question using a field-based manipulation of the assembly history of wood-inhabiting fungi as a model system. Ten different species of fungi were inoculated onto wood disks in 8 different arrival histories and at two nutrient levels, then placed into the forest floor for a 13-month incubation. We found stronger assembly history effects on individual species than on community properties, but

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no attenuation in effect size from community to ecosystem properties such as wood decomposition and carbon and nitrogen concentration. Furthermore, assembly history affected ecosystem properties more strongly than an experimentally imposed 3-fold difference in initial wood nitrogen concentration did. These results indicate that assembly history effects may attenuate from species- to community-levels of organization, but can be equally strong on community- and ecosystem-level properties even under natural environmental variability.

van Diepen, Linda TA^{1*}, Frey, Serita D.¹, Pringle, Anne², Sthultz, Christopher M.², Morrison, Eric W.¹, and Pérez, Samuel². ¹Department of Natural Resources & the Environment, University of New Hampshire, Durham, NH 03801, ²Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138. lvdiepen@gmail.com. **Evolution of decomposer fungi in a changing climate.**

Fungi are ubiquitous in terrestrial ecosystems and play an important role in biogeochemical cycling because of their function as litter decomposers. It has been demonstrated that increased nitrogen (N) deposition decreases fungal biomass, reduces their diversity and changes relative abundance of particular groups and species. In addition increased N can slow litter decomposition and reduce lignolytic enzyme activity. To understand the relationship between fungal community dynamics and changes in litter decay in response to climate change we made use of an existing long-term study in which a northern hardwood forest has been exposed to simulated increased N deposition for over 20 years (Chronic N Addition plots, Harvard Forest, Petersham, MA). The Chronic N Addition Experiment consists of 3 treatments (ambient, 5 and 15 g N m⁻² y⁻¹). Fungi were isolated from fresh litter collected at each of the treatments, and a subset of the same fungal species isolated from each of the three treatment plots were tested for their growth rate and decomposition ability under three different nitrogen levels. An isolate from the high N treatment of the fungal species *Epicoccum* sp. had a faster growth rate in a high N environment compared to the *Epicoccum* sp. isolated from the control and low N treatments, indicating that this isolate might have adapted to its new environment. In contrast, high N isolates of two other fungal species did not show any increase in growth, indicating that these species are physiologically plastic. The decomposition experiment resulted in decreased decomposition by isolates from high N treatment plots compared to control and low N isolates. The observed changes in growth rate and decomposition rate indicate that even if fungal species persist in a high N environment, their functioning might be affected, which in turn can affect the functioning of the ecosystem they inhabit.

Dowie, Nicholas J.* and Miller, Steven L. Department of Botany, University of Wyoming, Laramie, WY 82071. ndowie@uwyo.edu. **Fungal symbiont overlap in two mycoheterotrophic taxa (*Pterospora andromedea* and *Sarcodes sanguinea*).**

Pterospora andromedea has been shown to form obligate symbioses with only three species of *Rhizopogon* in section *Amylopogon*: *R. salebrosum*, *R. arctostaphyli* and an undescribed molecular taxon. *Sarcodes sanguinea*, another mycoheterotroph in the Ericaceae, and sister taxon to *Pterospora andromedea*, has been found to form symbioses with two species of *Rhizopogon* section *Amylopogon*: *R. ellena* and *R. subpurpurascens*. Until now no fungal symbiont overlap has been recorded between these two achlorophyllous plants and their associated mycobionts. Ectomycorrhizal tissue from nearly 200 *P. andromedea* rootballs were collected from the south-central Rocky Mountains and the mycobionts were identified using sequence analysis of the ITS locus compared with sequences of *Rhizopogon* section *Amylopogon* obtained from GenBank. An almost exclusive *P. andromedea*/*R. salebrosum* association occurred within this region, however, *P. andromedea* was found in association with *Rhizopogon ellena* in the Greater Yellowstone Ecosystem. Two additional loci, ATP6 and RPB2, supported this relationship. Overlap in obligate mycobionts between closely related mycoheterotrophs provides interesting new information on the phylogenetic history and co-evolution of mycoheterotrophs in Monotropeae (Ericaceae) and the discovery of a new mycobiont may provide evidence for an undiscovered, perhaps ancestral, lineage of *P. andromedea* inhabiting the Yellowstone area.

Doyle, Vinson P.^{1,2*}, Oudemans, Peter V.⁴, Rehner, Stephen A.³, Little, Damon P.^{1,2}, and Litt, Amy^{1,2}. ¹The New York Botanical Garden, 200th St and Southern Blvd, Bronx, New York, NY 10458, ²The Graduate Center, The City University of New York, New York, NY 10016, ³USDA Systematic Mycology and Microbiology Laboratory, 10300 Baltimore Ave., Beltsville, MD 20705, ⁴P.E. Marucci Center for Blueberry and Cranberry Research and Extension, 125a Lake Oswego Rd., Chatsworth, NJ 08019. vdoyle@nybg.org. **Diversity and population genetics of the *Colletotrichum gloeosporioides* complex in North America: understanding dispersal patterns in agricultural and wild populations.**

Colletotrichum gloeosporioides is a broadly circumscribed fungal species that is a widespread pathogen of diverse plant hosts including cranberry (*Vac-*

cinium macrocarpon). Early reports of *C. gloeosporioides* from cultivated cranberry in eastern North America date to the late 1800s and it is now common throughout the North American cranberry-growing regions. We employed multilocus sequence data to (1) investigate the diversity of *Colletotrichum* species from cranberry and sympatric host species and (2) to identify a clade within the *C. gloeosporioides* complex that is broadly distributed on cranberry. Phylogenetic analysis of DNA sequence data from nrITS1-5.8S-ITS2, beta-tubulin, apn2, and apn2-matIGS of *C. gloeosporioides* from North American hosts resolved multiple clades within the complex, with some containing representatives from both temperate and tropical regions. Three distinct clades infect cultivated and wild cranberry. The most broadly distributed clade on cranberry is closely related to isolates from the sympatric host *Rhexia virginica* and to the coffee berry pathogen, *C. kahawae*. Isolates from this clade were used to develop microsatellite markers to (1) infer fine-scale population structure and gene flow within and between native (wild) and cultivated cranberry bogs and (2) assess the role of outcrossing in field populations. Isolates were sampled from cranberry growing regions in British Columbia, Washington, Wisconsin, Massachusetts, Delaware and New Jersey as well as wild populations in Delaware and Pennsylvania. The most evident barriers to gene flow are between wild and cultivated populations separated by a minimum of 71 kilometers. Despite the presence of recombinant genotypes, homothallic and clonal reproduction predominates and clonal haplotypes are present in cultivated populations separated by more than 4000 kilometers. The broad distribution of clonal haplotypes among cultivated cranberry populations suggests *C. gloeosporioides* is dispersing with plant material as latent pathogens or endophytes.

Durall, Daniel M.^{1*}, Grelet, Gwen-Aëlle², Ba, R.², Alexander, Ian JA², and Taylor, Andy FS³. ¹University of British Columbia Okanagan, Dept. of Biology, 3333 University Way, Kelowna, BC V1V 1V7, Canada, ²Institute of Biological and Environmental Sciences, University of Aberdeen, Aberdeen AB24 3UU, UK, ³Department of Forest Mycology and Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden. daniel.durall@ubc.ca. **Linkages between taxonomy and ecology in root-inhabiting *Mycena* spp.**

Recent studies support the view that mycoheterotrophic plants may obtain their carbon not only from ectomycorrhizal or arbuscular mycorrhizal fungi, but also from saprotrophic *Mycena* spp. This view is widely accepted, but the interpretation of the results relies heavily on the unquestioned assumption that *Mycenas* are always saprotrophic. We provide 3 independent lines of evidence showing that some *Mycena* species can behave as plant-beneficial root endophytes in green Ericaceae plant species: (1) Direct isolation of *Mycena* from ericoid mycorrhizal roots; (2) analysis of the occurrence of *Mycena* sequences in global sequence databases and (3) a laboratory study based on the inoculation of ericaceous seedlings (*Vaccinium corymbosum*) with an isolate of *Mycena*, which examined both colonisation of root cells and the effects on plant growth. Our results suggest that some taxa currently recognised as members of the genus may represent transitional phases between full saprotrophic taxa and root symbionts. In evolutionary terms, ericoid mycorrhizas are probably the youngest mycorrhizal type, and recruitment of potential fungal symbionts may be more active in these associations than in those with a longer evolutionary history.

Eberhart, Joyce L.* and Luoma, Daniel L. Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR 97331. joyce.eberhart@oregonstate.edu. **Effects of varying levels of forest thinning on *Tricholoma magnivelare* (American matsutake).**

Commercial matsutake mushroom harvest in the Pacific Northwest is common in lodgepole pine forests. Insufficient ecological knowledge of the mycorrhizae and mycelium has challenged monitoring this resource. Among many management issues are concerns over logging practices, a lack of information on the ecology and habitat requirements of American matsutake, and the potential effects of the type and intensity of matsutake harvest on future mushroom productivity. Lodgepole pine and mixed conifer stands provide habitat for growing and harvesting matsutake mushrooms, but these stands have developed dense understories that can increase the risk of wildfire and disease. The Deschutes National Forest is implementing a plan to reduce the risk that insects, disease, and wildfire will lead to large-scale loss of forest resources. Our study will monitor the effects of the vegetation treatments (tree thinning) on shiros of *Tricholoma magnivelare* by directly sampling soil and mycorrhizae obtained from plots established throughout the project area. To minimize impact on soil hyphae, all tree-thinning experimental areas were designated for logging with snow cover present and by use of a feller-buncher to yard whole trees to landings. Four blocks were established. Each block contained 3 forest cover-types with treated and un-treated areas. Thirty shiros of matsutake per experimental unit were identified, and four soil samples were taken from each shiro. Due to volcanic glass in these soils, it was not possible to amplify DNA using extraction techniques that require bead beating or vortexing. In response, we devel-

Continued on following page

oped a quick, inexpensive modification of Xin's plant extraction methods. These extractions were then PCR'd using unpublished primers developed by B. Bravo that specifically amplify *T. magnivelare*. To date, only pretreatment samples have been collected. Logging over snow was completed the winter of 2010/2011, post-treatment sampling will occur in fall 2011.

Ebrahimi, Leila*, Aminian, Heshmatolah, Etebarian, Hasan Reza, and Sahebani, Navazolah. Dept. of Plant Pathology, Tehran University, Aboueyhan campus, Tehran, Iran. leila_ebrahimi2000@yahoo.com. **Torulasporea delbrueckii in biocontrol of *Penicillium expansum* on apple fruits.**

Penicillium expansum causes severe rots on apple fruit during storage, reduces shelf life, and can produce the hazardous mycotoxin, patulin. Synthetic fungicides are primarily used to control postharvest decay loss. However, concerns about public health and the development of resistant pathogens have increased the search for alternative methods. Recently developed biological control using antagonistic microorganisms for controlling post-harvest diseases has achieved considerable success. Use of the microbial antagonists like yeasts, fungi, and bacteria is quite promising and gaining popularity. Recently, researchers discovered that some yeasts are antagonists of *Penicillium expansum*. In this study, antagonistic activity of *Torulasporea delbrueckii* was evaluated against *Penicillium expansum*. Strains of *T. delbrueckii* were recognized for their extreme osmotic and freeze tolerance and resistance to several other types of physiological stresses. We tested *in vitro* the antagonistic effects of *T. delbrueckii* in controlling mycelial growth of *P. expansum* on PDA in dual cultures, and growth of *P. expansum* alone with cell free metabolites and volatile components of *T. delbrueckii*. The growth of the pathogen in dual culture compared to control were 70.64% and 63.56% for *T. delbrueckii* with isolates A4 and A6 of *P. expansum*, respectively. The percentages were 43.17% and 9.67% in tests of volatiles, and 15.49% and 7.7% in tests of non-volatile metabolites. Effects of the yeast on pathogen damage to 'Golden Delicious' apples in storage were also tested. 20 µl of antagonist suspension (1×10^8 cell/ml) was applied to wounds and incubated for 24 h, followed by application of 20 µl of pathogen conidial suspension (1×10^5 cell/ml). Fruits were then transferred to storage at either 20°C or 5°C. All treatments had four replicates. The area of decay was decreased by the yeast at both temperatures. The characteristics and antagonistic efficacy of this yeast show strong potential for use in biocontrol.

Ebrahimi, Leila*, Etebarian, Hasan Reza, Aminian, Heshmatolah, and Sahebani, Navazolah. Dept. of Plant Pathology, Tehran University, Aboueyhan campus, Tehran, Iran. leila_ebrahimi2000@yahoo.com. **Biocontrol of apple blue mold disease with *Metschnikowia pulcherrima* in combination with silicon.**

Penicillium expansum is the most common postharvest rot of pome fruits that with produced patulin on apple affect human health. The use of synthetic fungicides is a primary method of control of disease causing fungi in crop plants. However, concerns about public health and the development of resistant pathogens have increased the search for alternative methods. The new strategies include the biocontrol by means of natural compounds or antagonistic microorganisms. *Metschnikowia pulcherrima* alone and in combination with silicon (Si) was applied to control of *Penicillium expansum*. *in vitro*, Si at different concentrations was added to PDA culture, then a plug of *P. expansum* was placed on centre of plates for evaluation of Si direct effect on mycelia growth. Effect of Si on population of yeast in NYDB was determined after 24 and 48h. Si significantly decreased mycelia growth of pathogen and in 0.6 and 1% (wt/vol) completely inhibited mycelia growth of pathogen and decreased population of yeast low. For effect of *M. pulcherrima* alone and in combination with Si in control of disease in storage condition, apple fruits were wounded using a sterile nail. Each wound was treated with 20µl of: *M. pulcherrima* suspension (1×10^8 cell/ml), solution of Si in different concentration of 0, 0.2, 0.4, 0.6 and 1% (wt/vol), antagonist suspension amended by Si at different concentrations and sterile distilled water as the control. After 24h, 20µl of conidia suspension (1×10^5 cell/ml) of pathogen were applied. Then fruits were transferred to storage with 5°C. After 45 days the lesion diameter was measured and the population of yeast in the wound was determined by serial dilution. Si at 1% (wt/vol) in combination with yeast significantly inhibited the decayed area in compare with control. The results indicated that combination of Si with antagonistic yeast reduced the blue mold of apple better than Si and yeast alone.

Ellison, Christopher E.1*, Hall, Charles1, Kowbel, David1, Welch, Juliet1, Brem, Rachel2, Glass, Louise1, and Taylor, John W.1 1Department of Plant & Microbial Biology, University of California at Berkeley, Berkeley, CA 94720, 2Department of Molecular and Cell Biology, University of California at Berkeley, Berkeley, CA 94720. jtaylor@berkeley.edu. **Population genomics of divergence and adaptation in wild isolates of *Neurospora crassa*.**

Discovering the genetic basis behind adaptive phenotypes has long been considered the holy grail of evolutionary genetics. Thus far, most instances where adaptive alleles have been identified involved targeting candidate genes

based on their having a function related to an obvious phenotype such as pigmentation. This forward-ecology approach is difficult for most fungi because they lack obvious phenotypes. We have used a reverse-ecology approach to identify candidate genes involved in local adaptation to cold temperature in two recently diverged populations of *Neurospora crassa* by performing high-resolution genome scans between populations to identify genomic islands of extreme divergence. We find two such islands containing genes whose functions, pattern of nucleotide polymorphism, and null phenotype are consistent with local adaptation. We additionally explore patterns of gene expression variation within and between these two populations and identify suites of coregulated genes and genes that exhibit strong differences in expression level between populations.

Fernández Mendoza, Fernando1,2*, Domaschke, Stephanie1,2, and Printzen, Christian1,2. 1Biodiversität und Klima Forschungszentrum, Frankfurt am Main, Germany, 2Department of Botany and Molecular Evolution, Forschungsinstitut Senckenberg, Senckenberganlage 25, 60325, Frankfurt am Main, Germany. ffernando@senckenberg.de. **Which alga, how and where? Decoupling geography, ecology and evolution of photobiont use in the *Cetraria aculeata* group (Parmeliaceae, Ascomycota).**

We present a study in which a broad phylogenetic and geographical sampling is used to disentangle the spatial, climatic and evolutionary extent of the known trends of photobiont use in the lichen *Cetraria aculeata*. *C. aculeata* is a widely distributed lichen species that grows at high latitudes in both hemispheres, as well as in tropical and temperate highlands, and in Temperate and Mediterranean lowlands of Europe and Asia. *C. aculeata* is often found growing together with other closely related species, which we address here as *C. aculeata* group: *C. aculeata* (Schreb.) Fr., *C. crespoae* (Barreno & Vázquez) Kärnefelt, *C. steppae* (Savicz) Kärnefelt, *C. muricata* (Ach.) Eckfeldt and *C. odontella* (Ach.) Ach. Some of these species also have a wide distributional pattern; and all of them are selectively associated with photobiont strains belonging to the green alga *Trebouxia jamesii*. We used phylogenetic and genealogical reconstructions as a base to infer the evolution of the interaction between both symbionts, in terms of climate niche and trait evolution. In this work lichens belonging to the *C. aculeata* group were studied from the perspective of evolutionary genetics mainly on a transect joining South and North poles along the Andes and the Rocky mountains. The relative importance of long range dispersal, and its magnitude in space and time will be discussed, and the current distribution and genetic structure will be discussed from a phylogeographic perspective. The photobiont use will be reviewed from the point of view of phylogeography, codispersal history and climate envelope reconstruction.

Floudas, Dimitrios*, Binder, Manfred, and Hibbett, David S. Clark University, Worcester, MA, USA. dfloudas@clarku.edu. **Parallel losses of cellulose binding modules (CBMs) in carbohydrate-active enzymes (CAZs) in brown rot Agaricomycotina inferred from genome sequences.**

Saprotrophic species in Agaricomycotina are a major component of the wood degradation process in nature, having a great impact on carbon cycling. Two major wood degradation types have been recognized in this group, named white and brown type of rot. The two mechanisms show major differences in the biochemistry involved, the successive anatomical changes caused on the wood and the composition of the residue after degradation is completed. The genomes of the brown rot species *Postia placenta* (Polyporales) and *Serpula lacrymans* (Boletales) revealed parallel gene losses in gene families involved in wood degradation along with a reduced number of recognized CBM1 fungal domains, which participate in interactions of carbohydrate active enzymes with crystalline cellulose. More recently, the Saprotrophic Agaricomycotina project in collaboration with the Joint Genome Institute has generated the genome sequences of 11 white and brown rot species from 8 orders across the Agaricomycotina, with the aim of understanding the functional diversity and evolution of wood degradation mechanisms in this group. Preliminary results not only indicate that gene losses have taken places in all the brown rot lineages sampled in comparison to the white rot species sequenced, but also reveal that parallel losses of the CBM1 fungal domains have taken place without loss of the gene initially containing the domain, thus highlighting another aspect of convergent evolution on the molecular level among the brown rot lineages.

Foltz, Matthew J.*, Perez, Kathryn E., and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, 1725 State Street, La Crosse, WI 54601. foltz.matt@uwlax.edu. **Molecular phylogeny reveals cryptic species within the *Cantharellus cibarius* complex in the United States.**

Chanterelle mushrooms are highly sought-after choice edibles in many countries around the world because of their delicious taste and fruity odor of apricots. Once considered a single species, the common yellow-golden chanterelle (*Cantharellus cibarius sensu lato*) that can be found in many parts of the world is now known to be a complex of several species that look physi-

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cally similar in many ways. We compared chanterelles collected in Wisconsin to chanterelles from other areas of the United States, including freshly collected specimens and herbarium specimens, as well as sequences from well-defined *Cantharellus* species on Genbank. Nuclear ribosomal DNA from the LSU and SSU loci provided better taxonomic resolution in *Cantharellus* than the mitochondrial SSU DNA. Molecular phylogeny of the nLSU locus provided evidence for at least two cryptic species in Wisconsin that also match specimens from other locations in the Eastern U.S. In addition, nLSU data reveal a greatly expanded range for *Cantharellus cibarius* var. *roseocanus*, which had previously only been reported from the Pacific Northwest. Several other cryptic lineages exist within *C. cibarius sensu lato*, including one that was collected during the 2010 MSA foray in Kentucky. This study also suggests that cryptic lineages exist in other species of *Cantharellus* including *C. cinnabarinus*, and *C. perisicinus*.

Fox, Amy T.[†] and Schilling, Jonathan. University of Minnesota Bioproducts and Biosystems Engineering 203 Kaufert Laboratory 2004 Folwell Ave St. Paul, MN 55108. schilling@umn.edu. **The battle for birch: competitive outcomes between ubiquitous wood-degrading fungi can have long term consequences.**

Wood degrading fungi are largely responsible for the breakdown of persistent lignocellulosic material in temperate and boreal forest ecosystems. Two principal types of wood decay, brown rot and white rot, are distinguished by their unique degradative mechanisms, and the residues generated differ among these broad groups in metal binding capacities, redox reactions, permeability, soil sorption, and long-term residence time on the forest floor. Shifts in wood degrading communities can thus have meaningful consequences for soil formation, forest health, and carbon cycling. In our study, *Piptoporus betulinus* and *Fomes fomentarius* were selected to test effects of priority and temperature on the outcome of interactions between a brown rot and a white rot fungus, respectively, using a soil jar microcosm approach. Segments of small diameter (3.5-5.5 cm) paper birch with bark intact were used for the decay trials. Some segments were exposed to either *F. fomentarius* or *P. betulinus* (n=20 for each) for 5 weeks and then secondarily inoculated with the other fungus to test priority. Other segments (n=20) were exposed to both fungi simultaneously for the duration of the experiment. Equal proportions of jars were kept in 25°C or 33°C incubation and maintained at constant 80% RH. To incorporate a treatment of the natural community residing in the standing trees cut for this study, the above design was replicated on segments that were not autoclaved prior to addition to jars. This allowed us to observe the development of unknown fungal propagules latently present in the wood in conjunction with the activity of the inoculated species. At harvest (26 weeks), we will follow protocols from previous work to analyze pH, alkali solubility, and carbohydrate and lignin fractions of the wood residues as indicators for the type of decay that occurred under treatment conditions.

Frank, Robert^{*}, Urbina, Hector, and Blackwell, Meredith. Louisiana State University, Baton Rouge, LA 70803. mblackwell@lsu.edu. **Yeast species richness associated with the wood roach *Cryptocercus* sp.**

The gut of insects has been described as a microhabitat for novel species of yeasts. The presence of the xylose-fermenting (X-F) yeast *Scheffersomyces stipitis* and closely related species was confirmed in a study characterizing the gut flora of wood-feeding insects *Odontotaenius disjunctus* (Passalidae) and *Plagionotus arcuatus* and *Leptura rubra* (Cerambycidae) respectively, results that suggest a consistent association between X-F yeasts and wood-feeding insects. The objective of this study was the characterization of the yeast gut flora of the wood roach *Cryptocercus* sp. (Blattodea: Cryptocercidae) in order to confirm the presence of X-F yeasts. We isolated 25 yeast strains from the digestive track of 5 individuals of *Cryptocercus* sp. collected along the Appalachian Trail near New Found Gap on the border between Tennessee and North Carolina. The yeasts were characterized using three molecular markers in the ribosomal RNA repeat unit [small subunit (SSU); internal transcribed spacer (ITS1&2) and the region D1/D2 of the large subunit (LSU)] and DNA-directed RNA polymerase II subunit 1 (RPB1) genes. The species *Candida lignohabitans*, *Candida paludigena*, and *Candida shehatae* as well as two novel species closely related to these species, were identified from the gut of the individual tested. Both *Candida paludigena* and *C. lignohabitans*, a recently described asexual member of the *Sugiyamaella* clade, have been isolated from rotten wood. The isolation of the X-F yeast *C. shehatae* from the roach gut confirmed a relationship between wood-feeding insects and this rare biochemical ability.

Gaya, Ester^{1*}, Holguin, Angela², Ramirez-Mejia, Martin^{1,2}, and Lutzoni, François¹. ¹Duke University, Department of Biology, Box 90338, Durham, North Carolina 27708, USA, ²University of Los Andes, Department of Biology, Carrera 1, 18A-12, Bogotá, Colombia. ester.gaya@duke.edu. **Resolving phylo-**

genetic relationships within the lichen-forming order Teloschistales and the evolutionary history of Teloschistaceae with a seven-locus supermatrix.

The resolution of the phylogenetic relationships within Teloschistales (Ascomycota, Lecanoromycetes), with nearly 2,000 known species and an outstanding phenotypic diversity, has been hindered by the limitation in the resolving power that single-locus and two-locus phylogenetic studies have provided so far. In this context, an extensive taxon sampling within the Teloschistales with more loci (especially nuclear protein-coding genes) was needed to confront the current classification, and to improve our understanding of evolutionary trends within this order. Comprehensive maximum likelihood and Bayesian analyses were performed based on seven loci using a supermatrix approach, and including protein-coding genes *RPB1* and *RPB2* in addition to nuclear and mitochondrial ribosomal RNA-coding genes. We report here that the *incertae sedis* family Brigantiaeaceae and *Lecania sulphureofusca* are members of the suborder Teloschistiales. Within this suborder, one lineage led to the diversification of the epiphytic crustose Brigantiaeaceae and Letrouitiaceae, with a circum-pacific center of diversity and found mostly in the tropics. The other main lineage led to another epiphytic crustose family, mostly tropical and with an Australasian center of diversity - the Megalosporaceae - which is sister to the mainly rock-inhabiting, cosmopolitan, and species rich Teloschistaceae, with a diversity of growth habits ranging from crustose to fruticose. Although the progressive addition of taxa with missing data of our supermatrix approach did not affect dramatically the loss of support and resolution, the monophyly of the Teloschistales was inconsistent, depending on the loci-taxa combination analyzed. Based on these results we propose a new, but provisional, classification for the order Teloschistales.

Gazis, Romina O.^{*} and Chaverri, Priscila. Department of Plant Sciences and Landscape Architecture, University of Maryland, 2112 Plant Sciences Building, College Park, MD 20742. rgazis@umd.edu. **Sampling effect on tropical fungal endophyte diversity estimation: are we under-sampling fungal endophytes?**

Fungal endophytes are considered to be hyperdiverse and ubiquitous among all kinds of habitats and plant hosts. Ecological studies attempting to estimate their diversity constantly face the problem of insufficient sampling. Low sample size can affect not only the accuracy of the diversity estimation but also the ecological questions and hypotheses that may arise from those measurements. Unfortunately, attempts to standardize the sampling design are rare, limiting the comparative utility of published reports. Furthermore, the effects of the several layers of heterogeneity, intrinsic to any endophyte community such as host genetic background and spatial heterogeneity have not yet been explored. Using the sapwood endophytic fungal community inhabiting *Hevea brasiliensis* as a model, we set the following objectives: (1) to investigate the effects of sample size on the estimation of diversity parameters and confidence intervals, (2) to estimate the sampling effort necessary to reach the asymptote of a species accumulation curve, and (3) to estimate the loss of phylogenetic diversity when sampling is low. We used a combination of parametric, non-parametric, and phylogenetic approaches to estimate the diversity at different sample sizes (up to N=50). We found that all the diversity indices were strongly influenced by sample size and by the elimination of singleton species. We calculated that with a sample size of 50 individuals we covered 50% and 40% of the overall estimated diversity for the managed and wild habitat respectively, and that in order for the species accumulation curve to achieve a plateau, sample size needs to be increased more than 10 times. Results from this research are intended to contribute in the standardization of endophyte surveys and propose the inclusion of the estimated diversity coverage when comparing habitats.

Geml, József^{*} and Noordeloos, Machiel E. National Herbarium of the Netherlands, Netherlands Centre for Biodiversity Naturalis, PO Box 9514, 2300RA Leiden, Netherlands. jozsef.geml@gmail.com. **Contribution of metagenome pyrosequencing of soil fungi to nature conservation: a case study from sand dune communities in the Netherlands.**

There are serious concerns among researchers and the public alike related to the future of biodiversity. Although current conservation efforts focus on vascular plants and vertebrates, these groups only make up a small portion of biodiversity. Fungi are still poorly understood and appreciated compared to plants and animals. Nonetheless, significant advances have been made in the taxonomy, distribution and conservation status of macrofungi in the last two decades. Collecting such data has been particularly successful in the Netherlands, where a nationwide network of amateurs, paraprofessionals, and professionals have been mapping mushrooms since 1980, coordinated by the Werkgroep Paddenstoelenkartering Nederland (WPN). An official national Red List of fungi was published in 1996, then revised in 2008. Traditionally, our knowledge of fungal diversity and distribution has been based almost entirely on collection of sporocarps. In recent years, however, DNA-based studies of soil fungal commu-

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nities have provided valuable insights into the biodiversity and ecology of fungi. Building upon the data accumulated by the WPN, we have begun a series of 454 sequencing projects to supplement long-term sporocarp records with DNA-based species identification from soil samples for mapping purposes. The first of our fungal diversity assessments has focused on *Salix repens* sand dune communities along the North Sea coast, because these areas are highly important for nature conservation, water resource management, and recreational purposes. In the more than 600 000 ITS sequences generated from 10 sampling sites, we detected 1222 fungal 97% sequence similarity OTUs. Besides the providing the first kingdom-wide diversity assessment for this coastal ecosystem, we detected numerous red listed species in our samples, often from previously unknown locations. In addition, we found several species that had never been reported from the Netherlands. This project provides examples for the potential contribution of high-throughput soil sequencing studies to fungal mapping and nature conservation.

Geml, József^{1*}, Timling, Ina², Robinson, Clare³, Lennon, Niall⁴, Nusbaum, Chad⁴, Brochmann, Christian⁵, Noordeels, Machiel¹, and Taylor, D Lee². ¹National Herbarium of the Netherlands, Netherlands Centre for Biodiversity Naturalis, Leiden University, PO Box 9514, 2300RA Leiden, Netherlands, ²Institute of Arctic Biology, University of Alaska Fairbanks, PO Box 757000, Fairbanks, AK 99775-7000 USA, ³School of Earth, Atmospheric and Environmental Sciences, The University of Manchester, Williamson Building, Oxford Road, Manchester, M13 9PL, UK, ⁴Genome Sequence and Analysis Program, Broad Institute of MIT and Harvard, Cambridge, MA 02141, USA, ⁵National Centre for Biosystematics, Natural History Museum, University of Oslo, PO Box 1172 Blindern, NO-0318 Oslo, Norway. geml@nhn.leidenuniv.nl. **An arctic community of symbiotic fungi assembled by long-distance dispersers: phylogenetic diversity of ectomycorrhizal basidiomycetes in Svalbard based on soil and sporocarp DNA.**

Despite their key roles in arctic ecosystems, the phylogenetic diversity and phylogeography of arctic ectomycorrhizal (ECM) fungi remain scarcely known. Here, we assess phylogenetic diversity of ECM communities in an isolated, formerly glaciated, high arctic archipelago and provide explanation for their phylogeographic origins. We generated and analyzed ITS rDNA sequences from both curated sporocarp collections (from Svalbard) and soil PCR clone libraries (from Svalbard and the North American Arctic) and estimated the phylogenetic diversity of ECM fungi in Svalbard. Despite Svalbard's geographic isolation and arctic climate, ECM fungi are surprisingly diverse, with at least 72 non-singleton OTUs (soil) and 109 phylogroups (soil + sporocarp). The most species-rich genera were *Thelephora/Tomentella*, *Cortinarius*, and *Inocybe*, followed by *Hebeloma*, *Russula*, *Lactarius*, *Entoloma*, *Sebacina*, *Clavulina*, *Laccaria*, *Lecaninum*, and *Alicicola*. Our results indicate numerous recent colonization events and suggest that long-distance dispersal is widespread in arctic ECM fungi, which markedly differs from the currently prevailing view on the dispersal capabilities of ECM fungi in general. We argue that arctic fungi, particularly the keystone taxa with circumpolar distribution, likely have been selected for mobility during the glacial cycles, similar to arctic plants. This study reports among the first molecular evidence that long-distance dispersal has likely played a major role in the phylogeographic history of some ECM fungi in the Northern Hemisphere, and our results may have implications for studies on the biodiversity, ecology and conservation of arctic fungi in general. Inferred high mobility of arctic ECM fungi suggests that many of them have strong potential to adapt to the changing Arctic by tracking their ecological niche through long-distance dispersal.

Gladieux, Pierre. Ecologie, Systematique, Evolution. Batiment 360. Univ. Paris Sud. 91405 Orsay, France. pierre.gladieux@u-psud.fr. **Short- versus long-term natural selection in *Microbotryum* pathogens.**

Pathogens are attractive systems for the study of adaptive divergence: recently diverged species specialized on different hosts allow investigation of the early stages of specialization and speciation. *Microbotryum violaceum* is a complex of highly specialized sibling species responsible for anther-smut disease on many plant species in the Caryophyllaceae. Here, we aimed at investigating whether the genes showing signs of positive selection between *Microbotryum* species specialized on different hosts were also subject to recent positive selection, as expected if the same genes were involved both in specialization onto a novel host and in coevolution with a current host. Because methods for testing for selection assume that samples were collected in a nonstructured, constant-sized population, we first analyzed population structure, focusing on the species *M. lychnidis-dioicae* infecting *Silene latifolia*. Clustering analyses revealed a clear-cut example of European phylogeography reflecting recolonization from southern refugia after glaciation. The genetic structures of the pathogen and the host were congruent, suggesting dependence of the migration pathway of the anther smut fungus on its host. The fungus, however, appeared to have persisted in more numerous and smaller refugia than its host. For analyses of selection, we focused on two divergent clusters to minimize the effect of population struc-

ture. We used classical tests based on polymorphism and divergence to search for selection in the short-term. The focal genes tested were chosen because they showed a significant signal of positive selection in the long-term in a previous study based on d_n/d_s analyses and putative functions likely involved in host-parasite interactions. Comparison with control (housekeeping) genes revealed that all focal genes were subject to strong purifying selection and we found no footprints that would indicate recent positive selection. This suggests that genes that went through episodes of recurrent adaptive diversification during host shifts may subsequently be under strong functional constraint.

Glaeser, Jessie A.* and Norton, Kyah L. USDA-Forest Service, Northern Research Station, One Gifford Pinchot Dr., Madison, WI 53726. jglaeser@fs.fed.us. **In vitro growth of *Chlorociboria aeruginascens*, the green-stain fungus.**

The "green stain fungi," *Chlorociboria aeruginascens* and *Chlorociboria aeruginosa* (Helotiales), produce spectacular blue-green pigments *in vivo* and *in vitro*. Such pigmentation greatly increases the value of otherwise low-value hardwoods. Since medieval times, craftsmen have produced intricate inlays, termed "intarsia," from colonized, pigmented wood; affected wood continues to be in high demand by woodworkers. In culture, the fungi are notoriously slow-growing and often lose vigor and ability to produce pigment. As part of a feasibility investigation for the controlled production of green-stained timber, certain cultural requirements were defined for *C. aeruginascens*. The fungus appears to be extremely sensitive to pH, with optimal growth at pH 3.5 - 4.0. Minimal or no growth occurred at pH 5.0 and above. Most rapid growth occurred on pH 4.0 citrate-buffered 2% malt extract agar (MEA), cornmeal agar, prune agar, and oatmeal agar. Poor growth occurred on similarly buffered commercial and freshly-prepared potato dextrose agar, and gallic acid, tannic acid, sabouraud dextrose, nutritive caseinate, and czapek dox agars. Supplementing nonbuffered MEA with surface applications of small splinters of sterilized aspen, or hemlock, aspen, and sweetgum sawdust, stimulated pigment production. The addition of peptone to MEA was detrimental to both growth and pigment development. Temperatures of 23 - 25 C appeared optimal for growth and pigment production. These results will be used to develop inoculation techniques for the production of green-stained timber.

Glass, Daniel* and Taylor, D. Lee. Institute of Arctic Biology, University of Alaska Fairbanks, PO Box 757000, Fairbanks, AK 99775-7000. djglass@alaska.edu. **Determination of novel environmental DNA gene authenticity by modeling ribosomal RNA secondary structure.**

Both the number of formally described species and the number of uncollected environmental sequences deposited in the International Nucleotide Sequence Database have increased substantially over the last two decades. Although the majority of these sequences represent functional gene copies there is evidence of non-functional DNA in these databases as well. These include artifacts, such as chimeras, and non-functional gene-copies, such as numts and pseudogenes. To our knowledge, no environmental fungal ribosomal sequences have had their secondary structure analyzed. This is surprising considering secondary structure analyses are one of the best ways to determine if a sequence represents a functional gene copy. Phylogenetic analyses suggest that five novel sequences found in a boreal forest soil clone library belong to the fungal kingdom. In order to determine if one of these potentially novel fungal sequences (NS1) coded for a functional ribosomal RNA gene-copy, ribosomal secondary structure was modeled for four gene regions (ITS1, 5.8S, ITS2, partial LSU). These foldings were analyzed for the presence compensatory base changes, conserved domains and conserved nucleotide motifs. Minimal free energy (MFE) foldings and GC contents of sequences representing the major fungal clades, as well as NS1, were compared. Linear regression was used to determine if a relationship between ITS lengths and MFE was present. Together these findings support that NS1 does represent a functional gene-copy. These methods can be used on any potentially novel rRNA coding sequence, not just fungal sequences. As next-generation sequencing methods that yield shorter sequences become more widely implemented, methods such as those described here that validate sequence authenticity, should also be more widely implemented. Our findings suggest prioritizing the adjacent 5.8S and ITS2 gene-regions. This region is not only suited to distinguishing between closely related species, but it is also more informative regarding the authenticity of a sequence.

González, María C.* and Hanlin, Richard T.² ¹Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, DF 04510, México, ²Museum of Natural History Annex, University of Georgia, Bogart, GA 30622, USA. mcgv@ibiologia.unam.mx. **Potential use of marine arenicolous ascomycetes as bioindicators of ecosystem disturbance on sandy Cancun beaches: *Corollospora maritima* as a candidate species.**

We developed a quantitative scale for estimating disturbance level on 10

Continued on following page

public-access tourist beaches. For this purpose, we estimated frequency of occurrence values for sand-inhabiting obligate ascomycetes annually through 10 years (2000-2009). In particular, we determined the presence of *Corollospora maritima* on each beach. A positive correlation between sandy beach disturbance level and fungal species frequencies of occurrence was demonstrated. Progressively higher frequencies of occurrence for *C. maritima* were obtained from increasingly less disturbed beaches. Hence, intertidal autochthonous species have potential use as bioindicators, and we selected *C. maritima* to represent this group of marine obligate fungi as a bioindicator of sand beach degradation.

Grand, Larry F.^{*}, Vernia, Caroline S., and Cubeta, Marc A. North Carolina State University, Department of Plant Pathology, Campus Box 7616, Raleigh, NC 27695-7616. larry_grand@ncsu.edu. **Educational Outreach Workshop: Using Fungi in High School Classrooms.**

As part of a National Science Foundation-funded project investigating the biodiversity of fungi in North Carolina, an outreach program for teachers was offered focusing on introducing fungi into high school biology and environmental science curricula. In the standard course of study for high school biology, fungi are often only mentioned briefly in a review of the domains of life. Nonetheless, fungi play important roles in nutrient cycling in ecosystems, are being intensively studied for potential uses in biotechnology, bioremediation and medicine, and are useful model organisms for inquiry-based learning. Workshops were offered in July of 2010 and 2011 with five and eight North Carolina high school teacher attending the sessions in 2010 and 2011, respectively. The three day workshop (1) introduced teachers to fungal groups and structures and presented laboratory activities aligned to the North Carolina Standard Course of Study; (2) proposed a method for students to become collaborators in the North Carolina biodiversity of wood decay fungi study; and, (3) in collaboration with the North Carolina Museum of Natural Sciences, exposed teachers to the benefits of informal education opportunities. Teacher responses were positive and post-workshop communications have indicated that all have included components of the workshop in their classrooms.

