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— In This Issue —

— Important Dates —

August 15 Deadline:
Inoculum 57(5)

August 21-26, 2006:
8th International Mycological Congress, Cairns, Australia

Please send the editor notices about upcoming important events.

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Systematic Botany & Mycology Laboratory: Home of the U.S. National Fungus Collections

By Amy Rossman

At present the USDA Agricultural Research Service' Systematic Botany and Mycology Laboratory (SBML) in Beltsville, Maryland, serves as the research base for five systematic mycologists plus two plant-quarantine mycologists. The SBML is also the organization that maintains the U.S. National Fungus Collections with databases about plant-associated fungi. The direction of the research and extent of the fungal databases has changed over the past two decades in order to meet the needs of U.S. agriculture. This invited feature article will present an overview of the U.S. National Fungus Collections, the world's largest fungus collection, and associated databases and interactive keys available at the Web site and review the research conducted by mycologists currently at SBML.

Essential to the needs of scientists at SBML and available to scientists worldwide are the mycological resources maintained at SBML. Primary among these are the one-million specimens in the U.S. National Fungus Collections. Collections Manager **Erin McCray** ensures that these specimens are well-maintained and can be obtained on loan for research projects. Data associated with the specimens are available on the Internet so that researchers can order exactly the specimens needed. Recent data additions include specimen data for the Agaricales as well as the type, rust, smut, ascomycete, and asexual fungal specimens from Pennsylvania State University collections, which are now part of the U.S. National Fungus Collections.

Mycological Resources

A number of database resources primarily on plant-associated fungi are available to mycologists through the SBML Web site (www.ars.usda.gov/ba/psi/sbml). One of these is the database of fungi reported on plants worldwide in the literature. Following the completion of

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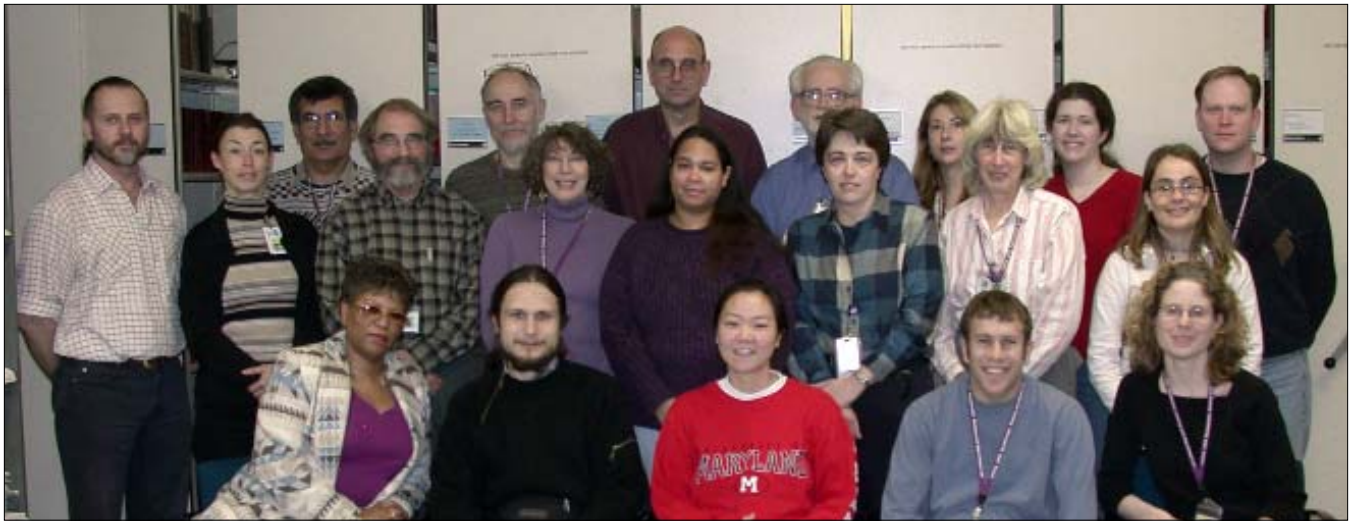
Lisa Castlebury



First row: Tee Yerby, Misha Sogonov, Cindy Park, Jim Cohen, Erin McCray. Second row: Jose Hernandez, Mary Palm, David Farr, Carole Ritchie, Jelia Tarrent, Lisa Castlebury, Amy Rossman, Priscila Chaverri. Third row: Adnan Ismaiel, John Wiersema, Gary Samuels, Joe Kirkbride, Cathie Aime, Aimee Hyten, John McKemy.

the project on *Fungi on Plants and Plant Products in the U.S.*, the SBML was asked to create a similar project for the world! When the laughter died down, we decided to at least attempt to provide these data and have gleaned the literature both past and recent for reports of the fungi on plants. At present these reports exceed 600,000 and, as such, are extremely useful for finding the host range and distribution of plant-associated fungi. In addition, a continuously updated database to the literature for the identification of plant pathogenic fungi is available. All names of fungi are included in the list based on the Saccardo index combined with *Index Fungorum*. Used in combination, these databases are very useful for determining the host range and geographic distribution of plant-associated fungi. A tool called "Quick Search" allows all databases to be searched at once. As some can appreciate, the impediment to synthesizing these data is the complex nomenclature of fungi. With funds partially contributed from APHIS, research associate **Erica Cline** updates the nomenclature of fungi and has, for example, updated the nomenclature for *Phoma* based on the recent monograph and has started to tackle *Phytophthora*.