Grelet, Gwen-Aëlle^{1,2*}, Dickie, Ian A.², Smart, Catherine³, Alexander, Ian J.¹, and Nilsson, Henrik R.⁴ ¹University of Aberdeen, Institute of Biological and Environmental Sciences, Cruickshank Building, AB24 3UU, Aberdeen, UK, ²Landcare Research – Manaaki Whenua, Gerald Street, PO Box 40, 7640, Lincoln, NZ, ³The James Hutton Institute, Craigiebuckler, AB15 8QH, Aberdeen, UK, ⁴University of Gothenburg, Department of Plant and Environmental Sciences, Box 461, 405 30 Göteborg, Sweden. GreletG@LandcareResearch.co.nz. **Ericoid mycorrhizal fungi: surfing INSD all the way to New Zealand.**

Ericoid mycorrhizas are typical of green Ericaceae plant species. They harbor highly diverse fungal communities but we know virtually nothing of the mechanism maintaining this diversity. Ericoid fungal community structure can change significantly at the metre scale, but such changes are not always linked to habitat characteristics. Furthermore, despite multiple attempts, no one has yet found any evidence of host specificity. Here we investigate whether broad biogeographical patterns and / or host preference could be teased out of the International Nucleotide Sequence Database, in an attempt to understand the factors driving the maintenance of high fungal diversity in ericoid mycorrhizas. We compiled a global meta-database comprising 1749 fungal ITS sequences, including sequence taxonomical affinity and quality, and all associated traceable published information. Several patterns emerged from this meta-data analysis, including the preponderance of one group of insufficiently classified fungal taxa, with highest identified blast matches to *Leptodontidium* and *Hyphodiscus* spp. We also found that the “true” ericoid mycorrhizal clades in the *Rhizoscypha ericae* aggregate have not been recovered from the Ericaceae subfamily Stypelioideae, restricted to Australasia and SE Asia. Because plant phylogeny and geographical effects are mostly confounded in our database, we could not test whether this pattern was due to true host specificity or biogeographical fungal community divergence. So we sampled in New Zealand, where ericoid mycorrhizal fungal sequences have never been collected, and characterised the fungal community hosted in the roots of exotic Northern hemisphere Ericaceae invading a stand of endemic NZ Ericaceae species (*Dracophyllum*) since the 1920s. Our results tell an unexpected tale of host specificity at the subfamily level, and of undesirable plant-fungus co-invasion in native stands of high conservation value.

Grubisha, Lisa C.^{1*} and Cotty, Peter J.^{1,2} ¹School of Plant Sciences, University of Arizona, Tucson, AZ 85721, ²United States Department of Agriculture, Agriculture Research Service, Tucson, AZ 85721. lisa.grubisha@gmail.com. **Genetic diversity and population structure of *Aspergillus flavus* in the southern USA.**

Aspergillus flavus is a fungal pathogen of animals and wild and domesticated plants with a global distribution. During infection by *A. flavus*, crops are

frequently contaminated with highly carcinogenic aflatoxins. *A. flavus* populations are composed of numerous vegetative compatibility groups (VCGs), however, not all VCGs produce aflatoxin. In a series of studies, several types of genetic markers (24 microsatellite loci, mating-type loci, SNPs) were used to assess genetic diversity, population structure and reproductive mode in *A. flavus* populations in the southern USA, including a study of YV36, the VCG to which the biocontrol fungus AF36 belongs. In all studies VCGs formed lineages of genetically similar individuals, with few exceptions. The results of analyses of 21 microsatellite loci from across the genome support the hypothesis that VCG YV36 is a clonal lineage with one dominant haplotype distributed both spatially and temporally in fields not treated with AF36. Furthermore, all isolates of YV36, including isolates from fields previously treated with AF36, had *MATI-2* and the SNP in the *aflC/pksA* gene resulting in a defective polyketide synthase and responsible for the lack of aflatoxin accumulation in YV36. Results from these studies did not support the hypothesis of random mating among VCGs of *MATI-1* and *MATI-2* in populations in the southern USA. These results have important implications for development of biological control programs using indigenous, nonaflatoxin-producing VCGs.

Grubisha, Lisa C.^{1,2*}, Taylor, D Lee¹, and Olson, Matthew M.¹ ¹Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK 99775, ²School of Plant Sciences, University of Arizona, Tucson, AZ 85721. grubishl@cals.arizona.edu. **Host, geography and climate change effects on population structure of the Holarctic *Populus*-associated ectomycorrhizal fungus, *Tricholoma populinum*.**

Tricholoma populinum is an ectomycorrhizal fungus that forms symbiotic associations only with the genus *Populus* (poplars, cottonwoods, aspens). *Populus* species have either a Palearctic or Nearctic distribution, while *T. populinum* has a Holarctic distribution. In this study we tested the hypothesis that *T. populinum* has a panmictic population structure across Europe and North America. Additionally, we tested the hypothesis that the present North America distribution of *T. populinum* with *P. balsamifera* and *P. trichocarpa* resulted from range expansion from Beringian refugia following the last glacial maximum (~18,000 years before present). Bayesian analyses of sequences from six nuclear loci from samples from Scandinavia associated with *P. tremula*, and North America (Alaska, Canada, Pacific Northwest) with *P. balsamifera* and *P. trichocarpa*, revealed genetically divergent lineages between continents. We are investigating whether this is the result of allopatric divergence followed by genetic drift or co-speciation with the hosts. Within North America, we did not find evidence to support range expansion from a Beringian refugium, which is consistent with recent phylogeographic studies of *P. balsamifera*. These studies add to the growing number of studies of epigeous ectomycorrhizal fungi demonstrating intercontinental divergence despite Holarctic distributions.

Grupe, Arthur C., II^{*}, Uehling, Jessie K.¹, Smith, Matthew E.², and Henkel, Terry W.¹ ¹Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, ²Department of Biology, Duke University, Durham, NC 27708. twh5@humboldt.edu. **A first record for the genus *Sarcodon* in the lowland South American tropics.**

Sarcodon pakaraimensis sp. nov., ined. is the first record for *Sarcodon* (Bankeraceae, Thelephorales, Basidiomycota) from the lowland Neotropical rainforests of South American. In the Pakaraima Mountains of western Guyana, *S. pakaraimensis* was discovered in forests dominated by the ectomycorrhizal (ECM) tree *Pakaraimaea dipterocarpaceae*, which is only one of two dipterocarp species known from the New World. The finding is significant given that the majority of the ~75 described species of *Sarcodon* are north temperate in distribution and frequently in association with coniferous ECM hosts. The new species is morphologically consistent with accepted generic diagnostic characters for *Sarcodon*, including pileate-stipitate stature with determinate development, dentate hymenophore, fleshy context, dark brown, tuberculate basidiospores, and regularly clamped hyphae. Analysis of DNA sequences corroborates the generic placement of *Sarcodon pakaraimensis*. Macromorphological, micromorphological and habitat data are provided for the new species, along with comparisons with phenotypically allied *Sarcodon* species. Observations on other genera of Thelephorales occurring in Guyana will be given.

Gryganskyi, Andrii^{*}, Humber, Richard A.², Smith, Mathew E.¹, Bonito, Gregory¹, Rodríguez-Carres, Mariana¹, Anishchenko, I³, Savytskyi, Oleksandr³, Colquhoun, A¹, and Vilgalys, Rytas¹. ¹Biology Dept., Mycology Lab, Duke University, Box 90338, Durham, NC 27708, ²Insect Pathology Research Unit, US Plant, Soil and Nutrition Lab, USDA-ARS, Tower Road, Ithaca, NY 14853-2901, ³Institute of Botany, National Academy of Sciences of Ukraine, 54 Volodymyrska St., Kyiv-30, 01601, Ukraine. apg10@duke.edu. **Molecular phylogeny for the subphylum Entomophthoromycotina incertae sedis.**

The recently elevated subdivision Entomophthoromycotina includes zy-

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gomycetous saprotrophs and parasites of diverse arthropod hosts. Ubiquitous species in this group play an important role as the pathogens of invertebrates and organic decomposers. Many of them are of special interest as biological control agents for economically important insect pests. Over 180 described species are known, however, the actual number of species belonging to this group is likely to be much greater. In this study we present ongoing research to resolve phylogenetic relationships within the order Entomophthorales. Bayesian and ML analyses of three genes (nuclear 18S and 28S rDNA, mitochondrial SSU and protein coding *RPB2*) and nonmolecular data showed consistent separation of 30 entomophthoralean taxa from other zygomycetes and flagellate fungi with good statistical support. Using the molecular tree as a backbone, we built the most comprehensive rDNA phylogeny of known entomophthoroid taxa. Entomophthoromycotina comprises five main groups: saprobic *Basidiobolus* and *Conidiobolus* and parasitic *Baikoa*, *Entomophthora* and *Zoophthora*. A newly described enigmatic snake parasite, *Schizangiella serpentis*, is a sister group to *Basidiobolus* clade, which is basal to the rest of the Entomophthoromycotina. The genus *Conidiobolus* appears polyphyletic and forms three distinctive groups with good statistical support: *C. coronatus*, *C. thombooides* and *C. pumilus*. Our data suggests the genus *Conidiobolus* is in need of revision. The *Entomophthora* clade is comprised of the genera *Entomophaga*, *Massospora* and *Eryniopsis*. The zoophthoroid clade consists of the genus *Zoophthora* s.s. and three other genera with poorly defined generic boundaries. Ancestral stage reconstruction indicates the ancestor of the entomophthoroid fungi was a *Conidiobolus*-like fungus.

Hallen-Adams, Heather E.*, Martinez, Ines, Kim, Jaehyoung, and Legge, Ryan. Department of Food Science and Technology, University of Nebraska, Lincoln, NE. hhallen-adams2@unl.edu. **Fungal profiling and ecology of the healthy human gut.**

The human digestive tract, providing warmth, shelter and nutrients, is home to an extensive microbial community. To date, most research has focused on characterizing the prokaryotic members of this community. Fungi have long been known to inhabit the mammalian digestive tract; however, the nature and composition of fungal GI tract communities has been little studied (with some exceptions, e.g. the rumen chytrids of cattle, and fungi associated with certain disease states). We used fungal-specific ITS primers to perform 454 amplicon sequencing on DNA isolated from feces of 40+ healthy humans. A variety of fungi were detected; ascomycete yeasts predating the whole genome duplication predominated. While some species were detected in the majority of humans sampled, relative abundances varied considerably, with individuals possessing unique fungal profiles and few species suitable candidates for "universal" human GI tract inhabitants. The possibility of competitive exclusion between *Candida* species, and the stability of fungal communities over time, will be discussed.

Hampton-Miller, Celia J.¹, Ickert-Bond, Steffi¹, and Spribille, Toby^{2*}. ¹University of Alaska Museum Herbarium, Fairbanks, AK 99775, USA, ²Institute of Plant Sciences, University of Graz, Holteigasse 6, A-8010 Graz, Austria. cjmiller3@alaska.edu. **Disentangling fistulose *Ramalina* species in northwest North America (Ramalinaceae, lichenized Ascomycota).**

The lichen genus *Ramalina* is notoriously difficult, on account of its large number of species and wide range of morphological variation. The *R. dilacerata* group, including several fistulose species around the Pacific rim, has long remained unresolved. One species in the Pacific Northwest recognized by its large thallus, less-branched form, convex apothecia and pale color was long given the name *R. inflata* or *R. geniculata*. Revisions of those species restricted their ranges to Australia and New Zealand, respectively, and the Pacific Northwest material has since been included in *R. dilacerata*. In a sampling of material from Alaska to Oregon and inland to Montana, we found strong evidence based on nuclear ribosomal DNA data to support its distinction from *R. dilacerata*. Our new species (*R. neopacifica* ined.) is further distinct in its ecology, and its current day distribution barely overlaps the range of the mainly boreal *R. dilacerata*, which is found in western North America from central British Columbia northwards.

Hart, Andrew* and Volk, Thomas J. Dept. Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601. hart.andr@uwlax.edu. **Poisons in my food? An educational poster about mycotoxins.**

Mycotoxins are fungal secondary metabolites that are relevant to our well being, medicine, and economy. Secondary metabolism (SM) is separated from primary metabolism in that products of SM are not required for normal growth and function. Despite this definition, SM can benefit the fungus by inhibiting competition or protecting the fungus or its host by making it taste bad to grazers. These toxins cause a wide range of ailments including gastrointestinal complications, tremorgenic and wasting diseases of livestock, and even cancers. This poster presents a summary of the most common and well known my-

cotoxins that are found mainly in *Fusarium*, *Penicillium* and *Aspergillus* species. *Fusarium* species are agriculturally important due to their affinity to grow endophytically on grain, making their way into animal feed and human foodstuffs. *Fusarium* mycotoxins include trichothecenes, deoxynivalenol, zearalenone, satratoxins, and fumonisins. *Penicillium* species are ubiquitous and thus are some of the most common food contaminants. *Penicillium* mycotoxins include mycophenolic acid, patulin, roquefortine C, and various neurotoxins. *Aspergillus* species are also a ubiquitous group most commonly contaminating grains. *Aspergillus* mycotoxins include many forms of aflatoxin and their precursors. Due to the recent advances in SM regulation research, it is timely to take a step back and look at advances that have been made, including understanding how to identify and activate silent SM gene clusters, a huge step in the hunt for novel SM compounds. Research in epigenetics has added another layer to SM regulation. SM spatial and temporal regulation, more specifically compartmentalization by specialized vesicles. Since *Aspergillus* genetics has been researched more than others, mechanistic examples are included for this genus. This educational poster was developed for use in various classes including, Mycology, Food Microbiology, Botany, Ecology, Nutrition and General Biology.

Hassett, Maribeth O.^{1*}, Sugawara, Zachary T.¹, Fischer, Mark WF², and Money, Nicholas P.¹ ¹Department of Botany, Miami University, Oxford, OH, 45056, ²Department of Chemistry and Physical Sciences, College of Mount St. Joseph, Cincinnati, OH 45233. hassetmo@muohio.edu. **Biomechanics of peridiole ejection and function of the funicular cord in bird's nest fungi.**

The bird's nest fungi (Agaricales, Nidulariaceae) package hundreds of millions of spores into sporangia (referred to as peridioles) that are splashed from their basidiomata by the impact of raindrops. This study examines the mechanism of peridiole ejection and funicular cord function in *Cyathus* using high-speed video. The funicular cord is a highly-extensible bundle of hyphae whose tensile strength is maximized by the modification of clamp connections. Peridioles are splashed from their flute-shaped basidiomata at speeds of 1 to 5 meters per second (11 mph). The funicular cord remains in a condensed form during flight with an adhesive pad exposed on the projectile surface. The cord unravels when the pad sticks to surrounding vegetation and acts as a brake that quickly reduces the velocity of the projectile. If the cord attaches to a grass culm, or to the petiole of a leaf, it is wrapped around the vegetation by the momentum of the decelerating peridiole. This elaborate mechanism tethers the peridiole in a perfect location for browsing by an herbivore and is viewed as a beautiful adaptation for a coprophilous fungus.

Healy, Rosaria A.^{1*}, Smith, Matthew E.², Bonito, Gregory², Vilgalys, Rytas², and McLaughlin, David J.¹ ¹Department of Plant Biology, University of Minnesota, St. Paul, MN 55108, ²Department of Biology, Duke University Durham, NC 27708. healy089@umn.edu. **Phylogenetic diversity and molecular ecology of asexual spore mats in ectomycorrhizal Pezizales.**

The ectomycorrhizal lifestyle has evolved independently in at least 16 lineages of the Pezizales (*Ascomycota*), an order rich in truffle species. While ascomycetes in general are notable for asexual propagation, this reproductive strategy is rarely observed in ectomycorrhizal fungi of any phylum. While studying the truffle genera *Pachyphloeus* and *Tuber*, we searched for their asexual spore mats (anamorphs) on the soil surface of woodlands in the eastern USA, Mexico, and China. We sequenced their ITS and 28S rDNA and then compared the sequences with our unpublished truffle sequence database and with GenBank. We found a high diversity of *Pachyphloeus* anamorphs in each location and more anamorphic *Tuber* species than were previously known. Two novel findings are that the truffle genera *Hydnobolites* and *Hydnotrya* produce anamorphs and that there is an unnamed clade of Pezizaceae that commonly produces anamorphs with no known sexual state. These five anamorphic clades are independent monophyletic groups and their anamorphs differ morphologically. Anamorphic spore mats were most common on bare soil after rainfall events and were found from March through November in the USA. Truffles are assumed to reproduce sexually and be dispersed primarily through mycophagy. However, the frequency, abundance, geographic range and phylogenetic diversity of anamorphs among these ectomycorrhizal *Pezizales* suggests that there may be a cryptic asexual cycle for these organisms. These findings have important implications in regards to mating, reproduction, and dispersal strategies in the ectomycorrhizal Pezizales.

Henkel, Terry W.^{1*}, Aime, M Catherine², Smith, Matthew E.³, Miller, Steven L.⁴, and Vilgalys, Rytas³. ¹Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, ²Department of Plant Pathology & Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, ³Department of Biology, Duke University, Durham, NC 27708, ⁴Department of Botany, University of Wyoming, Laramie, WY 82071. twh5@humboldt.edu.

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Ectomycorrhizal fungal diversity of *Dicymbe*-dominated forests in the Guiana Shield.

It was once widely believed that ectomycorrhizal (ECM) fungi were poorly represented in Neotropical forests. However, in the central Guiana Shield substantial areas are dominated by ECM leguminous trees. In Guyana ECM fungi were systematically sampled from 2000-2008 in three 1-ha plots in monodominant forests of the ECM canopy tree *Dicymbe corymbosa* (Fabaceae subfam. Caesalpinioideae). Over nine years 630 100 m² subplots were surveyed for fruiting body occurrence, and 127 morphospecies of putatively ECM fungi were recovered from among 13 families and 25 genera of primarily Agaricomycotina (Basidiomycota), but also Ascomycota (e.g. Elaphomycetaceae). Among these families, Russulaceae contained the most species (22 *Russula* spp.; 8 *Lactarius* spp.), followed by Boletaceae (6 genera, 24 spp.), Amanitaceae (17 *Amanita* spp.) and Clavulinaceae (15 *Clavulina* spp.). Approximately 70% of these species are new to science, and many of these have been formally described. While most of the species appear endemic to the Guiana Shield, some exhibit affinities with taxa distributed more widely in the Neotropics, Southeast Asia, or central Africa. This is the first long-term macrofungal dataset from an ECM-dominated Neotropical forest, and the ECM fungal species diversity is comparable to that recorded for temperate ECM forests. Species accumulation curves indicate that ECM fungal diversity was not fully recovered over the nine-year sampling period. This is reinforced by efforts to enhance taxon recovery by using molecular methods; internal transcribed spacer region rDNA (ITS) data from ECM rootlets of *D. corymbosa* suggest that ≥ 50% of ECM fungal diversity remains undiscovered as fruiting bodies in these plots, with a conservative estimate of 200+ species present. *Dicymbe* forests in Guyana are a hotspot for ECM fungal diversity in the Neotropics, and a putative center of diversity for a number of genera (e.g. *Clavulina*).

Herr, Joshua R.^{1,2*}, Buee, Marc², Coince, Aurore², Wagner, Tyler K.¹, Martin, Francis², and Carlson, John E.^{1,3} ¹Schatz Center for Tree Molecular Genetics, School of Forest Resources, Pennsylvania State University, University Park, PA, USA, ²INRA, UMR1136, INRA-Nancy Université, Interactions Arbres/Microorganismes, 54280 Champenoux, France, ³Department of Bioenergy Science & Technology, Chonnam National University, Gwangju, 500-757, South Korea. jherr@psu.edu. **Diversity of temperate forest soil fungi measured by pyrosequencing techniques.**

It has long been understood that fungi contribute to many key ecosystem processes. This is particularly important in forest soils, where saprotrophic fungi are the main drivers of plant organic matter decomposition and ectomycorrhizal fungi facilitate nutrient uptake for their host plants, thereby affecting plant growth and fitness. Additionally, the presence of soil fungi shape seedling establishment and evidence suggests that ectomycorrhizal fungi may contribute to the distribution of carbohydrates from one tree to another, directly regulating the survival of nurse seedlings. Despite their important ecological roles, there is a paucity of information regarding taxonomic diversity and abundance associated with plant host. Largely this is due to the fact that many fungi are unculturable, lack known sexual structures, and are known only by nucleotide identification. In order to understand the diversity of fungi associated with differing forest types, we have utilized next-generation sequencing techniques (454/Roche and Illumina/Solexa for re-sequencing efforts) to probe soil fungal diversity. Monoculture planted and mixed natural forest types, all at various ages, were sampled from locations in Eastern North America, Central-France, and South Korea. Next-generation sequencing showed extreme diversity in fungal taxa. Approximately one quarter of taxonomic sequence reads were able to be identified with existing fungal databases. This finding agrees with recent studies employing new sequencing techniques to probe fungal diversity. Our sequencing shows an average of more than 2000 unique fungal taxa in as little as four grams of forest soils. This presentation will present diversity data across the forest types surveyed and across seasonal sampling for some forest types.

Herrera, Cesar S.^{1*}, Samuels, Gary², Rossman, Amy Y.², and Chaverri, Priscila¹. ¹University of Maryland, Department of Plant Sciences and Landscape Architecture, 2102 Plant Sciences Building, College Park, MD 20742, ²United States Department of Agriculture, Systematic Mycology and Microbiology Lab, Rm. 304, B-011A, 10300 Baltimore Ave., Beltsville, MD 20705. csherrer@umd.edu. **Phylogenetic position and epitypification of the fungicolous species *Cosmospora vilior* sensu Starbäck.**

Cosmospora vilior (Nectriaceae, Hypocreales, Ascomycota) is a nectroid fungus, whose name has been applied incorrectly to collections that occurred on xylariaceous species. Based on the analysis of the type specimen from Brazil, *C. vilior* should be restricted to collections found on valsaceous fungi. The objectives of this research were (1) to designate an epitype for *C. vilior* based on a recent collection made from Brazil, (2) to determine the phylogenetic position of *C. vilior sensu stricto* within the genus and the Nectriaceae, and (3) to determine the phylogenetic relationships of *Cosmospora* species occurring on *Valsa*

species including the Brazilian collection as well as collections made from temperate forests. A multilocus phylogeny was constructed based on six loci (ITS, LSU, *rpb1*, *act*, *tub*, and *tef1*). Results from the phylogenetic analyses indicated a clade of various lineages that parasitizes valsaceous fungi and have an *Acremonium*-like anamorph. This clade is not closely related to *Cosmospora sensu stricto* (*C. coccinea*) or other recently segregated genera and thus may require new generic rank consideration.

Hesse, Cedar N.* and Spatafora, Joseph W. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR. hesssec@science.oregon-state.edu. **Fungal, Bacterial, and Archaeal soil communities associated with ectomycorrhizal mat-forming fungi in old-growth forests of the Pacific Northwest.**

Hyphal mats formed by some ectomycorrhizal fungi cover a substantial proportion of the forest floor in old-growth sites of the HJ Andrews Experimental Forest LTER, Oregon. The presence of ECM mats has been shown to alter both physical and chemical properties of the soil in which they grow, relative to adjacent non-mat soil. Additionally, studies have shown increased soil respiration from ECM mat soils suggesting a localized increase in microbial activity. We hypothesized that the abiotic differences between ECM mat soils and non-mat soil may provide unique niche-environments for soil microbes creating differences in the biotic microbial communities. We utilized two next-generation sequencing technologies (Illumina Hi-Seq 2000 and Roche 454-FLX Titanium) to comprehensively survey the fungal, bacterial, and archaeal communities present in the hyphal mats formed by two common ectomycorrhizal genera (*Piroloderma* and *Ramaria*) as well as the adjacent non-mat soils. To the authors' knowledge, this study represents one of the few surveys of microbial communities to capture high-resolution data for both fungi and prokaryotes in the same sample. Differences in microbial communities were visualized using community ordination techniques and phylogenetic placement. Presented here are initial comparisons of the fungal and prokaryotic communities associated with ECM mats and the utilization of next-generation sequence data to elucidate ecological questions.

Hewitt, Rebecca E.^{1*}, Chapin, F S., III¹, Hollingsworth, Teresa N.², and Taylor, D Lee¹. ¹Institute of Arctic Biology, University of Alaska Fairbanks, AK, ²Boreal Ecology Cooperative Research Unit PNW Research Station, Fairbanks, AK. rehwitt@alaska.edu. **Resprouting tundra shrubs may act as refugia for ectomycorrhizal fungi during wildfires, facilitating boreal tree seedling establishment at treeline.**

Soil microbes are key drivers of ecosystem processes, yet their roles in regulating landscape-scale vegetation change is poorly known. In the boreal forest climate-induced changes in fire regimes may be more critical drivers of landscape processes than the direct effects of warming. Studies of treeline position have noted that ectomycorrhizal fungi (EMF) may be an important factor delineating the boundary between forest and tundra. Fire could promote tree seedling colonization in burned tundra beyond treeline by improving seedbeds. However EMF, which are critical to seedling establishment are sensitive to wildfire. We investigated the role of resprouting ectomycorrhizal tundra shrubs in facilitating boreal tree seedling establishment after fire through the provision of EMF. We sampled pairs of spruce, birch, and aspen tree seedlings and adjacent birch or willow shrubs at alpine treeline sites (n=48 pairs) in Interior Alaska. Root tips from each seedling were sampled from each seedling, randomized, and pooled into one sample per seedling. We extracted DNA from the pooled sample and analyzed fungal community structure using ITS-ARISA. We also created clone libraries for pooled species x site combinations. We amplified clones and performed RFLP digestions using Hae III. We identified unique RFLP patterns and selectively sequenced these amplicons. Preliminary results indicate that most species of tree seedlings can have overlapping fungal taxa with adjacent resprouting shrubs. Preliminary analysis of the identity of the EMF suggests that later successional fungi may be maintained on the roots of the tundra shrubs after fire. These fungi may then be available to colonize establishing tree seedlings. Synergistic interactions between resprouting tundra shrubs and newly established tree seedlings after fire could either maintain boreal tree community dynamics at the limit of tree establishment or provide a mechanism for treeline expansion under future scenarios of warming and fire.

Hobbie, Erik A. Complex Systems Research Center, University of New Hampshire, Durham, NH 03824. erik.hobbie@unh.edu. **Functional classification of ectomycorrhizal fungi provides new insights into transfers of carbon and nitrogen among soils, fungi, and plants.**

Over the last 20 years, genetic techniques on ectomycorrhizae and extraradical hyphae have revolutionized our views of the diversity of the ectomycorrhizal community. However, understanding of fungal functioning has not advanced as quickly, as extracting functional attributes from genetic information

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is challenging. One promising approach to assess functional differences among ectomycorrhizal taxa is to correlate a morphological classification system of how ectomycorrhizal fungi explore the soil (termed exploration type) with various functional traits (carbon demand, enzymatic capabilities, insoluble versus soluble nutrient use, and sensitivity to nitrogen deposition). Exploration type appears to be generally consistent within a genus, and can be broadly separated into two categories, based on whether ectomycorrhizae are hydrophobic or hydrophilic. Ectomycorrhizal hydrophobicity in turn correlates with the use of insoluble and patchily distributed resources, as nutrient uptake directly by hydrophobic mycorrhizae is not possible, but instead occurs in associated (and hydrophilic) extraradical hyphae. Similarly, long-distance transport requires hydrophobic rhizomorphs to prevent resource loss during transport. Although carbon demand appears greater with hydrophobic than with hydrophilic exploration types, few potential markers of resource use have been surveyed in adequate detail for general patterns to emerge. One marker, nitrogen isotope ratios in sporocarps, appears to correlate with proteolytic capabilities, ammonia uptake (such as by 'ammonia' fungi), soil exploration depth, rhizomorph development, and the functioning of mycotrophic ectomycorrhizae (pick-a-back exploration type, e.g., *Gomphidius*). ¹⁴C from 1950s and 1960s thermonuclear testing can be used to probe the age of fungally-acquired organic nitrogen, with hydrophobic ectomycorrhizae acquiring older nitrogen than hydrophilic ectomycorrhizae. Comparisons between known functionalities and potential genetic markers of those functionalities are needed, so that we can better judge function from genomic information (e.g., metabolomics). Surveys are needed across taxa of differing enzymatic capabilities, abilities to access specific nutrients, nutrient concentrations, weathering capabilities, and levels of carbon demand.

Hoge, Brianna L.*, Wang, Xiao, Du, Wenbin, Loprete, Darlene M., Jackson-Hayes, Loretta, and Hill, Terry W. Departments of Biology and Chemistry, Rhodes College, Memphis, TN, 38112. hill@rhodes.edu. **Myosin-II is necessary for septum formation in *Aspergillus nidulans*.**

Cytokinesis in filamentous fungi involves the progressive inward growth of the cell wall and plasma membrane, resulting in a series of functionally connected multinucleate compartments, delimited by crosswalls termed septa. The process of septation, despite intensive study, is still incompletely understood. What is clear, however, is that the mechanism is complex, involving a wide variety of proteins acting in concert. By screening chemically mutagenized strains of *Aspergillus nidulans*, we have identified several isolates with impaired septum formation, and complementation studies using previously-identified *Aspergillus nidulans* "sep" mutations show that three of these strains contain mutations in novel loci. Here we report that the mutation in one of these strains (RCH-2) occurs in the gene that encodes the fungal homologue of mammalian myosin II (*MyoB*, AN4706). The RCH-2 mutation maps to the same region of Chromosome III where *MyoB* is located, and a cross between a strain bearing the RCH-2 mutation and one bearing a GFP-tagged allele of *MyoB* (provided by Naimeh Taheri-Taresh and Berl Oakley) resulted in zero percent recombination. Sequencing of the *MyoB* allele in the RCH-2 mutant strain reveals a point mutation that is predicted to result in a glycine-to-aspartate amino acid substitution at residue 843 in the myosin-II converter domain. This residue is conserved in all fungal, plant, and animal myosin-II sequences that we have examined. Down-regulation of wild-type *MyoB* expression under control of the *A. nidulans* *AlcA* promoter replicates the septation-minus phenotype of the RCH-2 mutation. A GFP-tagged version of *MyoB* localizes to constricting septal rings in a manner consistent with the protein's involvement in the process of septation.

Hoppe, Björn^{1*}, Kahl, Tiemo², Gminder, Andreas³, Schmidt, Martin³, Karasch, Peter³, Buscot, François^{1,4}, and Krüger, Dirk¹. ¹UFZ - Helmholtz Centre for Environmental Research, Department of Soil Ecology, Theodor-Lieser-Str. 4, D-06120 Halle (Saale), Germany, ²University of Freiburg, Institute of Silviculture, Tennenbacherstr. 4, D-79085 Freiburg i. Brsg., Germany, ³o UFZ - Helmholtz Centre for Environmental Research, Department Of Soil Ecology, Theodor-Lieser-Str. 4, D-06120 Halle (Saale), Germany, ⁴University of Leipzig, Institute of Biology I, Johannisallee 21-23, D-04103, Leipzig, Germany. bjoern.hoppe@ufz.de. **Dead wood fungal and bacterial diversity along different forest management types in coniferous and European beech stands in Germany.**

Coarse woody debris (CWD) is a key habitat in forest ecosystems. Mainly Agaricomycotina and some Pezizomycotina can most completely mineralize its lignocellulose complex. The increased CWD amount of extensively used forests with variable substrate quality and nutrient availability tends to sustain more diverse fungal communities. Project FunWood of the DFG (German Science Foundation) Biodiversity Exploratories investigates fungal diversity on CWD along a gradient of forest management types and its correlations with ecosystem processes. Dense sampling of sporocarps over the last two years on a well-characterized set of 202 logs (*Fagus sylvatica*, *Picea abies*, *Pinus sylvestris*) of different decay stages was done alongside applying PCR-based

techniques on wood DNA extractions of the same logs. 740 wood samples from 30 plots from three geographically distant sites in Germany have been processed using the F-ARISA (fungal automated ribosomal intergenic spacer analysis) fingerprint method that targets the ITS region of rDNA. Preliminary ARISA results covering one complete sampling site entailed 250 different OTUs (operational taxonomic units). Water content and decay stage have a significant influence on fungal community structure as well as tree composition and management type. In addition to ARISA we accumulated 195 BLAST-identified ITS sequence types from PCR clone libraries from 9 plots so far. Interestingly there is only an 11% overlap between the 195 cloned sequence types and 189 morphologically identified species, showing the complementarity of both molecular and traditional techniques in studying fungal diversity. The study will be complemented by describing bacterial diversity in the same samples, utilizing the ARISA variant targeting the IGS of bacterial rDNA. Initially we focused on the presence of nitrogen fixing bacteria in expectedly nitrogen poor CWD samples. We hitherto found 26 different *nifH* (nitrogenase) sequences. None was closer than 97% similarity to any on GenBank, indicating the presence of uncharacterized, potentially unknown bacteria.

Houseknecht, Janice, Suh, Sung-Oui, and Zhou, Jianlong J.* Mycology & Botany Program, American Type Culture Collection (ATCC), 10801 University Blvd, Manassas, VA 20110. jzhou@atcc.org. **Evaluation of cryopreservation parameters on the post-thaw viability of fastidious *Phytophthora* organisms.**

Cryopreservation parameters were evaluated in this study for improving the post-thaw revival of fastidious *Phytophthora* strains, a group of pathogens that attack many economically important crops and fruits. Three freezing protocols, three thaw conditions, fifteen cryoprotective solutions, as well as other treatments were assessed. It is found that (1) 5.0% Me₂SO aqueous solution is the best cryoprotective for *Phytophthora* among 15 cryo-solutions tested; (2) the Mr. Frosty freezing protocol is better than our current standard fungal freeze protocol or WPC freeze protocol for slow-growing strains; (3) post-freeze thawing condition (37C for 2 min) is better than 25C for 5min, while 55C for 90 seconds gave lowest viability. Overall, we found that the optimal cryopreservation conditions are largely species or even strain specific in virtually all parameters tested, with robust strains maintaining nearly perfect post-freeze, post-thaw viability while fastidious strains showing very poor recovery under all test conditions. Additionally, we noticed that apparently identical mycelium plugs in a vial going through the same freezing and thawing condition could show either robust growth or no growth at all, a phenomenon currently wanting an explanation.

Hustad, Vincent P.^{1*} and Miller, Andrew N.² ¹Department of Plant Biology, University of Illinois at Urbana-Champaign, 1816 South Oak Street, Champaign, IL 61820, ²Illinois Natural History Survey, University of Illinois at Urbana-Champaign, 1816 South Oak Street, Champaign, IL 61820. vhustad@illinois.edu. **Phylogenetic studies in the Geoglossomycetes.**

The class Geoglossomycetes encompasses a widespread and diverse group of fungi known from every continent except Antarctica. Commonly referred to as earth-tongues due to their morphology and terrestrial habitat, these fungi have long been the subject of mycological interest, although few molecular systematic studies have been conducted within the group. This study represents the first modern attempt to generate a multi-gene, species level phylogeny within the Geoglossomycetes. Sequences of the partial nuclear ribosomal 28S large subunit, internal transcribed spacer, RPB1, and Mcm7 genes were generated for numerous species in the genera *Geoglossum*, *Trichoglossum*, *Thumentidium*, *Sarcoleotia*, and *Nothomitra*. Results of maximum parsimony, maximum likelihood, and Bayesian analyses confirmed previous findings that the Geoglossomycetes form a well-supported monophyletic clade. Polyphyletic genera within the Geoglossomycetes were also observed and suggestions for redescription of these genera will be presented. The genus *Nothomitra*, previously classified as incertae sedis within the Helotiales, was shown to belong in the Geoglossomycetes.

Hwang, Yueh-Jiang (Irene)^{1*}, Forman, Mike¹, Gray, Melissa¹, Miller, Gabriel¹, Shi, Ben¹, Slessareva, Janna¹, Spivey, Rody¹, Walters, Don¹, Wilkinson, Jack¹, Schlagnhauser, Carl², and Romaine, C. Peter^{1,2}. ¹Intrexon Corporation, AgBio Division, 104 TW Alexander Dr. Bldg 4A, Research Triangle Park, NC 27709, ²Department of Plant Pathology, Pennsylvania State University, University Park, PA 16802. ihwang@intrexon.com. **Recombinant protein production using the button mushroom, *Agaricus bisporus*.**

We are developing the button mushroom, *Agaricus bisporus*, as a rapid, high-capacity, and low-cost system for the manufacture of recombinant proteins (i.e., industrial enzymes, biopharmaceuticals, etc.). *Agaricus bisporus* produces predominantly two-spored basidia, with a majority of the spores (ca. 95%) yield-

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ing a heterokaryotic hypha that is capable of forming fruiting bodies without the need for sexual crossing. Using this mushroom species, we devised a high-throughput *Agrobacterium*-mediated transformation and in-lab fruiting methods and efficient recombinant protein expression assays. The ability of *A. bisporus* to integrate a wide range of heterologous genes, totaling more than 30 unique sequences thus far, has allowed for the production of a broad range of protein classes, including bioactives (aprotinin, interleukin-2, insulin-like growth factor 1, beta-interferon, Protein A, Protein G), immunoglobulins (mAbs, Fabs), reporters (green fluorescent protein, red fluorescent protein, beta-glucuronidase) and enzymes (acetylcholinesterase, butyrylcholinesterase, carboxylesterase, trypsinogen, laccase). Expression levels for the various proteins ranged from <1 to 250 mg/kg fresh weight of fruiting body biomass. Moreover, several mushroom-made recombinant proteins have been extracted from the high-biomass fruiting body, purified, and shown to be fully active. The commercial-scale manufacture of several proteins is now in development.

Hynson, Nicole A.^{1*}, Merckx, Vincent², and Treseder, Kathleen¹. ¹Department of Ecology & Evolutionary Biology, University of California Irvine, Irvine, CA 92697-2525, ²Netherlands Centre for Biodiversity Naturalis, 2300RA Leiden, The Netherlands. nhynson@uci.edu. **Partners in crime: ectomycorrhizal introductions and the underground ecology of pine invasion on oceanic islands.**

Global commerce has caused thousands of invasions of species into ecosystems around the world through the transport and trade of plants and animals. Invasive organisms are the second-leading cause of species extinctions, and they produce large economic costs. Recently, interest has turned to the introduction of non-pathogenic symbiotic microbes, such as mycorrhizal fungi, to new environments. For instance, it is clear that ectomycorrhizal (EM) fungi must be co-introduced for non-native EM trees to establish into new habitats where they have no suitable fungal symbionts. However, the repercussions of these introductions to native ecosystem function are largely unknown. This project seeks to determine how mycorrhizal fungi affect tree invasions. To achieve this, we are using pine invasion on the islands of Hawaii as a model system to examine the feedbacks between plants and microbes in invaded ecosystems. We hypothesize that pines' interactions with non-native EM fungi enables pines to occupy a unique functional niche within their new habitats, thus increasing their ability to invade. To test this hypothesis we are using a combination of molecular and physiological techniques in a series of field and greenhouse experiments. So far we have identified the primary EM fungi that facilitate pine establishment, and determined these fungi's current geographic limits on the islands of Maui and Hawaii. As a next step in this research we are using quantum dots as nutrient tracers to compare the physiologies of EM fungi and native Hawaiian arbuscular mycorrhizal fungi. From this study we will gain new information about the functional ecology of plant-fungal symbioses that will provide a predictive framework for plant-microbe community assemblies and distributions. In addition, this project adds valuable information to the small body of research regarding EM fungal invasions in the Pacific Rim.

Jovan, Sarah E.^{1*}, Riddell, Jennifer A.², and Padgett, Pamela². ¹Forest Inventory and Analysis Program, USDA Forest Service, Portland Forestry Sciences Lab, 620 SW Main, Suite 400; Portland, OR 97205, ²USDA Forest Service, Pacific Southwest Research Station, 4955 Canyon Crest Drive, Riverside, CA 92507. sjovan@fs.fed.us. **Predicting N inputs to forest ecosystems using only characteristics of lichen community composition.**

Studies of nitrogen (N) impacts to epiphytic lichen communities of Mediterranean, temperate, and boreal forest ecosystems reveal a remarkably consistent pattern: increasing N cause significant losses of N-sensitive, oligotrophic lichen species, while populations of N-tolerant, eutrophic species increase. Eventually the more moderately N-tolerant mesotrophic species are lost as well. From an ecological perspective, this shift entails a serious loss of diversity, losses in species important to wildlife, and increases in "weedy," fast-growing lichens of relatively insignificant ecological importance. We surveyed epiphytic lichens at 22 long-term monitoring sites in the extremely N-polluted Los Angeles Basin where N deposition can range as high as 70 kg N ha⁻¹ yr⁻¹. We had an unprecedented variety of N measurements to compare against lichen community composition, including concentrations of major gases (NH₃, NO₂, HNO₃, O₃), and various measures of wet and dry N deposition. We used non-metric multidimensional scaling (NMS) ordination to resolve major community composition gradients. The most prominent gradient, characterized by increasing eutroph dominance, was closely related to throughfall N (R² = 0.94, p < 0.0001), a measure of the flux of NH₄⁺ and NO₃⁻ carried in runoff from the tree canopy. A response index based on the NMS ordination was able to predict throughfall N to forested sites in the Basin with decent accuracy (± 4.57 kg N ha⁻¹ yr⁻¹). Lichens predicted surprisingly high N deposition to forests in the Palomar Mt. Area of the Cleveland National Forest, prompting us to focus future biomonitoring work there. The ability to predict N inputs using only character-

istics of lichen community composition greatly enhances our ability to monitor N impacts on forest health. The expense and logistical difficulty of directly measuring air quality limits our knowledge to a small number of forests.