Systematic Mycologists

Each of the five systematic mycologists at the SBML is an expert in a different group of fungi and conducts research on peer-reviewed projects planned on a five-year cycle. **David Farr** conducts research on the Diaporthales and other agriculturally important fungi but also develops and maintains the databases of plant-associated fungi mentioned above. The database framework for interactive keys was developed by Dave, and in collaboration with Erin and SBML scientists, keys to a number of fungal groups have been developed. Interactive keys to *Hypomyces*, *Trichoderma*, hypocrealean fungi of the southeastern US, *Tilletia,* and the rust genus *Ravenelia* complete with descriptions and illustrations are now available. An interactive key to the rust fungi that occur on legumes in or near the United States was developed as a consequence of the discovery of soybean rust in the US in 2004. These keys are linked to the databases so that, for example, as one identifies a species of *Nectria* in the key to the hypocrealean fungi of the southeastern United States, one can click on the host-fungus databases to reveal the host range and geographic distribution of that species as well as accurate nomenclature, specimens in the U.S. National Fungus Collections, and recent literature.

Gary Samuels's specialty is the systematics of fungi used in biological control. Most recently he has tackled the difficult genus *Trichoderma* and its sexual state *Hypocrea*. He has published several monographs of sections of *Hypocrea-Trichoderma* and is continuously uncovering new species. These studies have linked numerous *Hypocrea* states with their *Trichoderma* anamorphs. Gary's research has been embraced by those working with cacao because several newly discovered species of *Trichoderma* are effective in controlling cacao diseases. These plant pathologists recognize the importance of using well-defined and characterized species as biocontrol agents.

M. Catherine Aime joined the group at Beltsville to work on the systematics of rust fungi. Collaborating extensively, she has collected and obtained rust fungi from throughout the world for an overview of phylogeny of rust fungi. This phylogeny has proven useful in responding to outbreaks of new rust fungi in the United States, most recently on *Rubus* in Oregon where the rust fungus being considered as a potential control agent for the invasive blackberry plant was found to exist there already. Postdoctoral associate **Daniel Henk** works with Cathie to explore the molecular biology of virulence in the bean rust fungus, *Uromyces appendiculatus*.

Because of her background in tropical agarics one of Cathie's projects has been to study the biology and relationships of the two most serious pathogens of cacao (chocolate) in the western hemisphere. One causes witches' broom of cacao in South America producing a mushroom fruiting

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body while the other causes frosty pod rot of cacao in South and Central America. Cathie has demonstrated that these pathogens are congeneric members of the Marasmiaceae. Knowing the close relationships of these pathogens is essential for those seeking control strategies and resistant germplasm against these diseases. Cathie is now working to elucidate aspects of the biology of the frosty pod rot pathogen, as well as collaborating with other ARS and international scientists to identify endophytes of cacao and coffee, in hopes that some of these may have potential as biocontrol agents of disease for these tropical crops.

Lisa Castlebury serves as the expert on smut fungi at SBML. She initially came to Beltsville in response to the crisis of Karnal bunt of wheat and has specialized in the systematics of bunt fungi, *Tilletia* spp. Although the Karnal bunt crisis has passed, Lisa responded to an incident last year in which Algeria alleged that *Tilletia indica*, cause of Karnal bunt, occurred in a shipment of wheat from Minnesota and North Dakota. Lisa flew to Algeria and was met by officials from the US State Department and the USDA Agricultural Attaché. She consulted with their scientists and diplomatically explained the intricacies of differentiating teliospores of *T. indica* from other look-a-like fungi. Lisa continues to explore the relationships of species of *Tilletia* especially on cereal and turf grass crops.

In addition to working with bunt fungi, Lisa collaborates with Amy and Dave on the systematics of the Diaporthales with emphasis on *Diaporthe* and its anamorph *Phomopsis*. Following receipt of a PEET grant with co-P.I. **Jim White** at Rutgers University, and Amy and Lisa supervise postdoc **Mikhail (Misha) Sogonov** tackling the very large genus *Gnomonia* and graduate student **Luis Mejia** working on the genus *Cryptosporella*. Other projects have involved various hypocrealean fungi such as species of *Neonectria* causing beech bark canker and *Stachybotrys* and *Myrothecium*, which form a new lineage in the Hypocreales, and lots of miscellaneous plant-associated fungi.