Jovan, Sarah¹, Root, Heather², Holt, Emily², Geiser, Linda⁴, Neitlich, Peter³, and McCune, Bruce^{2*}. ¹USDA Forest Service, 620 SW Main, Suite 400, Portland, OR 97205, ²Dept. of Botany & Plant Pathology, 2082 Cordley Hall, Oregon State University, Corvallis, OR 97331-2902 USA, ³Western Arctic National Parklands, National Park Service, 41A Wandling Rd, Winthrop, WA 98862, ⁴US Forest Service, Pacific Northwest Region Air Program, PO Box 1148, Corvallis, OR 97339-1148. mccuneb@onid.orst.edu. **Macrolichen diversity along climatic gradients from southern California to the Arctic: Do lichens follow the classic latitudinal gradient in diversity?**

Widespread use of a standard method for field sampling of macrolichens has opened doors to answering ecological questions of large geographic scope, including the relationships of lichens to large-scale macroclimatic gradients. We compiled lichen data from 1,571, 0.38 hectare plots, spanning 33-70 degrees N latitude along the Pacific coast, including California, Oregon, Washington, and Alaska (no data from BC). The area includes woodlands, oceanic and suboceanic conifer forests, taiga, and tundra. Forests in the lower 48 states and SE Alaska were sampled for epiphytes as part of the U.S. Forest Inventory and Analysis program. In northern areas (managed by NPS and BLM), sampling shifted to include both epiphytes and ground-dwelling lichens. Because patterns of diversity are often better resolved for specific functional groups rather than for overall diversity, we modeled richness of specific functional groups (N-fixers, epiphytic forage lichens, cladonioid lichens, other chlorolichens, and eutrophs) against climate. We regressed richness against climatic variables derived from WorldClim. We chose nonparametric multiplicative regression over linear regression to accommodate any response surface shape, including nonlinearities and interactions among predictors. Models with geospatial coordinates as predictors were consistently stronger than those with climatic variables as predictors, suggesting the importance of historical spatial processes such as dispersal limitations and past climates. Lichen diversity did not show decreasing diversity at higher latitudes. Considering only climatic predictors, response surfaces were strongly nonlinear and interactive. Diversity of epiphytic forage lichens peaked at cool mean annual temperatures over a broad range of precipitation. N-fixers peaked in areas with cool summers and were lowest in areas with low precipitation and warm to hot summers. Overall richness had a more complex pattern than individual functional groups, in warm areas peaking in areas with higher precipitation, while showing a pronounced additional peak in low precipitation and cold climates.

Jusino, Michelle A.^{1*}, Lindner, Daniel L.², and Walters, Jeffrey R.¹ ¹Department of Biological Sciences, Virginia Polytechnic Institute and State University, 2119 Derring Hall, Blacksburg, VA, 24061, ²CFMR, USDA-Forest Service, Northern Research Station, One Gifford Pinchot Drive, Madison, WI 53726. mjusino@vt.edu. **Heart rot hotel.**

Federally endangered red-cockaded woodpeckers (*Picoides borealis*) are primary cavity excavators in the longleaf pine system, and only excavate their cavities in the heartwood of live pine trees - a trait unique to this species. This process takes years to complete, but certain types of heartwood infecting fungi can decrease excavation time. Incomplete excavations are termed cavity starts and are gaping wounds in the trunks of trees. Thus, cavity starts are possible infection courts for the fungi that are thought to facilitate excavation. Additionally, red-cockaded woodpeckers may carry fungi from their roost cavities into cavity starts. We have designed a project to specifically test if red-cockaded woodpeckers facilitate heartwood infection of longleaf pine trees by the transmission of fungi in the early stages of cavity excavation (cavity starts), and if man-made cavity starts also facilitate fungal infection, given that they are red-cockaded woodpecker accessible. Thus far, the data from this experiment are promising, and show high (95%) fungal infection rates within the heartwood surrounding naturally excavated, complete cavities; medium (54%) rates of infection within the heartwood surrounding naturally excavated cavity starts; and very low (5%) rates of fungal infection within the heartwood of control trees. We will show how the infection rates in naturally excavated and experimental (man-made) cavity starts change through time. In addition to these data, we will present preliminary results from a cloning study that seeks to explore the communities of fungi within the trees that comprise our experiment. We have found that red-cockaded woodpeckers carry fungi on their beaks and feet that are similar to the fungi found fruiting on their cavity trees. However, our preliminary cloning results point to a much more complex story than that presented in current red-cockaded woodpecker literature.

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Justo, Alfredo* and Hibbett, David S. Biology Dept., Clark University, 950 Main St. 01610, Worcester, MA. ajusto@clarku.edu. **Phylogeny and taxonomy of *Trametes* (Basidiomycota, Polyporales): one genus or too many?**

The phylogeny of *Trametes* and related genera was studied using molecular data from ribosomal loci (nLSU, ITS) and protein-coding genes (RPB1, RPB2, TEF1-a). Molecular analyses recover a highly supported clade that includes most of *Trametes* species (including the type *T. suaveolens*, the *T. versicolor* group, and mainly tropical species as *T. maxima* and *T. cubensis*) together with *Corioloopsis polyzona*, *Lenzites* and *Pycnoporus*. Our data confirm the positions of *Trametopsis cervina* in the Phlebioid clade and of *Trametes trogii* outside the *Trametes* clade, closely related to *Corioloopsis gallica*. The genus *Corioloopsis* as currently conceived is polyphyletic with at least three independent lineages occurring in the Core Polyporoid clade. In view of these results there are mainly two possible taxonomic arrangements of the *Trametes* clade: (i) classify all members of this clade under one single generic name. A formal proposal to conserve *Trametes* against *Lenzites* would be necessary to use the name *Trametes* for this clade and avoid a large number of new combinations in *Lenzites*. That would imply that the genera *Corioloopsis*, *Pycnoporus* and *Lenzites*, as currently typified, would become synonyms of *Trametes*; (ii) To split the *Trametes* clade into several smaller genera. That would imply resurrecting old names that have been practically absent from the mycological literature of the past century (*Artolenzites*, *Cubamyces*, *Cyclomyces*, *Pseudotrametes*) and probably erecting new genera for some of the clades recovered in the analyses. Separation of these smaller genera from each other based on morphological characters would be, in most cases, very difficult. These two options are briefly discussed under the framework of the phylogenetic results.

Kellner, Harald. Environmental Biotechnology, IHI-Zittau, Germany. mail@haraldkellner.com. **Expression of genes encoding fungal lignocellulolytic enzymes in forest soils.**

Fungi are the main organisms responsible for the degradation of biopolymers such as lignin, cellulose and hemicellulose in forest ecosystems. Soil surveys largely target fungal diversity, paying less attention to molecular fungal activity. In several studies in different forest ecosystems we used soil cDNAs and PCR with degenerate primers to detect the expression of fungal genes encoding important lignocellulolytic enzymes (e.g. ligninolytic: laccase and diverse secretory peroxidases; cellulose- and hemicellulolytic: endoglucanase, cellobiohydrolase, xylanase and others). In one study, altogether 26 enzyme groups were detected in the organic horizon of a sugar maple (*Acer saccharum* Marsh.) dominated US-hardwood forest, which was manipulated in the nitrogen deposition. Sequences were identified belonging to asco- and basidiomycetes. Using quantitative PCR, a distinct transcriptional regulation of laccase and cellobiohydrolase genes was detected. In a second survey, we followed the detection of fungal secretory peroxidases (i.e. manganese peroxidase, heme-thiolate peroxidases/peroxygenases and dye-decolorizing peroxidase) in different forest ecosystems, like aspen, aspen-birch, beech, maple and spruce forests. Finding many of them expressed, we conclude that these peroxidases are widespread and important agents of lignin and aromatic compound conversion in the litter horizon of forest soils. The methods used here could be widely applied in future forest soil research, linking fungal activities to ecosystem functioning.

Kennedy, Aaron H.^{1*}, Minnis, Andrew M.², Grenier, Daniel B.³, and Bischoff, Joseph F.³ ¹Molecular Diagnostics Laboratory, USDA-APHIS-PPQ, B-580, Powder Mill Rd., Beltsville, MD, 21075, ²Systematic Mycology & Microbiology Laboratory, USDA-ARS, B-010A, 10300 Baltimore Ave., Beltsville, MD, 20705, ³National Identification Services, USDA-APHIS-PPQ, B-010A, 10300 Baltimore Ave., Beltsville, MD, 20705. aaron.h.kennedy@aphis.usda.gov. **Phylogenetic placements of *Asperisporium* and *Pantospora* based on rDNA sequence data from their generic types (Mycosphaerellaceae).**

The family Mycosphaerellaceae includes thousands of species and displays remarkable morphological diversity, which is recognized by the inclusion of numerous anamorphic genera. Many are plant pathogens and the known diversity has been documented on most, if not all groups of embryophytes. Recent progress to review the known familial diversity and produce a natural classification has led to a period of taxonomic instability as many genera have been shown to be non-monophyletic, and the utility of morphological characters used to differentiate them has been challenged. Reaching a stable classification will require increased sampling from hosts across the embryophytes and phylogenetic placements of key generic types. Here, we contribute towards this goal through study of the generic types of the anamorphic *Asperisporium* and *Pantospora*. Cultures from recent interceptions were studied and described. DNA sequence data from the ITS and nLSU were obtained and analyzed phylogenetically in an effort to place these generic types within existing phylogenies. Lastly, and to stabilize the application of these generic types, detailed morphological studies were conducted of herbarium specimens that will be proposed as epitypes associated with living cultures and DNA sequence data. *Asperisporium*

caricae, the type of *Asperisporium* and cause of a leaf and fruit spot disease of papaya, is closely related to species of *Passalora*. This result supports the hypothesis of others who postulated that *Asperisporium* is a later synonym of *Passalora*. Since *Passalora* is polyphyletic, a final conclusion can not be reached until the generic type of *Passalora* is placed phylogenetically. *Pantospora guazumae* is the synnematous representative of the monotypic genus. Previous workers suggested that *Pantospora* is a later synonym of *Pseudocercospora*. Our results refute this and support the hypothesis that this genus represents a distinct lineage.

Kennedy, Peter. Lewis & Clark College, Dept. of Biology MSC 53, 0615 SW Palatine Hill Rd., Portland, OR, 97219. pkennedy@lclark.edu. **Colonization-competition tradeoffs and successional dynamics among ectomycorrhizal fungi.**

Colonization-competition tradeoffs have been shown to be important determinants of succession in plant and animal communities, but their role in ectomycorrhizal (ECM) fungal communities is not well understood. To test the hypothesis that strong spore-stage competitors may not remain dominant on plant root tips as competition shifts to mycelial-based interactions, we investigated the mycelial competitive interactions among three naturally co-occurring ECM species (*Rhizopogon occidentalis*, *R. salebrosum*, and *Suillus pungens*). Each species was grown alone and in all pair-wise combinations on *P. muricata* seedlings in experimental microcosms and culture assays. Competitive outcomes were assessed from ECM root tip colonization, soil mycelial abundance, and mycelial growth. In the microcosm experiment, we observed a clear competitive hierarchy of *R. salebrosum* > *R. occidentalis* > *S. pungens*. Competitive effects were also apparent in the culture assays, however, no similar hierarchy was present. These results contrast with our previous findings from spore-based competition, strongly suggesting that ECM competitive outcomes can be life-stage dependent. The differing competitive abilities observed here also corresponded with patterns of ECM succession in *Pinus muricata* forests, indicating that competitive interactions may significantly influence temporal patterns of ECM community structure.

Kernaghan, Gavin* and Patriquin, Glenn. Biology Department, Mount Saint Vincent University, Halifax, Nova Scotia, B3M 2J6, Canada. Gavin.kernaghan@msvu.ca. **Fungal root endophytes of boreal trees.**

Fungal root endophytes colonize root tissue concomitantly with mycorrhizal fungi but their identities and host preferences are largely unknown. We studied fungal endophyte assemblages co-colonizing *Cenococcum geophilum* ectomycorrhizae of *Betula papyrifera*, *Abies balsamea* and *Picea glauca* from two boreal sites in eastern Canada by culturing and direct PCR. Pure cultures isolated from surface-sterilized roots were identified by ITS rDNA sequencing. For direct PCR, ITS rDNA was amplified, cloned and sequenced. Sequencing of pure cultures revealed 31 distinct phylotypes; mainly members of the ascomycete families Helotiaceae, Dermateaceae, Myxotrichaceae and Hyaloscyphaceae, with *Phialocephala fortinii sensu lato* dominating. Multivariate analyses of the pure culture data revealed a clear separation among the assemblages of fungal endophytes colonizing the different host tree species. Direct PCR detected many of the same fungi seen with pure culture isolation, but in very different proportions with an unidentified clade within the Helotiaceae dominating. Direct PCR also revealed a number of co-colonizing ectomycorrhizal fungi which were not detected by the pure culture technique.

Kohn, Linda M.¹, Parreiras, Lucas S. and Anderson, J.B. Department of Biology, University of Toronto Mississauga, Mississauga, Ontario, Canada L5L 1C6. linda.kohn@utoronto.ca. **Mechanisms of adaptation and epistasis in experimental yeast populations.**

Ecological speciation, fixation of adaptive alleles in two or more populations under divergent selection, is one of several speciation models. The genetic mechanism of reproductive isolation (and species cohesion) can be epistasis, when the effect of two alleles together is greater than the sum of the effects of each allele independently. Our previous work has demonstrated this phenomenon in 500 generations under strong selection for either high salt or low glucose, among replicated experimental yeast populations originating from a single cell (Dettman et al. 2007, Nature). Based on whole genome sequences, genetic reconstruction of strains carrying single and combined evolved alleles, and expression studies, key evolved loci are now known to be, *PMATe*, evolved under high salt, encoding a proton efflux pump and known to play a central role in pH homeostasis, and under low glucose, two global regulators: *MKT1e* regulating mRNAs encoding mitochondrial proteins and *MDS3* required for growth in alkaline media and a negative regulator of early meiotic gene expression (Anderson et al. 2010, Current Biology). Here we present new data showing that in low glucose (1) *MKT1e* and *MDS3* synergistically increase mitochondrial gene expression in the shift from fermentation to oxidative respiration, (2) the fitness effect of *MKT1e* in low glucose is enhanced in the *MDS3e* background, (3) reca-

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pitulation of the emergence and fixation of *MKT1e* in experimental populations depends on a *MDS3e* genetic background and (4) *PMA1e* is impaired in maintaining intracellular pH, the likely source of negative epistasis. Importantly, the *MKT1e* mutation (89G) evolved from the laboratory-standard (89A) is the form fixed in wild populations of *S. cerevisiae* and *S. paradoxus* (Liti et al., 2009, Nature); it is likely an important fitness determinant and target of natural selection.

Knudson, Alicia G.* and McLaughlin, David J. Department of Plant Biology, University of Minnesota, 250 Biological Sciences Center, 1445 Gortner Ave., St Paul MN 55108. knud0260@umn.edu. **Species diversity of *Ramaria* in the Laurentian mixed and eastern broadleaf forests of Minnesota.**

The genus *Ramaria* produces upright coral mushrooms in summer and fall months all across the USA. These fungi are important decomposers in many forests systems and some are known to form mycorrhizal associations with oak and pine species. Despite their widespread occurrence, the genus has been researched largely on the eastern and western coasts of the USA with moderate collecting in some central states. Most of the Midwestern states have very few documented collections. The University of Minnesota herbarium contains 13 species and many unidentified *Ramaria* specimens, focusing on a limited number of state parks and other collection sites. In 2010, collections of *Ramaria* were made to assess the species diversity in Minnesota, sampling eight state park and Scientific and Natural Areas. Collection sites for this study were in a transect from northwest to southeast, representing two of the major vegetation biomes of Minnesota, the conifer and mixed hardwoods of the Laurentian Mixed Forest and the oaks, maples, and basswoods of the Eastern Broadleaf Forest. Gross morphology, microscopic characters and ITS (internal transcribed spacer region) sequences were used to determine species. Newly documented *Ramaria* species will be discussed and compared to current information on Midwestern species.

Kokaew, Jitra¹*, Manoch, Leka¹, Visarathanonth, Nipon¹, Singburadom, Narong¹, Chamswang, Chiradej², Piasai, Onuma¹, and Strobel, Gary A.³ ¹Department of Plant Pathology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand, ²Department of Plant Pathology, Faculty of Agriculture Kamphaeng Saen, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom 73140, Thailand, ³Department of Plant Science, Montana State University, Bozeman, MT 59717, USA. agrlkm@ku.ac.th. **Diversity of endophytic fungi from Mu Koh Aung Thong and Mu Koh Similan National Parks and the efficacy to control plant pathogenic fungi *in vitro*.**

Thirty samples of healthy plants were used to isolate endophytic fungi. Plants were collected from Mu Koh Aung Tong National Park, Suratthani Province and Mu Koh Similan National Park, Phangnga Province in April 2009 and April 2010 for isolation of endophytic fungi. For surface sterilization, the leaf samples were cut into small pieces and put in 10% sodium hypochlorite for 3 min and 70% ethanol for 30 sec. The treated leaves were placed on water agar (WA). Stems were thoroughly treated with 95% ethanol and flamed until the alcohol was eliminated and the bark was removed with a sterilized sharp blade. The bark and inner pieces of the stem were plated on WA and glycerol arginine media (GAM). Plates were incubated at 28 °C for 7-21 days. A total of 191 isolates of endophytic fungi were found including *Colletotrichum gloeosporioides* (9 isolates), *Colletotrichum* spp. (17), *Fusarium* sp. (1), *Guignardia* sp. (1), *Neosartorya* spp. (2), *Periconia* sp. (3), *Pestalotiopsis* spp. (6), *Phomopsis* spp. (20), *Phyllosticta* spp. (18), xylariaceous fungi (17) and non-sporulating endophytic fungi (97). We selected four isolates of non-sporulating fungi for testing antagonism against plant pathogenic fungi *in vitro*. Potential fungal antagonists and pathogens were placed 0.5, 1.0 or 1.5 cm apart on potato dextrose agar (PDA) and incubated at 28 °C for 10-14 days. The results revealed that 4 isolates of non-sporulating endophytic fungi KUFC6253, 6257 from *Pandanus odoratissimus* and KUFC6198, 6203 from *Hopea pierrei* inhibited mycelial growth of *Rhizoctonia solani*. However, these four isolates failed to inhibit mycelial growth of *Pythium aphanidermatum*, *Phytophthora palmivora* and *Sclerotium rolfsii*.

Kropp, Bradley R. Biology Department, 5305 Old Main Hill, Utah State University, Logan, Utah 84322 USA. brad.kropp@usu.edu. **Endophytes from pines and dwarf mistletoe: are they shared by their hosts?**

Previous studies on host specificity of endophytic fungi have shown that, except for grass symbionts, many endophytes have low host specificity. One question that has received relatively little attention is whether endophytic fungi are shared between parasitic plants such as mistletoes and their hosts. This preliminary study examined the host specificity of endophytic fungi colonizing Dwarf Mistletoe (*Arceuthobium americanum*) and its host Lodgepole Pine (*Pinus contorta*) in a montane habitat in northern Utah. Eighteen different endophytic fungi were cultured from samples of mistletoe and the pines that they were parasitizing. The pine samples yielded 10 different endophytes whereas the mistletoe yielded 11 different fungi. Of these fungi, only 3 were shared by the

mistletoe and its host tree, indicating that most of the endophytes were not shared by these intimately associated plants.

Krüger, Dirk¹*, Pavic, Aleksandar², Yurkov, Andrey³, Hommel, Kerstin¹, Begerow, Dominik³, Arnold, Norbert⁴, Marjanovic, Zaklina², and Tarkka, Mika¹. ¹UFZ-Helmholtz-Centre for Environmental Research, Department of Soil Ecology, Theodor-Lieser-Str. 4, D-06120 Halle (Saale), Germany, ²Institute for Multidisciplinary Research, Department for Life Sciences, Kneza Viseslava 1a, 11 000 Belgrade, Serbia, ³Geobotany Section, Ruhr-Universität Bochum, Universitätsst. 150, D-44801 Bochum, Germany, ⁴IPB-Leibniz Institute of Plant Biochemistry, Department of Bioorganic Chemistry, Weinberg 3, D-06120 Halle (Saale), Germany. dirk.krueger@ufz.de. **Ectomycorrhizal mushrooms *Xerocomus*, *Paxillus*, *Tuber* - aspects of multipartite interactions between soil yeasts, bacteria and filamentous fungi.**

Boletales basidiocarps are commonly associated with non-parasitic microorganisms and infected by mycoparasitic ascomycetes (*Sepedonium*, teleomorph *Hypomyces*). We tested *in-vitro* if non-parasitic cultures influenced the growth of the mycoparasite or the host fungus. Yeast cultures from *Paxillus* and *Xerocomus* included *Rhodotorula*, *Rhodospiridium*, *Mastigobasidium*, *Cryptococcus*, *Cystofllobasidium*, *Holtermanniella*, *Trichosporon* and *Khyveromyces*. Several yeasts stimulated the growth of *Sepedonium chrysospermum* var. *paxilli* but inhibited the host, indicating that the yeasts may have an adverse effect on basidiocarp health. Bacteria from *Xerocomus* basidiocarps belonged to diverse groups. We observed that streptomycetes were particularly strong inhibitors of the *Xerocomus* mycoparasite, *Sepedonium microspermum*, but had no or little influence on host growth. Most potent inhibitors expressed higher chitin degrading activity than a non-antagonistic strain. This suggests that basidiocarp-associated streptomycetes may protect the mushrooms from mycoparasite infection. White truffle (*Tuber magnatum*) ascocarps also host diverse bacterial communities, including numerous Actinobacteria. 66 bacterial isolates were screened for their ability to grow on nitrogen poor media. Two Actinobacteria resembling *Curtobacterium flaccumfaciens* and *Rhodococcus* sp. were characterized by *in vitro* bioassays. $\text{Ca}_3(\text{PO}_4)_2$ solubilisation activity of both strains was at its highest under ammonium nutrition and with mannitol as sole carbon source. Neither bacteria degraded phytate, but both bacterial strains produced siderophores. Apart from growing on carbohydrates known from ascocarps (mannitol, trehalose, β -glucan) offered as sole carbon source, *C. flaccumfaciens* degraded chitin and pectin, and showed lipase and protease activities, while *Rhodococcus* sp. expressed cellulase and urease activities. Three parasitic fungi (*Verticillium leptobactrum*, *Bionectria ochroleuca*, *Trichoderma tomentosum*) were isolated from ascocarps and the bacteria tested against them displayed species-specific effects. Characterization of phosphate and iron solubilizing bacteria utilizing carbohydrates from ascocarps thus suggests that some symbiotic bacteria may improve truffle nutrition during the formation of the ascocarp, and protect it from potential mycoparasites.

Kumar, Arun¹, Healy, Rosaria A.¹, Spatafora, Joseph W.², Blackwell, Meredith³, and McLaughlin, David J.¹ ¹Department of Plant Biology, University of Minnesota, St. Paul, MN 55108, ²Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, ³Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803. davem@umn.edu. **Ultrastructure of *Orbilbia auricolor* and the phylogeny of Pezizomycotina.**

Molecular phylogenetic analyses indicate that the monophyletic classes Orbiliomycetes and Pezizomycetes are among the earliest diverging branches of Pezizomycotina, the largest subphylum of the Ascomycota. Although Orbiliomycetes is resolved as the most basal lineage in some analyses, molecular support for the node resolving the relationships between the two classes is low and topologies are unstable. We provide ultrastructural evidence to inform the placement of Orbiliomycetes by studying *Orbilbia auricolor*, a representative species of the only order (Orbiliales) of the class. The truncate ascus apex in *O. auricolor* is thin-walled except at the margin, and an irregular wall rupture of the apex permits ascospore discharge. Ascus, ascogenous and non-ascogenous hyphae were simple septate, with septal pores plugged by unelaborated electron-dense, non-membranous occlusions. Globose Woronin bodies were located on both sides of the septum. Nuclear division was characterized by the retention of an intact nuclear envelope, and a two-layered disc-shaped spindle pole body. The less differentiated nature of the spore discharge apparatus and septal pore organization support the earliest diverging position of Orbiliomycetes within the subphylum, while the closed nuclear division and disc shaped spindle pole body are interpreted as ancestral state characters for Ascomycota.

Lamit, Louis J.¹*, Sthultz, C M.², Wooley, S C.³, Lindroth, R L.⁴, Whitham, T G.¹, and Gehring, C A.¹ ¹Department of Biological Sciences and Merriam-Powell Center for Environmental Research, Northern Arizona University, Flagstaff, AZ 86011, ²Organismic and Evolutionary Biology, Harvard University, 16 Di-

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vinity Ave, Cambridge, MA 02138, ³Department of Biological Sciences, California State University Stanislaus, Turlock, CA 95382, ⁴Department of Entomology, University of Wisconsin, Madison, WI 53706. ljl47@nau.edu. **Twig endophyte communities respond to *P. angustifolia* genotype: community heritability and correlations with tree traits.**

Endophytic fungi often exhibit specificity to plant species, however the influence of genotypic differences within host species on endophytes is poorly understood. We hypothesized that communities of endophytes in twigs of *Populus angustifolia* (narrowleaf cottonwood) would vary among tree genotypes. Additionally, we examined relationships with tree growth traits and chemistry to identify links between tree genetics and endophytes. Culturable endophytes were isolated from twigs of replicated *P. angustifolia* genotypes growing in a common garden, during two sampling dates. Shoot growth, aboveground biomass, and condensed tannins were also quantified. Several lines of evidence supported our hypotheses. 1.) On both sampling dates, endophyte composition and isolation frequency varied significantly among tree genotypes, whereas richness did not. 2.) Aboveground tree biomass, shoot growth, and twig condensed tannins all varied among genotypes, but only biomass showed a relationship with endophytes. 3.) Tree genotypes that grow fast support the largest numbers of endophytes, but the species present (i.e. composition) are not directly affected by productivity. These results indicate that twig endophytes are sensitive to differences among tree genotypes and identifies an important link between tree growth and endophytes.

Landolt, John C.¹, Cavender, James C.², Rollins, Adam W.³, Ndiritu, George G.⁴, and Stephenson, Steven L.^{5*} ¹Department of Biology, Shepherd University, Shepherdstown, WV 25443, USA, ²Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA, ³Department of Biology, Lincoln Memorial University, Harrogate, TN 37752, USA, ⁴National Museums of Kenya, Nairobi, Kenya, ⁵Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. slsteph@uark.edu. **Dictyostelid cellular slime molds of Kenya.**

Dictyostelid cellular slime molds (dictyostelids) are an understudied group in Kenya, but samples collected during the period of 2005–2011 have yielded at least nine described species and a number of other forms that appear to be species new to science. In January 2011, small sets of samples were collected from two study sites in the extensive grasslands of the Maasai Mara and a single study site on each of two mountains (Aberdare and Mt. Kenya). These samples were processed using the standard “Cavender” method to isolate dictyostelids. The grassland samples (a total of 10) were almost completely devoid of dictyostelids, and only a single clone was recovered. As such, dictyostelids appear to be much less common in the grasslands of Kenya than is the case for grasslands in the central and western United States. The samples from montane forests on Aberdare and Mt. Kenya were relatively more productive (8 of 13 samples yielded dictyostelids), but only a few species were present. All of the species recorded in this most recent survey were members of the genus *Dictyostelium*. This work was supported by a grant from the National Science Foundation.

Larsson, Karl-Henrik^{1*}, Læssøe, Thomas², Yorou, Nourou S.³, and Ryvarde, Leif⁴. ¹Natural History Museum, PO Box 1172 Blindern, 0318 Oslo, Norway, ²Natural History Museum of Denmark, Øster Voldgade 5-7, 1350 København K, Denmark, ³LMU Department of Biology, Systematic Botany and Mycology, Menzinger Strasse 67, 80638 München, Germany, ⁴Department of Biology, University of Oslo, PO Box 1066 Blindern, 0316 Oslo, Norway. k.h.larsson@nhm.uio.no. **The phylogenetic position of *Hydnodon* and *Scytinopogon*.**

Scytinopogon is a genus of clavarioid fungi with mainly tropical-subtropical distribution. Species are characterized by richly branched, light coloured basidiomata with flattened branches, a monomitic hyphal system with clamped, non-inflated, colourless hyphae, total lack of vegetative organs, four-sterigmate basidia, and white to ochraceous, densely aculeate basidiospores. The same morphological properties are also found in the stipitate, hydroid genus *Hydnodon* and in the effused corticioid genus *Trechispora*. We used nuclear rDNA sequences to infer the phylogenetic position of *Scytinopogon* and *Hydnodon*. Both genera occur nested within *Trechispora* but do not seem to be related. The results support the transfer of the type of *Hydnodon* to *Trechispora* already made (Ryvarden 2002). *Trechispora* is a large genus containing species with a smooth, hydroid, or poroid hymenophore. The *Trechispora*-*Hydnodon*-*Scytinopogon* clade is strongly supported but the selected genetic markers do not resolve the relationships within the clade. *Scytinopogon* and *Hydnodon* grow on the forest floor while *Trechispora* species form basidiomata on strongly decayed wood and other debris on the ground. *Trechispora* species are sometimes reported from mycorrhiza studies but proof of a mycorrhizal habit is lacking.

Lawrence, Daniel P.* and Pryor, Barry M. School of Plant Sciences, University of Arizona, P.O. Box 210036, Tucson, AZ 85721-0036. bmpryor@email.ariz

ona.edu. **Systematics of *Alternaria* and related genera: a genomics approach.**

The genus *Alternaria* contains 100 to several hundred morphologically diverse species that occur worldwide and occupy a variety of ecological niches. For analysis of relationships within *Alternaria*, the variable ITS region has commonly been used. While other studies have revealed the utility of the ITS region for resolving relationships among species that exhibit conspicuous morphological diversity, little sequence variation was detected among species exhibiting few and subtle morphological differences. Similar results were obtained with analysis of mitochondrial rDNA large subunit (mtLSU) and small subunit (mtSSU) genes. Collectively, the loci chosen for these analyses may be inappropriate for species resolution within *Alternaria*, thus the need for analyses based upon more divergent loci. The genus *Alternaria* is comprised of eight species-groups (the infectoria, panax, brassicicola, sonchi, radicina, gypsophila, alternata, and porri species-groups) based on a previous three gene phylogeny of ITS, *gpd*, and *Alt a1* genes. In order to clearly resolve taxa within each species-group, a five gene phylogenetic approach was implemented, which included the *actin*, *gpd*, *Alt a1*, *plasma membrane ATPase*, and *calmodulin* genes. In order to assess relationships at the species-population interface, a hierarchical sequencing effort was employed that first generated 6X coverage for a representative species from the two largest species-groups, the alternata and porri species-groups, followed by 1X coverage for 12 additional species from each group. Data from these taxa will be aligned to the *A. brassicicola* genome for assessments of homology. This will allow the development of addition primers that will enable the utilization of more divergent loci for the production of more robust phylogenies at a lower-order phylogenetic scale.

Leavitt, Steven D.¹, Esslinger, Ted L.², and Lumbsch, H. Thorsten^{1*}. ¹Department of Botany, Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, IL 60605–2496, USA, ²Department of Biological Sciences, North Dakota State University, Fargo, ND 58105–5517, USA. sleavitt@fieldmuseum.org. **Species delimitations in lichen-forming fungi – are cosmopolitan brown parmelioid lichens (Parmeliaceae, Ascomycota) really cosmopolitan?**

There is an increasing body of evidence that in many cases morphology-based taxonomic circumscriptions misrepresent fungal diversity in lichen associations, particularly in lichens thought to be broadly distributed. In this study we address species circumscription in two notoriously challenging parmelioid lichen genera (*Melanelixia* and *Melanohalea*) with broad distributions throughout the northern Hemisphere. Using DNA sequence data from ca. 500 individuals we address current morphological/chemical species circumscriptions, identify previously unrecognized lineages, and discuss biogeographical patterns. Although many clades are largely congruent with traditionally circumscribed taxa, some morphologically indistinguishable groups (cryptic species) are recovered within multiple, distinct genetic lineages in both *Melanelixia* and *Melanohalea*. Strong nodal support and overall congruence among independent loci suggest long-term reproductive isolation between most lineages. While many lineages are truly widespread, a limited number of clades appear to have much more restricted distributional ranges. These results provide an important contribution to understanding distributional patterns and species delimitation in common lichen-forming fungi.

Leewis, Mary-Cathrine C.*, Taylor, D Lee, and Leigh, Mary Beth. Institute of Arctic Biology, University of Alaska – Fairbanks, PO Box 756100, Fairbanks, AK 99775. mcleewis@alaska.edu. **Microbial community structure and functional genes associated with four boreal vegetation types.**

The boreal forest is a major global carbon reservoir, the flux of which is governed largely by microbial decomposition of litter and soil organic matter. Understanding the fate of this carbon, including under changing climatic conditions, requires a greater understanding of the microbial processes involved and the environmental factors controlling them. Vegetation type is one important factor affecting soil microbial community structure and function. The aim of this study is to characterize the bacterial and fungal community structure and function associated with several vegetation types within the Alaskan boreal forest. The GeoChip microarray enables the study of bacterial, fungal and archaeal functional genes involved in biogeochemical and ecological processes in a rapid, high throughput and semi-quantitative fashion. This technique was used to screen the microbial functional potential of root zone soils associated with four vegetation types dominated by either *Picea glauca* (white spruce), *Picea mariana* (black spruce), *Populus tremuloides* (quaking aspen), or *Betula neoalaskana* (Alaskan paper birch), located within the Bonanza Creek Long Term Ecological Research Site (BNZ LTER) in interior Alaska. The same microbial community structure in these soils was then assessed using Sanger sequencing of the fungal ITS region, bar-coded 454-pyrosequencing of bacterial 16S rRNA genes and GeoChip functional gene microarray analyses. Prelimi-

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nary results indicate that the microbial community and functional metagenome varies in abundance and diversity in accordance with the dominant tree species present.

Liimatainen, Kare* and Niskanen, Tuula. Plant Biology, Department of Biosciences, P.O. Box 65, 00014 University of Helsinki, Finland. kare.liimatainen@helsinki.fi. **A comparison of rDNA IGS1, ITS, RPB2 and LSU regions in the species delimitation and identification of *Cortinarius* (Basidiomycota, Agaricales).**

The most commonly used regions in the species level taxonomy of Agaricales (Basidiomycota) are the rDNA ITS1 and ITS2 regions. They have been used as species-identifier sequences in *Cortinarius* although in fungi no barcode region has not yet been formalized. Some morphologically delimited *Cortinarius* species, however, have nearly identical ITS-sequences. We studied some of these species pairs more in detail based on their IGS1, RPB2, ITS, and LSU regions. Of these IGS1 has rarely been used in Agaricales. Our results show that IGS1 was the only region containing enough variation for separating the species pairs. The variation in RPB2 region was comparable to ITS regions and the variation in LSU lower. This challenges the current dominance of ITS regions in fungal taxonomy and barcoding and clearly shows the potential of IGS1 as an additional region for species level studies.

Lilleskov, Erik A.^{1*}, Romanowicz, Karl J.², Chimner, Rodney A.², Kane, Evan S.², Pypker, Thomas G.², Kolka, Randall K.³, Daniels, Aleta L.², and Potvin, Lynette R.¹ ¹USDA Forest Service, Northern Research Station, Houghton, MI 49931, ²School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI 49931, ³USDA Forest Service, Northern Research Station, Grand Rapids, MN, 55744. elilleskov@fs.fed.us. **Role of ericoid mycorrhizal fungi in peatland carbon cycling.**

Ericaceae are ecologically successful plants, and may owe much of their success to a unique mycorrhizal mutualism. Members of this small guild of fungal symbionts have extracellular enzymes able to depolymerize a number of complex organic polymers, presumably to gain access to organically bound nutrients, but are only able to partially decompose lignin. Given their ready access to host carbohydrates and broad enzyme potentials it has been postulated that they could be effective competitors for nutrients with free-living saprotrophs, and hence constrain C mineralization. Exoenzyme potentials have been demonstrated in the lab, but it is unclear to what extent ericoid fungi regulate community enzyme activity and carbon mineralization in the field. We have initiated an experiment designed to provide insights into the impact of Ericaceae and their symbionts on carbon cycling in the context of climate change. This study, called the PEATCosm experiment, is taking place at the US Forest Service's Houghton, MI Mesocosm Facility. One meter cubed experimental units are filled with monoliths from a bog ecosystem and subjected to a vegetation manipulation (unmanipulated, removal of sedges, removal of Ericaceae) and precipitation manipulation (average precipitation, summer drought). Our goal is to understand the extent to which the plant communities drive divergent microbial community structure and function as mediated by their fundamentally different adaptations to the unique stresses of peatland ecosystems. We hypothesize that communities dominated by Ericaceae will exhibit lower populations of free-living saprotrophs, lower activity of lignolytic enzymes, and lower C mineralization than in the absence of Ericaceae. We are examining the impact on a number of parameters, including carbon mineralization, methane flux, fungal and prokaryote communities, DOC quantity and quality, and enzyme activities. We present preliminary results from the first growing season of manipulations.

Lindahl, Björn*, Clemmensen, Karina, and Bödeker, Inga. Swedish University of Agricultural Sciences, Dept. Forest Mycology & Plant Pathology, Uppsala, Sweden. Bjorn.Lindahl@slu.se. **Ectomycorrhizal fungi both supply and degrade organic matter in humus layers.**

Root derived carbon is known to be a major driver of microbial processes in forest and heathland soils, but the roles of mycorrhizal fungi in building and degrading organic matter are still unresolved. We have studied humus formation, mycelial production and fungal community composition at three Swedish field sites; two boreal forests and one at the sub-arctic birch forest - alpine heath transition. Analysing organic matter dynamics using ¹⁴C dating in combination with stable isotope analyses, we found that the humus layers at a boreal forest site originated largely from mycorrhizal mycelium, and that mycelial turnover rates rather than plant litter decomposition appear to determine long term carbon sequestration. Counter-intuitively, the thickest humus layers were found at sites of low productivity, whereas the highest production of plant litter and fungal mycelium were found at sites with thin humus layers. Isotope data suggest that accumulation of nitrogen in growing humus stocks may restrict plant productivity. We used 454-sequencing to analyze fungal communities in humus layers and found striking differences in community composition between sites with contrasting humus accumulation rates. At sites with thin humus layers, species

assemblages seemed optimized to avoid accumulation of fungal mycelium and humus, while maximizing nitrogen delivery to the plant community. For example, high abundances of certain *Cortinarius* species were observed at sites with thin humus layers. These ectomycorrhizal species produce peroxidase enzymes with capacity to degrade recalcitrant organic compounds. At other sites, slow but persistent mycelial accumulation seems to promote humus build-up, due to hitherto unknown biochemical stabilization mechanisms. Our results indicate a central role of mycorrhizal mycelium in long term carbon sequestration in boreal and sub-arctic ecosystems. This view is in sharp contrast with current carbon cycling models, in which carbon balances are explained solely on the basis of plant litter production and degradation.

Lindner, Daniel L.^{1*}, Lorch, Jeffery^{2,5}, Foster, Jeffery T.³, Gargas, Andrea⁴, and Blehert, David⁵. ¹Center for Forest Mycology Research, US Forest Service, One Gifford Pinchot Dr, Madison, WI 53726, ²Molecular and Environmental Toxicology Center, University of Wisconsin - Madison, Medical Sciences Center, 1300 University Avenue, Madison, WI 53706, ³Center for Microbial Genetics and Genomics Northern Arizona University, Flagstaff, AZ 86011, ⁴Symbiology LLC, Middleton, WI 53562, ⁵US Geological Survey - National Wildlife Health Center, 6006 Schroeder Road, Madison, WI 53711. dlindner@wisc.edu. **Discovery and whole-genome sequencing of close relatives of *Geomyces destructans*, the fungus associated with White Nose Syndrome in bats.**

Since the winter of 2006, bats in eastern North America have been experiencing unprecedented mortality from White Nose Syndrome, a previously unknown disease. Efforts are underway to characterize the putative causal agent, the recently named fungus *Geomyces destructans*, and to develop DNA-based methods to detect *G. destructans* in environmental samples (e.g. soil, bat feces, air samples). Initial attempts at developing DNA-based detection methods were hampered by the presence of many closely related, uncharacterized *Geomyces* species in cave soils. In order to differentiate *G. destructans* from closely related species, *Geomyces* isolates were cultured from a range of cave soils from eastern North America. Many *Geomyces* species were recovered, including isolates with ITS regions >99% similar to *G. destructans*. Whole genome sequencing of close relatives of *G. destructans* is underway to determine which DNA regions can be used to differentiate species and to identify regions necessary for pathogenicity

Lodge, D Jean^{1*}, Cantrell, Sharon A.², and Pérez Jiménez, José R.² ¹Center for Forest Mycology Research, USDA-Forest Service, Northern Research Station, PO Box 1377, Luquillo, PR 00773-1377, ²Department of Biology, School of Science and Technology, Universidad del Turabo, PO Box 3030, Gurabo, PR 00778. djlodge@caribe.net. **Forest floor fungal community changes with simulated hurricane disturbance components.**

Hurricanes commonly disturb forests in the Caribbean, opening the canopy and depositing leaves and branches onto the forest floor. Our objective was to determine the separate and combined effects of canopy opening and debris addition or removal on relative abundance and diversity of microorganisms in leaf litter using a simulated hurricane experiment. The treatments were applied to subtropical wet forest in the Luquillo Mountains of Puerto Rico using a 2 x 2 factorial design (with and without debris, with and without canopy opening; three complete replicate blocks). Weighed senesced and green leaves were decomposed in baskets placed on the soil, and litter cohorts were demarcated using 1 mm mesh screens. Green leaves were added only in debris addition treatments. Five replicate baskets were harvested from each plot at 3-month intervals for 12 months. Microbial community succession was monitored using fatty acids and DNA markers, and fungal connections between litter cohorts were counted. Microbial community changes were analyzed with Principal Components Analysis. Canopy opening reduced while debris additions accelerated decomposition. Faster decomposition rates were associated with more diverse fungal and bacterial TRFLP phylotypes, number of fungal connections between litter cohorts and phosphorus accumulation via fungal translocation. In both green and senesced leaves, fungal phylotypes decreased while bacterial phylotypes increased during microbial community succession. Generally, succession and decomposition were arrested by canopy opening when debris was removed. Microbial community succession was correlated with microclimate, early abundance of fungi (indicated by high fatty acid content and number of fungal connections between litter cohorts), and availability of labile compounds. Microbial communities follow different trajectories depending on whether there is early colonization by fungi, primarily white-rot basidiomycetes that degrade lignin. These early leaf decomposer fungi are inhibited by canopy opening but the negative effects of canopy opening are moderated by debris deposition.