Mary Palm

Amy Rossman serves as the Research Leader of the SBML and Director of the U.S. National Fungus Collections. Although drawn back to the Hypocreales on occasion, she has migrated to research on the Diaporthales obtaining and isolating any and all specimens in that order. Working with Lisa these isolates have served as the basis for an evolving phylogenetic overview with an increasing number of families to be recognized in the order. In addition Amy provides the morphological aspects from projects on the Diaporthales, Hypocreales, and anamorphic fungi and is a co-P.I. on the NSF PEET grant in the Gnomoniaceae with Lisa. With Gary she recently completed a user-friendly account of the hypocrealean fungi in the southeastern United States that is also available as an interactive key with descriptions and illustrations available on the SBML Web site.

David Farr and Erin McCray

Two plant quarantine mycologists, **Mary Palm** and **John McKemy**, working for the USDA Animal and Plant Health Inspection Service (APHIS), are co-located at the SBML using the mycological resources that include the incredible library, collections, database re-

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sources and expertise. Both Mary and John must respond immediately to identify fungal specimens taken from shipments of agricultural commodities waiting at the ports. Based on their identification, the shipment may or may not be allowed entry into the U.S. In these situations, thousands, even millions, of dollars in trade may depend on the accurate identification of a fungal specimen. Increasingly they are called upon to respond to crises caused by invasive fungi inside the U.S. Both are involved in confirming identifications of *Phytophthora ramorum*, cause of sudden oak death, as a national survey for this pathogen is implemented. The presence of soybean rust, *Phakopsora pachyrhiza*, in the southeastern U.S. was also cause for rapid response and accurate identification of this pathogen. In the near future several plant pathologists will be hired to form the Molecular and Biochemical Diagnostics Lab, lead by Mary, that will identify pathogens using validated molecular and biochemical tests.

Now you know a little more about what goes on at Beltsville! We feel privileged to conduct research on fungi that are important to the American public while thoroughly enjoying the chance to reveal the relationships of these interesting organisms. To some scientists this research may seem applied because it relates directly or indirectly to solving real-life problems while to others especially plant pathologists our research in the field of systematics appears to be basic because it does not always relate to a plant disease. We straddle the line between applied and basic research and hope that our research and databases are useful to mycologists, plant-pathologists, and many others.

Questions or comments should be sent to Amy Rossman, Systematic Botany & Mycology Lab, Rm 301, B011A, 10300 Baltimore Ave., Beltsville, MD 20705 United States. Email: arossman@nt.ars-grin.gov

Myxomycetes (True Slime Molds): Educational Sources for Students and Teachers Part II (Cont. 57-3)

By Harold W. Keller and Sydney E. Everhart

Publications are available that describe experimental protocols for high school or college students using myxomycetes (Alexopoulos and Koevenig 1964; Gray and Alexopoulos 1968; Keller and Braun 1999; Spiegel et al 2004). Laboratory exercises using myxomycetes in classroom teaching at the high school (Braun) and university (Keller) level (Keller and Braun 1999, pages 33-37) provide additional ideas for classroom observations and research projects. A recent book on the biodiversity of fungi includes a chapter on Mycetozoans that covers the Protostelia, Myxogastria, Dictyostelia, and Acrasids (Spiegel et al 2004). This book chapter highlights phylogenetic relationships, taxonomy, diversity, distribution, inventory, and sampling methods. Sampling methods described for myxomycetes include collection and culturing methods of different substrata: wood, litter, soil, bark, dead plant parts, and dung. This is a good resource for groups interested in both Fungi and the Mycetozoans.

Field and technical guides: Field guides (Farr 1981; Keller and Braun 1999; Stephenson and Stempen 1994; and more technical monographs on Myxomycetes (Mycetozoans) (Martin and Alexopoulos 1969; Olive 1975) provide information to collect, culture, and identify "the biological jewels of nature". The world monograph on the myxomycetes by Martin and Alexopoulos (1969) is still the taxonomic standard, although more recent evidence has increased our understanding of evolutionary relationships and almost doubled the number of species (near 1,000) now recognized since 1969.

Future educational materials: Stephenson and Nelson (2005) announced the production of PowerPoint programs that will cover the biology, ecology, and identification of myxomycetes. One of the authors (SEE) is working on a project to create a laminated, a two-sided picture key of selected species of myxomycetes for Great Smoky Mountains National Park (GSMNP), including easily identified common and rare species and one species new to science only found in GSMNP. The field guide will include 47 color photos of selected myxomycete species, represented by distinctive shapes, colors, external markings, and size large enough to be seen with the naked eye. One side of the guide will include photos of common species, some rare species, and the species new to science (*Diachea arboricola*) from GSMNP. The field guide text on the backside will include educational information of interest to summer campers, educational workshop participants, amateur naturalists, parataxonomists, and the general public. Heavy stock paper with a protective lamination will enable hikers, visitors, and workshop users to carry the picture field guide in their backpacks, in their hands on nature trails, and in their cars without damage due to normal wear and tear or rain or stain. This picture field guide will increase public interest, knowledge, and appreciation for biodiversity in general and myxomycetes in particular.