Luoma, Daniel L.* and Eberhart, Joyce L. Department of Forest Ecosystems and Society, Oregon State University, Corvallis OR 97331. luomad@fsl.orst.edu. **Response of ectomycorrhizae to Swiss needle cast disease.**

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Characteristics of the ectomycorrhiza community can be used to monitor forest health and may be useful in predictive models. We have determined levels of ectomycorrhizae (EM) in forest stands with moderate to high levels of Swiss needle cast (SNC) disease. The levels of EM diversity found indicated that the below-ground ecosystem was strongly affected by SNC, by the previous removal of mature trees during timber harvest, by post-harvest silvicultural practices, or by a combination of all three. There was also indication that some EM fungi (EMF) may be “stress tolerators” (*sensu* Grime). Common Douglas-fir EM types such as *Cenococcum* and *Rhizopogon* were less widespread in SNC stands than has been found in other studies from western Oregon. Because the SNC affected trees were mycorrhizal (at low densities) we hypothesized that certain (EMF) have become more predominant on the roots that remain and are filling the important functional roles that EMF play in tree nutrition. Twenty-four of the 31 EM types found in this study were recorded from one soil core each. An additional 4 EM types were recorded from only 2 soil cores each. Rather than a few EMF species dominating because they are particularly tolerant of a reduced carbon supply on highly impacted SNC sites, we may be seeing a “survival of the survivors” scenario. With this concept, the remaining EMF species supporting Douglas-fir growth on these sites are able to persist simply because other EMF species have dropped out at a locally patchy scale. Stand-level, aggregate species richness (50% reduction) has not been impacted as severely as local, soil-core species richness (80% reduction). The highly patchy soil environment may provide opportunities for particular EMF species to persist due to each species’ unique adaptive advantages in a given location.

Lutzoni, François^{1*}, Jolanta Miadlikowska¹, Valerie Reeb¹, Michael Nowak¹, Katalin Molnar¹, Jana U’Ren², Frank Kauff³, Ester Gaya¹, Michael Alfaro⁴, Susana Magallon⁵, and A. Elizabeth Arnold². ¹Department of Biology, Duke University, Durham, NC 27708 USA, ²School of Plant Sciences, University of Arizona, Tucson, AZ 85721 USA, ³Molecular Phylogenetics FB Biologie, TU Kaiserslautern, 67653 Kaiserslautern, Germany, ⁴Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA 90095 USA, ⁵Universidad Nacional Autónoma de México, México D.F. 04510, Mexico. flutzoni@duke.edu. **A comprehensive phylogenetic overview of spatial and host distribution of endolichenic and endophytic fungi based on 15,000 tissue samples.**

Endophytic fungi s.l. are now well established as one of the most species-rich guilds in the fungal kingdom. Increasing evidence suggests that many of these cryptic but universal symbionts of plants and lichens contribute meaningfully to host fitness in little-known ways. Yet the great majority of endophytic fungal species have not yet been described, and for the most part their phylogenetic placement within the fungal tree of life has not been inferred. We have integrated representative endophytes from >15,000 host tissue samples, representing phylogenetically diverse plants and lichens from four distinct bioclimatic regions in North America, into ITS-LSU and multilocus phylogenetic analyses restricted to the endophyte-rich Pezizomycotina. Results reveal a complex and intertwined evolution of endolichenic and endophytic fungi, with strong signals of geography and local radiations of symbiont diversity as well as trends in host specificity. This comprehensive phylogenetic study confirms our earlier inferences of their evolutionary history, suggesting that the evolution of endolichenic fungi preceded that of endophytes. Extant endophytes reflect an early origin among endolichenic fungi followed by multiple instances of colonization of plants, which occurred through host switches and lichen-independent origins of endophytism as land plants diversified and transformed the terrestrial landscape. To independently assess the validity of these results, we estimated the chronosequence of the evolution of endolichenic and endophytic fungi and their respective hosts based on estimates of divergence and diversification times of fungi and plants. Our study shows that a comprehensive understanding of the evolution of endophytic fungi and their ecological, evolutionary, and trophic transitions can be achieved only in light of large-scale sampling and robust reconstruction of their macroevolutionary history.

Lynnaun, Johnson^{1*}, Stonewall, Jason¹, McCleery, Robert², McClanahan, Rod³, Kath, Joseph⁴, and Porras-Alfaro, Andrea¹. ¹Biological Sciences, Western Illinois University, Macomb, IL 61455, ²Wildlife Ecology and Conservation PO Box 110430, University of Florida, Gainesville, FL 32611-0430, ³USDA Forest Service, Shawnee National Forest, Harrisburg, IL 62946, ⁴Illinois Department of Natural Resources, Springfield, IL 62702-1271. a-porras-alfaro@wiu.edu. **A survey of the psychrophilic fungi associated with Illinois bats including *Geomyces destructans*.**

Geomyces destructans is a psychrophilic fungus causing the deaths of almost a million bats to date. This infection by *G. destructans* is known as Geomycosis or White Nose Syndrome (WNS), started 2006 in New York. WNS has spread towards other states including Canada and threatens Illinois. Hibernacula during the winter months, when bats are hibernating, support the growth of *G. destructans* (optimal growth temperature ranges from 4 - 10 °C) but a lack

of information on the diversity of other psychrophilic fungi associated with bats prevents our understanding on adaptations, dispersal and survival of this group of fungi and their effect on the susceptibility of bats to WNS or other fungal infections. Using a modified bat swabbing technique (USDA protocol), we isolated psychrophilic fungi from *Myotis sodalis*, *Myotis septentrionalis* and *Perimyotis subflavus*. Four hibernacula were surveyed using a harp trap. A total of 30 bat wings were swabbed, inoculated in situ and incubated at 6 °C producing 170 fungal isolates from bat wings. The majority of these isolates came from *M. septentrionalis* (89 isolates). Classification based on morphospecies indicates that we obtained in pure culture at least 47 species. Temperature tests showed three potential true psychrophilic fungi and the other 167 were psychrotolerant. Direct amplification from wing punches using *Geomyces* specific primers showed no presence of *G. destructans* in IL by March 2011. Direct amplification of wing punches using general fungal primers showed a diverse fungal community including fungi closely related to Ascomycota fungi in the genus *Sphinctrina*, *Metschnikowia*, *Trichoderma*, and other unidentified fungi in the order Pleosporales as well as the Basidiomycota fungus *Crepidotus*. The presence of this high number of potential fungal competitors that are found in bat wings opens new opportunities to evaluate biocontrol strategies to control the spread of WNS in IL and other states.

López-Giráldez, Francesc^{*}, Wang, Zheng, and Townsend, Jeffrey P. Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520. francesc.lopez@yale.edu. **Assessing phylogenetic information content in fungal genomes with PhyDesign, a web application for smart marker selection.**

Molecular phylogeny has shown great advances since the field was established in the 1970s with development of sequencing techniques, genomic research, and computational biology. However, one of the enduring issues in molecular phylogeny is the lack of connection between the theory and practice of marker selection; specifically, many markers used for phylogenetic analysis have been chosen somewhat randomly in a “blind-date” way which does not necessarily maximize scientific discovery, particularly under limited resources. The genomes of nearly 150 fungi are now or are in the process of being sequenced. Most of these organisms have thousands of genes, yet only a few of those have been commonly used as markers for phylogenetic studies. The Townsend (2007) phylogenetic informativeness provides a unique empirical metric for locus prioritization optimizing cost-effectiveness of sequencing for phylogenetic purposes, as well as increasing the accuracy of phylogenetic studies. Recently, we have expanded the phylogenetic informativeness methodology to quantify the effects of sequence convergence and the relative utility of increased taxonomic versus character sampling. To facilitate the use of this methodology and obtain phylogenetic informativeness profiles, we have also developed PhyDesign, a user-friendly web application. We evaluated and applied this methodology in different fungal datasets, including a collaborative work with the AFtoL project. This collaboration revealed the existence of numerous orthologous markers that are significantly more informative than standard loci currently in use in fungal phylogenetics. Phylogenetic informativeness framework offers explicit quantitative procedures for judicious experimental design about which genes and taxa one should sequence for a given phylogenetic hypothesis.

Ma, Li-Jun. 204C Fernald Hall, 270 Stockbridge Rd, Amherst MA 01003. lijun@psis.umass.edu. **Genomic plasticity and niche adaptation – comparative genomics of plant pathogenic fungi.**

Over 400 genomes of fungi have been produced, which makes fungi the most sequenced eukaryotic taxon. Comparative genomics among these fungal genomes revealed clear correlation between genetic plasticity enabled through flexible genomic features and the rapid adaptation of the organisms, specifically reflected as pathogenicity in pathogenic fungi. Among the plant diseases, vascular wilts caused by fungal pathogens are widespread and very destructive, causing enormous economic losses. Distinctively, strains of *F. oxysporum* that cause Fusarium wilts exhibit wide host range and are pathogenic to both plant and animal species, reflecting remarkable genetic adaptability. Through comparative analysis, we identified a set of proteins that are uniquely shared among wilt pathogens, including homologs of a bacterial glucosyl transferase that synthesizes osmoregulated periplasmic glucans and plays important roles in pathogenicity. The acquisition of these genes through horizontal transfer events from Rhizobiales bacteria likely contributed to the niche adaption of these wilt fungi. Comparative study also revealed greatly expanded lineage-specific (LS) genomic regions in *F. oxysporum* that include four entire chromosomes that harbor many full-length and highly similar copies of retroelements and DNA transposons, providing genetic flexibility. These LS chromosomes also enriched in genes involved in host-pathogen interactions, including known effectors, enzymes targeting plant substrates or processes, and genes involved in lipid sig-

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nalling and gene silencing. We found evidence for the acquisition of the LS chromosomes through horizontal transfer. The mobility of these LS chromosomes probably is one of the many examples that illustrate how organism acquire genetic plasticity and adapt to its novel ecological niche and may explain the rapid emergence of new pathogenic lineages in distinct genetic backgrounds.

Madsen, Thomas P. Integrative Biology, University of California Berkeley, Berkeley, CA. tmadsen@berkeley.edu. **Ex situ seed baiting for host fungi of North American terrestrial orchids.**

All orchids are mycoheterotrophic for a portion of their lives, relying on fungal hosts to provide them with fixed carbon. Orchids that remain partially or fully myco-heterotrophic for their full life cycle typically maintain specialized relationships with their host fungi; such fungi may be readily identified from mycorrhizal tissue of adult plants. In contrast, most orchid species are myco-heterotrophic only at the seedling stage, while adult plants frequently acquire additional fungal symbionts that are incapable of supporting heterotrophic seedling development. Therefore, to infer that a fungus supports heterotrophic seedling development, it must be documented in heterotrophic seedlings. While such seedlings are most commonly obtained via *in situ* seed baiting (i.e., from seed packets buried in the field), they may also be obtained via *ex situ* seed baiting - with seed sown in the lab on field-collected soil samples. The latter approach offers protection of seeds/seedlings from environmental perturbation, as well as the ability to regularly monitor seed germination and seedling growth with out disturbing their progress. Despite the successful use of this technique with a number of Australian terrestrial orchids, it has yet to be widely adopted elsewhere. A modified approach to *ex-situ* seed baiting has yielded myco-heterotrophic seedlings of North American terrestrial orchids from the Orchidoideae, Epidendroideae and Cypripedioideae subfamilies. A variety of Tulasnelloid and Ceratobasidioid fungi have been identified in association with these seedlings.

Mallepally, Rika R.*, Mijalis, Alexander J., and de Figueiredo, Paul. Borlaug Advanced Research Center, Dept. of Plant Pathology & Microbiology, TAMU 212, Texas A&M University, College Station, TX 77843. rika.mallepally@gmail.com. **Invisible Jungle.**

Invisible Jungle is a radio program that promotes STEM education by providing interesting and relevant information to the public about the "invisible" world of microbes. An interdisciplinary group of honors students at Texas A&M University (College Station, Texas) manages all facets of research and broadcast production of the show, which started in the Fall of 2009. To date, Invisible Jungle has produced and broadcast over 60 two minute-long shows with a weekly listenership of 20,000 listeners across east central Texas. It has established itself as a regular presence within local radio and promotes access to materials via various e-media channels. We describe the genesis and development of the show, breaks with traditional STEM education banks, and our plans for expanding Invisible Jungle Radio and e-media into becoming a premier resource for educating the public about the microbial sciences.

Malloure, Brian D.* and James, Tim Y. Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109. malloure@umich.edu. **Estimating inbreeding in the bird's nest fungus *Cyathus stercoreus* using microsatellites and mating type allele distribution.**

Inbreeding leads to the loss of heterozygosity and may decrease mean population fitness. Inbreeding can result from a reduced dispersal distance among potential mates. Mushroom fungi (Agaricomycetes) generally have widely dispersed spores, which reduce the potential for inbreeding. However, within the bird's nest fungi (Nidulariaceae) spores are packaged in peridioles for dispersal, which increases the likelihood of inbreeding among siblings. Furthermore, unlike other Basidiomycetes studies on mating type numbers and distributions have shown that bird's nest fungi have a low number of mating type alleles, suggesting that they have small effective population sizes as predicted for a species undergoing a high level of inbreeding. In order to test whether the unique dispersal strategy of bird's nest fungi has led to inbreeding, we sought to estimate the degree of inbreeding using both mating type genes and neutral markers. We analyzed the allele frequencies of microsatellite and mating type alleles from three Michigan populations (n=34) of the coprophilous bird's nest fungus *Cyathus stercoreus*. We scanned an Illumina GAIx genome sequence of *C. stercoreus* to derive 78 putative microsatellite loci. We are currently screening these loci in order to estimate inbreeding coefficients and population structure in *C. stercoreus*. Additionally, we are performing a complete diallel cross on 43 isolates to determine the distribution of mating type alleles. Our results will inform how dispersal relates to inbreeding at multiple geographic scales.

Martin, Francis M. Ecogenomics of Interactions Lab, INRA-Nancy, 54280 Champenoux, France. fmartin@nancy.inra.fr. **Blurred boundaries: lifestyle lessons from ectomycorrhizal fungal genomes.**

Soils contain a multitude of fungi with vastly divergent lifestyles ranging from saprotrophic to ectomycorrhizal symbionts (ECM) and parasites. It is unknown if all classes of symbiotic fungi share a common core set of genes required for the formation of symbiosis, or if the genetic mechanisms required for mutualism were reinvented each time it developed in evolutionary history. The study of symbiosis between ECM fungi and trees has seen some significant advances with the availability of the sequenced genomes of two symbiotic fungi, that of the Basidiomycete *Laccaria bicolor* and that of the Ascomycete *Tuber melanosporum*. The genomes of these fungi are proving especially useful in characterizing the genetic foundation of mutualistic symbiosis. New insights gleaned from these genomes, as compared to their saprotrophic and pathogenic cousins, have helped to redefine and shape our understanding of the nature of the symbiotic lifestyle. It would appear, based on the different molecular 'tool-boxes' of these two ectomycorrhizal genomes, that the evolution of the symbiotic lifestyle is quite divergent. Although commonalities exist, such as a reduction in plant cell wall-degrading enzymes, large differences are also seen, such as the secretion of effector-like small secreted proteins that are present only in *L. bicolor*. To understand if the differences between these two species are due to their origins in the Ascomycota, versus the Basidiomycota, the genomes of more mycorrhizal fungi are currently being sequenced to serve as a comparison. The fact that mycorrhizal fungi appear to be independently derived from multiple saprobic lineages means that genomic data generated by current sequencing projects of saprotrophic agarics will provide independent assessments of the genetic underpinnings of mycorrhizal competence.

Matheny, P Brandon^{1*}, Bougher, Neale L.², Gates, Genevieve M.³, and Ryberg, Martin¹. ¹Department of Ecology and Evolutionary Biology, University of Tennessee, Hesler Biology Building 332, Knoxville, TN 37996, USA, ²Department of Environment and Conservation, Western Australian Herbarium, Bentley Delivery Centre, Perth, WA, Australia, ³School of Plant Science, University of Tasmania, Sandy Bay Campus, Life Sciences Building 2, Private Bag 55, Hobart, Tasmania 7001, Australia. pmatheny@utk.edu. **Patterns of diversity in Australian Inocybaceae (Agaricales).**

Australia at present features 17 species of the ectomycorrhizal family Inocybaceae in two genera, *Auritella* and *Inocybe*. This assessment is based on a revision of all available type materials of species described from the continent. However, within the past two years, exploration of different forest habitat types primarily in Tasmania and southwest Western Australia-including monographic revisions of herbarium specimens-reveals rich and diverse assemblages in the family in these areas. To date, we have detected at least 89 phylogenetic species of Inocybaceae distributed across 28 lineages based on nLSU-rRNA phylogenetic analysis. Sequences from an alternative gene, *rpb2*, uphold this pattern. The overall species number (89) is an under-estimate because not all herbarium specimens have yet been molecularly annotated and fieldwork is incomplete. Phylogenetically, Australian lineages of Inocybaceae are species-poor, containing one to three (rarely up to five) species that are highly polyphyletic throughout the family tree. This pattern would suggest that dispersal is the major mode that has produced Australia's high diversity in this group. In contrast, a single major clade has undergone extensive diversification in temperate Australia-the Smooth-spored, Temperate, Austral Clade (STAC). STAC contains at least 42 Australian species to date, plus an additional 12 *Nothofagus* or Myrtaceae-associated species from New Zealand and southern South America. STAC may be a useful clade to study the evolution of southern hemisphere ectomycorrhizal symbiosis and to test the hypothesis that *Nothofagus*-associated symbionts (putative ancient rainforest relicts) switched to Myrtaceae-associations.

May, Georgiana^{1*}, Haight, Robert², Nelson, Paul¹, and Rodríguez-Estrada, Alma¹. ¹Dept. of Ecology, Evolution & Behavior University of Minnesota, St. Paul, MN, ²Northern Research Station, US Forest Service, St. Paul, MN. gmay@umn.edu. **A defensive mutualist affects the evolution and expression of pathogen virulence.**

All pathogen's interactions with their hosts are set in a context of the community of co-occurring symbiotic organisms. Although we know that symbionts such as endophytic fungi may act as defensive mutualists, their impact on the evolution of pathogen virulence is not well understood. In this work, we use results of lab and field studies together with simulation modeling to show that endophytic fungi of maize such as *Fusarium verticillioides* may slow the evolution of virulence in pathogen's such as *Ustilago maydis*. Under deterministic models, competition from a co-occurring symbiont will often drive increasing virulence. However, with variation in either the spatial occurrence of such endophytic, or with varying effects by the endophyte on the expression of virulence by the pathogen, defensive mutualists will slow virulence evolution. We consider whether the extreme diversity in endophytic fungi might in part be explained by finding that related endophytic species, such as the *Fusarium* species in maize, apparently play very similar ecological roles.

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Mayerhofer, Michael S.^{1*}, Kernaghan, Gavin G.^{1,2}, and Harper, Karen A.³ ¹Department of Biology, Saint Mary's University, 923 Robie Street, Halifax, Nova Scotia, Canada B3H 3C3, ²Department of Biology, Mount Saint Vincent, 166 Bedford Highway, Halifax, Nova Scotia, Canada B3M 2J6, ³School of Resource and Environmental Studies, Dalhousie University, 1459 Oxford Street, Halifax, Nova Scotia, Canada B3H 4R2. michael.mayerhofer@mail.mcgill.ca. **Meta-analysis on the response of plant biomass and nitrogen concentration to non-systemic ascomycetous root endophytes.**

Meta-analysis was used to quantitatively assess the response of plant growth (root, shoot and total biomass) and nitrogen concentration to the inoculation of non-systemic ascomycetous root endophytes. This was done at three taxonomic levels: Ascomycetes, Helotiales and *Phialocephala fortinii sensu lato*. One-hundred and thirty-three studies derived from 29 publications were used in the analyses. Increases of 13.8%-27.5% in shoot biomass and 6.7%-9.8% in nitrogen concentration were observed for all taxonomic groups. Also, increases of 4.3% in total biomass and 29% in root biomass were estimated in the Helotiales and *P. fortinii* s.l. analyses, respectively. When significant heterogeneity was observed, the data were further analyzed using categorical factors. Factors describing the greatest amount of heterogeneity were publication, host species, fungal strain and type of carbon. The type of carbon added to the media or exclusion of carbon altogether caused contrasting results between biomass responses. However, the addition of carbon more frequently generated a positive response. An increase of 83.9% to 88.1% in root biomass was estimated in the Ascomycetes and the Helotiales analyses when the inoculated endophyte was isolated from the same host. Generally, the exclusion of peat moss and the addition of organic nitrogen resulted in significant increases in plant biomass ranging from 134.6% to 191.4% and as high as 692.1% when considering the addition of protein and amino acids specifically (although this latter calculation was based on a limited number of studies). Conversely, nitrogen concentration increased by 16.8% when excluding and decreased by 8.5% when including protein and amino acids. The meta-analysis indicates that plant response to the inoculation of root endophytes varies considerably depending on host plant species, endophyte species and experimental conditions. Overall, the effect seems to be neutral to slightly positive, with a limited number of studies demonstrating very high growth responses.

McDonald, Jennifer V.* and Thorn, R Greg. University of Western Ontario, Biological and Geological Sciences Building, 1151 Richmond St. N, London Ontario, N6A 5B7, Canada. mcdonald.jennifer@gmail.com. **A preliminary phylogenetic analysis of cyphelloid *Resupinateae*.**

Cyphelloid fungi (small, cup-shaped Agaricomycetes with a smooth spore-bearing surface) are, compared to their gilled relatives, very poorly studied and understood. Within the tribe *Resupinateae* (which includes *Resupinatus*, *Stigmatollemma*, *Aphyllotus* and *Stromatocypella*), little is known about the evolution of the cyphelloid fruit body form. How many times has this reduced morphology evolved within the group? Do all cyphelloid members that are currently treated in this group belong? Are there other species of cyphelloid fungi currently treated in other genera that belong within the *Resupinateae*? I will present a preliminary phylogeny of the cyphelloid and small lamellate members of the *Resupinateae* based on rDNA sequences (ITS1, 5.8S, ITS2 and the D1/D2 region of the large nuclear ribosomal subunit) to illustrate the evolution of reduced basidiomata in the *Resupinateae*. I will also provide traditional morphological characters used to distinguish species (fruit body colour and size, and spore size, shape, ornamentation and colour) and compare morphological and DNA-based classifications to illustrate a common problem in cyphelloid taxonomy: because these forms are so rarely studied, the incidence of synonymy within the group is high. The few herbarium specimens associated with many species names (for some, only the type specimen) may lead to false impressions of host specificity or restricted geographic ranges for species that are more generalist or cosmopolitan. In contrast, some previously suggested synonymies and reports based on misidentifications mask genuine patterns of hosts and geographic range.

McTaggart*, Alistair R. Department of Plant Pathology & Crop Physiology, 302 Life Sciences Building, Louisiana State University Agricultural Center. alistair.mctaggart@gmail.com. **Systematics of the *Ustilago-Sporisorium-Macalpinomyces* complex.**

Smut fungi are important pathogens of grasses, including the cultivated crops maize, sorghum and sugarcane. Typically smut fungi infect the inflorescence of their host plants. Three genera of smut fungi, *Ustilago*, *Sporisorium* and *Macalpinomyces*, form a complex with overlapping characters that makes species placement problematic. Previous attempts by others to more accurately define these genera using morphology and molecular phylogenetics have been unsuccessful and highlighted the polyphyletic nature of the genera. A systematic analysis of 137 smut species in the *Ustilago*, *Sporisorium* and *Macalpinomyces* complex was completed. Morphological and molecular data from five

loci were phylogenetically analysed by maximum likelihood and Bayesian analysis. The phylogenetic hypotheses generated were used to indicate morphological synapomorphies, which had previously been dismissed as homoplasious within the complex. These synapomorphic characters are the basis for a new taxonomic classification of the *Ustilago-Sporisorium-Macalpinomyces* complex, which takes into account their morphological diversity and coevolution with their grass hosts. The new classification is based on (i) a redescription of the type genera of *Ustilago* and *Sporisorium*, and (ii) the establishment of four new genera based on monophyletic groups to accommodate the species that are expelled from *Ustilago* and *Sporisorium*.

Mejia, Luis C.^{1,2*}, Herre, Edward A.¹, Maximova, Siela N.¹, Van Bael, Sunshine¹, and Guiltinan, Mark J.¹ ¹Smithsonian Tropical Research Institute, Balboa, Ancon, Panama, ²The Pennsylvania State University, University Park, PA, USA. mejialc@si.edu. **Microarray analysis uncovers host differential response to endophyte and pathogen infections in the tropical tree *Theobroma cacao*.**

Theobroma cacao, the source of raw material for chocolate, is a Neotropical forest tree species for which a complete genome is available. Our work has shown that fungal endophytes establish asymptomatic infections within plant tissues and help protect them against pathogens. The mechanisms by which fungal endophytes protect their host are poorly known. Here we use a *T. cacao* 17247-element Nimblegen microarray to: 1) Analyze gene expression in *T. cacao* leaves infected with *Colletotrichum tropicale*, the dominant endophyte in *cacao* and 2) Compare these to the gene expression in leaves infected with the oomycete pathogen, *Phytophthora palmivora*. We find that both endophyte and pathogen regulate genes involved in host defense pathways (ethylene signal transduction) and that the pathogen regulates double the number of genes regulated by the endophyte. Several phenotypic changes in the host can be related to the genetic changes and the benefits (increased pathogen resistance) trade off against costs i.e. reduced photosynthesis.

Methven, Andrew S.^{1*} and Nuytinck, Jorinde². ¹Department of Biological Sciences, Eastern Illinois University, Charleston, IL 61920, USA, ²Department of Biology, Universiteit Gent, Gent, Belgium. Jorinde.Nuytinck@UGent.be. **Sharing the same name: North American and European species of *Lactarius*.**

Historically, North American literature in systematic mycology has used scientific names for mushrooms based on the work of four great European mycologists: Fries, Persoon, Bulliard and Scopoli. Descriptions and illustrations of mushrooms in early North American mycological writings were compared with European literature even though abbreviated descriptions and stylized illustrations made such comparisons superficial. The result is a body of literature in which names have been loosely applied, and even 20th century workers have attached European names to American mushrooms based on tradition rather than on meticulous examination. As a result, a large number of names in use for mushrooms in the Appalachian Mountains originated in Europe. For example, a survey of the list of mushroom species in the Great Smoky Mountains National Park (GSMNP) revealed that more than one third of the 1500 mushroom names in the list originated in Europe. In the genus *Lactarius*, more than two dozen of the 100+ species of *Lactarius* reported from the GSMNP feature names of European origin. The proposed project is intended to: 1) determine if European and Appalachian species of *Lactarius* are the same; 2) establish concepts and neotypes for European taxa of *Lactarius* where necessary; 3) name and establish types for Appalachian taxa of *Lactarius* where appropriate; and, 4) assess the mycogeography of European and Appalachian species of *Lactarius*.

Miller, Stephen J., Jr.^{1*}, Masuya, Hayato², and Zhang, Ning¹. ¹Department of Plant Biology and Pathology, Rutgers University, 59 Dudley Rd, New Brunswick NJ 08901 USA, ²Department of Forest Microbiology, Forestry & Forest Products Research Institute, Matsunosato 1, Tsukuba, Ibaraki 305-8687, Japan. zhang@aesop.rutgers.edu. **Metagenomic analysis reveals hidden fungal diversity in dogwood (*Cornus*) foliage.**

The diversity of microorganisms on earth remains poorly understood. Unculturable fungi inhabiting rhizosphere, phyllosphere, and other less studied niches are thought to represent a large fraction of the unknown diversity. In this study, we used both traditional culture-dependent method and culture-independent metagenomic approach to explore the endophytic fungal communities associated with dogwood (*Cornus*) foliage. Healthy dogwood leaves were sampled from the U.S. and Japan. In culture, endophytes were recovered from 258 of the 940 leaf tissue segments resulting in 121 OTUs. *Pleuroceras*, *Elsinoe*, *Verticillium* and *Alternaria* were dominant in North American samples. *Colletotrichum* and *Penicillium* were the dominant genera in the Asian samples. A wild *Cornus kousa* sample from northeast Japan was analyzed using an Illumina GA-IIX. The metagenomic analysis yielded 284,111 unique OTUs from the

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resulting 13,117,130 sequences. Ascomycota, Basidiomycota and unassigned fungal isolates represented 48%, 28% and 24% of the OTUs identified from the metagenomic data, respectively. Ascomycota was dominant as indicated by both the culture and metagenomic methods. However, the metagenomic analysis revealed *Taphrina*, *Phaeomoniella*, and *Curreya* as the dominant taxa. Illumina metagenomic sequencing has allowed for greater coverage and detection of unculturable fungi, which helps us to better understand the diversity and role of fungi in the ecosystem.

Miller, Steven L.^{1*}, Henkel, Terry W.², and Aime, M. Catherine³. ¹Department of Botany, University of Wyoming, Laramie, WY 82071, ²Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, ³Department of Plant Pathology & Crop Physiology, 302 Life Sciences Building, Louisiana State University Agricultural Center, Baton Rouge, LA 70803. fungi@uwyo.edu. **Diversity of the ectomycorrhizal genus *Russula* in forests of the Guiana Shield.**

Legume-dominated forests (Fabaceae subfam. Caesalpinioideae) and scattered trees of the Polygonaceae, Nyctaginaceae, and Dipterocarpaceae of the central Guiana Shield harbor a rich diversity of ectomycorrhizal (ECM) Agaricomycotina and Ascomycota. At least 170 morphologically distinct ECM fungal species have been documented so far. In this assemblage, *Russula* is the most diverse genus, represented by at least 30 species; approximately 70% of these species are new to science, and are in the process of being formally described. In contrast to the many *Russula* spp. from temperate regions with deep yellow spore prints, species from Guyana produce white spore prints. This is consistent with *Russula* spp. from the tropics in general, and suggests that tropical species may be more ancient. *Russula* spp. from Guyana are morphologically diverse, with pleurotoid, annulate and agaricoid species, and both brightly and cryptically colored species. There is a diminutive stipitate species less than one cm in diameter, numerous “mycenoid” species with thin flesh and striate pileus features, and many with velutinous, hispid or gossypinoid stipe and/or pileus surfaces. These fungi are also microscopically diverse, with unusual cuticular structures and cystidia, microchemical staining reactions, and spore ornamentation. At least one species produces cells in the dermis that are attractive to ants; the ants preferentially graze on the pileus and stipe cuticle. Evidence from morphological and molecular analyses indicates close ties of several Guyana *Russula* spp. to taxa from central Africa and tropical Asia, while others appear to be unique to the Guiana Shield. A number of species in three common and widespread subsections intergrade morphologically, and are difficult to reliably distinguish. Additional population-level study in concert with critical morphological examination will be necessary to fully elucidate the species boundaries.

Moebius-Clune, Daniel J.^{1*}, Moebius-Clune, Bianca N.², Anderson, Zoe¹, and Pawlowska, Teresa E.¹ ¹Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853, ²Department of Crop and Soil Sciences, Cornell University, Ithaca, NY 14853. djc74@cornell.edu. **Arbuscular mycorrhizal fungal communities in maize fields are diverse, strongly dominated, and likely shaped by soil textural characteristics.**

Arbuscular mycorrhizal fungi (AMF) are of interest to agroecology due to the numerous potential benefits their presence can provide. But, while mycorrhizal host plants are non-specific in association with AMF fungi, the functional outcome of the interaction varies depending on the identities of the partners. So, it is important to understand the composition of the AMF community in agroecosystems, and to identify the features of these environments that may influence the fungal community structure. We explored the AMF community in a selection of maize fields across a landscape in eastern New York State and characterized their diversity, dominance, and species abundance distribution. Species abundances were distributed lognormally, suggesting that several factors influence community structure. We observed strong dominance across the landscape and in multiple fields of one taxon, while other taxa were frequent but never dominant. This abundance distribution, diversity, and pattern of strong dominance, are consistent with observations for AMF communities in other, non-agricultural ecosystems. We used indirect gradient analysis, using NMDS ordination of both taxon-based (Bray-Curtis) and phylogeny-based (UniFrac) dissimilarity measures, to identify edaphic factors shaping the AMF community. The two approaches revealed different, but complementary, indications that soil textural components, rather than phosphorus or pH, are associated with compositional differences in the AMF community structure.

Mohatt, Katherine R.^{1*}, Dillman, Karen L.², Trudell, Steve³, and Cooper, Erin⁴. ¹USDA Forest Service, Girdwood, AK, 99587, ²USDA Forest Service, Petersburg, AK, 99833, ³College of Forest Resources, University of Washington, Seattle, WA, 98195, ⁴USDA Forest Service, Cordova, AK, 99574. kmohatt@fs.fed.us. **Expanding our knowledge of Southern Alaska's macrofungi through fungus-themed events.**

Southern Alaska contains the two largest National Forests in the Nation, and a majority of the State's population is located near these Sitka Spruce and Mountain/Western Hemlock dominated forests. Each fall these forests host prolific fruitings of mushroom-producing species similar to those found in the Pacific Northwest. To accommodate growing public interest, the Chugach and Tongass National Forests have hosted a series of events celebrating fungi during the peak of fruiting season since 2007. The first of these events is the Fungus Fair just outside of Anchorage in the small resort town of Girdwood which occurs the last weekend in August. This is followed by the Fungus Festival in Cordova in western Prince William Sound on Labor Day weekend. The final event is the Tongass Rainforest Festival in Petersburg on Mitkof island in Southeast Alaska the following weekend. Many out-of-state guest mycologists have contributed to these events over the years including Dr. Steve Trudell, Dorothy Beebe, Dr. Matt Trappe, Dr. Thom O'Dell, Dr. Lawrence Millman and mycochef Patrick Hamilton in addition to participation by local clubs and enthusiasts. Activities throughout these events include talks, forays, display tables, workshops for dyeing and growing edible species, and lavish five-course mushroom feasts. Prior to these festivals, there was little information on fungi from the coastal rainforest belt of Southern Alaska. Thanks to visiting mycologists and local collectors, knowledge of locally occurring fungi in these areas has been greatly expanded by the accumulation of annual records produced by these events. Further, attendance has risen steadily each year indicating a growing interest in fungi by residents. These events are an important interface between amateur and professional mycologists that benefits our knowledge of fungal biodiversity.

Moore, Geromy G.^{*}, Beltz, Shannon B., and Cary, Jeffrey W. Southern Regional Research Center, USDA, ARS, New Orleans, LA. geromy.moore@ars.usda.gov. **Molecular investigations of *Aspergillus ochraceoroseus* and *Aspergillus rambellii*.**□

Aspergillus ochraceoroseus and *A. rambellii* are two species that are full of mystery. To current knowledge they have only been sampled once, from the Tai National Park, in an African nation experiencing great civil unrest, the Côte d'Ivoire (Ivory Coast). Having only a single isolate for each species, previous investigations revealed that there exists a cluster of secondary metabolite genes in *A. ochraceoroseus* and *A. rambellii* that has homologues to both sterigmatocystin and aflatoxin gene clusters. In fact, both species produce sterigmatocystin (ST) and aflatoxin (AF), but the genes are not organized in the order usually observed in pathways which produce either ST or AF. *A. rambellii* reportedly produces B1 aflatoxin in excess of most measured toxigenic isolates. Since the characterization of the *A. ochraceoroseus* “gene cluster”, there is interest in determining the relative ages of the *A. ochraceoroseus* and *A. rambellii* cluster genes compared to homologues in species that only produce ST or AF. Utilizing population genetic analyses, we hope to discover whether or not *A. ochraceoroseus* and *A. rambellii* formed from hybridization across sub-genera. Alternatively, these species may be the progenitors of modern-day ST and AF producers in the Aspergilli. Various cluster amino acid/gene sequences will be comparatively analyzed using the SNAP Workbench. As well, investigating the presence of a *MAT* locus might help elucidate why these unique species are found in such low frequency.

Moreau, Pierre-Arthur^{1*}, Rochet, Juliette^{2,3}, Jargeat, Patricia^{2,3}, Manzi, Sophie^{2,3}, Gryta, Hervé^{2,3}, Roy, Mélanie^{2,3}, and Gardes, Monique^{2,3}. ¹Laboratoire de Botanique, Faculté des Sciences Pharmaceutiques et Biologiques, Université Lille, Nord de France, B. P. 83, F - 59006, Lille Cedex, France, ²Université de Toulouse, UPS, UMR 5174 EDB, 118 route de Narbonne, 31062 Toulouse Cedex 4, France, ³CNRS, UMR 5174 EDB, 31062, Toulouse Cedex 4, France. pierre-arthur.moreau@univ-lille2.fr. **How to become an *Alnus*-associated basidiomycota: a phylogenetic approach in eight ectomycorrhizal genera.**

Alnus (Betulaceae), a tree genus of temperate to subarctic distribution, is known to host an exceptional species-poor and specialized ectomycorrhizal (ECM) fungal community compared to other trees. Recent studies in Europe and America have recently documented the composition of these fungal communities, but the host-specificity pattern and its significance in terms of fungal diversification and speciation remain poorly documented. Relationships between fungal species and host specialization were especially explored in eight ECM genera of Basidiomycota, based on both sporocarp and mycorrhiza samplings: *Alnicola* and *Cortinari* (Agaricales), *Alpova*, *Gyrodon*, *Melanogaster* and *Paxillus* (Boletales), *Lactarius* and *Russula* (Russulales), and dominant species of *Tomentella* (Thelephorales). Multigene phylogenetic reconstructions in these groups define 47 phylogenetic species, also characterized by morphological and ecological data. Only 7 species are identified as alnicolous without tree specificity. Amongst the 19 lineages here identified as only including *Alnus*-specific fungi, at least 9 of them contain species strictly associated with *Alnus* subgen. *Alnus* in basal position, which suggests a relatively recent origin of the associa-

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tion with alder trees of this subgenus, followed or not by a speciation on the same hosts (host-dependent radiation). Only 3 lineages are clearly identified (and 2 are suspected) to have basal species associated with *Alnus* subgen. *Alnobetula* (the first which was differentiated from tropical ancestors). But many more species are currently associated with *Alnus* subgen. *Alnobetula*; most of them (at least 11) are found within *Alnus* subgen. *Alnus*-associated lineages in derived position, suggesting a recent speciation process driven by host shift. These global results give a preliminary overview of the history of this singular ECM symbiosis, the most specific described so far, and suggest a few number of events (host specialization from unspecialized species, host-dependant speciation, and late host-shifts) which can be responsible of the composition of the currently known communities.

Morrison, Eric W.^{1*}, Frey, Serita D.¹, Thomas, W Kelley², and Bik, Holly M.²
¹Department of Natural Resources, University of New Hampshire, Durham, NH 03824, ²Hubbard Center for Genome Studies, University of New Hampshire, Durham, NH 03824. ewj4@unh.edu. **Effects of nitrogen fertilization on fungal community composition in hardwood forests of the northeastern USA.**

Nitrogen deposition from fossil fuel combustion has the potential to affect important ecosystem processes and is regulated under Title IV of the Clean Air Act. The soil microbial community regulates decomposition in soils, and changes in this community affect the global carbon cycle and the global N cycle. Simulated N deposition has been observed to reduce fungal:bacterial biomass ratios, decrease the activity of ligninolytic enzymes, and decrease rates of litter decomposition, leading to an accumulation of C in the forest floor of a northeastern hardwood forest ecosystem. Chronic N deposition may decrease fungal biodiversity and cause a shift in fungal community composition in this ecosystem. Pyrosequencing of fungal ITS sequences may allow deep coverage of fungal diversity in highly diverse soil environments. The Harvard Forest Chronic Nitrogen Addition experiment was established in 1988 to test the effects of chronic N additions on a mixed hardwood forest ecosystem. Plots receive ambient N deposition (control), 50 kg N ha⁻¹ yr⁻¹ (low N), or 150 kg N ha⁻¹ yr⁻¹ (high N). Three replicate organic soil samples were taken from each plot in November 2009 to test the effects of chronic N deposition on fungal community diversity and composition. DNA was extracted and ITS2 was amplified using ITS4 and 5.8s primers with MID tags and Roche 454 FLX Titanium A and B adaptors. Amplicons were sequenced in two lanes of a Roche 454 sequencing reaction. Sequences were parsed and clustered at various sequence similarity levels using the OCTUPUS pipeline for 454 data processing developed at the University of New Hampshire. Preliminary results indicate a decrease in Shannon diversity with N fertilization and significant changes in relative abundance of dominant taxa. OTUs with BLAST hits against two *Russula* species were dominant. One of these species increased with increasing N fertilization while the other declined.