Myxomycetes are ideal organisms for use in teaching and learning because the materials needed for the collection and preservation of myxomycete fruiting bodies are readily available as homemade. Identification of myxomycetes can be learned quickly because fruiting body terminology is relatively simple. Specimens can be examined using tools such as dissecting needles, handheld blowers, and hand lenses that are inexpensive to purchase or are homemade (Sundberg and Keller 1996). Microscopic slide preparations do not require complex chemicals, tap water is sufficient. Moist chamber bark cultures are simple to prepare using materials available at hardware stores. Bark cultures yield plasmodia, plasmodial tracks, and developing fruiting bodies easily observed at 10 to 100 times magnification (Keller and Braun 1999). Educational materials using myxomycetes were first pro-

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duced in 1961 and are available for all levels, from elementary and middle school, high school, college and university, and for field and technical use. Due to the nature of myxomycetes and the curiosity that surrounds their origin and life cycle, it is not likely that this is a complete list or includes every use of myxomycetes for education.

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Correction to Part I: Hirano Bodies are found in a cellular slime mold, *Dictyostelium discoideum*.

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MSA BUSINESS

MSA Secretary Email Express — June 15, 2006

MSA Council approved the following three motions since my last report.

(1) MSA poll 2006-2. Council approved the nomination of the **2006 Karling Lecturer, Franz Oberwinkler**, as proposed by the Karling Lecture Committee, chaired by Michelle Momany.

(2) MSA poll 2006-3: Council approved the nomination of **Scott Kroken as Mycologia Associate Editor** for the term 2006-2009, as nominated by Editor-in-Chief Donald Natvig.

(3) MSA poll 2006-4. Council approved the nomination of **Michael Wingfield for the award of Honorary Member 2006** as put forward by the MSA Honorary Awards Committee, chaired by John Taylor**.**

New Members: The MSA extends a warm welcome to new (or returning) members: New memberships will be formally approved by the Society at the Annual Meeting, 29 July - 2 August 2006, Québec City, Québec, Canada.

Argentina: Leonor Carrillo
France: Pierre-Arthur Moreau
India: Pawan K. Kasera
Japan: Shinnosuke Miyauchi
United States: Vincent P. Hustad, Tami R McDonald, Kevin Mccluskey, Angela Swerdlove Moss, Kara Lynn Pivarski, Les J. Szabo, Susan A. Thomas, Kimberly L. Vernier, Debbie Viess, Daniel Voltz Peter D. Voth.

With great sadness I report that the Society received notices of the deaths of two colleagues: **Dr. William (Bill) Cibula** passed away on Nov 30th 2005. **Dr. Orson K Miller**, **Jr**., MSA Past-President (2000-2001), died on June 9th, 2006. They will be missed and celebrated by family, friends and colleagues.

—***Faye Murrin***
MSA Secretary
fmurrin@mun.ca

Minutes of the MSA 2006 Midyear Council Meeting

Saturday, March 4, 2006,
Glen Erin Inn, Mississauga, Ontario

CALL TO ORDER AND APPROVAL OF MINUTES

(1) The 2006 mid-year Executive Council Meeting was called to order at 8:40 am by President *James B Anderson*. MSA Executive members present were President *Anderson*, President-Elect *Gregory Mueller*, Vice-President Don Hemmes, Treasurer *Karen Snetselaar*, and Past-President *David J McLaughlin*. Secretary *Faye Murrin* was delayed due to inclement weather in Newfoundland and arrived at approximately 10:05 am. *Mycologia* Editor-in-Chief, *Donald Natvig* and *Mycologia* Managing Editor, *Jeffrey Stone*, were also present as invited participants. President *Anderson* distributed hard copies of the Executive Council Packets sent by email prior to the meeting which included the Agenda, updated MSA Roster, midyear reports and minutes of the 2005 Executive and General Council meetings. Managing Editor *Stone* gallantly took minutes up to the point of Secretary *Murrin*'s arrival after which the following motion was approved.
MOTION 1: (approved unanimously) Moved by Secretary *Murrin* and seconded by President *Anderson* that the minutes of the MSA 2005 Executive Council meeting be approved as published in *Inoculum* 56(3).

OFFICERS' REPORTS (excluding financial matters)

(2) **President *Anderson*** presented his report [*Inoculum* 57(4)]. The President has been acting as local organizer for the up-coming annual meeting in Quebec City. He has also held discussions with the *ad hoc* "Blue Sky" Committee concerning the future of the MSA. In particular questions from that committee arose on how best to manage the publication of *Mycologia* to be more profitable, the need to maintain membership and the need to include in our Society other mycologists such fungal geneticists, those studying fungi as model organisms, and other groups of professionals. A discussion followed on the need for a membership committee (see motion 4 below).

(3) **President-Elect *Mueller*** reported that he is continuing to prepare **materials for advertising the Society** at other meetings including a brief power point presentation, poster etc.

(4) **Vice-President *Hemmes*** reported on the progress of the **nominations** for the spring ballot. While there were numerous nominations for some positions, the position of Secretary is proving the greatest challenge.

FINANCIAL AND PUBLICATION REPORTS

(5) **Treasurer *Snetselaar*** presented her report (please see the next issue of *Inoculum*), the highlights of which included the following. There *appears* to be a budget surplus presently but this appearance is misleading; the present budget reflects the payment for only four of the six issues of *Mycologia*. There needs to be more coordination between the Treasurer and the annual meeting conference centers/organizers: despite appearances the meetings last year and this coming year are operating at a loss as the reported meeting expenses do not cover all of the actual costs. On the publishing side, income from memberships and subscriptions is slowly declining. There followed further discussion of the need for a membership committee that would cover a number of areas including international memberships. The need for a traveling display for MSA members to take to other meetings to advertise the Society and *Mycologia* was reiterated (see item 3 above) and it was suggested that this should be on the website so that it could be readily downloaded.

(a) **MOTION 2 (approved unanimously): Moved by Treasurer *Snetselaar* and seconded by President *Anderson* that the Society close the "Endowment Receiving" account and return to depositing new endowment funds directly into the Endowment Money Market Account.** Background: The accounting system of the Society is a complex one, although transparent in the sense that it is accessible and open to scrutiny. The original purpose of the Endowment Receiving account, for increased transparency, is not being met but is making extra work for the Treasurer. All these funds must pass into the Money Market Account regardless, thus rendering the Endowment Receiving account redundant.

(b) **MOTION 3: (approved in principle, unanimously) Moved by Treasurer *Snetselaar* and seconded by Past-President *McLaughlin*, that the Society change the Endowment section in the Society By-laws (Article IX, section E) to better describe the differences between the Restricted and General En-**

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dowment funds as follows (the original wording is appended at the end of this report)**:**
"Receipts from membership dues shall be used exclusively for the stated purposes of the Society and serve as the primary source of revenues, along with Mycologia subscriptions. The Endowment Fund shall be comprised of the Restricted Endowment and the Uncommitted Endowment. The Restricted Endowment is a permanently restricted account maintained for the purpose of providing earned investment income to support specific activities of the society, as designated by those making donations to these funds. The Restricted Endowment Subfunds include the Alexopoulos Prize Fund, the Alexander H. and Helen V. Smith Award Fund, the Martin-Baker Research Award Fund, the Myron P. Backus Award Fund, the Karling Lecture Fund, and the named Mentor Travel Award funds. As required by law, the principal of each of these funds must be maintained by the Society in perpetuity, and the income can be used only for purposes designated by the donors. Establishment of a new Restricted Endowment Fund requires the approval of Council. The Uncommitted Endowment is used to support activities of the Society and special projects (e.g., special publications, workshops) that enhance mycology as a discipline and serve the other goals of the Society, as approved and allocated by vote of Council. Council may vote, on an annual basis, to use income from the Uncommitted Endowment to supplement income from the Restricted Endowment named funds when making annual awards. Council may vote to commit part of the principal of the Uncommitted Endowment for special purposes and these must be reviewed every three years."

Background: Current language in the By-laws does not adequately describe the differences between the Restricted and General Endowment funds. Legally, the named funds are considered to be **Permanently Restricted** net assets because the donors have imposed restrictions on these funds such that the principal must be maintained by the society and cannot be used. Only the income generated by these funds can ever be used, and it must be used only for the specific purpose for which the fund was established. This cannot be changed except if the donor(s) agree to the changes. These types of funds, while crucial to the Society, should only be established after careful consideration because of the restrictions on their use as outlined above. It would be wise to change the By-laws to make it clear how these funds are to be established. Further, what is now called the General Endowment (proposed "Uncommitted Endowment) has to be considered part of the **Unrestricted** net assets of the Society for tax purposes. Principal in the General/Unrestricted Endowment includes, for example, donations made directly to that fund, and auction proceeds. There has been much confusion over the years on Council decisions because of the ambiguity in the By-laws. In addition, in the past, Councils have added to the principal of some of the named Permanently Restricted funds with money from the General Endowment; however, this should never be done as it is not in the best interest of the Society to willingly tie up such funds forever. These funds must remain part of the General (Uncommitted) Endowment for tax purposes.
Action to be taken by Treasure *Snetselaar*: that this change in wording of the By-Laws be reviewed by legal council prior to final approval by Council and prior to inclusion in the Sprint ballot. [Note added: legal council obtained.]
Action to be taken by Treasure *Snetselaar*: to investigate if an accountant could revise the layout of the MSA Treasurer's books to make them more efficient.