Mouriño-Pérez, Rosa R.^{*}, Callejas-Negrete, Olga A., Delgado-Alvarez, Diego L., and Bartnicki-Garcia, Salomon. Departamento de Microbiología. Centro de Investigación Científica y Educación Superior de Ensenada. Ensenada, B.C. Mexico. rmourino@cicese.mx. **Chronology of actin structures during septum formation in *Neurospora crassa*.**

Filamentous actin (F-actin) plays essential roles in filamentous fungi, as in all other eukaryotes, in a wide variety of cellular processes including cell growth, intracellular motility, and cytokinesis. We visualized F-actin organization and dynamics in living *Neurospora crassa* via confocal microscopy of growing hyphae expressing GFP fusions with homologues of the actin-binding proteins, namely fimbrin (FIM) and tropomyosin (TPM-1), a subunit of the Arp2/3 complex (ARP-3), coronin (cor1), and Lifeact, a recently developed actin marker. All these GFP fusion proteins were transiently localized at septa in the following sequence. Lifeact-GFP first appeared as a broad ring during early stages of contractile ring formation and later coalesced into a sharper ring. TPM-1-GFP was observed in maturing septa, and after a few seconds FIM-GFP/ARP3/COR1-GFP labeled cortical patches formed a double ring flanking the septa. Our observations suggest that each of these F-actin-binding proteins associates with a different subset of F-actin structures, presumably reflecting distinct roles in F-actin organization and dynamics during all the stages of septation. Actin is present from the early stages of septum formation, the contractile force of the actomyosin ring is related to the presence of tropomyosin and it seems that there is a need of plasma membrane remodeling as deduced by the presence of endocytic patches labeled by fimbrin, coronin and Arp2/3 complex.

Mueller, Olaf^{1*}, Blanc, Guillaume², Collart, Frank³, Larsen, Peter³, Martin, Francis⁴, Morin, Emmanuelle⁴, Lutzoni, François¹, and Armaleo, Daniele¹. ¹Department of Biology, Duke University, Durham, NC 27708 USA, ²Information Génétique et Structurale (IGS), CNRS-UPR2589, IFR-88, Marseille, France, ³Argonne National Laboratory, 9700 S. Cass Avenue, Argonne, IL 60439, USA, ⁴UMR 1136, INRA-Nancy Université, Interactions Arbres/Microorganismes,

INRA-Nancy, 54280 Champenoux, France. olaf.mueller@duke.edu. **Evolutionary insights from comparative genomics of lichen symbioses.**

Mutual recognition of plants and fungi remains a vital question in cellular communication of either pathogenic or mutualistic relationships. The genomes of the lichen-forming ascomycete *Cladonia grayi* (mycobiont) and its photoautotrophic symbiont, the single-celled green alga *Asterorochloris* sp. (photobiont), were sequenced and analyzed to identify and study genes crucial for establishing lichen symbiosis. To achieve this goal annotated gene models of *C. grayi* were compared to 10 reference genomes of species representing the closest related Ascomycota taxa, i.e., representing Eurotiomycetes, Leotiomycetes, Sordariomycetes and Dothideomycetes. An initial mutual best-hit blast approach was performed to identify similarities and differences in gene inventories, and to provide a scaffold for detailed phylogenetic analyses. Additional Markov cluster (MCL) studies compiled extended and contracted gene families in the *Cladonia* mycobiont and photobiont, and were investigated separately phylogenetically. Because the origin of the lichen symbiosis exemplified by *C. grayi* dates back at least to the divergence of the Lecanoromycetes from other classes of fungi composing the Leotiomycota, a major shift in selection pattern is expected for genes essential to the establishment and maintenance of this symbiosis. Candidates genes identified in this manner, will be discussed in light of results from transcriptomic and metabolomic analyses derived from RNA isolated from the mycobiont and photobiont growing separately, and together in early lichen symbiosis reconstitution experiments.

Mujic, Alija B.^{1*}, Hosaka, Kentaro², and Spatafora, Joseph W.¹ ¹Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA, ²Department of Botany, National Museum of Nature and Science (TNS), Tsukuba-shi, Ibaraki, 305-0005, Japan. mujica@science.oregonstate.edu. **Mycorrhizal discoveries in Japan support monophyly of *Pseudotsuga* ectomycorrhizal host relationships within the genus *Rhizopogon*.**

Rhizopogon (Basidiomycotina: Boletales) is a large genus of ectomycorrhizal (EM) fungi that produces hypogeous, truffle-like, basidiocarps in association with host trees of the family Pinaceae. Generic level host association is a polyphyletic trait across *Rhizopogon* with the exception of *Rhizopogon* subgenus *Villosuli*, which possesses an apparently monophyletic host relationship with the genus *Pseudotsuga*. *Pseudotsuga* species are naturally distributed around the northern Pacific Rim but the monophyly of the *Rhizopogon-Pseudotsuga* EM symbiosis is currently demonstrated only from North America for the host tree *P. menziesii*. We sampled hypogeous sporocarps and EM root tips from *Pseudotsuga japonica* (Togawara) forests on the Japanese Islands of Honshu and Shikoku. These field surveys produced the first account of *Rhizopogon* species associated with Asian *Pseudotsuga* hosts. Molecular and morphological analysis distinguish basidiocarps discovered under *P. japonica* as a new species of *Rhizopogon* subgenus *Villosuli* which is provisionally described here as *Rhizopogon togasawarensis* nom. prov. The monophyly of *Rhizopogon-Pseudotsuga* symbiosis, the ecological significance of the symbiosis in North America and hypothesized processes of *Pseudotsuga* speciation support a single evolutionary origin for the symbiosis. These factors make the *Rhizopogon-Pseudotsuga* symbiosis an excellent model system for the study of the evolutionary biology of EM host specificity and its role within host evolution and ecological interaction. *Pseudotsuga menziesii* is a tree of great ecological and economic importance in North America and *P. japonica* is listed as "vulnerable" on the Red List of Threatened Plants of Japan. An understanding of the systematics of the *Rhizopogon-Pseudotsuga* symbiosis provides valuable information useful in forest ecosystem conservation and management of harvested stands that are under growing pressures presented by global climate change.

Nakasone, Karen K.¹ and Burdsall, Harold H., Jr.^{2*}. ¹CFMR, USDA-FS, Northern Research Station, Madison, WI, ²Fungal & Decay Diagnostics, LLC, Black Earth, WI. knakasone@fs.fed.us. **A new genus/species of wood inhabiting resupinate from Alaska.**

More than 250 species of wood inhabiting basidiomycota are reported from Alaska. Several collecting trips to Alaska during the past 20 years by the second author resulted in the collection of many of these species, as well as some that are new to science. Herein, we present an undescribed taxon that is found exclusively on the bark of living *Tsuga mertensiana*, mountain hemlock. Although morphologically similar to the genus *Dendrothele*, this new taxon is shown by molecular sequence analysis of the large subunit of the nuclear ribosomal gene to be in the Hymenochaetales and not with *Dendrothele* in the Agaricales. A new genus will be proposed to accommodate this new taxon. Both will be described formally in the near future.

Nelsen, Matthew P. Committee on Evolutionary Biology, University of Chicago, Chicago, Illinois, Department of Botany, The Field Museum, Chicago, Illi-

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nois. mpnlsen@gmail.com. **Patterns and processes of diversification in lichen-forming ascomycetes.**

The disparity in species richness across fungal lineages is striking. Within the subclass Lecanoromycetidae (Lecanoromycetes: Ascomycota), this unevenness is especially pronounced, with the number of species per family ranging from under 15 to nearly 2500. Here potential explanations for this imbalance, focusing on clade age and diversification rate, are explored. Net diversification rates are estimated for individual families and clades with exceptionally high or low diversification rates are identified. Additionally, I discuss whether the observed levels of diversity are consistent with a diversity dependent pattern of diversification.

Nelson, Peter R. Department of Botany and Plant Pathology Cordley Hall 2082 Oregon State University Corvallis, Oregon 97331-2902. nelsopet@science.oregonstate.edu. **Mapping lichens using satellite imagery.**

Lichens are a ubiquitous vegetation component across high latitudes and a large portion of the overall vegetation community diversity. Lichens are also important winter food for caribou. Mapping lichens using satellite imagery is possible because they are spectrally distinct from other surfaces but requires accurate, spatially extensive vegetation data. We mapped the abundance of 3 different lichen groups (total lichen, all usnic acid lichens and usnic acid caribou forage lichens (*Cladonia* sp.) in Denali National Park and Preserve, Alaska using vegetation abundance data from >500 plots in the NPS vegetation monitoring system, LANDSAT 7 ETM+ satellite data and physiognomic variables for each plot. Maps were made from models of lichen abundance using the satellite imagery and physiognomic variables as predictors. Models of lichen abundance had hump or sloped ridged-shaped response surfaces, with highest lichen abundance at medium brightness values of selected satellite bands. Elevation was negatively related to usnic and caribou forage lichen abundance. The expected spectral signatures of the lichens were corroborated by the model predictor selection for the usnic and caribou lichens, after accounting for elevation. In contrast, best model for total lichen lacked elevation and had different predictors than the best models for the other two groups. The total lichen models differed from the other two lichen models likely because total lichen incorporates groups that are spectrally heterogeneous. All the best models for each lichen group had cross-validated $R^2 > 0.30$. The solar radiation index was not selected as important for any of models for the three lichen groups. We compare the maps of the 3 lichens groups and interpret their differences based on ordination of plots in spectral space and the spatial patterns between the maps. These maps could be used for mapping caribou food resources and describing patterns lichen communities across vast inaccessible landscapes.

Nguyen, Nhu H. Dept. of Plant and Microbial Biology, 111 Koshland Hall, UC Berkeley, Berkeley CA 94720. xeranthum@berkeley.edu. **Longevity, dormancy, and a fiery re-awakening of ectomycorrhizal fungal spores.**

Some ectomycorrhizal fungi follow a similar pattern to plants in leaving dormant and long-lived propagules in the soil. However, few studies have examined the longevity of spores beyond 1 year. Using pine seedlings, we bioassayed 6 year old forest soils where we recovered species in the genera *Rhizopogon*, *Suillus*, and *Wilcoxina*. The spores in this spore bank await certain signals from the environment to break their dormancy. This signal could come from the host plant or other environmental conditions. Previously, we showed that spores of *Rhizopogon* species can persist in the soil for at least four years and all species exhibited increased viability (Bruns *et al* 2009). However, after two years the viability of *Rhizopogon olivaceotinctus* decreased noticeably. By heat-treating the spores, we show that heat is a stimulatory factor that breaks the dormancy of *R. olivaceotinctus*, an observation that had never been reported for any ectomycorrhizal fungi. These data together suggest that spores of some ectomycorrhizal fungi can persist in the soil for long periods of time and that other environmental factors in addition to host signals are required to break dormancy.

Niskanen, Tuula^{1*}, Liimatainen, Kare¹, Ammirati, Joe², and Kytövuori, Ilkka³. ¹Plant Biology, Department of Biosciences, PO Box 65, 00014 University of Helsinki, Finland, ²Department of Biology, 351330, University of Washington, Seattle, WA 98195, USA, ³Botanical Museum, PO Box 7, FI-00014 University of Helsinki, Finland. tuula.niskanen@cortinari.us. **Diversity of *Cortinarius* in boreal North America and Europe.**

Fungi play a significant role in the boreal ecosystems. Species diversity and richness are high, the fungi are poorly known, and many commonly encountered macrofungi are undescribed species. Consequently very little is known about species distributions or differences in intercontinental species composition across the boreal region. This study is focused on *Cortinarius*, the most species rich genus of Agaricales. Both morphological and molecular (ITS) data are being used to study the different subgenera of *Cortinarius* in boreal North America and Europe. Based on our studies endemic species occur in

Western North America, Eastern North America and Europe. Also these regions have many, presumably circumboreal species, in common. Most similar is the species composition of Eastern North America and Europe as compared with that of Western North America. In the majority of taxonomic groups the number of species is greater in North America than in Europe likely due to the larger geographical area, climate and geological history. New information about species host specificity was also gained. For example, in Europe many species seem to be locally host specific, e.g. *C. luteo-ornatus* (sect. *Armillati*) is associated with conifers in the boreal zone while in the subalpine zone it occurs with birch. In all the taxonomic groups undescribed species were found, e.g. in the section *Armillati*, the number of new species is as high as the number of known species. Our studies included a careful evaluation of *Cortinarius* types; mainly species of *Telamonia* described from North America. Interestingly, almost fifty percent of the North American type species were the same as European species, and most of the names were synonyms of already described species. The results show that considerable work remains to be done on *Cortinarius* and underscores our lack of current knowledge of this important ectomycorrhizal genus in boreal ecosystems.

Olarte, Rodrigo A.^{1*}, Horn, Bruce W.², Monacell, James T.^{1,3}, Singh, Rakhi¹, and Carbone, Ignazio¹. ¹Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695, ²National Peanut Research Laboratory, Agricultural Research Service, US Department of Agriculture, Dawson, GA 39842, ³Bioinformatics Research Center, North Carolina State University, Raleigh, NC 27695. ignazio_carbone@ncsu.edu. **Recombination and cryptic heterokaryosis in *Aspergillus flavus*.**

Aspergillus flavus is a pathogen of many agronomically important crops worldwide and can also cause human and animal diseases. *A. flavus* is the major producer of aflatoxins (AFs), which are carcinogenic secondary metabolites. In the United States, mycotoxins have been estimated to cause agricultural losses totaling upwards of \$1.66 billion annually. In 1974, an AF poisoning epidemic resulted in 106 human deaths in western India, and more recently, in 2004, 125 deaths were reported in Kenya, East Africa. We recently described *Petromyces flavus*, the sexual state of *A. flavus*, from crosses between strains of the opposite mating type. We demonstrated that sexual reproduction in *A. flavus* is heterothallic and occurs between individuals belonging to different vegetative compatibility groups, which suggest that the vegetative compatibility system is not a barrier to genetic exchange and recombination. In the present study, we genetically examined the F1 offspring from several successful crosses. Linked loci within the AF gene cluster on chromosome 3 and unlinked loci on different chromosomes were analyzed to detect crossovers and independent assortment. Our data indicate that recombination increases the effective population sizes of aflatoxigenic fungi and may be driving genetic and functional hyperdiversity in *A. flavus*. We also observed non-Mendelian inheritance of extra-genomic AF cluster alleles in crosses with partial AF cluster parents, which suggests a possible role of cryptic heterokaryosis, in addition to sexual recombination, in modulating AF production.

Oliver, Jason P. University of Minnesota, Department of Bioproducts & Biosystems Engineering, 203 Kaufert Lab, 2004 Folwell Avenue, St. Paul, MN 55108. oliv0328@umn.edu. **Fishin' Chips: Characterizing the role of fungi in gas-phase wood chip biofilters.**

Confined animal feeding operations (CAFOs), like swine farms, are one of many examples of diffuse point sources of gaseous pollution locally (odor) and globally (greenhouse gases). Recently, low-cost wood chip biofilters (WCBs) have shown potential to mitigate emissions of NH₃, reduced sulfides, CH₄, N₂O, odor, and VOCs while reducing dust and bioaerosols. To date, however, the microbial communities in WCBs are poorly characterized. Understanding these communities will enable better control of the biofilters, improving reliability and robustness; e.g. by reducing lag time following media replacement. Our work is focused on the role of fungi in WCBs. Fungi are hypothesized to improve WCB performance by tolerating desiccation and acidification, and by accelerating the phase-transfer and capture of emissions via high surface area hyphae with hydrophobic properties. At an active swine facility in Morris, MN, we are using defined wood chip baits to explore the microbial communities in two WCBs using different size birch chips (2" & 4" mesh). Bulk sampling of biofilter media is also being conducted in Morris and at other WCBs in Minnesota counties where biofilter use is mandated. Chips baited at the time of WCB construction are being collected through a 3 yr. period to look at community development in the media at shallow and deep depths and at close and far proximities to inlet emissions. Emissions (H₂S, NH₃, CH₄, CO₂, N₂O) are being monitored continuously before and after biofiltration using a series of regularly calibrated gas analyzers. Total microbial biomass determination by chloroform fumigation extraction has been developed targeting wood surfaces, and is complemented by ergosterol determination to assess fungal: total microbial

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biomass ratios. Correlating these data with sampled gaseous emissions and wood characterization over time, and with microscopy and molecular methods being developed, we can better describe the role of fungi in WCBs.

Oono, Ryoko^{1,2*}, Arnold, A. Elizabeth³, May, Georgiana⁴, Lutzoni, François¹, and Carbone, Ignazio². ¹Department of Biology, Duke University, Durham, NC 27708, ²Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695, ³School of Plant Sciences, The University of Arizona, Tucson, AZ 85721, ⁴Department of Ecology, Evolution, and Behavior, University of Minnesota, St. Paul, MN 55108. ryoko.oono@duke.edu. **Population structure in *Lophodermium* sp., a dominant fungal endophyte of loblolly pine.**

Foliar fungal endophytes of woody plants are usually horizontally transferred and frequently comprise phylogenetically diverse communities within single host plants. However, endophyte species are not typically equally represented in a host. In central North Carolina, endophyte communities within mature foliage of loblolly pine (*Pinus taeda*) are markedly dominated by a single species of *Lophodermium* (Rhytismatales). Haplotype analyses of the nuclear ribosomal internal transcribed spacers and 5.8S gene (ITS) suggest cryptic structure within our study population with uncertain implications for local-scale host-endophyte co-evolution. Here we present results of fine-scale population analyses of *Lophodermium* endophytes based on 1) microsatellites developed using 454 sequencing and 2) various intra-population parameters, such as genetic diversity, rates of recombination, linkage disequilibrium, and different selection pressures. This study provides new insight into the capacity of ITS data to capture population-level structure and highlights the cryptic structure in host affiliations that may underlie many endophyte-plant associations.

Padamsee, Mahajabeen* and McKenzie, Eric HC. Biosystematics Team, Landcare Research, Auckland 1072, New Zealand. padamsee@landcareresearch.co.nz. **Towards a comprehensive phylogeny of New Zealand rust fungi.**

New Zealand can be considered to have a depauperate representation of Pucciniales. Of the 166 recognized genera worldwide, only 22 have been recorded from New Zealand. Although these rust fungi have been well characterized morphologically, they have barely been studied using molecular data. We have set out to comprehensively study and construct a preliminary phylogeny of the approximately 250 species of rust fungi found in New Zealand. We sampled native and introduced rust species to generate sequence data from the nuclear large subunit gene. Amongst the first set of specimens sequenced were isolates from the Chatham Island forget-me-not (*Myosotidium hortensium*). Despite its *Uredo*-like morphology, the position of this fungus in the phylogeny suggests that it may represent a new, undescribed genus of rust fungi. Further investigations using additional genes may reveal other unique lineages of Pucciniales and will enable a better understanding of the evolution of New Zealand rust fungi.

Padamsee, Mahajabeen¹, Binder, Manfred^{2*}, Kumar, TK Arun³, Riley, Robert⁴, Boyd, Alex⁵, Calvo, Ana⁶, Furukawa, Kentaro⁷, Hesse, Cedar⁸, Hohmann, Stefan⁷, James, Timothy Y.⁸, LaButti, Kurt⁴, Lapidus, Alla⁴, Lindquist, Erika⁴, Lucas, Susan⁴, Miller, Kari³, Shantappa, Sourabha⁶, Hibbett, David S.², Spatafora, Joseph W.⁵, Grigoriev, Igor V.⁴, McLaughlin, David J.³, and Aime, M Catherine¹. ¹Louisiana State Univ. Agricultural Center, Dept. Plant Pathology & Crop Physiology, Baton Rouge, LA, USA, ²Clark Univ., Dept. Biology, Worcester, MA, USA, ³Univ. Minnesota, Dept. Plant Biology, St. Paul, MN, USA, ⁴US Dept. of Energy Joint Genome Institute, Walnut Creek, CA, USA, ⁵Oregon State Univ., Dept. Botany & Plant Pathology, Corvallis, OR, USA, ⁶Northern Illinois Univ., Dept. Biological Sciences, Dekalb, IL, USA, ⁷Univ. of Gothenburg, Dept. Cell & Molecular Biology/Microbiology, Gothenburg, Sweden, ⁸Univ. of Michigan, Dept. Ecology & Evolution, Ann Arbor, MI, USA. maime@agcenter.lsu.edu. **The *Wallemia sebi* genome: small in size but reveals clues to surviving an osmotically challenging environment.**

Wallemia (Wallemiales, Wallemiomycetes) is a genus of xerophilic Fungi that is of uncertain phylogenetic position within the Basidiomycota. Most commonly found as food contaminants, species of *Wallemia* have also been isolated from hypersaline environments. The ability to tolerate low water environments is rare in the Basidiomycota and suggests several adaptations involving osmoregulation. We sequenced the genome of *Wallemia sebi* in order to test whether it possesses any unique genomic adaptations for surviving osmotically challenging environments, and coupled genome and phylogenetic analyses with ultrastructural studies aimed at addressing other questions about its biology. Compared with other Basidiomycota, *W. sebi* has a compact genome (9.8 Mb), with few repeats and the largest fraction of genes with functional domains. *In silico* analyses identified >90 putative osmotic stress proteins, the domains of which possess a relatively high number of transporters that may be correlated with the ability to live under osmotic stress. Despite the seemingly reduced genome, several gene family expansions were revealed that also provide clues

to the ability of *W. sebi* to colonize harsh environments. Phylogenetic analyses of 71 single protein datasets support the position of *Wallemia* as the earliest diverging lineage of Agaricomycotina, which is confirmed by septal pore ultrastructure. Mating type gene homologs were identified although we found no evidence of meiosis during conidiogenesis, suggesting there may be aspects of the life cycle of *W. sebi* that remain cryptic.

Park, Hyun*, Ka, Kang-Hyeon, and Sou, Hong-Duck. Korea Forest Research Institute 57 Hoegiro, Dongdaemungu, 130-712, Seoul, Korea. hyunpark@korea.kr. **Cultivation of Chaga mushroom (*Inonotus obliquus*) on a living tree of *Betula* species.**

We attempted to obtain fruiting bodies of *Inonotus obliquus* through artificial inoculation of *Betula platyphylla* var. *japonica* trees that are planted widely in Korea. The inoculum was prepared using a strain isolated from *Betula ermani* from Mt. Odae in Korea grown in a sawdust-based medium mixed with sawdust of *Quercus mongolica* and rice bran (8:2 on weight basis). The inoculum (spawn) was injected using a spring-inoculator, and the surface was covered by a styrofoam stopper. We isolated the same fungus from the inoculated site 14 months later, demonstrating that the inoculation was successful. About 30 months after the inoculation, we observe several sclerotia 3-4 cm on trunks of host trees. The sclerotia resembled those collected from natural habitats, but were smaller than natural ones. About 35 months after the inoculation, the sclerotia were 1.1-4.8 cm wide and 0.5-2.0 cm thick. We expect that more than 10 years will be needed to obtain commercial conks (sclerotia) from these artificial infections. The growth rate of the sclerotia will be monitored to determine the suitable time for obtaining the greatest economic value.

Peay, Kabir G.^{1,2*}, Beslisle, Melinda², and Fukami, Tadashi². ¹Dept. of Plant Pathology, University of Minnesota, St. Paul, MN 55108, ²Dept. of Biology, Stanford University, Stanford, CA 94305. peay0001@umn.edu. **Phylogenetic relatedness predicts priority effects in nectar yeast communities.**

Priority effects, in which the outcome of species interactions depends on the order of their arrival, are a key component of many models of community assembly. Yet much remains unknown about how priority effects vary in strength among species in a community and what factors explain this variation. We experimented with a model natural community in laboratory microcosms that allowed us to quantify the strength of priority effects for most of the yeast species found in the floral nectar of a hummingbird-pollinated shrub at a biological preserve in northern California. We found that priority effects were widespread, with late-arriving species experiencing strong negative effects from early-arriving species. However, the magnitude of priority effects varied across species pairs. This variation was phylogenetically non-random, with priority effects stronger between closer relatives. Analysis of carbon and amino acid consumption profiles indicated that competition between closer relatives was more intense due to higher ecological similarity, consistent with Darwin's naturalization hypothesis. These results suggest that phylogenetic relatedness of potential colonists may explain the strength of priority effects and, as a consequence, the degree to which community assembly is historically contingent.

Perry, Brian A.* , Datlof, Erin, and Kodis, Mali'o. Biology Department, University of Hawaii at Hilo, 200 W Kawili St., Hilo, HI 96720. baperry@hawaii.edu. **Foliar endophytic community structure in wild and cultivated stands of Hawaiian 'ohi'a lehua (*Metrosideros polymorpha*).**

Although associated with all plants that have been investigated, the taxonomic, genetic and functional diversity of endophytic fungi remains undocumented for many regions, including the Hawaiian Islands. Fungal endophytes have been shown to confer such benefits as increased draught tolerance, resistance to pathogens, and anti-herbivory properties. Additionally, fungal endophyte composition has been shown to play a large role in altering vegetation dynamics and plant community composition. Given the potential roles of fungal endophytes, it is clear that a detailed understanding the taxonomic and genetic diversity of these symbionts should be addressed as conservation and management plans for host species are developed. To assess such diversity in a native Hawaiian taxon, we examined foliar fungal endophytic community structure in elevational phenotypes of wild and cultivated *Metrosideros polymorpha* ('ohi'a lehua) using environmental PCR methods. Preliminary results based on ITS sequence data indicate that low and high elevation populations on Hawai'i Island harbor disparate endophytic communities. Additionally, seeds collected from high and low elevation populations and reared together in a mid-elevation garden harbor endophytic communities similar to those of their parent populations, suggesting strong host selection and/or vertical symbiont transmission.

Petersen, Ronald H.* , Dunlap, John, and Hughes, Karen W. Ecology & Evolutionary Biology, University of Tennessee, Knoxville, TN 37996-1100. repete@utk.edu. **Reticulate spore ornamentation in *Strobilomyces*.**

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As part of a study of *Strobilomyces* (Boletaceae, Basidiomycotina) in eastern North America, comparison of spore ornamentation was necessary. Moreover, a project to typify some early European names attributable to *Strobilomyces* has involved comparison of many European collections. As part of the general comparison it was thought efficacious to explore the fine structure of reticulate spore ornamentation. Reticulate spore ornamentation in *Strobilomyces* is visible under light microscopy (bright field and phase contrast) up to 2000 \times . While some distinctions can be made at this magnification, ontogeny and fine structure of the ornamentation cannot be discerned. Scanning electron microscope images, conversely, reveal significant additional structure from which the ontogenetic process can be traced. This paper attempts to outline the ontogeny of reticulate spore ornamentation in *Strobilomyces*.

Piasai, Onuma*, Manoch, Leka, Kokaew, Jitra, Sudsanguan, Manorat, Dang-goman, Apiraporn, Kamnerdngam, Arada, Kamsorn, Wanvisa, and Taboon-pong, Kopathai. Department of Plant Pathology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand. agromj@ku.ac.th. **Diversity of soil fungi from Mu Ko Similan National Park in Thailand.**

Soil samples from Mu Ko Similan National Park, Phang Nga Province in Southern Thailand were collected in April 2010. Soil plate method as well as alcohol and heat treatment techniques and Gochenaour's glucose ammonium nitrate agar were used for isolation of microfungi. Identification of the fungal isolates were based on morphological characteristics as colony growth on different agar media. Fruiting bodies and spore ornamentations were examined under stereo and light microscopes. A total of 98 fungal isolates of microfungi belonging to 21 species in 15 genera were recorded comprising *Aspergillus*, *Chaetomium*, *Curvularia*, *Emericella*, *Eupenicillium*, *Eurotium*, *Fusarium*, *Gongronella*, *Hamigera*, *Neosartorya*, *Nigrospora*, *Penicillium*, *Phialophora*, *Sordaria* and *Talaromyces*. Pure cultures of microfungi are deposited at the culture collection at the Department of Plant Pathology, Faculty of Agriculture, Kasatsart University, Bangkok.

Piriyaprin, Siangjeaw^{1*}, Sunantapongsuk, Vanlada², and Somrang, Ard². ¹Department of Plant Pathology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand., ²Land Development Department, Ministry of Agriculture and Cooperatives, Bangkok 10900, Thailand. agrlkm@ku.ac.th. **Utilization of halophilic fungi as biological agents for controlling *Fusarium moniliforme* and *Pythium aphanidermatum*.**

Decaying leaf residue was collected from the rhizosphere soil and roots of Lam phu, *Sonneratia caseolaris* (Sonneratiaceae) and Kongkang, *Rhizophora apiculata* (Rhizophoraceae) in mangrove forest at the Kung Krabaen Bay Royal Development Study Center, Chumphuri Province, Eastern Thailand. For isolation of fungi, organic residue were diluted using the soil dilution plate method on Gochenaour's glucose ammonium nitrate agar with 70% sea water and incubated at 30 c for 3 days. *Rhizomucor variabilis* could degrade cellulose and protein. Soil samples were collected from moderately saline soil at Amphur Kham Talay Sor, Nakhonratchasima Province, northeastern Thailand. For isolation of fungi, the samples were diluted using the soil dilution plate method on Gochenaour's glucose ammonium nitrate agar with 10% sodiumchloride and incubated at 30 c for 5 days. *Termitomyces cartilagineus* could degraded cellulose, protein, lipid and calciumphosphate. Plates for antagonism tests of these fungi against *Fusarium moniliforme* that causes bakane of rice and *Pythium aphanidermatum* that causes damping-off of sunnhemp were incubated at 30 C for 5-7 days. The halophilic fungus; *T.cartilagineus* inhibited 56% and 71% mycelium growth of *F.moniliforme* and *P.aphanidermatum*, respectively, after 7 days incubation. The estuarine fungus, *R.variabilis*, suppressed 68% and 76% mycelium growth of *F.moniliforme* and *P.aphanidermatum*, respectively, after 5 days incubation.

Ponchart, Julien P.^{1,2*}, Piche, Yves¹, and Berube, Jean A. ¹Centre d'Etude de la Foret, Faculte de Foresterie de Geographie et de Geomatique, Universite Laval, Quebec, QC, G1V 0A6, Canada, ²Laurentian Forestry Centre, Canadian Forest Service, 1055 du PEPS, PO Box 10380, Succ Ste-Foy, Quebec city, QC, G1V 4C7, Canada. julien.ponchart.1@ulaval.ca. **454 pyrosequencing of a single *Abies balsamea* host tree reveals endophytic fungi are highly tissue specific.**

We used 454 pyrosequencing to study the fungal endophytic microbiome of a single balsam fir tree from the boreal forest. Buds, bark and wood from 7 branches at 4 heights were surface sterilized, subjected to whole DNA extraction, PCR amplified with primers ITS1F and ITS4 and then pyrosequenced to reveal fungal biodiversity distribution patterns within the tree. We obtained 98579 clean sequences (median ~450pb) distributed in 1752 OTUs (1141 contigs and 612 singletons) for a single tree and the 25 most common OTUs represented about 70% of the total number of sequences. The 3 most common OTUs were not tissue specific and were found in all tissues, while 17 of the 25 most common OTUs showed specificity for a single tissue (incidence superior to 95%). Ten OTUs had specificity for the buds, 7 for the bark but none for the

wood, revealing a specialisation of fungal distribution in different parts of the same host tree.

Presley, Gerald N.* and Methven, Andrew S. Department of Biological Sciences, Eastern Illinois University, Charleston, IL 61920. gnpresley@eiu.edu. **Comparison of atrazine degradation by several lignocellulose degrading fungi.**

Atrazine is an herbicide widely used in the cultivation of corn, sorghum, and sugar cane. Several recent studies have identified atrazine as a potential human endocrine disruptor and correlated atrazine exposure with altered sexual development in amphibians. Although atrazine slowly degrades in nature, it is persistent enough to make its way into the water supply via agricultural runoff. Bioremediation has been considered as a technique to de-contaminate areas with severe atrazine accumulation. Lignocellulose degrading fungi are good candidates for use in bioremediation because they have evolved adaptable enzyme systems capable of deriving organic carbon from complex, heterogeneous plant polymers. A number of fungal species have been studied for their potential to metabolize xenobiotics, including atrazine. In this study, several species of wood degrading fungi were tested for their ability to degrade atrazine. Fungi were grown in liquid basal medium containing atrazine (30ppm) and 1% glucose for 21 days at 25°C on a rotary shaker (150rpm). The culture medium was analyzed using HPLC and putative atrazine metabolites were detected in all species tested. The quantity and identity of the putative metabolites will be determined using GC-MS and compared between species.

Pringle, Anne. Harvard University, Organismic and Evolutionary Biology, 16 Divinity Avenue, Cambridge, MA 02138. pringle@oeb.harvard.edu. **Life and death in a Petersham Cemetery: the demography of *Xanthoparmelia* lichens.**

Global change is reshaping the geographic ranges of organisms. Demographic processes will affect how fungi move and establish across landscapes, and data to parameterize basic models of population biology are critically needed. In October 2005 I began a survey of *Xanthoparmelia* lichens growing on tombstones of a New England Cemetery. Each year I recorded births and deaths, along with growth rates of established individuals. I am currently tracking near to 1,000 individuals. Lichens are an ideal demographic model because thalli are visible and easily counted. Although lichens are symbioses of fungi and photosynthetic microbes, in this work I am focused on the filamentous fungus enclosing the photobiont. I am using data to explore a series of fundamental questions, including: are birth rates equivalent each year, or are births more common in a subset of particularly favorable years? Is a fragmenting lichen senescing? How is reproduction apportioned across the lifespan of a lichen? Is the probability of death equivalent across years, and does the probability of death increase with age or size? I am also using genetic data to explore past demographic shifts in the populations of these species. Preliminary analyses suggest *Xanthoparmelia* lichens experienced a massive increase in numbers in the recent past, coincident with the advent of intensive farming across New England and construction of miles of stone walls. Births are not equivalent across years, and smaller lichens easily recover from mechanical damage and fragmentation. Reproduction increases with the size and age of an individual. Although lichens experience "infant" mortality, as lichens grow larger and older the probability of death decreases. Data suggest humans have influenced the population biology of *Xanthoparmelia* lichens since at least the 18th C, and life history patterns of these modular, indeterminate organisms may be poorly served by traditional demographic models.

Pérez-Jiménez, José R.* and Laureano-Córdova, Diana L. Interdisciplinary Research institute, Universidad del Turabo, PO Box 3030, Gurabo, PR 00778. ut_jperezjm@suagm.edu. **Molecular biogeography of fungi across tropical coastal ecosystems.**

Mangroves, as a biome, sustain highly productive ecosystems while been subjected to coastal dynamics. On the coast, estuarine sediments constitute an unusual habitat for fungi. Puerto Rico is bordered by mangroves and has the second largest estuary (Jobos Bay) managed as a national reserve. As fungi are considered primary decomposers of complex organic matter, we aimed to describe the heterogeneity and biogeography of fungi in those tropical coastal ecosystems. The composition of fungal communities was characterized by amplification of partial ITS from soil and sediment samples for Terminal Restriction Fragment Length Polymorphism (TRFLP). DNA extraction was performed on 91 samples, but the ITS was amplified in only 24 positive samples. A total of 1329 phylotypes (TRFs) were detected, representing 345 different TRFs (richness). Fungal community in mangroves oscillated between 23 (Vieques) and 152 (Maunabo) TRFs whereas in Jobos Bay oscillated between 18 (CNT18) and 79 (OTR37). Currently, no TRF was found in common among all samples. Only one sample detected 29% of the picks, suggesting potential endemism. Similar-

Continued on following page

ity analyses, based on the Sorensen index, illustrate the association with geographic proximity. The similarity index fluctuated between 19% and 72%, and was highest among neighboring sites. The application of TRFLP provides information on fungi diversity, and shows that the fungal community is distinctive for mangrove and sediments ecosystems.

Radwan, Ghada L.* and Magill, Clint W. Dept. Plant Pathology & Microbiology, Texas A&M University, College Station, TX 77843-2132. ghadalotfy3000@tamu.edu. **Molecular Characterization of a-mating type loci of *Sporisorium reilianum* and genotyping analysis of newly emerged races.**

Sporisorium reilianum (Kühn) Langdon & Fullerton, a dimorphic basidiomycete, causes head smut on maize and sorghum. Phylogenetic analysis of ITS and large sub unit ribosomal DNA showed that *S. reilianum* is closely related to *U. maydis*, the head smut pathogen in maize, but *S. reilianum* differs from *U. maydis* in disease etiology. Although *S. reilianum* has been known as a pathogen on maize and sorghum for a long time, molecular data were previously lacking. Mating type genes play an important role in formation of the infectious filamentous form and consequently, pathogenicity. We are characterizing mating type loci in isolates that differ in pathotype through sequence analysis and expression levels as part of an effort to verify the ploidy level of the cultures and if crosses can be made between pathotypes. We also are working on genotyping analysis of recent emerged races of *S. reilianum*. Sequences of the known alleles of *a*-loci *a1*, *a2*, and *a3* of *S. reilianum* are being compared to gene bank public sequence databases. We are still working to complete the entire sequences and alignments for the three alleles. Pheromone genes are designated *mfa1.2* and *mfa1.3* for the *a1* allele, *mfa2.1* and *mfa2.3* for the *a2* allele and *mfa3.1* and *mfa3.2* for the *a3* allele. The pheromone receptor genes are designated *pra1*, *pra2* and *pra3* for the respective alleles. QRT-PCR data revealed that in compatible strains the expression level of *mfa1.2* is greater (Ct values) than expression of B-tubulin, and *para1* is considerably higher than the level of pheromone receptor gene *pra1*. For our ongoing work, we are studying the functionality of a mating type locus by transformation in non-mating strains, and characterizing the genetic diversity among new emerged races using AFLP.

Ratekin, Angela K.*¹, Taylor, Bernadette¹, and Volk, Thomas J.² ¹Department of Microbiology, Cowley Hall, University of Wisconsin-La Crosse, La Crosse, WI 54601, ²Department of Biology, Cowley Hall, University of Wisconsin-La Crosse, La Crosse, WI 54601. ratekin.ange@uwlax.edu. **The immune response of human neutrophils to virulence factor BAD1: comparing two genetic groups of the human pathogen, *Blastomyces dermatitidis*.**

Blastomycosis, a systemic fungal infection, presents with a variety of disease states. The causative agent, *Blastomyces dermatitidis*, a thermally dimorphic fungal pathogen continues to pose many questions regarding its mechanisms of invasion and the evasion of the immune response mounted by the human host. The yeast form, a broad based budding yeast, is large making it difficult for the phagocytic cells of the human immune system to engulf. Neutrophils are the predominant immune cell involved in phagocytosis and the predominant cell populating the initial defense of the human immune system. *Blastomyces* adhesin factor (BAD1) is a virulence factor associated with *B. dermatitidis*. BAD1 attaches to the CR3 receptor found on phagocytic cells resulting in immunomodulation, a change in chemical messaging. The attachment to the CR3 receptor alters the cytokine production, specifically Tumor Necrosis Factor- α (TNF- α). This change in messaging may result in an increased activation of neutrophils resulting in an increase in neutrophil extracellular traps (NETs) production. The yeast cells are too large to be readily engulfed by the neutrophils; however a net with a DNA backbone embedded with antimicrobial peptides and enzymes may aid in the containment and elimination of pathogens. However, the activation of neutrophils may become overzealous resulting in excess lung tissue damage; presenting as Acute Respiratory Distress Syndrome (ARDS). We will measure the BAD1 expression of *B. dermatitidis* isolates with known clinical presentation using an Enzyme-linked immunosorbent assay. We will determine the production of NETs with the same isolates. Our hypothesis is that the level of BAD1 expression correlates with neutrophil activation and NET production, which in turn plays a part in determining the type of clinical manifestation resulting in the human host. A high level of BAD1 expression results in tissue damage, ARDS, whereas a lower level results in dissemination of the organism.