(c) **MOTION 3: (approved unanimously). Moved by President *Anderson* and seconded by Past-President *McLaughlin* that the Society form a pro-active, broad-ranging membership committee to counteract the drop in Society membership.** This is to be on an *ad hoc* basis for the first year with the intention of it becoming a permanent committee in the following year.
Action to be taken President *Anderson*: to contact folks to set up this membership committee.
Action to be taken by Managing Editor *Stone*: to ask Highwire to link directly to the Allen Business page / Membership site
Action to be taken by Treasurer *Snetselaar*: to develop a list of advantages of being an MSA member for the Highwire website (eg. free reprints) and to give this to the new *ad hoc* membership committee.

(d) A discussion followed on the **cost of producing hard copies of the newsletter, *Inoculum***, which has been available on-line in the first instance for a number of years. Printing costs approximately $12,000 per year for 1400 copies which are sent out with all *Mycologia* hard copies and those memberships with *Inoculum* only. The idea of having the default option of *Inoculum* as on-line only was discussed, a topic raised a number of times in previous Council meetings. The question also arose as to who would be responsible for copying and distributing the hard copies if this were approved.
Action to be taken by Secretary *Murrin*: to prepare a motion to be put to full Council to have on-line only as the default option for subscription to *Inoculum* and that this commence with the new editor in January 2007. Further, if a member wants to continue receiving the hard copy, they will need to contact the *Inoculum* Editor. It was suggested that, if this is approved, a notice be put in last two hard copies of *Inoculum*.
Action to be taken by Secretary *Murrin*: to ask *Kay Rose* about the numbers of people without email addresses and thus gain an estimate of how many people would require hard copies of the newsletter. [Note added: A good estimate was obtained during the spring ballot in May and was approximately 200].
Action to be taken by Secretary *Murrin*: to present this idea to the present and incoming editors of *Inoculum* for their input.

(6) **Finance Committee Chair *Stone*** apologized for the lack of a written report and proceeded with a summary of the financial status of the Society. The Endowment Receiving Account is set up so that if that balance should never go over $1000, the extra will automatically be transferred to the Endowment Account. A $25,000 Treasury Note will be converted to a Certificate of Deposit (CD). Overall the investment strategy is defensive, making use of, for example, short term CDs (at ~4.5%) for a year. The next bond matures in May and this $20,000 will likely go into a CD. The investment portfolio is still sound and strong but it is a different climate that five years ago when we were able to support awards at a more lavish level from Endowment income. Mutual funds make up about one third of total Endowment balance and should not be much more. He noted further that the Endowment Principal does not increase (except through new donations) and all interest income is spent on awards etc.

The meeting broke for lunch from 12:15 -1:15 pm.

(7) **Editor-in-Chief *Natvig*** presented his report ((please see the next issue of *Inoculum*) highlighting the good news that ***Mycologia* is now included in PubMed**, a long-time goal of the Society, but also presenting the bad news concerning the lateness of the last two issues. The latter was due in part to fallout from Hurricane Katrina, health of the Assistant Editor, and changes in account managers at Allen Marketing and Management. The journal should be back on schedule quickly with issue 97-6 recently completed, 98-1 in production and 98-2 well along. The length of the issues has been returning to the normal number of pages following a year of longer issues which were produced in an effort to accommodate the manuscripts on hand; the extra costs associated with those lengthier issues will no longer be incurred.

(a) MOTION 5: (approved unanimously) Moved by Secretary *Murrin* and seconded by President *Anderson* that Council formally and enthusiastically extend its thanks to those who were in-

Continued on following page

volved in the successful bid to have *Mycologia* accepted for inclusion in Medline and PubMed: Editor-in-Chief *Don Natvig,* Editorial Advisory Committee Chair *David Geiser,* Managing Editor *Jeffrey Stone* and Past-President *John Taylor* (2002-2003).

(b) There followed a detailed discussion of the concerns associated with the **costs of producing *Mycologia***, including the broader implications of going to on-line publishing only. There was a general agreement that there should be a detailed review of our association with Allen Press and a comparison with other, similar societies. The low percentage of authors paying the page charges, the need to enforce the page limits, the need for activation of on-line subscriptions and the low subscription rate for *Mycologia* were other issues identified as areas of concern. Past-President *McLaughlin* stressed the need for analysis of the data and not a reliance on anecdotal discussions in order to make sound decisions.
Action to be taken by Managing Editor *Stone*: to contact [a suggested member] and ask if he would agree to spear-head a broad review of *Mycologia* publication.
Action to be taken by Managing Editor *Stone*: to ask Allen Press for information on the cost differences with reduction in the numbers of hard-copies of the journal, and if appropriate, to follow up this with an article in *Inoculum* stressing the advantages of the choice of *Mycologia* as on-line only.

(8) **The report of the Managing Editor *Stone*** included the following items. The **activation of institutional subscriptions is problematic** and high on list of priorities for the Managing Editor. This involves merely filling in IP ranges by the institution one-time only but it is difficult to contact the correct people to have this done. There was a suggestion that the list be parceled out to members of the Editorial Advisory Committee to contact individuals at the approximately 210 institutions. It was noted again that the **institutional price for *Mycologia* is very low** at $213/230 compared with MYCOL RES at $1220/1148. Other items discussed for increasing journal subscriptions/membership were to place ads in competing journals, to recruit reviews, to publish the Presidential and Karling Lectures, and promotion of the Deep Hypha issues. There are some problems remaining with **page charge payment** including the fact that Managing Editor *Stone* has not been getting all of the forms which have been sent to past Managing Editor *James Ginns* but that error is now fixed. There was general agreement that the submission of this form should be required prior to publication, and that the form should be attached to the letter to the author and not have to be downloaded.
Action to be taken by Managing Editor *Stone*: to change copy on Allen publicity site by adding PubMed and the impact factor.
MOTION 5: (approved unanimously) Moved by President-Elect *Mueller* and seconded by Past-President *McLaughlin* that *Mycologia* 98 (6), the issue dedicated to Deep Hypha manuscripts, be accepted at the cost of $25,000.

Other Committee Considerations

(9) In response to **the report from the Mycological Memoirs Committee Chair, *Keith Seifert***, (*Inoculum* 57(4)) and earlier discussions with him, the following motion was approved.
MOTION 3: (approved unanimously) Moved by President *Anderson* and seconded by Secretary *Murrin* that the status of the *Mycologia* Memoirs Committee be changed from a Standing Committee to an *ad hoc* committee to be reconstituted on submission of future manuscripts to the Editor-in-Chief of *Mycologia.*
Action to be taken by Secretary *Murrin*: to investigate any required changes to By-laws and subsequent inclusion in a ballot to the membership.
Action to be taken by Editor-in-Chief *Natvig*: to follow the final approval up with a short article on-line and in *Mycologia*.

(10) Past-President *McLaughlin* inquired about the status of the ***ad hoc* Committee on Permits**, emphasizing its importance to mycologists.
Action to be taken by Vice-President *Mueller*: to check with the Chair of the Committee on Permits to see if any progress has been made and on the advisability of reappointment of that committee.

(11) **MOTION 5: (approved unanimously) Moved by Past-President *McLaughlin* and seconded by Editor-in-Chief *Natvig* that authors publishing in *Mycologia* be required to deposit ultrastructural data into the AFTOL structural data base.** Background: This structural data base is to parallel the sequence data bases. Authors will use *Mycologia* to file on-line data. To publish in *Mycologia* authors will need to deposit data into the data base with a link from the *Mycologia* manuscript to the supplemental data base. The data base is presently with Past-President *McLaughlin* and responsibility for monitoring the process will be AFTOL's.

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(12) Past-President *McLaughlin* inquired about letter for **BSA 100th anniversary** and for the **MSJ 50th anniversary** this summer. President *Anderson* reported that he had already sent the letter to MSJ although he cannot attend the event, and that he will draft a letter with Past-President *McLaughlin* for BSA.

Upcoming Meetings

(13) **MSA 2006.** President *Anderson* reported on the good progress being made on **MSA/APS/CPS 2006** *Quebec City* (*Inoculum* 57(4)). There was some discussion of the 75th Anniversary of the MSA and it was decided to initiate the celebration in Quebec City and then carry to celebrations forward to Louisiana in 2007. The report of the **Foray Coordinator, *Donald Ruch***, was gratefully received (*Inoculum* 57(4)); it was noted that the Foray this year will be held on Saturday July 29th and will be hosted by the local mushroom club (CMAQ).
Action to be taken by President *Anderson*: to contact 2007 Local Organizer, *Meredith Blackwell* regarding possible 75th Anniversary celebrations.

(14) **MSA 2007-2010**. President-Elect *Mueller* reported on the MSA 2007 meeting in **Louisiana** informing council that he has viewed the venue and that they are aiming for the weekend of July 21st- 22nd in order not to overlap with APS or BSA meetings that year. The report for MSA 2008 in **Pennsylvania** submitted by Local Organizer, *David Geiser*, was gratefully received by Council (*Inoculum* 57(4)). Vice-President *Hemmes* reported that he has been discussing the possibility of holding the Annual Meeting in 2010 in **Fairbanks, Alaska** with potential Local Organizer, *Gary Laursen*.

Other Business

(15) Secretary *Murrin* asked about the progress on **Memorials** and Editor-in-Chief *Natvig* reported that the memorial for *Dr. Jorge Wright* is being edited for publication. Suggestions for two other memorials were briefly discussed prior to adjournment at 4:48pm.