Reithmeier, Laura C.*¹ and Kernaghan, Gavin^{1,2}. ¹Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, ²Biology Department, Mount Saint Vincent University, Halifax, Nova Scotia, Canada. lr868512@dal.ca. **Facilitation of ectomycorrhizal colonization of black spruce by alternate host plants above treeline.**

Ectomycorrhizal fungi (ECMF) are critical for woody plant establishment in high elevation and high latitude habitats due to their ability to enhance nutrient acquisition and water absorption. The availability of ECMF to conifer

seedlings above the present treeline is likely related to the presence of alternate ECMF host plants, including *Betula*, *Arctostaphylos* and *Salix*. We assessed the ECMF inoculum potential of alpine and tundra soils by using black spruce seedlings as bait plants grown under controlled conditions in soils from the Mealy Mountains of Labrador, Canada. Soils either supported or lacked one of *Betula glandulosa*, *Arctostaphylos alpina* or *Salix herbacea*. Colonizing fungi were identified by microscopy and ITS rDNA sequencing. Seedlings became colonized when grown in soils supporting and lacking alternate host plants, but ECMF percent colonization, species richness, and species diversity were higher for those grown in alternate host soils. Growth of black spruce bait plants varied among the three different soil types, and also between soils supporting and lacking an alternate host. The results suggest that soils lacking alternate host plants may contain ECMF spores and/or facultative mycorrhizal fungal species. Also, seedlings germinating proximal to alternate host plants may benefit from higher ECMF percent colonization and species diversity.

Reynolds, Hannah^{1*}, Castellano, Michael², Hosaka, Kentaro³, and Vilgalys, Rytas¹. ¹Dept. of Biology, Duke University, Box 90338, Durham, NC 27708, ²USDA Forest Service, Center for Forest Mycology Research, Northern Research Station, Corvallis OR 97331, ³National Museum of Nature & Science, Tsukuba, Japan. hannah.t.reynolds@gmail.com. **Investigating Elaphomycetaceae phylogeography.**

Because of their apparent dispersal limitation, a general hypothesis for truffles is of limited species ranges and relatively rare long-distance dispersal. Contrary to this hypothesis, a phylogeographic study of a broadly distributed truffle family, the Elaphomycetaceae (Eurotiales) indicates frequent long-distance dispersal. The Elaphomycetaceae are a family consisting of two ectomycorrhizal genera: the false truffle *Elaphomyces* and the above-ground genus *Pseudotulostoma*. *Elaphomyces* has been found in all continents save Africa and Antarctica in temperate to subtropical forests on numerous host genera. *Pseudotulostoma*, a recently discovered genus, has been found so far only in Guyana and Japan on *Dicymbe* and *Quercus* respectively. We conducted a multi-gene phylogenetic study of over 60 species of the Elaphomycetaceae collected from its known range from several hosts. The study uncovered 4 major morphological clades of *Elaphomyces*, each with a broad distribution. We estimated node ages in BEAST to test whether a scenario of continental vicariance could explain the biogeographic pattern and found an early to mid-Cretaceous origin for the family and a Paleocene to Miocene origin for the *Elaphomyces* subgenera.

Riddle, Jakob M.* and Arnold, A. Elizabeth. School of Plant Sciences, 1130 E. South Campus Drive, Forbes 303, The University of Arizona, Tucson, AZ 85721. arnold@ag.arizona.edu. **Diversity and phylogenetic affinities of endohyphal bacteria associated with foliar fungal endophytes of the Sonoran Desert.**

Foliar fungal endophytes frequently harbor endohyphal bacteria that appear to be distinct from those previously known in rhizosphere fungi, but to date these endohyphal symbionts have been investigated in only a few endophyte species and in the context of only a few localities and host associations. Increasing evidence suggests that some endohyphal bacteria can confer heat tolerance on endophytes, as well as alter endophyte growth in response to particular nutrients and change plant-endophyte interactions. To broaden our understanding of the diversity, phylogenetic relationships, and forces structuring communities of endohyphal bacteria we examined the bacterial symbionts associated with a diverse community of endophytes isolated from representative plants in the Sonoran Desert in the southwestern USA. Endophytes from multiple plant species, localities, and classes of Pezizomycotina were screened for endohyphal symbionts using PCR, and 16S rRNA sequences were integrated into broader phylogenies to test hypotheses regarding host associations and geographic heterogeneity. The results provide a new perspective on the diversity of endohyphal bacteria occurring within foliar endophytes and reveal clues as to the origins on this common but largely unexplored symbiosis.

Riquelme, Meritxell, Verdin, Jorge, Sánchez-León, Eddy, Fajardo-Somera, Rosa, and Bartnicki-Garcia, Salomon*. Department of Microbiology, CICESE-Ensenada Center for Scientific Research and Higher Education, Ensenada, Baja California, Mexico. bartnick@cicese.mx. **Mapping the traffic of wall-build-up vesicles during hyphal morphogenesis.**

Molecular tagging with fluorescent proteins (GFP or mCherry) has made it possible to follow the dynamics of organelles and molecular complexes believed to be involved in specific morphogenetic processes. Case in point, the polarized growth of the hyphal apex. Separate experimental and theoretical studies had previously: 1) implicated microvesicles (chitosomes) as the internal containers and conveyors of chitin synthase (CHS) in the fungal cells, and 2) predicted that the Spitzenkörper (Spk) regulates the traffic of vesicles by functioning as a vesicle supply center. By tagging the different putative *chs* genes of

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Neurospora crassa with either GFP or mCherry, it was possible to map the intracellular localization of the corresponding CHS proteins in living hyphae. Although all seven CHS of *N. crassa* participated in septum formation, only four of them were found to participate in apical growth. The most conspicuous finding was the congregation of CHS-GFP in the central, microvesicle-rich, region of the Spk. Thus fluorescent tagging provides definite confirmation of the involvement of the Spk in the traffic of chitin-building enzymes, i.e. in the construction of the microfibrillar skeleton of the wall. Dual labeling of different CHS pairs gave clear evidence of distinct populations of chitosomes moving toward the Spk. By tagging GS-1, a β -1,3-glucan synthase related protein, we showed that it also congregates in the Spk but it does it on the outer macrovesicle-rich region forming what we have called the Spitzenring. The stratification of these two biochemical activities in the Spk poses intriguing questions about the cause for such spatial segregation, and its consequences on vesicle traffic to the cell surface and its possible impact on cell wall assembly.

Rivera, Yazmin* and Horton, Thomas R. State University of New York – College of Environmental Science and Forestry, Syracuse, NY 13210. yarivera@syr.edu. **Ectomycorrhizal pine invasion on Puerto Rico: who are the partners in crime?**

Commercial plantations of pines were established throughout the southern hemisphere with the help of ectomycorrhizal (EM) fungal associations. After many failed attempts introducing pines to Puerto Rico, plantations of *Pinus caribaea* were successfully established in 1955 with soil from the United States as the source of EM inoculum. However, the introduced EM fungal species in the soil were unknown. Subsequently, fruiting bodies of various EM fungi (exotic to the island) have been observed in plantations and under pines colonizing areas outside plantations. EM fungi used in agroforestry can have negative consequences by contributing to the spread of their introduced host plant beyond plantation sites into neighboring habitats. Characterizing the EM communities on Puerto Rico is an important step to understanding the invasion of pines on Puerto Rico and elsewhere. The main goal of this study was to describe the EM communities inside three original plantations and those establishing at 100m, 500m and 1000m outside the plantations. At each of these distances two trees were selected and four soil cores were collected surrounding each tree. Pine roots were separated and EM root tips were sorted by morphology and identified by BLAST search of the ITS sequences in GenBank. The EM community associated with *P. caribaea* is characterized by its low diversity (7 species). Species and groups identified include *Pisolithus tinctorius*, *Rhizopogon* sp., *Wilcoxina mikolae*, *Suillus* sp., *Amanita rubescens*, *Clavulinaceae* and *Thelephoraceae*. Interestingly, the epigeous species *R. rubescens* was found up to 1km from plantations, suggesting the potential role of a dispersal agent. The role of EM fungal dispersal should be further studied as an important driver of invasions when plants are unable to associate with local symbionts.

Rosling, Anna^{1,3*}, Cox, Filipa², Cruz-Martinez, Karelyn¹, Ihrmark, Katarina¹, Grete, Gwen-Aëlle⁴, Lindahl, Björn D.¹, and James, Timothy Y.⁵ ¹Department of Forest Mycology and Pathology, Uppsala BioCentre, SLU, Uppsala, Sweden, ²Kew, Jodrell Laboratory, Imperial College London and Royal Botanic Gardens, London, UK, ³Department of Biology, Indiana University, Bloomington, IN, USA, ⁴Institute of Biological and Environmental Sciences, The University of Aberdeen, Cruickshank building, Aberdeen, UK, ⁵Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA. arosling@indiana.edu. **Archaeorhizomycetes - a new class of ancient, widespread soil fungi.**

Although over 100 000 species of fungi have been described, these are predicted to represent less than one tenth of the true species diversity. Studies of environmental DNA identify many new lineages that are only known by their DNA sequences and thus cannot be described. Among the most ubiquitous of these novel lineages, the Soil Clone Group 1 (SCG1) has been hypothesised to comprise unculturable obligate biotrophs. Phylogenetically unrelated to any described fungi based on ribosomal sequences, these fungi sometimes dominate fungal communities identified from total soil DNA extracts. Using the first cultures of these species, we are able to firmly place these fungi as a new class within the subphylum Taphrinomycotina, adding a prominent new basal branch to the Ascomycete tree. We propose the new class Archaeorhizomycetes because all fungi in this class appear to be restricted to roots and rhizosphere soil. Based on DNA sequence similarity, this novel class is likely to comprise hundreds of cryptic species. We show that species have a wide geographical distribution, occurring in several continents, but that many species show strong specificity towards host and habitat. The Archaeorhizomycetes colonize roots and soil in forests, grasslands and alpine habitats but their ecological niche and dispersal remains a mystery.

Roy, Mélanie H.^{1*}, Juliette, Rochet¹, Manzi, Sophie¹, Jargeat, Patricia¹, Gryta, Hervé¹, Moreau, Pierre-Arthur², and Gardes, Monique¹. ¹Laboratoire Evolution

et Diversité Biologique. Université Toulouse III Paul Sabatier - CNRS Bâtiment 4R3 118, route de Narbonne 31062, Toulouse Cedex 4, France, ²Laboratoire de Botanique et de Mycologie Faculté de Pharmacie 3, rue du Professeur Laguesse BP83 - 59006, Lille Cedex, France. mroy@cict.fr. **Does host evolution shape alder-associated ectomycorrhizal fungi communities?**

When considering ectomycorrhizal fungi (EMF), one would expect the host tree to be an important factor influencing fungal community structure or diversity, even for generalist species. Most studies have investigated the role of host, soil or abiotic factors in shaping EMF communities, but the host is treated as a fixed factor, *id est*, not as an evolving or co-evolving factor. The role of plant-fungi coevolution in shaping EMF communities can be investigated either by comparing host and fungal phylogenies, or by comparing related host species and their respective EMF communities. If EMF and host co-evolved, one would expect the difference between communities to be ordered as host phylogenies. To test this hypothesis, *Alnus* spp. constitutes an adequate model as (1) patterns of specificity of several alder-associated EMF genera have recently been described, unravelling a fine level of recognition of EMF towards host sub-genera, and (2) alder-associated EMF communities are known to be highly specific and less diverse than for other host trees. In the present study, we have investigated EMF communities associated with four *Alnus* species (representing two sub-genera), from 39 locations in France. In parallel, we have intensively collected fruitbodies around *Alnus* spp. to build an ITS database, and allow comparisons of EMF from geographically distant communities. Communities were less specific than expected, but still dominated by alder-associated taxa, suggesting a higher competitive ability or active selection process. However, such a specificity does not prevent a few generalist species from forming ectomycorrhizae. The host was the most important factor differentiating communities when taking occurrences into account, but not abundances. Soil and habitat characteristics were also significant factors structuring communities. Finally, differentiation between communities did not reflect host phylogeny, partly explained by possible host shifts and habitat filtering.

Rush, Tomas A.* and Aime, M. Catherine. Department of Plant Pathology and Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA 70803. trush2@lsu.edu. **The genus *Meira*—phylogenetic placement and description of a new species.**

The genus *Meira* currently contains three recently described species from Israel and Japan and is placed in the Exobasidiomycetes (Ustilaginomycotina, Basidiomycota) *incertae sedis*. A previously undescribed species of *Meira* was isolated as a ballistospore phylloplane yeast from a magnolia leaf in Louisiana, USA in 2008. We describe this species and provide phylogenetic analyses from three genes to resolve the placement of *Meira*. Phylogenetic analyses of the D1/D2 region of the nuclear large subunit, internal transcribed spacer region, and the 18S small subunit of the rDNA repeat confirm placement of the new species within *Meira* and the placement of *Meira* within the Exobasidiales. Furthermore, we provide evidence that the genus *Meira* belongs to the family Brachybasidiaceae. Other species in the genus are known to be mite pathogens and possible biocontrol agents against powdery mildew. The new species was also tested for antagonism against several plant pathogens found commonly on commercial and agriculturally important ornamentals and crops. To our knowledge, this is the first record of a member of the genus *Meira* in the United States.

Ryberg, Martin^{1*}, Nilsson, R Henrik^{2,3}, and Matheny, P. Brandon¹. ¹Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996-1610, USA, ²Department of Plant and Environmental Sciences, University of Gothenburg, Box 461, 405 30 Göteborg, Sweden, ³Institute of Ecology and Earth Sciences, University of Tartu, 40 Lai St., 51005 Tartu, Estonia. kryberg@utk.edu. **The diversification of ectomycorrhizal Agaricales: dealing with incomplete taxon sampling.**

Ectomycorrhizal (ECM) mushrooms form a diverse and ubiquitous group including about 5000 described species of Agaricales, distributed in at least 10 separate evolutionary lineages. The process by which this diversity arose is essentially unknown, largely due to lack of fossil evidence. However, insights into patterns of diversification can be studied using time calibrated molecular phylogenetic trees. Unfortunately, missing taxa will bias the inference. We use three approaches to address the problem of missing taxa: 1) simulate the effect of missing taxa on the gamma value, which describes the distribution of branching points through time; 2) simulate the effect of missing taxa on the maximum likelihood estimate of a basic model of species diversification; and 3) use a Bayesian framework to add lineages, with prior distributions instead of data, that substitute the missing taxa. We show that ECM lineages in the agaricoid clade started to diversify during the Paleogene, while *Amanita*, *Catathelasma*, *Hygrophorus* and *Tricholoma* originated in the Cretaceous, and that the diversification within each lineage has not departed from rate constancy. These results suggest a staggered origin of ECM lineages of Agaricales and that the present day di-

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versity of each lineage is not the consequence of rapid adaptive radiations into new niche spaces following the switch from saprotrophic to ECM habits.

Schardl, Christopher L.^{1*} and Young, Carolyn A.² ¹Department of Plant Pathology, University of Kentucky, Lexington, KY 40546, ²Forage Improvement Division, Samuel Roberts Noble Foundation, Ardmore, OK 73401. schardl@uky.edu. **Structure and dynamics of alkaloid biosynthesis gene clusters in plant-associated Clavicipitaceae.**

The fungal family, Clavicipitaceae, includes plant pathogens and heritable (seed-borne) mutualistic plant symbionts. The abilities of these fungi to produce psychoactive and anti-insect alkaloids contribute to the protective qualities of the mutualists. For example, many produce ergot alkaloids, which accumulate in fungal resting structures (ergots on ears of cereals) or in host seeds and foliage, and have been used for millennia as pharmaceuticals, but are historically linked to mass poisonings (St. Anthony's fire) and witch hunts. The epichloae (*Epichloë* and *Neotyphodium* species), symbionts of grasses (Poaceae), are especially diverse chemotypically, producing ergot alkaloids, tremorgenic indole-diterpenes, or anti-insect lolines and peramine. Similarly, the recently described *Periglandula* species are heritable symbionts of Convolvulaceae responsible for the famously high levels of ergot alkaloids in morning-glory seeds. We sequenced genomes of several heritable epichloae (*Neotyphodium gansuense*, *Epichloë brachyelytri*, and two isolates of *E. festucae*), a more pathogenic relative (*Epichloë glyceriae*), a morning-glory symbiont (*Periglandula ipomoeae*), a systemic parasite of bamboo (*Aciculosporium take*), and three pathogenic ergot fungi (*Claviceps purpurea*, *C. fusiformis* and *C. paspali*). In most genera, clusters of genes for ergot alkaloids (*EAS*) and indole-diterpenes (*IDT*) showed similar arrangements, particularly in the core genes for the alkaloid skeleton structures. In contrast the epichloae clusters had large segments of AT-rich retroelement-derived repeats, and exhibited a propensity for rearrangements, deletions, duplications and neofunctionalization. Two novel *IDT* genes in *E. festucae* were responsible for the particularly potent lolitrems, and genes for lolines (*LOL*) and peramine (*PER*) were unique to the epichloae. In contrast to their alkaloid gene clusters, the epichloid genomes had no greater abundance of repeats or tendency for recombination than the other Clavicipitaceae, suggesting that the grass symbionts are under selection for diversification of their alkaloid profiles. Their diversity reflects the diverse roles of epichloae, often providing host protection under varied ecological circumstances.

Scharnagl, Klara^{1*} and Stephenson, Steve L.² ¹13001 SW 106 Street Miami, FL 33186, ²Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701. klara.scharnagl@gmail.com. **Surveying fungal biodiversity in Thailand: the student perspective.**

In summer 2011, I and three other interns from the United States will spend a month in the tropical forests of northern Thailand surveying fungal biodiversity. Tropical forests are recognized hotspots for fungal biodiversity, and there is much yet to be discovered. This opportunity is funded through a grant from the National Science Foundation, and the program is co-directed by Dr. Steve Stephenson of the University of Arkansas, and Dr. Steve Miller of the University of Wyoming. While in Thailand, student interns will learn to recognize and collect fungi in the field, and to analyze them in the lab. Students will be encouraged to initiate mini studies within the larger survey, and to then present their findings to colleagues and fellow mycologists at Chiang Mai University. Apart from gaining important skills as aspiring mycologists, student interns from the United States will also have the invaluable opportunity to work alongside graduate students and professors from Chiang Mai University, Mae Fah Luang University, and the Mushroom Research Center in Thailand. The poster will include some of our findings and discoveries, but will also highlight the importance of learning within an international setting. This poster will reflect upon the experience, both in the field and in the lab, of working with a diverse international team with a common passion - mycology.

Schilling, Jonathan S. University of Minnesota, Bioproducts and Biosystems Engineering, 108 Kaufert Laboratory, 2004 Folwell Ave, St. Paul, MN 55108. schilling@umn.edu. **Wood-degrading fungi in long-term wood decay studies in northern forests.**

Wood is a resource for lumber, fiber, and, increasingly, for fuel. The long-term research necessary to understand and manage commercial timber, often spanning many decades, is not adequately complemented by long-term research on the role of wood left behind on the forest floor. This is in spite of renewed efforts to utilize more wood from each tree harvested, particularly from the crown. This presentation will overlay projects at several northern forest sites, including two new sites in the Alaskan boreal forest, to better define the role of wood on the forest floor. Specifically, we are using repeated measures of logs and small-diameter boles and branches in soil contact and under relevant canopy, including thorough time zero characterization. We use wood density and wet chemistry to characterize lignin and holocellulose fractions, as well as

physiochemical variables that differ relative to rot type and have consequence on residue quality. Inductively-coupled plasma spectroscopy is used to track the import/export of cations, including their exchangeability over time in woody tissue versus adjacent soils. Dilute alkali solubility (DAS) is used as a general measure of brown versus white rot in tissues to be coupled with lignin content information. Nitrogen, extractives content and pH are also measured. In most cases, data are expressed relative to time zero contents and not per gram, in order to compensate for density lost over time. We are also using species-specific primers and quantitative PCR (qPCR) to track individual fungi in multi-species lab trials. By freezing field samples over the time series (>10 years), this offers potential to isolate and "back-track" to assess historical colonization and dominance dynamics. The overall goal is to gain a better understanding of the biology and consequence of woody debris decay in forests and to use this information to better target debris requirements for forest certification.

Schoch, Conrad L.^{1*}, Seifert, Keith A.², Spouge, John¹, Robert, Vincent A.³, Bolchacova, Elena⁴, Crous, Pedro W.³, and Schindel, David⁵. ¹NIH/NLM/NCBI, Bethesda, MD, USA, ²Agriculture and Agri-Food Canada, Ottawa, Ontario, Canada, ³CBS-KNAW Fungal Biodiversity Center, Utrecht, Netherlands, ⁴LifeTech, Foster City, CA, USA, ⁵CBOL, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA. schoch2@mail.nih.gov. **The last steps towards an official barcode for Fungi.**

The DNA barcode movement has established strict criteria to enable standardized application of DNA sequences for identification of all living organisms. In order for GenBank to apply the barcode tag to a standardized set of sequences, the Consortium for the Barcode of Life (CBOL) laid down specific conditions that workers in all taxonomic disciplines should meet. Although mycologists have a long history of using sequence-based markers to aid fungal identification, to date no official barcode matching these conditions has been declared for Fungi. Following successful sessions at two conferences in 2010 and engagement with a broad group of researchers from across the globe, we assembled a sample set that will allow for a broad comparison across the kingdom Fungi for four different markers: the large and small nuclear ribosomal subunits (LSU, SSU), a sequence spanning the two flanking internal transcribed spacers of the 5.8S nuclear ribosomal gene (ITS), and part of the largest subunit of the ribosomal polymerase II enzyme (RPB1). We will report on the progress towards the designation of an official barcode for Fungi and discuss the analyses of this set of sequences provided by numerous collaborators.

Sekimoto, Satoshi^{1*}, Inaba, Shigeaki², and Honda, Daisuke³. ¹Department of Botany, 6270 University Blvd., University of British Columbia, Vancouver, BC, V6T 1Z4, Canada, ²NITE Biological Resource Center (NBRC), National Institute of Technology and Evaluation (NITE), 2-5-8 Kazusakamatai, Kisarazu, Chiba 292-0818, Japan, ³Department of Biology, Faculty of Science and Engineering, Konan University, 8-9-1 Okamoto, Higashinada, Kobe, Hyogo 658-8501, Japan. sekimoto@mail.ubc.ca. **Taxonomical examination of the genus *Olpidiopsis* (Oomycetes, Stramenopiles) based on molecular phylogeny and ultrastructural data.**

With 55 described species, *Olpidiopsis* is one of the largest endobiotic oomycete genera. It is characterized by a unicellular, spherical sporangium producing stramenopile-type biflagellate zoospores. It includes obligate endoparasites of wide range of eukaryotes including freshwater hyphal oomycetes, chytrids, freshwater diatoms, as well as green, brown and red algae. We hypothesized that *Olpidiopsis* might not be monophyletic based on the variation in morphology and wide host range of its species. We recently described two new *Olpidiopsis* species parasitizing marine red algae (*O. porphyrae* and *O. bostrychiae*). They were morphologically identical to the genus *Olpidiopsis*, but unlike most of other *Olpidiopsis* species (including the type *O. saprolegniae*), oosporeogenesis was not observed. Fortunately, we recently succeeded in establishing isolates of three terrestrial *Olpidiopsis* species (including two *O. saprolegniae*). To test the monophyly of *Olpidiopsis*, we used the SSU rRNA gene phylogeny and a comparison of the ultrastructure of the terrestrial and marine isolates. In the maximum likelihood tree, the three terrestrial *Olpidiopsis* formed a monophyletic group supported by high bootstrap values, as did the two marine species. However, the marine and terrestrial clades did not group together in any of our analyses. Our marine *Olpidiopsis* shared ultrastructural characters with other marine endoparasitic oomycetes rather than terrestrial *Olpidiopsis* species. These results clearly showed that the genus *Olpidiopsis* is not monophyletic, and we conclude that the marine species should be placed in a new genus.

Seminara, Agnese^{1,2*}, Fritz, Joerg², Amselem, Gabriel², Roper, Marcus³, Brenner, Michael P.², and Pringle, Anne². ¹Institut Pasteur, 28 rue Dr Roux, 75015, Paris, France, ²Harvard University, 02138, Cambridge, MA 02138, USA, ³Dept of Mathematics, University of California, Berkeley, CA 94720, USA. semi-

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nara@seas.harvard.edu. **An organizing principle for the morphological diversity of Ascomycete spore shooting apparatuses.**

The morphological diversity of fungal spores has been used as a tool to delineate species for more than two centuries. Spore shapes, sizes, and ornamentation remain an essential element/tool of modern identification and description. Ascomycetes are the largest phylum of fungi and are defined by the ascus, a fluid-filled sac which launches spores to new habitats. In forcibly ejecting species mature spores inside the ascus excrete osmolites greatly increasing ascus pressure. At a critical pressure spores and sap are explosively discharged through an opening. Spores enable dispersal, and to escape the parent fungus, spores must use a lot of energy to travel across the boundary layer of still air surrounding a fruit body. Although ascomycete spores are launched with accelerations of up to 180000 g, among the fastest recorded in nature, they are rapidly decelerated to rest due to their microscopic size. The morphologies of different ascii and spores may vary in diameter from 2 to 30 microns; typically these features are considered as unrelated parameters in the taxonomic literature. We present a simple physical model of spore ejection to predict and then test a novel correlation between ascus and spore morphologies. We target our analysis to poricidal ascomycetes - species where the ascus opening takes the form of a pore or ring. The need for an efficient energy conversion leads us to predict a non-trivial relationship between the morphology of the ascus ring and the spore. We test our hypothesis by plotting morphological data of an enormous diversity of spores and apical rings from several species sampled from phylogenetically distant families. In fact these data confirm that the morphologies are restricted to the predicted subspace of possible geometries. We argue that natural selection, and not phylogenetic constraint, guides the collapse of geometries.

Sepúlveda-Chavera, German F.¹, Pereira-Carvalho, Rita C.², Inácio, Carlos A.², Souza-Armando, Eliane A.², and Dianese, José C.^{2*} ¹Depto. de Recursos Ambientales, Fac. de Ciencias Agronómicas, Univ. de Tarapacá, 058-205507 Tarapacá, Chile, ²Depto. de Fitopatología, Universidade de Brasília, Campus Darcy Ribeiro, Asa Norte, 70910-900 Brasília, DF, Brazil. jcarmine@unb.br. **A new coelomycete on leaves of *Gomidesia pubescens* from the Brazilian Cerrado.**

Several specimens of a coelomycete were found on leaves of *Gomidesia pubescens* (Myrtaceae) in Cerrado vegetation near Brasília (accession numbers 15840, 10031, and 7528, Herbarium UB, Mycol. Collection). Comparisons of conidiomata and conidia revealed that this fungus is a new species not previously described. The coelomycete was characterized as follows: *conidiomata* pycnidial, cylindrical to lageniform, unilocular; superficial, 75-100(-147) mm in the wider basal portion × 290-575 mm high, on a thin subiculum, hypophyllous, mostly located on top of leaf veins, rostrate; *rostra* 50-90 mm tall; *wall* 8-13 mm thick, with few filamentous hyphal appendages; *conidiogenous cells* 5-6 × 3-5 mm, holoblastic, ampulliform to short cylindrical, hyaline; *conidia* 97-148 × 19-29 mm, appendiculate, cymbiform to cylindrical, muriform with several transverse, oblique and longitudinal septa; *conidial appendages* cellular, 7-12 × 3-5 mm. The material studied showed some similarities with species belonging in *Callistospora*, *Orphanocoela*, *Urohendersoniella*, *Rieleya* and *Scolecosporiella*, but clearly insufficient to justify its inclusion in any of the known coelomycete genera, including those noted here. Thus the specimens will be used to describe a new genus.

Sheedy, Elizabeth M.^{1,2*}, Van de Wouw, Angela P.¹, Howlett, Barbara J.¹, and May, Tom W.² ¹School of Botany, The University of Melbourne, Parkville, Victoria 3010, Australia, ²Royal Botanic Gardens Melbourne, Private Bag 2000, South Yarra, Victoria 3141, Australia. esheedy@pgrad.unimelb.edu.au. **Cryptic speciation within Australian *Laccaria* (Hydnangiaceae, Basidiomycota) and apparent widespread homozygosity at microsatellite loci of *Laccaria* sp A.**

Laccaria is a cosmopolitan ectomycorrhizal fungus that is common in Australian forests and heathlands. Species of Australian *Laccaria* are notoriously difficult to identify due to the paucity and variability of morphological characters. Species boundaries of Australian *Laccaria* were investigated using consensus trees based on parsimony analyses of the internal transcribed spacer (ITS) of ribosomal DNA repeat unit, beta subunit of RNA polymerase II (RPB2), and translation elongation factor-1 alpha (*tef*-1alpha). Individual gene trees produced the same terminal taxa as in the concatenated tree. Comparisons were made to species defined using macro- and micro-morphological characters. Most terminal taxa in the phylogenetic trees are congruent with the delimitation of species by multivariate analysis of macro- and micro-morphological characters. However, cryptic speciation is evident in two morphologically defined species, which contain two and three phylogenetic species. These cryptic species are not sister taxa. The truffle-like genus *Hydnangium* is also supported as a member of *Laccaria*. Populations of one well-defined species that is easily identified by field characters (*Laccaria* sp A) are being analysed. Eight species-specific microsatellite loci were amplified from 50 individuals. Size polymor-

phisms were present between individuals, including individuals from the same localities, with between two and ten alleles detected per locus. However, almost all individuals had single alleles at each locus on agarose gels, suggesting heterozygotes are extremely rare. Analysis of combined samples showed that preferential amplification of one allele was not the cause of the paucity of heterozygotes. *Laccaria* sp A exclusively inhabits cool temperate rainforest dominated by *Nothofagus cunninghamii*, a very stable environment that may favour survival of highly suited individuals with a strong competitive edge. Although the life-history of the species could explain the extreme level of homozygosity, the underlying genetic mechanism is unknown.

Simmons, D Rabern* and Longcore, Joyce E. School of Biology & Ecology, University of Maine, 5722 Deering Hall, Orono, ME 04469. david.r.simmons@umit.maine.edu. **Phylogeny of Powellomycetaceae fam. nov. in Spizellomycetales.**

Powellomyces was described to accommodate monocentric chytrid species from soil that develop exogenously and possess zoospore ultrastructure similar to other members of the order Spizellomycetales. Despite *Powellomyces*-like chytrids being common in gross culture and showing diversity in molecular phylogenies, the genus has contained only two species. I amassed 49 isolates of *Powellomyces*-like chytrids, including the cultures upon which species types were based and new isolates from pollen-baited water cultures of soils, plant detritus, or manure. I sequenced portions of nucSSU and nucLSU rDNA regions and the *EF-1a*-like gene from each isolate to produce a molecular phylogeny and examined zoospore ultrastructure of pertinent isolates by transmission electron microscopy. Molecular and ultrastructural evidence indicated that these chytrids represent a diverse and distinct spizellomycetalean clade, which I describe as Powellomycetaceae fam. nov. Groupings based on zoospore ultrastructure, which is used for genus recognition in this order, corroborate the molecular phylogeny, and the family contains four genera. This study adds additional taxa to Spizellomycetales to reflect the diversity indicated by molecular and ultrastructural examinations of this morphologically-conserved chytrid lineage.

Sjökvist, Elisabet^{1*}, Pfeil, Bernard E.¹, Larsson, Ellen¹, Miettinen, Otto², and Larsson, Karl-Henrik³. ¹Dept. of Plant and Environmental Sciences, University of Gothenburg, PO Box 461, SE 405 30 Göteborg, Sweden, ²Botanical Museum, Finnish Museum of Natural History PO Box 7, FI-00014 University of Helsinki, Finland, ³Natural History Museum, University of Oslo PO Box 1172, Blindern 0318 Oslo, Norway. elisabet.sjokvist@dps.gu.se. **Molecular phylogeny of the Polyporales.**

Polyporales is a fungal order comprising roughly 1800 species of wood-decaying basidiomycetes. These are primarily polyporoid and corticioid, but a few species have lamellae. Previous studies with main focus on the polyporoid clade have only used sequences from one or a few rDNA genes, resulting in phylogenies with low support on branches. This study aims to identify higher-level relationships within Polyporales using multi-locus phylogenies. Preliminary results will be presented from a concatenated dataset using both protein coding genes, nrDNA and mitochondrial DNA.

Skaltsas, Demetra^{1*}, Castlebury, Lisa², and Chaverri, Priscila¹. ¹University of Maryland, Department of Plant Sciences and Landscape Architecture, 2102 Plant Sciences Building, College Park, MD 20742, ²U.S. Department of Agriculture, Agricultural Research Service, Systematic Mycology and Microbiology Laboratory, Beltsville, MD 20705. dskaltsa@umd.edu. **Delimitation of tropical endophytic *Phomopsis* species from three euphorbiaceous hosts: *Hevea brasiliensis*, *H. guianensis*, and *Micandra* sp.**

Phomopsis (Valsaceae, Diaporthales, Ascomycota) includes a wide array of species that are endophytes, saprobes, opportunistic pathogens, as well as aggressive pathogens of economically important crops. *Phomopsis* has been reported as one of the most frequent endophyte genus in many plant hosts. One hundred and eight *Phomopsis* samples were collected from Cameroon, Mexico and Peru. The fungi were isolated from asymptomatic leaves and bark of three different wild hosts (*Hevea brasiliensis*, *H. guianensis* and *Micandra* spp., Euphorbiaceae), as well as cultivated *H. brasiliensis* trees. The objective of this study was to determine the identity of the species associated with these trees in the wild and in plantation. In this study we used ecological, morphological and multigene (ITS nrDNA, *tef*1) phylogenetic approaches to delimit *Phomopsis* species. Preliminary phylogenetic analyses of the ITS nrDNA regions resulted in ca. 40 "phylogenetic species." However, when using a multigene approach many more species were detected. Several of the species are most likely new. Results of this study also show that *Phomopsis* is more abundant in plantations than in wild trees. This research will aid in the understanding the biology of endophytic *Phomopsis* and its relationship with pathogenic species, as well as its distribution and ecological function.

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Skogen, Marte Jertine^{1*}, Davey, Marie L.^{1,2}, Kauserud, Håvard², and Ohlson, Mikael¹. ¹Department of Ecology and Natural Resource Management, Norwegian University of Life Sciences, N-1432 Ås, Norway, ²Molecular Evolution Research Group, Department of Biology, University of Oslo, N-0316 Oslo, Norway. skogen.marte@gmail.com. **Amplicon pyrosequencing of bryophilous fungal communities in a nitrogen enriched boreal forest in Norway.**

Anthropogenic nitrogen deposition in Norway is expected to increase by 10 percent in the coming century, and the impact this change will have on the boreal forest is not well understood. Despite their presumed importance in bryophyte dominated ecosystems, bryophilous fungi are an understudied group, partly due to their inconspicuous and cryptic nature. *Hylocomium splendens*, *Pleurozium schreberi* and *Dicranum scoparium* were collected in a boreal spruce forest in Norway from control and experimental plots established in 2003 that have been fertilized with 150 kg N ha⁻¹ y⁻¹. 454 amplicon pyrosequencing was used to characterize the fungal communities associated with these mosses, and the effect of nitrogen fertilization on community composition and diversity. In addition, we examined host specific and above- and below-ground responses to fertilization. Amplicon pyrosequencing can detect rare and inconspicuous species, allowing us to characterize these minute and discreet communities in previously impossible detail. Our preliminary results suggest that the fungal communities differ significantly between the different moss hosts both in terms of species composition and overall species richness. The communities were dominated by Ascomycota (approximately 70%), followed by Basidiomycota (approximately 20%). Chytridiomycota, Glomeromycota and Zygomycota were also detected, but in very low numbers. Additionally nitrogen fertilization is associated with a slight increase in species richness within the fungal community associated with these bryophytes. There is also slightly higher species richness in the senescent versus the photosynthetic parts of the moss shoot.

Smith, Dylan P.* and Kennedy, Peter. Lewis & Clark College, Dept. of Biology MSC 53, 0615 SW Palatine Hill Rd., Portland, OR, 97202. pkennedy@lclark.edu. **High overlap between the mycorrhizal fungi present on *Arbutus menziesii* and coniferous hosts in Pacific Northwest, USA.**

To better understand the composition and diversity of the mycorrhizal communities associated with *Arbutus* and explore their potential role in the successional dynamics of Pacific Northwest forests, we conducted a molecular-based investigation of arbutoid mycorrhizas present in pure and mixed *A. menziesii* stands in southern Oregon, USA. 800 samples from *A. menziesii* roots were collected from two pure and two mixed sites and identified using ITS rDNA gene sequences. Mycorrhizal genera associated with *A. menziesii* roots included *Piloderma*, *Cenococcum*, *Rhizopogon*, *Russula*, *Cortinari*, and *Tomentella/Thelephora* among others. Our data indicate the mycorrhizal communities associated with *A. menziesii* have high overlap with those present on coniferous ectomycorrhizal host species in the same forests. Given the stump-sprouting ability of *A. menziesii*, this mycorrhizal host species may play an important role in the recovery of Pacific Northwest forests from fire, logging, and other disturbances.

Smith, Matthew E.^{1*}, Williams, Gwendolyn C.¹, Henkel, Terry W.², Aime, M. Catherine³, and Vilgalys, Rytas¹. ¹Department of Biology, Duke University, Durham, NC 27708, ²Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, ³Department of Plant Pathology & Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA 70803. trufflesmith@gmail.com. **Do different soil microhabitats associated with *Dicymbe corymbosa* trees harbor distinct communities of tropical ectomycorrhizal fungi?**

In the central Guiana Shield ectomycorrhizal (ECM) fungi are diverse and abundant in rainforests dominated by the ECM *Dicymbe corymbosa* Spruce ex Benth. (Fabaceae subfam. Caesalpinioideae). *Dicymbe corymbosa* is unique among Neotropical canopy tree species in exhibiting indeterminate reiterative shoot and root growth, which over many centuries results in large, stand-dominating trees with multi-aged stems, aerial adventitious roots, fused pseudotrunk, and basal root mounds. This complex physiognomy facilitates aboveground litter capture and soil microhabitat differentiation, including aerial litter caches between stem bases, decayed wood in heart-rotted stems, thick humic layers on root mounds, and underlying mineral soil. Previous fruiting body-based studies in *Dicymbe* forests have shown a preference by individual ECM fungal species for specific soil microhabitats as fruiting substrata. In this study we hypothesized that the different soil microhabitats, by providing greater overall ECM "niche space", host distinct ECM fungal communities and enhance ECM fungal alpha-diversity. We addressed this by sampling ECM roots from the four microhabitats on 20 *D. corymbosa* trees across four 1-ha plots in western Guyana. 100 ECM roots were pooled from each of 80 microhabitat samples and the mycobiont communities were characterized using either 454 pyrosequencing or PCR-cloning Sanger-sequencing. The effects of soil microhabitats

on ECM fungal community assembly and species diversity in *Dicymbe*-dominated forests will be discussed. We will also provide a comparison of results obtained with the different molecular methods.

Spribile, Toby. Institute of Plant Sciences, University of Graz, Holteigasse 6, A-8010 Graz, Austria. tspribi@gwdg.de. **Testing phylogeographic hypotheses in the mycobiont of a boreal lichen.**

Much of what is known today about post-Pleistocene dispersal patterns and genetic diversity of high latitude lichens is derived from a small number of species with enigmatic distributions. Little is known of how today's 'circumboreal' lichen species came to acquire their large, nearly continuous ranges. We studied phylogeographic patterns in the mycobiont of one of the common epiphytic crust lichens of the northern hemisphere, *Mycoblastus sanguinarius*, based on material from four major sectors of the northern conifer belt in Asia, Europe and eastern and western North America. Haplotype networks based on over 500 sampled individuals indicate a complex pattern of rapid range expansion and local bottlenecks with disjunction types that reflect those of taxa at higher taxonomic ranks (species, genera). We explore the most likely reasons for this by testing a variety of scenarios by which the observed patterns could have been arrived at, and what implications this may have for past assumptions about evolution and diversification of lichen fungi.

Stajich, Jason E.^{1*}, Joneson, Suzanne², James, Tim Y.³, Zamudio, Kelly⁴, and Rosenblum, Erica B.² ¹Department of Plant Pathology & Microbiology, University of California, Riverside, CA, ²Department of Biology, University of Idaho, Moscow, ID, ³Department of Ecology & Evolutionary Biology, University of Michigan, Ann Arbor, MI, ⁴Department of Ecology & Evolutionary Biology, Cornell University, Ithaca, NY. jason.stajich@ucr.edu. **Population genomics of the amphibian pathogen *Batrachochytrium dendrobatidis* from genome resequencing.**

Batrachochytrium dendrobatidis (*Bd*) is an emerging infectious disease linked to worldwide amphibian decline. Global genotypic variation appears to be low, but some private geographic-specific alleles are present suggesting genetic isolation of strains. Using the whole genome sequencing of strains JAM81 (Joint Genome Institute) and JEL423 (Broad Institute) as references we re-sequenced and identified polymorphisms in an additional 22 strains to compare variation among isolates from the Western & Eastern US and Central & South America. The *Bd* genome is diploid and previous work (James et al, 2009) has identified regions of loss of heterozygosity (LOH) from Multi Locus Sequencing markers. Analysis of whole genomes of multiple strains now identifies precise genomic locations of independent and shared LOH events. We have found that strains from Central and South America have lost alleles that are observed in North America due to reciprocal crossover of chromosome arms. The resequencing data from geographically and genetically diverse strains allow us to build a high-resolution inventory of genetic variation useful for future developments of high throughput sample genotyping and tracing origins of *Bd* outbreaks.

Stultz, Christopher M.^{1*}, Pringle, Anne¹, van Diepen, Linda TA², and Frey, Serita D.² ¹Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, MA 02138, ²University of New Hampshire, Department of Natural Resources, Durham, NH 03824. chris.stultz@gmail.com. **Influence of nitrogen deposition on saprophytic fungal community structure and the role of endophytes as latent decomposers.**

How global change will impact microbial community structures remains poorly understood. However, because microbes are important drivers of biogeochemical cycles, anthropogenically mediated changes in communities may impact ecosystem function. Saprophytic fungi are a diverse group of species and are primarily responsible for decomposition in temperate forest systems, yet relatively little is known about how factors of global change, including increased nitrogen deposition, will affect decomposer community assembly. In the first months of a multi-year litterbag/decomposition experiment, we focused on endophytic fungi. Endophytes are fungi that live asymptomatically in the tissues of plants, including the leaves of most temperate trees. Their function in ecosystems is still debated, and their interactions with hosts range from mutualism to parasitism. Here we test a recent hypothesis suggesting that endophytes may be latent decomposers, ready to start decomposition as soon as leaves senesce. We used a long-term experimental N addition plot, exposed to three levels of N deposition (ambient, 5 and 15 g N m⁻² y⁻¹) since 1990, and a combination of pyrosequencing and traditional cloning and sequencing techniques to test the following hypotheses: 1) Increased N deposition will alter the community composition and decrease the richness and diversity of fungal endophytes from freshly dropped leaves. 2) The most active fungi involved in early decomposition (5 days after leaf fall) will be a subset of species found in freshly dropped leaves. 3) The most active decomposer species will differ among the treatment

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plots. Testing these hypotheses will increase understanding of the ecology and evolution of saprotrophic fungi in a global change context, add to what is known about the biodiversity of decomposer fungi, and examine the role of endophytes as latent decomposers.

Stone, Daphne F. 30567 Le Bleu Rd., Eugene, OR 97405. daphstone@gmail.com. **Leptogium: the Importance of the Medulla.**

The structure of the medulla in *Leptogium* typically has been treated as one of two types: those with parenchyma-like cells and those with long, loose hyphae intertwined with long chains of the photobiont. However, thin cross-sections of the medulla of several *Leptogium* species show an array of different, distinguishable types of organization intermediate between these two categories, that appear to be consistent for each species. *Leptogium* is a difficult genus to work with because of plasticity in thallus structure and because lichen acids traditionally used for distinguishing species in other genera are lacking. Many *Leptogium* species do not often produce apothecia, and therefore are identifiable only by characters such as thallus color or shape of isidia, characters that are so variable that identification of a particular species may involve guesswork. Furthermore, the original descriptions of many *Leptogium* species are not sufficiently detailed to clearly separate one species from others that may be growing sympatrically. A review and documentation of the structure of the medullas of *Leptogium* species could provide a useful identification tool to help clarify known species and bring to light new species.

Stursová, Martina^{1*}, Kolarik, Miroslav¹, Leigh, Mary Beth², Vorisková, Jana¹, Zifčáková, Lucia¹, and Baldrian, Petr¹. ¹Institute of Microbiology of the ASCR, Videnská 1083, 14220 Praha 4, Czech Republic, ²Institute of Arctic Biology and Biology & Wildlife Department, University of Alaska Fairbanks, 211 Irving I Building, AK 99775, Fairbanks, USA. stursova@biomed.cas.cz. **Structure and activity of fungal decomposers reflect vertical stratification of spruce forest soil.**

Soils of coniferous forests are important for the global carbon cycle and the identification of active microbial decomposers is essential for understanding organic matter transformation in these ecosystems. We compared the total fungal community composition in two soil horizons of *Picea abies* forest soil, followed the distribution of functional genes active in cellulose decomposition and their transcripts, and tried to specifically identify cellulose-degrading microorganisms. We used 454-Titanium pyrosequencing of rDNA and rRNA to analyze community composition and to identify the genes and transcripts encoding for fungal cellobiohydrolase. DNA-SIP with ¹³C-cellulose was used to identify microorganisms deriving their biomass from cellulose. RNA-derived populations representing active microorganisms were largely different from DNA-derived populations but exhibited similar diversity. Fungal community members were often distinctly associated with a particular soil horizon. Most fungi (>1000 OTUs) belonged to Ascomycetes and Basidiomycetes. Ectomycorrhizal fungi strongly dominated the DNA pool (>80%) while the active community was enriched in saprotrophic and parasitic species. Litter had higher diversity (150–200 cbhl OTUs) and a higher proportion (40%) of the expressed sequences of *cbhl* than the organic horizon (80 and 25% respectively). Some of the most abundant transcripts were produced by fungi with very low occurrence in the ecosystem. *cbhl* genes showed distinct association with either litter or humic horizons suggesting that different fungal communities decompose cellulose at different soil depths. Analysis of microbes deriving their biomass from ¹³C-cellulose clearly showed that their community is distinct from the total community and also confirmed the idea that cellulose degradation is mediated by different populations in each soil horizon. Our results also show that there are many important cellulose-degrading microorganisms which were earlier not recognized as such.

Suh, Sung-Oui^{*}, Hart, Erica L., Houseknecht, Janice L., Gujjari, Pushpa, and Zhou, Jianlong J. Mycology and Botany Program, ATCC, 10801 University Blvd., Manassas, VA 20110. ssuh@atcc.org. **Fungi associated with wood-inhabiting insects in northern Virginia.**

Insects living on woody substrates are a good source of microorganisms which may be useful for biofuel production from agricultural and forest wastes. During a survey of microbial flora in wood inhabiting insects of northern Virginia, we isolated approximately 140 strains of bacteria and 175 strains of fungi from beetles, roaches, termites and their environment. *Penicillium* spp., *Trichoderma* spp., and *Mucor* spp. were the most popular species among the filamentous fungi isolated in this study. On the other hand, almost 60% of yeast isolates were identified as species near *Scheffersomyces stipitis* including a few novel xylose-fermenting yeasts. Several novel yeasts were also placed in the clades near *Sugiyamaella*, *Kazachstania*, *Trichosporon*, and *Cryptococcus*. As the result of physiological characterization, we found that more than 90% of fungal isolates were able to assimilate xylose, a pentose that forms the backbone of hemicellulose which is a major component of plant cell walls, and almost a half of those strains could ferment xylose to ethanol.

Supaphon, Orathai^{1*}, Phongpaichit, Souwalak¹, Sakayaroj, Jariya², Rukachaisirikul, Vatcharin³, and Spatafora, Joseph W.⁴ ¹Department of Microbiology and Natural Products Research Center, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla, Thailand, ²National Center for Genetic Engineering and Biotechnology (BIOTEC) 113 Thailand Science Park Phahonyothin Road, Klong 1, Klong Luang, Pathumthani, Thailand, ³Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR USA, ⁴Department of Chemistry, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla, Thailand. spatafoj@science.oregonstate.edu. **Antimicrobial activity and diversity of endophytic fungi isolated from the seagrass, *Cymodocea rotundata*.**

Endophytic fungi colonize the healthy tissue of their host plants and are a potential source of antimicrobial substances. Endophytic fungi from seagrasses have been rarely studied, with only few reports. Seagrasses, however, are important sources of primary production in marine ecosystem. The coastal areas of Trang Province, southern Thailand, have rich seagrass beds, especially *Cymodocea rotundata*. Therefore, this study aimed to evaluate the diversity of endophytic fungi from *C. rotundata* and screen for their ability to produce antimicrobial metabolites against human pathogens. Healthy *C. rotundata* samples were randomly collected from Trang Province. Endophytic fungi were isolated from surface-sterilized leaves, roots and rhizomes into axenic culture. Fungal identification was based on morphological features and molecular analysis using the ITS ribosomal DNA region. Crude ethyl acetate extracts of the culture broth (BE), crude hexane (CH) and ethyl acetate extracts (CE) from fungal mycelia were screened for their antimicrobial activity using a colorimetric broth microdilution method against ten pathogenic microorganisms. A total of 11 isolates of fungal endophytes were obtained from *C. rotundata*. Only three isolates sporulated in culture and they were identified by morphological characteristics as *Penicillium* (2 isolates) and *Nigrospora* (1 isolate). The remaining eight sterile mycelia isolates were identified by molecular method. Seven isolates belonged to the Sordariomycetes and Dothideomycetes (Ascomycota) and one isolate belonged to the Agaricomycotina (Basidiomycota). These isolates were classified as *Acremonium* sp., *Cladosporium* sp., *Fusarium* sp., *Leptosphaerulina* sp., *Phanerochaete* sp. and xylariaceous fungi. The endophytic fungus PSU-ES26 (*Acremonium* sp.) produced the best active extracts with MIC values less than 10 µg/ml. Its CH extract had the strongest activity against *Candida albicans* ATCC90028, *Candida albicans* NCPF3153, *Cryptococcus neoformans* ATCC90113 (MIC 8 µg/ml), and *Microsporium gypseum* clinical isolate (MIC 2 µg/ml).

Swanson, Michaela M.^{1*}, Ruess, Roger R.¹, Kiehl, Knut¹, Olson, Karl D.¹, McFarland, Jack W.², and Taylor, D. Lee¹. ¹Institute of Arctic Biology, Department of Biology and Wildlife, Fairbanks, AK, 99775, ²US Geological Survey, Menlo Park, CA 94025. m.swanson@alaska.edu. **Effects of resource availability on alder-associated ectomycorrhizal community structure and function in Alaskan boreal forests.**

Ecosystem processes depend heavily on inputs of biologically fixed nitrogen (N) from *Alnus tenuifolia*, which contributes the majority of N accumulated during succession in Alaskan boreal forests. Because of the high phosphorus (P) demands of this plant, we hypothesize that N-fixation inputs are controlled by the ability of alder to access P through associations with ectomycorrhizal fungi (EMF) that produce enzymes which mobilize organic and recalcitrant P forms. In this study we measured the activity of acid phosphatase, phosphodiesterase and phytase enzymes bound to the surfaces of individual mycorrhizally-infected alder root tips (n=1260), using fluorogenic substrates, over several gradients of resource availability. We expected shifts in alder-EMF communities and function to parallel changes in phosphorus availability between a) soil horizons, b) across successional stages and c) within plots whose soil P levels were experimentally manipulated. Potential rates of acid phosphatase and phosphodiesterase were highest in late successional stands (both <0.001) where on average these enzymes mobilized 2.50 and 0.18 µmol P mm² root tip surface area⁻¹ hr⁻¹, respectively. We also found evidence that the application of P caused strong significant differences (all p < 0.001) between treatments for acid phosphatase and phosphodiesterase enzymes (except phytase (p = 0.078)). This suggests a reduction in the alder-EMF communities' potential to mobilize organic phosphorus when P availability is high. Sequencing and ARISA (automated ribosomal intergenic spacer analysis) profiles of the fungal ITS region, isolated from root tips, are presently being used to match potential enzyme activities with a fungal identity and create community profiles. These analyses will be used to determine if the observed differences in enzyme activities across succession and between treatments were due to shifts in EMF community structure and assess if enzyme activities within a given EMF species varies across these spatial scales.

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Sweeney, Katarina^{1*}, Stone, Jeffrey¹, Sniezko, Richard², Kegley, Angela², and Schoettle, Anna³. ¹Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, ²USDA Forest Service, Dorena Genetic Resource Center, Cottage Grove, OR 97424, ³USDA Forest Service Rocky Mountain Research Center, Fort Collins, CO 80526. sweeneka@science.oregonstate.edu. **Hypersensitivity reactions in five needle pines in response to infection by *Cronartium ribicola*.**

Hypersensitive response-like (HR) needle reactions to infection by the white pine blister rust pathogen, *Cronartium ribicola*, have been reported for several species of five needle pines native to western North America. The best-studied examples are in *Pinus monticola* and *P. lambertiana*. In these species a “needle spot” phenotype has been identified in which HR-like needle reactions are related to disease resistance that is conditioned by a major gene. Conventionally it is believed that the HR-like needle reactions in resistant pines prevent spread of the pathogen to vascular stem tissue by HR mechanisms commonly seen in other plant-pathogen incompatibility interactions, i.e. a rapidly induced plant cell death and subsequent localized tissue necrosis. The dead cells present a barrier to colonization by biotrophic pathogens and cause degeneration of fungal hyphae to stop further pathogenic invasion. Structural analyses of early *C. ribicola* colonization in resistant *P. monticola* have shown, however, that these symptoms and their underlying physiology are fundamentally different from the clearly defined HR described in other host-pathogen systems. Contrary to the pattern of HR responses seen in most incompatible host reactions, onset of needle lesions was first seen several weeks after initial entry of *C. ribicola*. We observed extensive proliferation of fungal hyphae in the host and penetration of the needle endodermis and vascular tissue by the pathogen prior to the onset of a discernable HR. The amount of fungal tissue present and progress of needle colonization was similar for both resistant and susceptible *P. monticola*. Therefore, typical HR does not appear to function in needles as the mechanism of disease resistance in the “needle reaction” phenotype. We are also studying needle resistance reactions in other western North American pines, including *P. albicaulis* and *P. flexilis* in comparison with the reactions seen in *P. monticola*.

Sylvain, Iman A.* and James, Tim Y. Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109. isylvain@umich.edu. **Effects of production method and geography on the fungal community composition in green coffee beans.**

Plant products and their associated fungi are transported all over the world via the industrial food system. The globalization of food allows us to investigate whether fungi associated with agricultural commodities show cosmopolitan distribution or have a restricted geographic range due to dispersal limitation or mode of production/transportation. We are developing the coffee trade as a model system for testing the global distribution of crop-associated contaminant fungi and the impact of global transport of food. Through coffee we explore how modes of production can alter community structure and gene flow. Specifically, we are testing whether different methods of agricultural production lead to the assembly of distinct fungal communities on coffee, including mycotoxigenic fungi. Using both culture-dependent and culture-independent methods, we have assessed fungal communities of conventional and organic green coffee beans from multiple geographic regions. Culture-dependent methods involved plating 200 surface-sterilized beans per lot on Dichloran-glycerol 18 and Malt Extract Antibiotic agar media. Fungi were isolated into pure culture and identified by sequencing of the ITS ribosomal RNA. These results show that distinct fungal communities form on the same substrate of different geographic locations. Culture-independent methods of assessing fungal community assemblage involved extracting DNA from whole green beans from 20 conventional and organic bean samples from different geographic regions and the use of fungal specific universal primers (ITS1-F and ITS4) to amplify the fungal DNA found in the beans. Fungal species diversity appears to be affected by method of agricultural production, and communities of different geographic regions are composed of different species, suggesting that although food fungi may be cosmopolitan, they may not be ubiquitous.

Sánchez-García, Marisol^{1*}, Cifuentes Blanco, Joaquín¹, and Matheny, P. Brandon². ¹Biología Facultad de Ciencias, Universidad Nacional Autónoma de México, México DF, 04510, México, ²Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA. msanchezg@ciencias.unam.mx. **An overview of *Melanoleuca* (Agaricales) in Mexico.**

The genus *Melanoleuca* contains approximately 50 species distributed worldwide. Eight taxa have been previously reported in Mexico, including *M. yucatanensis*, a species described from the Yucatan Peninsula. A number of specimens housed at six Mexican herbaria were examined (ENCB, FCME, IBUG, MEXU, TLXM, XAL). We found several new species mainly distributed in the Transmexican Volcanic Belt, which has been recognized by its distinct geologic and biotic features that make it a unique region with great diver-

sity and high endemism. The Mexican taxa are distributed in grasslands, oak, coniferous and cloud forests. Most of them present morphology that resembles European species and this is why foreign names have been applied to these taxa. However, they are different phylogenetic species. The use of European names for Mexican species, the distinctive characters of the new taxa, and the need of more thorough analyses to study fungal diversity in Mexico will be discussed.

Talbot, Jennifer M.* and Treseder, Kathleen K. Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92617-2525. jtalbot@uci.edu. **Lignin, cellulose, and N control the activity and interactions between decomposer fungi.**

Litter decay rates often correlate with the initial ratios of lignin:nitrogen (N) or lignin:cellulose in litter. However, the chemical and microbial mechanisms that give rise to these patterns are still unclear. To identify these mechanisms, we studied the decomposition of a model plant system, *Arabidopsis thaliana*, in which plants were down-regulated in the biosynthesis of lignin or cellulose, or were grown to have low or high levels of litter N. Plants were decomposed in litterbags for one year in control and N-fertilized plots in an Alaskan boreal forest and analyzed for total mass loss, change in chemical composition of the litters, activity of extracellular enzymes, and fungal biomass. Initial litter chemistry had a strong effect on total litter mass loss and chemical changes in the litter. Litter N had a positive effect on total mass loss ($P = 0.0002$) due to greater losses of lignin, N, and soluble C. Lignin had a negative effect on rates of total litter mass loss due to lower losses of cellulose ($P < 0.0001$) and hemicellulose ($P = 0.0040$) from litter. Cellulose had a strong positive effect on lignin loss ($P = 0.0005$), indicating that cellulose was required for lignin breakdown. Low lignin litter had higher N-acetyl glucosaminidase (NAG) activity and higher fungal biomass, suggesting increased antagonism between decomposer fungi. N fertilization also increased NAG activity in the early stages of decay and then led to increased cellulase activity on the litters and reduced lignin losses in the later stages. The transition in fungal activity on the litters from antagonism to high cellulase activity and suppressed lignin loss suggested that differential effects of N fertilization on cellulose and lignin degradation in field studies may result from a community shift towards efficient N- and cellulose-degraders.

Timling, Ina^{1*}, Taylor, D Lee¹, Walker, D A.¹, Dahlberg, Anders², Gardes, Monique³, and Charcosset, J-Y³. ¹Institute of Arctic Biology, University of Alaska Fairbanks, 311 Irving I Building, AK 99775, USA, ²Dept. of Forest Mycology and Pathology, Swedish University of Agricultural Science, Box 7026, S-750 07 Uppsala, Sweden, ³Dept. of Evolution and Biological Diversity, University of Toulouse, 118 Route de Narbonne, 31062 Toulouse Cedex 4, France. itimling@alaska.edu. **Fungal diversity along a bioclimatic gradient from the Low to the High Arctic.**

Fungi are key components of terrestrial ecosystems that drive mineral and energy cycling, and influence the occurrence of other organisms. Ectomycorrhizal fungi form symbioses with a variety of plants in the Arctic. Nonetheless, their abundance, diversity, and functions in the arctic tundra and their potential responses to climate change are poorly understood. The goal of our study was to describe ectomycorrhizal fungal communities along a bioclimatic gradient from the Low to the High Arctic. Besides the identification and distribution of fungi, we are seeking an understanding of the key drivers shaping ectomycorrhizal fungal communities along this gradient. We collected roots from *Dryas integrifolia* and *Salix arctica* at 23 locations along this gradient. DNAs were extracted from ectomycorrhizal morphotypes and the ITS region was sequenced. Ectomycorrhizal communities associated with the two host-plants, are dominated by a few common and diverse families (*Thelephoraceae*, *Inocybaceae*, *Sebacinaceae*, *Cortinariaceae*, *Pyronemataceae*). A total of 242 OTUs were observed, with 203 OTUs belonging to the Basidiomycota and 39 to the Ascomycota. Both host plants show similar species richness along the gradient (154 OTUs on *Dryas integrifolia*, 176 OTUs on *Salix arctica*). Host-plant does not affect their fungal community composition in this study. A subset of locations was used to identify key drivers for fungal distribution along the gradient. We found, that fungal communities associated broadly with two floristic provinces of the Arctic. Furthermore, neighboring bioclimatic subzones and locations had the greatest similarity in fungal species composition. The most abundant fungal taxa observed in this study were also found in other regions of the Arctic as well as in temperate climates from a variety of different hosts. Abiotic factors correlated with fungal community composition include a complex of factors relating to geographic location, soil properties and temperature.

Tomas, Rush A.^{1*}, Raymond, Schneider W.¹, Glen, Hartman L.², Sarah, Hambleton³, Nicole, Ward A.¹, and Aime, M. Catherine¹. ¹Louisiana State University Agricultural Center, Department of Plant Pathology and Crop Physiology, Baton Rouge, LA 70803, USA, ²USDA-ARS, National Soybean Research Cen-

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ter, Department of Crop Sciences, University of Illinois, Urbana IL 61801, USA, ³Agriculture and Agri-Food Canada, Ottawa, ON K1A 0C8, Canada. trush2@lsu.edu. **Validation of diagnostic assays for *Phakopsora pachyrhizi* in the United States.**

There are an estimated 120 species in the genus *Phakopsora* (Pucciniales, Basidiomycota) worldwide, with 19 species reported in the continental United States. Of these, *Phakopsora pachyrhizi* is the most widely known and monitored species because of its potential impact on soybean production, its multiple alternative hosts, and its widespread distribution in the United States. In 2002, a quantitative PCR (qPCR) diagnostic assay was reported to identify and discriminate between the two soybean rust pathogens in infected leaf tissue. It was later used in spore trapping studies in which the qPCR diagnostic assay detected the presence of *P. pachyrhizi* in Ohio and other northern states where soybean rust was never reported. It is possible that these reports from spore traps may be the result of false positives because other *Phakopsora* spp. are known to exist in these states, such as *P. crotonis*, which has been reported in Indiana, Illinois, and Nebraska. In 2009 a new qPCR diagnostic assay was developed with sensitivity to detect single spores of *P. pachyrhizi* in rain wash spore collections. Both qPCR assays were tested against several *Puccinia* species and against *Phakopsora meibomia* (a less aggressive rust pathogen on soybeans); however, neither of these assays was tested against the other *Phakopsora* spp. known to occur in the continental United States. In our study we assessed the potential for both assays to generate false positives against several North American species of *Phakopsora* including *P. arthuriana*, *P. crotonis*, *P. meibomia*, *P. nishidana*, and *P. tecta*. Preliminary results indicated that the 2002 qPCR assay detected and discriminated between *P. pachyrhizi* and *P. meibomia*, and the 2009 qPCR assay only detected *P. pachyrhizi*. Neither assay gave positive results for other *Phakopsora* spp.

Toome, Merje^{1*}, Padamsee, Mahajabeen^{1,2}, and Aime, M. Catherine¹. ¹Plant Pathology and Crop Physiology Department, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, USA, ²Biosystematics Team, Landcare Research, Auckland 1072, New Zealand. mtoome@agcenter.lsu.edu. **Resolving phylogenetic relationships in Pucciniomycotina.**

Pucciniomycotina is one of three subphyla of Basidiomycota, containing more than 8000 known species. The majority of these fungi are plant parasites, known as rusts (Pucciniales), but Pucciniomycotina also includes saprotrophs, mycoparasites, animal parasites, and even mycorrhiza-forming fungi. The latter groups are less studied than the rusts and some have only very recently been recognized as belonging to Pucciniomycotina. Previous studies have identified eight supported monophyletic classes in this subphylum based on sequences of large and small subunits of nuclear rDNA: Pucciniomycetes, Atractiellomycetes, Cystobasidiomycetes, Microbotryomycetes, Classiculomycetes, Agaricostilbomycetes, Mixiomycetes and Cryptomycolacomyces. While tremendous progress has been made in circumscribing Pucciniomycotina, deeper nodes lack resolution with rDNA, limiting understanding of the evolutionary pathways that led to development of such unusual traits as obligate parasitism and heteroecism within this group. As part of the AFTOL (Assembling the Fungal Tree of Life) project we generated sequences for several protein coding genes (e.g. FAL1, EF1a, RPB2, EFT2, KRR1) that had previously been used to resolve poorly supported nodes in Ascomycota. Our preliminary results provide stronger support for several key clades that allow some inference about the evolutionary history of these early diverging Basidiomycetes.

Treseder, Kathleen K.^{*}, Whiteside, Matthew D., Allison, Steven D., and Talbot, Jennifer M. Ecology and Evolutionary Biology, University of California Irvine, Irvine CA 92697. treseder@uci.edu. **Do mycorrhizal fungi augment or reduce soil C sequestration?**

We investigated the role of mycorrhizal fungi in sequestering or releasing carbon from soils under global change, particularly anthropogenic nitrogen enrichment. Our goal was to determine whether fungi might form positive or negative feedbacks on climate change by mediating atmospheric carbon dioxide. We examined this issue in boreal soils in Alaska, where a significant portion of the Earth's carbon is stored. We used microscopy and DNA sequencing to characterize shifts in the abundance and diversity of fungi under nitrogen enrichment, and we found that ectomycorrhizal abundance and fungal diversity declined. In addition, soil CO₂ efflux slowed. To examine rates of uptake of organic compounds by fungi, we used nanotechnological "quantum dots" to visually track movements of (labile) glycine and (recalcitrant) chitosan through the soil and into ecto- and arbuscular mycorrhizal fungi in the field. We observed that ecosystem-level uptake rates of glycine as well as chitosan declined as nitrogen availability increased. It is possible that the use of organic nitrogen by mycorrhizal fungi may decrease as a result of nitrogen enrichment. Overall, our findings suggest that in the short term, mycorrhizal fungi may form a negative feedback on global warming owing to decreases in their abundance, use of recalcitrant organic nitrogen, and soil respiration.

Tretter, Eric D.^{1*}, Wang, Yan¹, Johnson, Eric M.¹, Guardia Valle, Laia², Strongman, Doug³, and White, Merlin M.¹ ¹Boise State University, Dept. of Biological Sciences, Boise, ID 83725 USA, ²Biologia Vegetal y Ecologia, Universitat Autònoma de Barcelona, 08193-Bellaterra, Spain, ³Unitat de Botànica, Dept. de Biologia Animal, Dept. of Biology, St. Mary's University, Halifax, NS, B3H 3C3, Canada. erictretter@u.boisestate.edu. **An expanded phylogeny of the Trichomycete fungi.**

The trichomycete fungi include two orders (Harpellales and Asellariales) that are obligate gut symbionts of arthropods. Many species within the Harpellales and all species within the Asellariales have yet to be isolated in axenic culture. This has hampered previous attempts to characterize these groups through molecular phylogenetics, as material for genetic analysis must be obtained through dissection of host arthropods, which presents genomic DNA that is frequently mixed with DNA from the host insect. We have developed novel primers and protocols for the amplification of trichomycete ribosomal DNA without amplifying the DNA of the host insect. With these new methods, we have placed in phylogenetic trees several genera of the Harpellales previously not characterized via molecular methods, such as *Graminella*, *Spartiella*, *Caudomyces*, *Legeriosimilis*, and *Legerioides*. Additionally, we have been working on amplify and sequence protein-coding genes to confirm the rDNA-based phylogeny and improve resolution. We have preliminary trees available for RPB1, MCM7 (for which we had to develop novel primers), and Beta-Tubulin. Congruence between these trees and the rDNA-based tree will be examined and the potential for each gene to improve our understanding of the early-diverging fungi discussed. Finally, we report on our attempts to amplify and sequence genes from the order Asellariales, for which no gene sequence has yet been published.

Trudell, Steve¹, Mohatt, Katherine R.^{2*}, and Dillman, Karen L.³ ¹College of Forest Resources, University of Washington, Seattle, WA, 98195, ²USDA Forest Service, Girdwood, AK, 99587, ³USDA Forest Service, Petersburg, AK, 99833. kmohatt@fs.fed.us. **Some interesting macrofungi from southern Alaska's Chugach and Tongass National Forests.**

The Tongass and Chugach National Forests are the first and second largest national forests in the United States and combined they cover a majority of southern Alaska. They are primarily composed of coastal temperate rainforests that are dominated by ectomycorrhizal conifers, mainly Sitka Spruce and Western and Mountain Hemlock. These forests produce prolific fruitings of macrofungi in late summer and fall, however, surprisingly little is known about species occurrence and distributions in southern Alaska. Since 2007, the Chugach and Tongass National Forests have supported a series of fungus-themed events aimed at expanding knowledge of the local macrofungi and their ecology in these habitats. These events have hosted numerous local experts, visiting mycologists, and a large number of mushroom enthusiasts and has resulted in annual records of fungal species occurrences in the two national forests. Here we report a combined species list from these events and illustrate and describe some of the characteristic species of the region.

U'Ren, Jana M.^{1*}, Lutzoni, François², Miadlikowska, Jolanta², and Arnold, A. Elizabeth¹. ¹School of Plant Sciences, University of Arizona, Tucson, AZ 85721, ²Department of Biology, Duke University, Durham, NC 27708. juren@email.arizona.edu. **Diversity and biogeography of endophytic and endolichenic fungal communities.**

Endophytic and endolichenic fungi occur in healthy tissues of every plant and lichen species surveyed to date. Phylogenetic analyses suggest a close evolutionary relationship between these guilds, but previous sampling has been insufficient to evaluate the distinctiveness of these symbiotrophs and has not comprehensively assessed the biogeographic and abiotic factors that structure their communities. Drawing from surveys of 105 species of phylogenetically diverse lichens and plants in four biogeographic provinces across North America (southwestern coniferous forest; eastern semi-deciduous forest; subtropical scrub forest; and coastal and inland tundra in Alaska), we examined the diversity, taxonomic composition, and biogeography of 4154 endophytic and endolichenic isolates of Pezizomycotina. Our surveys reveal that these symbiotroph communities differ significantly at the species level among sites, and that different classes of Pezizomycotina dominate related hosts in different locations. At the landscape scale fungal communities located closer together are more similar than communities located farther apart, with differences reflecting environmental heterogeneity more strongly than geographic distance alone. Abiotic factors such as mean annual temperature and precipitation contribute differently to endophyte and endolichenic abundance and diversity. Endolichenic fungi are distinctive relative to most endophytes of vascular plants, but genotypes occurring in lichens frequently are found in mosses as well. Finally, our study reveals the distinctiveness of boreal endophytic fungi relative to those found in other biomes, and reveals their high diversity and unique patterns of host affiliation.

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Uehling, Jessie K.^{1*}, Smith, Matthew E.³, Aime, M. Catherine², Henkel, Terry W.¹, and Vilgalys, Rytas³. ¹Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, ²Department of Plant Pathology & Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, ³Department of Biology, Duke University, Durham, NC 27708. tw5@humboldt.edu. **Is *Clavulina* hyperdiverse in the Guiana Shield? Species diversity and phenotypic variation in Guyana.**

Worldwide there are ~75 described species of the ectomycorrhizal (ECM), predominantly tropical coral fungus genus *Clavulina* (*Cantharellales*, *Basidiomycota*). In the central Guiana Shield of northeastern South America mycofloristic surveys and mycorrhizal sequencing demonstrate that *Clavulina* is a ubiquitous and speciose genus in rainforests dominated by ECM leguminous trees, and also associates with ECM hosts in the Polygonaceae and Dipterocarpaceae. Of the 170 morphospecies of ECM fungi collected over 13 years at a local site in Guyana's Pakaraima Mountains, ~25 belong to *Clavulina*, and belowground molecular studies indicate that at least 21 additional *Clavulina* species are currently undiscovered as fruiting bodies. This is the highest number of sympatric *Clavulina* species recorded at a single site, suggesting that western Guyana is a center of diversity for the genus. Nearly all of these species are new to science. Most strikingly, a number of these *Clavulina* taxa have macro- and micro-morphologies that differ radically from the traditional generic diagnostic features of coralloid basidiomata and bisterigmate basidia. Guyanese taxa have been described with infundibuliform, resupinate or effuso-coralloid basidiomata and basidia bearing from three to six sterigmata. Here we present the first large scale multi-locus phylogenetic analyses of the genus *Clavulina*. Insights into infrageneric structure, biogeographic patterns and evolution of unusual morphologies in *Clavulina* will be discussed.

Urbina, Hector* and Blackwell, Meredith. Louisiana State University, Baton Rouge, LA 70803. hurbina1@tigers.lsu.edu. **Diversity of novel xylose-fermenting yeasts associated with the gut of Guatemalan passalid beetles.**

Xylose is a major component of the plant cell wall carbohydrate hemicellulose, but the ability to ferment xylose is rare and in fermentations for production of bioethanol, xylose usually is not fermented and may even disrupt the fermentation process. Recently large numbers of yeast species have been isolated in association with plant-feeding insects from woody substrates that can ferment this sugar. Interest in discovering novel species of yeasts that carry out the fermentation of xylose is important in order to better understand this biochemical ability as well as to discover species with high production of ethanol to be used in industrial processes. The primary aim of this project was the isolation and characterization of xylose-fermenting (X-F) yeasts isolated from the gut of wood-feeding passalid beetles. Approximately 3000 yeast strains were isolated from the digestive system of 23 species of passalid beetles (Coleoptera, Passalidae) collected in Guatemala. The yeasts were identified using three molecular markers in the ribosomal RNA gene [small subunit (SSU); internal transcribed spacer (ITS1&2) and the region D1/D2 of the large subunit (LSU)]. Phylogenetic analysis was performed with MrBayes using a matrix of 3380 characters with MCMC running for 1,000,000 generations (four simultaneous runs). In agreement with previous studies, ascomycete and a few basidiomycete yeasts dominate the gut flora. Xylose-fermenting yeasts, members of the *Spathaspora* and *Scheffersomyces* clades, were consistently found in all passalids dissected. The inclusion of sequences from 13 undescribed Guatemalan yeast taxa in a phylogenetic analysis improved support for a phylogenetic reconstruction, and members in the *Scheffersomyces* clade were divided into two monophyletic groups corresponding to their competency to ferment xylose. These results provide indirect evidence to confirm a consistent relationship between yeasts and passalid beetles as well as the phylogenetic relatedness among X-F yeasts.

Urbina, Hector¹, Suh, Sung-Oui², Luangsa-ard, J Jennifer³, and Blackwell, Meredith^{1*}. ¹Department of Biological Sciences, LSU, Baton Rouge LA 70808, USA, ²Mycology Program, American Type Culture Collection, Manassas, VA 20110, USA, ³Phylogenetics Laboratory, National Center for Genetic Engineering and Biotechnology, Science Park, Pathum Thani, Thailand. mblackwell@lsu.edu. ***Candida tanzawaensis*: a diverse clade associated with basidiomata-feeding beetles.**

Candida tanzawaensis was discovered by Nakase in 1966, but he did not describe it until 1988, because he waited unsuccessfully to isolate a second strain of the yeast. Kurtzman described six additional members of the clade in 2001 from a variety of substrates including insect frass, wood, and mushrooms. Sixteen species were described in 2004 from Panama and the southern United States, all of which were isolated from associations with fungus-feeding beetles. The aim of this study was the isolation and characterization of yeasts from the gut of Thai fungus-feeding beetles. In 2010 we isolated 128 yeast strains from approximately 40 fungus-feeding beetles classified in the families Erotylidae, Nitulidae, Endomychidae, Tenebrionidae, and Scaphidiidae, members of the same insect families that were hosts of *C. tanzawaensis* clade members in Pana-

ma and the United States. These beetles were collected in fewer than 5 days in Khlong Lan and Kaeng Krachen National Parks, Thailand. Phylogenetic reconstructions using four loci were performed, and these indicate that 15 undescribed species are members of the *C. tanzawaensis* clade. Only three species, *C. panamericana*, *C. anneliseae*, and *C. chickasaworum*, that were common in the Western Hemisphere, also occurred in Thailand.

Vaughan, Michael Joe S.^{1*}, Maier, Raina M.², and Pryor, Barry M.¹ ¹School of Plant Sciences, University of Arizona, PO Box 210036, Tucson, AZ, 85721, ²Department of Soil, Water and Environmental Sciences, University of Arizona, PO Box 210038, Tucson, AZ, 85721. bmpryor@ag.arizona.edu. **Fungal community structure from speleothem and rock wall surfaces in Kartchner Caverns, Benson, AZ, USA.**

Kartchner Caverns, located near Benson, Arizona, is an actively forming carbonate cave renowned for its mineralogical and speleothem diversity. Since its discovery in 1974, special attention has been paid toward preserving the cave in a near-prediscovery condition. The cavern is the focus of numerous studies exploring the microbial diversity and ecology of carbonate speleothems. The research presented here aims to elucidate 1) the fungal richness among calcium carbonate stalactites, 2) the spatial distribution of fungal taxa among stalactites, and 3) to compare the fungal communities on these stalactites to rock wall fungal communities. This project uses GS FLX Titanium 454 sequencing of community DNA ITS1 amplicons to identify the members of the fungal communities on these substrates, capturing both culturable and culture recalcitrant species. Sampling was conducted in a low impact area of the cave (receiving < 3 visits per year from park rangers) across a distance gradient of 450 meters. Samples were taken from eight sites at intervals along this gradient. The location of each site was determined by the availability of formations which met the criteria to be included in that sampling. At each site, three speleothems and three adjacent rock wall sections were sampled. After sequencing, OTUs were defined based on sequence similarity at three levels, 95%, 97%, and 100%. It was found that speleothems do not harbor the same fungal communities across the distance gradient, and that there was a significant effect of site location on community composition. The relationships between fungal community composition and sample site proximity and in-depth characterizations of the comparison between rock walls and speleothems are also discussed. This research provides valuable information as to the structure of cave microbial communities in an oligotrophic environment.

Vellinga, Else C.* and Bruns, Thomas D. Department of Plant and Microbial Biology, University of California at Berkeley, Berkeley, CA. ecvellinga@comcast.net. **The mycota of two national parks in California - inventory, identification, sequencing, and data dissemination.**

Yosemite National Park (YNP) in the central Sierra Nevada range and Point Reyes National Seashore (PRNS) are icons of western landscapes and biodiversity. Their fungal diversity is presently under investigation. Five large scale inventories, so-called mycoblitzes, have been held in PRNS; small group forays have been organized for YNP in spring 2010 for the first time. Collections have been photographed (www.mushroomobserver.org and <http://pmb.berkeley.edu/~bruns/tour/mycoblitz1.html>), vouchered, and identified by experts in their field, and nrITS sequence data produced. So far in one year of collecting in YNP 130 species have been reported, and in PRNS we have over 500 species of macrofungi. Only 38% of YNP taxa were also found at PRNS, but the YNP collections are currently biased toward spring fruiters, often associated with snow melt and snow banks. A third of the PRNS species have only been found once in one location, whereas four species were collected more than 25 times. With nrITS sequence data for PRNS collections we can place our collections in a phylogenetic context, deduce distribution patterns, and determine whether the taxa are already described. Three new species have been discovered so far: one *Amaurodon* sp., *Pseudobaespora aphana*, and *Suillus quiescens*. Sequence data also revealed cryptic diversity: e.g. the commonly found "*Pluteus cervinus*" represents in fact three, undescribed, and widespread taxa. This project has only been possible because of the input by many collectors and identifiers, amateurs and professionals, and the general public. All data are available on the web, and we hope that this may serve as a model for other similar projects.

Walker, Allison K.* and Campbell, Jinx. The University of Southern Mississippi Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39564. a.k.walker@eagles.usm.edu. **Marine fungal diversity of US Gulf of Mexico barrier island beaches.**

Marine fungi play a significant degradative role in marine and estuarine environments and serve as an important food resource for invertebrates. Basic marine fungal distribution data are lacking in many parts of the world. This study sought to delineate the parameters shaping marine fungal distribution and

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biodiversity along latitudinal gradients, via a comparison of marine fungal communities of selected Florida and Texas barrier island beaches. Beach detritus (wood, seagrass, saltmarsh and mangrove) and sand were collected in winter and summer from the intertidal zone and incubated in the laboratory. Seafoam was also collected and examined for the presence of marine fungal spores. Morphological and molecular techniques (ITS T-RFLP community fingerprinting) were employed to compare intertidal fungal communities from the Florida Keys north to St. Vincent Island, Florida and from South Padre Island north to Galveston Island, Texas. Marine fungi from Ship Island, Mississippi are also being inventoried to investigate changes in marine fungal communities over shorter time scales. Collections were completed prior to the Deepwater Horizon oil spill of April 20, 2010, allowing this study to provide baseline data on marine fungal biodiversity of the U.S. Gulf of Mexico.

Walker, Donald M.^{1,2*}, Castlebury, Lisa A.², Rossman, Amy Y.², and White, James F., Jr.¹. ¹Department of Plant Biology and Pathology, Rutgers University, 59 Dudley Rd., New Brunswick, NJ 08901, ²Systematic Mycology and Microbiology Laboratory, USDA Agricultural Research Service, 10300 Baltimore Blvd., RM. 224, BLDG. 010A, BARC-WEST, Beltsville, MD 20705. dowalker@eden.rutgers.edu. **Environmental influences on speciation and role of the niche in the genus *Ophiognomonia* (Gnomoniaceae, Diaporthales).**

Species of *Ophiognomonia* are leaf- and stem-inhabiting perithecial fungi occurring mostly on host plants in the Fagales but also the Lauraceae, Rosaceae, Salicaceae, and Tiliaceae. In this study local ecological patterns were linked with a multi-gene phylogeny of all available species of *Ophiognomonia* to better understand speciation events and host associations in this genus. The impact of environmental variables on fungal speciation was also assessed. Individual specimen coordinates from 151 collections were linked with 56 quantitative precipitation and temperature environmental variables, which were extracted from GIS base layers and USGS base maps using Spatial Evolutionary and Ecological Vicariance Analysis (SEEA; Struwe et al., 2011). A total of 304 environmental variable comparisons were significantly associated with 42 nodes across the *Ophiognomonia* phylogeny. Eleven of these nodes independently displayed 13–48 associations. The two nodes representing one deep and one shallow relationship were associated with 48/40 environmental variables respectively and are the focal point of discussion. In summary, host plant specificity was correlated with deeper divergences in the phylogeny of *Ophiognomonia*. Temperature and precipitation were significant, but less important variables that influenced ecological divergences at deeper nodes. Quantitative environmental variables, such as precipitation during the wettest month and annual temperature range, were significantly associated with shallow divergences in sister species clades of *Ophiognomonia*. Host specificity and niche conservation were determined as mechanisms contributing to speciation in *Ophiognomonia*. Using this method of analyzing existing environmental data provides a better understanding of speciation events over broad geographic ranges and host associations.

Wang, Yan^{1*}, Tretter, Eric D.¹, Lichtwardt, Robert W.², and White, Merlin M.¹ ¹Department of Biological Science, Boise State University, Boise, ID, 83725-1515, ²Department of Ecology & Evolutionary Biology, University of Kansas, Lawrence, KS 66045-7534. yanwang@u.boisestate.edu. **Teasing apart the polyphyletic “*Smittium*” clade of gut fungi (Harpellales): merging multi-gene molecular and morphological margins.**

Gut fungi are endosymbiont microorganisms that live in the digestive tracts of insects and other Arthropoda. As one of the more studied and also the largest genus of Harpellales, various species of *Smittium* and related taxa have clustered loosely in phylogenetic analyses and been regarded as the “*Smittium*” clade. The genus has a culturable rate of 40%, which is much higher than most other taxa of gut fungi, and isolates of *Smittium* have been used in varied earlier studies relating to host specificity, growth parameters, thalial development as well as molecular phylogenetics. Currently, *Smittium* has 79 named species, and genomic DNA or isolates of some of them have been used by multiple labs and studies, but are often limited to a few representatives, such as *S. culisetae*, *S. culicis* or *S. simulii*. However, *Smittium* is polyphyletic based on previous molecular systematic analyses using DNA sequences (18S and 28S rDNA genes analyzed separately). Additionally, several lineages may well make up the “*Smittium*” clade and perhaps even require a new genus designation for phylogenetically distinct taxa like *Smittium culisetae*. We are building a multi-gene dataset for *Smittium* and related taxa including *Austrosmittium*, *Furculomyces*, *Stachylina* and *Trichozygospora*. Placing members of the “*Smittium*” clade amongst other Harpellales and early diverging fungi is one of the goals of our current research program. A snapshot of our ongoing efforts to infer a multi-gene (18S and 28S rDNA, with protein-coding RPB2 genes) phylogeny with emphasis on the “*Smittium*” clade will be highlighted here. Molecular studies, in combination with the assessment of traditional morphological traits will help to inform systematic revisions and reclassifications, especially amongst these early diverging sections of the fungal tree of life.

Wang, Zheng¹, Lehr, Nina¹, Sikhakolli, Usha², Trail, Frances², and Townsend, Jeffrey P.^{1*} ¹Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520, ²Department of Plant Biology, Michigan State University, East Lansing, MI 48824. Jeffrey.Townsend@Yale.edu. **Comparative transcriptomics of fruiting body development in environmental context.**

Fungal fruiting body size and form are influenced by the ecology of the species, including diverse environmental stimuli. The endophytic lifestyle has played an important role in the evolution of the morphology of reproductive structures (body) in one of the most problematic groups in fungal classification, the Leotiomycetes (Ascomycota). Mapping fungal morphologies to two groups in the Leotiomycetes, the Rhytismatales and Hemiphacidiaceae reveals significant divergence in body size, shape and complexity. Mapping ecological roles to these taxa reveals that the groups include endophytic fungi living on leaves and saprobic fungi living on duff or dead wood. Finally, mapping of the morphologies to ecological roles reveals that leaf endophytes produce small, highly reduced fruiting bodies covered with fungal tissue or dead host tissue, while saprobic species produce large and intricate fruiting bodies. Intriguingly, resemblance between asexual conidiomata and sexual ascomata in some leotiomycetes implicates some common developmental pathways for sexual and asexual development in these fungi. To reveal the shifts in gene expression that drive differentiation of tissues and the evolution of new morphologies, we have examined microscopic phenotype and assayed genome-wide gene expression during perithecial development of three species of the model saprobe, *Neurospora*, and two species of the plant pathogen, *Fusarium*. These developmental processes are fundamental to sexual reproduction, recombination, and to the adaptive dynamics of pathogens and hosts. This information, mapped to the phylogeny of the species, will be used to estimate the ancestral evolutionary transitions that resulted in the shifts in morphology and ecology.

Wang, Zheng*, Lopez-Giraldez, Francesc, Li, Ning, and Townsend, Jeffrey P. Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520. wang.zheng@yale.edu. **Diversification of light sensors and light responsive networks in fungi.**

Abstract: Light is an essential environmental factor conveying information of daily and seasonal time to all kind of organisms, and light also serves as a critical indicator of environmental structure for plants and fungi. Light responses, especially via genes sensing blue-light, have been extensively studied for decades in fungal models, especially *Neurospora crassa*. Light affects various physiological processes in *Neurospora*, including circadian clock adjustment, pigment production, as well as asexual and sexual development. About 340 early- and late- light responsive genes are identified in *N. crassa*. Recently, light sensors for red and green light have been also found in diverse fungi, and red light has shown variable impacts on sexual and asexual development in *Aspergillus* species. Nevertheless, phenotypes for red and green-light sensors have not yet been established. In our study of asexual and sexual development of *N. crassa*, different expression patterns for different light sensor genes and light-responsive genes have been observed for different development stages. Red- and green-light sensor genes show an opposite expression pattern to the blue-light sensor genes, implying complex light-regulation in *N. crassa*. We further investigated the distribution of these light sensor genes and light responsive genes in published fungal genomes. Phylogenetic reconstruction and functional structure prediction with clustering analysis for these genes provide hypotheses about how different light sensor genes have evolved and about the diversification of light responsive systems cross the fungal kingdom.

Weber, Carolyn F.^{1*}, Porter, Terri M.², Moya Balasch, Monica¹, Vilgalys, Rytas³, and Kuske, Cheryl R.¹ ¹Bioscience Division, Los Alamos National Laboratory, Los Alamos, NM 87545 USA, ²Department of Biology, McMaster University, Hamilton, Ontario, Canada, ³Department of Biology, Duke University, Durham, NC 27708 USA. webercarolynf@gmail.com. **Soil fungal metatranscriptomics and community shifts in response to elevated CO₂ and nitrogen fertilization.**

Increased levels of atmospheric CO₂ enhance rates of photosynthesis and inputs of complex carbon, such as cellulose, to soils. As key players in carbon cycling, fungi are expected to be among the most impacted soil microbes, which could significantly impact biogeochemical cycling of carbon and alter atmospheric CO₂ levels. In order to understand the response of soil fungal communities, it is necessary to characterize their composition and activity. In this study, we constructed high-resolution sequence profiles of the fungal large subunit gene (LSU) at four depth intervals (litter, 0–2 cm, >2–5 cm, >5–10 cm) of soil cores collected from U.S. DOE free air carbon dioxide enrichment (FACE) site located in a loblolly pine forest (Chapel Hill, NC). Triplicate cores were collected from plots exposed to four different carbon and nitrogen regimes: Elevated CO₂ (eCO₂), elevated CO₂ and nitrogen fertilization (eCO₂+N), ambi-

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ent CO₂ (aCO₂) and ambient CO₂ and nitrogen fertilization (aCO₂+N). From each of the 48 soil depth intervals, an average of ca. 4,000 LSU sequences was obtained. Annotation in MG-RAST indicated that the percentage of sequences from Basidiomycota increased in soil exposed to eCO₂. In the nitrogen fertilization treatments under both CO₂ regimes, the percentage of Ascomycota sequences increased. These impacts were most pronounced in the litter and 0-2 cm depth intervals. Metatranscriptome sequencing of 96,000 reads from the 0-2 cm interval in an aCO₂ plot, indicates that Basidiomycota dominate gene expression in these soils. In sum, our data show a response of fungal communities to elevated CO₂ and nitrogen fertilization treatments at the phylum level and demonstrate the need to examine both DNA and RNA-based sequence profiles in soil to better understand impacts of ecosystem perturbation on fungal communities.

Weir, Bevan S.* and Johnston, Peter R. Private Bag 92170, Auckland Mail Centre, Auckland 1142, New Zealand. weirb@landcareresearch.co.nz. **Defining Genetic Species Limits in *Colletotrichum*.**

Recent, coalescent-based 'species-tree' approaches to phylogenetic analysis use multi-gene data to account for evolutionary processes such as incomplete lineage sorting. These methods allow the recognition of groups that may more closely imitate the biological species concept than simply concatenating multigene data sets. Concatenation of multiple genes ignores discordance among genes, which may lead to poor clade support and bias topologies. We test the species-tree approach using *Colletotrichum*, a plant pathogen with a confused taxonomy. Many species in the genus have been described on the basis of host substrate. Using morphological characters, in the 1950's von Arx synonymised many early names leaving species such as *C. gloeosporioides* with extreme genetic and biological diversity - a species complex. We tested coalescent-based analysis methods on two known *Colletotrichum* species complexes. Although the resulting species-trees supported some current species (and revealed putative new species), others were poorly resolved. The groups that we recognised surely have evolutionary significance, but questions remain about how they can be handled taxonomically. Ultimately, species-tree approaches to phylogenetic analysis represent another tool for the systematist that may be helpful for testing novel species hypotheses in difficult genera such as *Colletotrichum* in an unbiased quantitative manner.

William, Robert. Biology Department, Saint Mary's University, Halifax, Nova Scotia, Canada. robertwilliam00@gmail.com. ***Pteromaktron timberleaense* sp. nov. isolated from heptageniid nymphs in Timberlea Nova Scotia, Canada.**

A new species of trichomycete within the order Harpellales is described from mayfly (Heptageniidae) nymphs from a stream in Timberlea, Nova Scotia, Canada. The new species *Pteromaktron timberleaense* R. T. William & Strongman adds another taxon to the formerly monotypic genus, *Pteromaktron*. Sexual reproduction has not been described in *Pteromaktron* but we present evidence to suggest this fungus may produce zygospores.

William, Robert T.^{1,2} and Strongman, Doug^{1,2*}. Biology Department, Saint Mary's University, Halifax, Nova Scotia, Canada. doug.strongman@smu.ca. **Two new genera of Harpellid trichomycetes from Nova Scotia, Canada.**

Two new trichomycete fungi, *Bactromyces fluminalis* gen. et sp. nov. and *Laculus insecticola* gen. et sp. nov., are proposed, from stonefly (Plecoptera:Capniidae) and mayfly (Ephemeroptera: Caenidae) nymphs respectively. The stonefly hosts were collected in a stream habitat while the mayflies came from a lake. The distinctive characteristics of each new genus and the morphological relationship to other harpellid fungi are described.

Williams, Gwendolyn C. Department of Biology, Duke University, Box 90338, Durham, NC 27708. gcw7@duke.edu. **From pine to oak: ectomycorrhizal host preference facilitates succession.**

The process of ecological succession comprises an interconnected web of biotic and abiotic factors that both affect and respond to changes in the community, but historically the study of succession has focused on plants and left other essential organisms, such as ectomycorrhizal (EM) fungi, largely ignored. EM fungi are both phylogenetically and functionally diverse, and often show host preference for particular plant taxa, but the effects of host preference on interspecies competition between trees are not known. Fungal host preference may either facilitate or hinder the succession of dominant tree species. To address this question, a reciprocal transplant of white oak (*Quercus alba*) and loblolly pine (*Pinus taeda*) seedlings was conducted in paired plots of oak-dominated and pine-dominated forest in the Piedmont region of North Carolina. EM root tips were collected from seedlings and adults for molecular identification of fungal species based on sequence similarity of the internal transcribed spacer region of ribosomal DNA. Most individual seedlings hosted only 1-2 species of EM fungi, though the identities of these species varied

widely among different seedlings within the same plot, indicating that seedling associations are primarily determined by the initial colonization of roots, rather than by any competitive advantage of seedling-adapted EM species. The fungal associations of adult trees determine which EM species are dominant in the soil and thus available for seedlings to associate with. Oak seedlings planted under pine proved significantly better able to form mycorrhizal associations with the available fungi than were pine seedlings planted under oak. The broad preference of oak seedlings may allow oaks to readily establish in mid-seral pine forests, facilitating succession.

Wilson, Andrew W.^{1*}, Zhang, Rui¹, Hosaka, Kentaro², and Mueller, Gregory¹. ¹Chicago Botanic Garden, Plant Conservation Science, 1000 Lake Cook Rd, Glenview, IL 60022, USA, ²Department of Botany National Museum of Nature and Science (TNS) Tsukuba-shi, Ibaraki 305-0005, Japan. awilson@chicagobotanic.org. ***Laccaria* from the eastern Himalayas.**

Specimens of the cosmopolitan ectomycorrhizal genus *Laccaria* were collected from the eastern Himalayas in the Chinese provinces of Yunnan and Xizang (Tibet) in the summers of 1998, 2002, 2006, 2007 and 2009. Additional material was obtained on loan from HKAS. Preliminary systematic analysis indicated that most of these *Laccaria* have not been previously described. The purpose of this study is to identify and describe these specimens to determine if they represent unique species of *Laccaria*. To date, results of systematic analysis have identified at least six distinct taxa. Only one of these occurs in a clade with species from western temperate forests. The remaining phylotaxa appear as distinct taxa at the species level. The final analyses will compare the systematic relationships of these specimens to representatives of *L. alba* and *L. angustilamella* recently described from Yunnan. The results of systematic analysis will be used to inform a taxonomic study of the genus from this region and will be documented in this poster.

Wilson, Emma R.^{1*}, Smalling, Kelly L.², Reilly, Timothy J.³, Steele, Lance¹, Kandel, Prasanna¹, Chamberlin, Alison B.¹, and White, Merlin M.¹ ¹Boise State University, 1910 University Dr, Boise, ID 83725-1515, ²U.S. Geological Survey, 6000 J Street, Placer Hall, Sacramento, CA 95819, ³US Geological Survey, 810 Bear Tavern Road, Suite 206 West Trenton, NJ 08628. emmawilson@u.boisestate.edu. **Beyond gut feelings - how are trichomycetes affected by fungicides in aquatic systems?**

Fungicides of various forms have been used for decades to control fungal diseases and play an important role in modern agriculture. However, they tend to be understudied and are not typically included in water quality monitoring programs. Chlorothalonil and other broad spectrum fungicides have been applied for over 50 years, but the use of newly developed or different classes of fungicides has been increasing. The development and registration of new fungicides and expansion of their use is driven by the onset of new diseases, the persistence of older diseases and increasing fungicide resistance by many fungal pathogens. Fungicides are moderately hydrophobic and their persistence has been documented in water and sediment as a result of non-point source pollution. Currently, there are limited data on the effects of fungicides on aquatic organisms and impacts on non-target fungal communities require much attention. Trichomycetes (gut fungi) are obligate endosymbionts of aquatic insect larvae. To better understand potential effects on these organisms, surface water samples and arthropod hosts of symbiotic gut fungi were collected from impacted and reference sites between April and December 2010 in southwestern Idaho, USA. Reference drainages in Boise, Idaho had no pesticide inputs, whereas agriculturally impacted waterways in Parma, Idaho were variably fungicide-impacted. Specifically, Azoxystrobin and Boscalid (the two most frequently detected, emerging fungicides) were detected in over 90 % of the surface water samples at impacted sites. Larval insect hosts from control sites contained gut fungi with higher density, diversity and spore production, while those collected from the two impacted sites typically had lower diversity and fecundity (spore production). We believe that preliminary results indicate that fungicides have the potential to affect non-target fungal communities in surface water systems.

Wong, Valerie L.^{*}, Ellison, Christopher E., Brem, Rachel B., Eisen, Michael B., and Lior, Pachter. University of California, Berkeley, CA. vwong@berkeley.edu. **Utilization of Assembly-Free Synteny Analysis to identify rearrangements in wild *Penicillium chrysogenum* strains.**

Strain acquisition and improvement has been an important tool for human bioproduct utilization. While traditional methods of mutagenesis and selection have been effective in improving production of compounds to commercial scale, the genetic changes behind the altered phenotypes have remained largely unclear. We utilized high-throughput Illumina short read sequencing of a wild *Penicillium chrysogenum* strain in order to make whole genome comparisons to a sequenced improved strain (WIS 54-1255). We developed an as-

Continued on following page

sembly-free method of identifying rearrangements and validated the in silico predictions with a PCR-based assay followed by Sanger sequencing. In addition to finding a previously published inversion in the penicillin biosynthesis cluster, we located several genes related to penicillin production associated with these rearrangements. By comparing the configuration of rearrangement events among several historically important strains known to be good penicillin producers to a collection of recently isolated wild strains, we suggest that wild strains with rearrangements similar to those in known good penicillin producers may be viable candidates for further improvement efforts.

Yeraballi, Sagar^{1*}, Gossage, Zachary¹, Porras-Alfaro, Andrea^{1,3}, Suding, Katherine², Farrer, Emily C.², and Sinsabaugh, Robert³. ¹Biological Sciences, Western Illinois University, Macomb, IL, ²Department of Environmental Science, Policy & Management, University of California Berkeley, CA, ³Department of Biology, University of New Mexico, Albuquerque, NM. a-porras-alfaro@uiw.edu. **Study of mycorrhizal and endophytic fungi associated with two co-dominant alpine tundra plants.**

Root-associated consortia are unknown for the majority of plant species in alpine tundra ecosystems. Nitrogen (N) enrichment can facilitate plant productivity and fungal growth, but in certain conditions can negatively affect diversity and survival. The main goal of this study was to describe fungal symbionts associated with two co-dominant plants (*Geum rossii* and *Deschampsia cespitosa*) and to evaluate the effect of N fertilization on fungal colonization and diversity. Forty-two plants were collected from four different treatments: control, N fertilized, N fertilized/*Deschampsia* removal, *Deschampsia* removal/no N added in 2008 and 2010. The study site was located at the Niwot Ridge Long Term Ecological Research (LTER) site in Colorado. Roots were harvested from each treatment and stained to quantify fungal colonization. Two hundred pure cultures of endophytic fungi were isolated on potato dextrose agar. Fungal isolates were identified by sequencing the Internal Transcribed Spacer rDNA. Plant-roots were highly colonized by arbuscular mycorrhizal fungi and dark septate endophytes. Microscopy data from 2008 and 2010 showed an increase in percentage of fungal colonization (primarily in vesicles and spores of arbuscular mycorrhizal fungi) in N fertilized plots when compared to control plots. Preliminary identification of root isolates showed that *Geum* is mainly colonized by ericoid mycorrhizal fungi in the order Helotiales including *Cryptosporiopsis ericae* and the dark septate fungus *Phialocephala fortinii*. Potential effects of these fungal symbionts on various seeds and young plants were also examined. High levels of fungal colonization in alpine tundra plants by mycorrhizal fungi (ericoid and AMF) indicate high plant-dependence on fungal symbionts.

Zahn, Geoffrey L.^{*}, Stephenson, Steven L., and Spiegel, Fred W. Department of Biological Sciences, University of Arkansas, Fayetteville, AR, 72701. gzahn@uark.edu. **The protosteloid amoebae of New Zealand.**

During the period of March 2004 to December 2007, numerous samples of aerial litter and ground litter were collected from a wide variety of ecosystem types and range of latitudes (34° S to 50° S) in order to survey the assemblage of protosteloid amoebae on the islands of New Zealand (including the Auckland Islands). Twenty-seven described species of protosteloid amoebae were recovered along with the myxomycete *Echinostelium bisporum* and the acrasid *Acrasis rosea*. Of these, *Protostelium mycophaga* was by far the most abundant, being found in more than half of all samples. Most species were found in less than 10% of the samples collected. There was some evidence of a general trend towards lower species richness and diversity with increasing latitude and a pronounced decrease in species richness and diversity from the North Island to the South Island and the Auckland Islands. (This project was supported in part by grants from the National Science Foundation and the National Geographic Society.)

Zhang, Ning^{1*}, Zhao, Shuang^{1,2}, and Shen, Qirong². ¹Rutgers University, Department of Plant Biology & Pathology, 59 Dudley RD, New Brunswick, NJ 08901, ²Nanjing Agricultural University, Nanjing, China. zhang@aesop.rutgers.edu. **Systematics of Magnaporthaceae based on a six gene phylogeny, morphology and mode of infection.**

The family Magnaporthaceae includes devastating fungal cereal and grass pathogens, such as *Magnaporthe oryzae* (rice blast fungus, formerly known as *M. grisea*), *M. poae* (summer patch pathogen of turf grasses), and *Gaeumannomyces graminis* (take-all fungus of various cereals and grasses),

which are popular model organisms in fungal biology and host-pathogen interaction studies. Despite their ecological and economic importance, the phylogenetic relationships among the constituent species remain ambiguous due to the lack of convincing morphological characters and paucity of molecular data for the majority of the non-model species in the family. In this study, our multilocus phylogeny suggests that both *Magnaporthe* and *Gaeumannomyces* are polyphyletic genera. The phylogeny also provides insights into fungal biology and pathogenesis. *Magnaporthe oryzae* formed a basal clade, while *M. poae* and *M. rhizophila* formed another well-supported clade with *G. incrustans* and *G. graminis*. The basal species infect both root and aerial parts of the plant host, while the aerial infection capacity seems to be lost in the taxa of the latter clade. The phylogeny is corroborated by evolution of the anamorphs and a cAMP-dependent protein kinase (*CPKA*) gene. *Magnaporthe oryzae* produces *Pyricularia*, while taxa in the latter clade all produce *Phialophora*-like anamorphs. *CPKA* is present in animals and many fungal lineages with various functions. In *M. oryzae*, *CPKA* is essential for the formation of functional appressoria for leaf penetration. In root-infecting *G. graminis* var. *tritici* and *M. poae*, however, only non-functional *CPKA* homologous pseudogenes were found in their genomes. The study indicates that anamorphic and ecological features are more informative than the teleomorphic characters in defining monophyletic groups among these taxa.

Zhao, Serena Y.^{*} and Pringle, Anne. Department of Organismic and Evolutionary Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138. serena.yz@gmail.com. **Infection rates of Laboulbeniales on beetles of the Boston Harbor Islands.**

The Laboulbeniales, a group of ascomycetes that undergo determinate growth, parasitize a wide range of arthropod hosts. While the exact mechanisms of nutrient uptake and dispersal are not yet known, they have been found to be particularly prevalent on beetles. The Carabidae and Coccinellidae beetle families are often carnivorous and exhibit aggregating behaviour, which mark them as particularly susceptible to infection by Laboulbeniales. The Boston Harbor Islands are 34 islands ranging in size from 3 acres to 274 acres, with varying ecologies based on size, distance from the mainland, and dispersal patterns. The rates of Laboulbeniales infection on beetle species on the islands varies by island, beetle lineage, and life history. Further inquiry into the specificity of Laboulbeniales and their hosts would provide tools for better estimating the global diversity of fungi.

Zimmerman, Naupaka B.^{*} and Vitousek, Peter. Department of Biology, Stanford University, Stanford CA 94305. naupaka@stanford.edu. **Landscape biogeography of foliar fungal endophytes in the tropics.**

Fungal endophytes are microfungi that inhabit the asymptomatic above-ground tissues of their host plants. Relatively little is known about endophytes in woody vegetation - especially in the tropics, where the few extant studies show endophytes to be ubiquitous and hyperdiverse. We used a model host within a model environmental system to evaluate patterns of tropical endophyte distribution at the landscape scale. *Metrosideros polymorpha*, a tree endemic to Hawai'i, occurs across an extraordinary range of elevation and rainfall. The Mauna Loa environmental matrix on the Island of Hawai'i includes *Metrosideros*-dominated ecosystems that vary in mean annual temperature from 10-23° C and mean annual precipitation from 500 to 5500 mm, while holding constant the physical and chemical properties of the soil matrix. Barcoded pyrosequencing of the rDNA ITS1 region was used to group fungi into Operational Taxonomic Units (OTUs) and quantify community composition in surface-sterilized leaves from trees within a matrix of sites across the landscape. Sequencing resulted in over 700,000 high-quality sequences from 130 trees, with an average of over 5,000 fungal sequences per tree. We found very high levels of both alpha and beta diversity across the environmental matrix. Grouping denoised sequences into OTUs at 95% similarity, per-tree richness ranged from 40 to 257, per-site from 401 to 829 OTUs, and overall fungal OTU richness across the landscape was more than 4,100. BLAST searches against Genbank suggest that a large portion of the identifiable sequences were from the Pezizomycotina. While the majority of matched sequences were Ascomycetes, we also observed, among others, sequences attributed to the Agaricomycotina and Pucciniomycotina. Nonmetric multidimensional scaling and partial mantel tests showed that community similarity is strongly correlated with environmental variables including temperature/elevation and rainfall.

MYCOLOGIST'S BOOKSHELF

We are pleased to welcome Bob Marra (Robert.Marra@ct.gov), Connecticut Agricultural Experiment Station, who has been appointed to serve as the new Inoculum Bookshelf Editor. Bob will take over for Barrie Overton starting with the August issue of Inoculum.

Love, Sex and Mushrooms

A memoir titled *Love, Sex and Mushrooms: Adventures of a Woman in Science*, by Cardy Raper, was published in March, 2011. The book describes Cardy Raper's quest to become a scientist starting at a time when such professions did not welcome women. Through the teachings of mycologist John (Red) Raper at the University of Chicago, Cardy falls in love with fungi—and Red. They

marry and together investigate the myriad ways in which fungi find mates for sexual reproduction. Cardy interweaves the personal and scientific aspects of her life in science over a period of half a century. See www.cardyrap-er.com for a description of the book, its author and how it can be ordered.

List of fungi recorded in Japan

List of fungi recorded in Japan. By Ken Katumoto. 2010. The Kanto Branch of the Mycological Society of Japan. (Contact: Toru Okuda <torula@lab.tamagawa.ac.jp>) North American distributor: Mycotaxon Ltd., P.O. Box 264, Ithaca, NY 14851-0264, USA. <info@mycotaxon.com>. Pp. xv + 1177. Softcover ed. ISBN 978-4-87974-624-5. Price (US) \$130, postpaid. Hardcover ed. ISBN 978-4-87974-625-2. Price (US) \$220, postpaid. Canada and Mexico delivery add US\$25 for postage.

Sometimes even reading lists of fungi can be interesting particularly when the list provides reliable information on names, authors, distributions and first reports. Distributional patterns of fungi have been explored only in the most rudimentary way and certainly lists of occurrences can tell us something about ranges of fungi and perhaps cast light on extinctions and introductions of fungi. With this checklist of fungi recorded in Japan, all 1177 pages of it, one has a healthy dose of data on which to reflect. The organisms included here are the kingdom Fungi, the Straminipila, the Plasmodiophoromycota, and those Trichomycetes formerly treated as fungi. Slime molds of various ilk, other than that mentioned above, are not included. The classification follows that of recent treatments such as found in the *Dictionary of Fungi*.

To test myself on how I could use this mammoth compilation presented in a mix of roman script and Japanese ideographs, I turned to some genera that I know. Generic names are listed in roman script along with their place of publication, also in roman script. The status of the name is indicated, conserved names, for example, are noted. If the genus is considered a synonym of another genus then one is referred to the accepted genus. The type species for each genus is listed, as is the family to which it is referred. The listings are arranged throughout alphabetically by genus but

a classification is provided as an appendix. Species are listed alphabetically under the genus; their place of publication or the citation for the place of publication of a new combination is given. This information is all in roman script. From here on the road gets a bit steep because much of the text is in ideographs. Common names are provided in Katakana ideographs; host plants also are listed in this way. Reports from journals of the fungus in Japan are given but in most cases the journal title is given in Kanji. Sometimes there seem to be lengthy commentaries on topics one cannot decipher without a knowledge of Japanese but in some spot-checking most of this seems to be listings of hosts. For the inquisitive non-Japanese reader this is frustrating. One wants to have all the information that the author has so diligently assembled in these pages. Most helpful are the cross referenced synonymies. For example, looking under *Coprinus* one is given the proper referral to *Coprinellus*, *Coprinopsis*, *Parasola* and the *Coprinus* species *sensu stricto*.

One bit of detective work done by Katumoto is apparent and valuable. Where a name has been used but later has been determined to be misapplied or incorrectly used there are cross-references. For example, when Imai and, later I, studied a *Wynnea* species from Japan we called it *W. americana* but subsequent workers recognized it, perhaps correctly, as *W. macrospora*. These interpreted or misinterpreted names are traced. Such information is very difficult to retrieve using standard bibliographic sources and search methods. Here it is laid-out neatly.

An important appendix gives the full names of Japanese mycologists with accepted abbreviations. These appear both in roman script and in Japanese ideographs. For example, one can sort the Japanese mycologists named Ito. There are 11 and 5 of them have T as a first initial or the 11 mycolo-

Continued on following page

gists with the name Sato. The proper abbreviations are given for these Japanese authors. To further help in the identification of authors it would have been helpful to have birth and death dates for them, only some dates are given, but, with this perhaps I am becoming greedy. This appendix is further expanded to correct those authors' names that have appeared in the literature erroneously.

Bibliographies are rarely appreciated and are often dismissed as mere compilations without intellectual merit. Yet the well-constructed bibliography reflects a thoughtful and

insightful author. Such works save investigators time — time that can be put to other work. This is one of those thoughtful and time saving bibliographies. Despite the focus on Japanese fungi it is not just for the investigator concentrating on fungi from Japan but it also serves as a quick reference to see names in current use, synonyms, and alternative or misapplied names. Surely Ken Katumoto deserves our thanks.

—Donald H. Pfister
Harvard University

MYCOLOGICAL JOBS

Postdoctoral Researcher: Adaptation of fungi to climate change

The *Biodiversity and Climate Research Centre* (BiK-F) is a joint venture between the Senckenberg Gesellschaft fuer Naturforschung, Goethe-University Frankfurt/Main, and additional partners. It is funded by the German Federal State of Hesse through the Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. Project Area C “Adaptation and Climate”, Schmitt Laboratory, invites applications for the position of a postdoctoral researcher in *Adaptation of fungi to climate change* (Project C2.6, Ref. #C43).

The successful applicant will investigate short-term evolutionary processes in fungal communities, species or populations as a response to climatic factors. He or she has the opportunity to independently develop a project on the above theme preferably using mutualistic fungi, e.g. lichens, endophytes or mycorrhizae as study systems. Experiments involving the use of terrestrial model ecosystems, genomic and metagenomic approaches including next generation sequencing are possible. The institute offers ample opportunities to interact with researchers focusing on modeling, statistics, genomics, or social sciences approaches to studying the relationships between biodiversity and climate.

The applicant should hold a Ph.D. in evolutionary biology, ecology or a related field, and have a strong background in some of the following areas: mycology, evolutionary theory, molecular community assessment, phylogenetics, population biology, and bioinformatics. Post-doc experience is preferable, but not necessary. A solid publication record,

good written and oral communication skills in English, the willingness to write research papers and research proposals, work productively in a team, and to learn at least basic German are required.

We offer a competitive salary (TV-H E 13, a public service position in Germany), full benefits, and training opportunities at Goethe University Frankfurt and international/national laboratories.

The position is available from August 15th 2011, but the start date is flexible. The initial contract will be for one year with the possibility of multiple year extensions for up to six years. Habilitation is possible.

The Biodiversity and Climate Research Centre advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

Please send your application by e-mail attachment, mentioning the reference of this position (#C43) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2-3 referees and a copy of your PhD thesis to: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de.

Review of applications will begin on July 1st, 2011, and continue until a suitable candidate is identified.

Informal inquiries to Imke Schmitt ([imke\[schmitt\]@senckenberg\[de\]](mailto:imke[schmitt]@senckenberg[de])) before application are welcome.

PhD student: Fungal communities on poplar

The *Biodiversity and Climate Research Centre* (BiK-F) is a joint venture between the Senckenberg Gesellschaft fuer Naturforschung, Goethe-University Frankfurt/Main, and additional partners. It is funded by the German Federal State of Hesse through the Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on

the interactions of biodiversity and climate change at the organism level. Project Area C “Adaptation and Climate” invites applications for the position of a PhD student for the project *Fungal communities on poplar* (Project C2.6, Ref. #C44).

Continued on following page

The successful candidate will have a Master of Science (MSc) or equivalent in evolutionary biology, molecular biology, molecular ecology or related fields, and a strong interest in plant-fungal interactions, mycology. Experience in molecular laboratory techniques and DNA sequence analysis, next generation sequencing, bioinformatics and statistics are an advantage. Furthermore, good written and oral communication skills in English, teamwork skills, the willingness to write research-funding proposals and to learn some German are essential for a rewarding research. Working language will be English.

We are applying metagenomics techniques to questions of evolution, climate change and fungal community composition. The focus of this position will be on the environmental influences and evolutionary processes acting on the communities of leaf associated fungi in balsam poplar. You will use standard molecular genetics techniques as well as next-generation sequencing technology. Within the Biodiversity and Climate Research Centre you will have ample opportunities to interact and collaborate with faculty, postdocs and PhD students specializing in a variety of topics, such as biogeography, phylogenetics, macroecology, genomics, modeling, and bioinformatics. Frankfurt am Main is an attractive city in beautiful surroundings, with a multicultural population, and many educational and recreational opportunities.

The Research Centre BiK-F advocates gender equality. Women and other underrepresented groups are strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

The contract shall start on August 15 2011 and will be limited to three years. The start date is somewhat flexible. Salary and benefits are according to a public service position in Germany (TV-H E 13, 50%). The employer is the Senckenberg Gesellschaft fuer Naturforschung, the place for work is Frankfurt am Main, Germany.

Please send your application by e-mail attachment, mentioning the reference of this position (#C44) and including (1) a letter outlining your interest in this kind of research, and your suitability for the post, (2) a detailed CV, (3) contact details of 2 referees and (4) a copy of your thesis and other relevant exams: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de.

Review of applications will begin on July 1, 2011, and continue until a suitable candidate is identified.

Informal inquiries to Imke Schmitt ([imke\[schmitt\]@senckenberg.de](mailto:imke[schmitt]@senckenberg.de)) before the application are welcome.

PhD in Food and Bioproduct Sciences

The Opportunity: A Ph.D. graduate student is sought to carry out a research project with financial support from the Natural Sciences and Engineering Research Council of Canada (NSERC) grant. The funded project will investigate the topic "Mycoparasites and Fusarium Mycotoxins."

Qualifications: The applicant should have a strong academic background in molecular biology, proteomics, mycology/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 75% 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: A stipend is available to aid in the completion of the Ph.D. program

Deadline: The project is to commence once a suitable candidate has been identified (September 2011)

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 #vv2011.02 and mail or email package to: Graduate Secretary (brenda.rebeyka@usask.ca), Department of Food and Bioproduct Sciences, College of Agriculture and Biore-sources, 51 Campus Drive, University of Saskatchewan, Saskatoon, SK, Canada, S7N 5A8.

MYCOLOGICAL CLASSIFIEDS

Mold and Fungus Testing and Identification Services

Identification of fungi in microfluidic devices, medical diagnostic fluids, buildings and plant & animal diseases. Epi-fluorescent microbial detection in industrial ultrapure water systems and medical diagnostics. Biochallenge tests for ink,

medical and pharmacological products. 10% discount for regular and sustaining MSA members. Email steve@pacificanalytical.com or visit www.pacificanalytical.com.

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Sponsoring a gift membership in MSA offers tangible support both for the recipient of the membership as well as for mycology in general. Providing both *Mycologia* and *Inoculum*, a gift membership is an excellent way to further the efforts of our mycological colleagues, especially those who cannot afford an MSA membership. In addition to a feeling of great satisfaction, you also will receive a convenient reminder for renewal of the gift membership the following year.

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*If this membership is given after June 1, please add \$10 to cover postage for past issues.

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 kröse@allenpress.com.

MYCOLOGY ON-LINE

Below is an alphabetical list of websites featured in *Inoculum*. Those wishing to add sites to this directory or to edit addresses should email dnatvig@gmail.com. **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/

ASCOFrance.com, a very useful site for illustrations of ascomycetes including anamorphs (accessible in both French and English)
ascofrance.com/?lang=us

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

Basidiomycete Research Group (University of Helsinki, Finland) studies systematics, ecology and evolution of fungi in forest environment.
www.basidio.fi

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

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)
<http://blog.mycology.cornell.edu/>

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

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

The Cybertruffle internet server for mycology seeks to provide information about fungi from a global standpoint (59-3).
www.cybertruffle.org.uk

Cyberliber, a digital library for mycology (59-3).
www.cybertruffle.org.uk/cyberliber

Cybernome provides nomenclatural and taxonomic information about fungi and their associated organisms, with access to over 548,000 records of scientific names (59-3).
www.cybertruffle.org.uk/cybernome

Dictionary of The Fungi Classification
www.indexfungorum.org/names/fundic.asp

Distribution Maps of Caribbean Fungi (56-2)
www.biodiversity.ac.psiweb.com/carimaps/index.htm

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

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

Fungi of Ecuador
www.mycokey.com/Ecuador.html

German Mycological Society DGfM
www.dgfm-ev.de

MYCO-LICH facilitates mycology and lichenology studies in Iran.
www.myco-lich.com

Mycologia
mycologia.org

Humboldt Institute — Located on the eastern coast of Maine, the institute is known for the extensive series of advanced and professional-level natural history seminars it has offered in Maine since 1987, along with ecological restoration seminars and expeditions to the neotropics. It publishes the *Northeastern Naturalist* and *Southeastern Naturalist*, two scholarly, peer-reviewed, natural history science journals.
www.eaglehill.us

Website relating to the taxonomy of the Hysteriaceae & Mytiliniaceae (Pleosporomycetidae, Dothideomycetes, Ascomycota) to facilitate species identification using a set of updated and revised keys based on those first published by Hans Zogg in 1962. 59(4)
www.eboehm.com/

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

Interactive Key to *Hypocreales* of Southeastern United States (57-2)
nt.ars-grin.gov/sbmlweb/fungi/keydata.cfm
ISHAM: the International Society for Human and Animal Mycology
www.isham.org

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/abbeylab.html

McCrone Research Institute is an internationally recognized not-for-profit institute specializing primarily in teaching applied microscopy. 59(4)
www.mcri.org

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

Mycology Education Mart where all relevant mycology courses can be posted. www2.bio.ku.dk/mycology/courses/

MycoKey
www.mycokey.com

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

New Electronic Journal about mushrooms from Southeast Mexico (61-4)
<http://fungavera.blogspot.com>

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

Pacific Northwest Fungi — A peer-reviewed online journal for information on fungal natural history in Alaska, British Columbia, Idaho, Montana, Oregon and Washington, including taxonomy, nomenclature, ecology, and biogeography.
www.pnwfungi.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/

Robigalia provides information about field observations, published records and reference collection specimens of fungi and their associated organisms, with access to over 685,000 records (59-3).
www.cybertruffle.org.uk/robigalia

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/

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

Trichomycete site includes monograph, interactive keys, a complete database, world literature, etc. (61-4)
www.nhm.ku.edu/~fungi

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

Valhalla provides information about past mycologists, with names, dates of birth and death and, in some cases, biographies and/or portraits (59-3).
www.cybertruffle.org.uk/valhalla

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

Wild Mushrooms From Tokyo
www.ne.jp/asahi/mushroom/tokyo/

CALENDAR OF EVENTS

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 Don Natvig at dnatvig@gmail.com.

July 18-21, 2011

VII Latin American Mycological Congress
San Jose, Costa Rica
www.almic.org

July 23-30, 2011

The International Botanical Congress (IBC 2011)
Melbourne, Australia
<http://www.ibc2011.com>

August 1-6, 2011

MSA Meeting
University of Alaska
Fairbanks, AK, USA
<http://mercury2.iab.uaf.edu/msa>

September 10-17, 2011

Seventh International Congress on the Systematics
and Ecology of Myxomycetes (ICSEM7)
Recife, Brazil
icsem7@gmail.com

September 19-23, 2011

XVI Congress of European Mycologists
Thessaloniki, Greece
www.xvicem.org

September 6-10, 2011

2011 UMS Congress: XIII International Congress of Mycology
Sapporo, Japan
<http://www.congre.co.jp/iums2011sapporo/index.html>

October 15-20, 2011

EMBO conference: Comparative Genomics of Eukaryotic
Microorganisms
Sant Feliux, Spain
<http://events.embo.org/11-comparative-genomics/index.html>

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 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)
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