Appendix to item 5b, above: Original By-laws (Article IX, section E) :

"Receipts from membership dues shall be used exclusively for the stated purposes of the Society and serve as the primary source of revenues for operational costs. The Endowment Fund shall be comprised of the Restricted Endowment and the General Endowment. The Restricted Endowment is a restricted account maintained for the purpose of providing earned investment income to support specific activities of the society: memorial lectures, graduate student fellowships, senior research awards, and student travel awards. Subfunds included within the restricted endowment include the Alexopoulos Prize Fund, the Alexander H. and Helen V. Smith Award Fund, the Martin-Baker Research Award Fund, the Myron P. Backus Award Fund, the Karling Lecture Fund, the named Mentor Travel Award funds and others, as established. The General Endowment is a restricted account with earned investment income used to support regular activities of the society and special projects (e.g., special publications, workshops) that enhance mycology as a discipline and serve the other goals of the Society, as approved and allocated by vote of Council."

Faye Murrin
MSA Secretary

MSA 2006 Midyear Reports

1. President's Midyear Report

The year has progressed unusually quickly, with a steady stream of MSA activity in Council and among Members. This report focuses on two areas: i) preparations for our upcoming annual meeting in Québec and ii) the longer-term health of our society, publishing practice, and member recruitment.

Meeting preparations. The MSA Annual Meeting with the American Phytopathological Society (APS) and the Canadian Pathological Society (CPS) in Québec City, July 29 - Aug. 2, 2006 is shaping up well. I have been working actively with local organizer, **Linda Kohn**, Meeting Manager **Paula Trenda**, and Director of Meetings **Betty Ford** at APS. The draft schedule of the meeting is as follows. MSA Council will meet on Friday, July 28, the day before the official opening of the meeting. The Foray, being organized by **Don Ruch,** is to be held on Saturday. The Opening Plenary Session on Sunday will feature three lectures of broad scope, each arranged by a participating society. **Jeff Townsend** (University of Connecticut) is the MSA invitee. The Presidential Address will be on Monday and the Karling Lecture on Tuesday. The MSA Business Breakfast will be on Tuesday. The Program Committee, chaired by **Tom Bruns**, has lined up four excellent MSA symposium sessions: Fungal Movement: Contemporary Experimental Analysis, Bacterial Symbionts of Fungi, Diversity of Zoosporic Fungi, and Population and Species Divergence; each session includes international participation from a diversity of research fields. A total of $6,000 was approved by Council to help support participation by non-members of the MSA. As usual, the MSA will have numerous contributed paper sessions, plus posters. **David Geiser** (Pennsylvania State University) has kindly set up the abstract submission web site for all MSA sessions with a deadline for submission of March 30 (abstract submissions for CPS and APS sessions are separate and are offered for a charge). The Social and Auction will be held on Tuesday evening in a venue adjacent to similar, but separate, activities for APS and CPS members, who may well opt to participate in our auction as the evening progresses. Inexpensive housing at Université Laval will be available with transportation to and from the meeting. I will visit the meeting venue, the Centre des Congrès de Québec, in June to check on the facilities and arrangements. By then, the full program will be complete.

Our financial arrangement with APS is that the MSA will not share in either the potential profits or losses from the meeting. This has already proved to be a good choice as the meeting appears poised to lose money overall, due mainly to an increase in the value of the Canadian dollar against the US dollar. Registration proceeds will cover the same events for the MSA as for the other two societies. The expenses of the three invited Plenary Session speakers will come from the registration proceeds, as will complementary registration for all non-member symposium speakers. Events special to the MSA, for example the Committee Reception and the Council meeting, will be billed to the MSA. The Foray and MSA breakfast will be offered as options with a charge on the registration form.

The longer term. Having been involved with MSA activities as a member of the Executive Council for 2.5 years, I see two issues that will strongly impact on the health of the MSA in the future and that urgently need our full attention now. First, the main expense by far for the MSA is that of printing Mycologia. Another aspect of printing is that the rate of expense has not always been predictable over time; this has introduced a huge element of uncertainty into our overall budget. Another looming problem is that if open-access policy in the US moves to the point where journals with federally-funded research must be available to readers without cost, then our present model for publishing Mycologia might become unsustainable.

As a publisher of Mycologia, the MSA urgently needs to do two things. At the mid-year executive meeting, we must make sure that printing costs are minimized as much as possible over the short term, following up on our extensive discussions among Executive Council members this past fall. Beginning at the mid-year meeting, we must also make plans for developing a long-term strategy for publishing. We cannot afford merely to default to the status quo. **The MSA needs a select group of members to thoroughly analyze our position with respect to printing Mycologia and to recommend action.**

The other pressing issue is that MSA membership is either declining gradually or remaining flat. We need a concerted effort to reverse this recent trend and increase our membership. To increase membership, it would undoubtedly help to make annual MSA meetings a higher priority for the thousands of de-facto mycologists world-wide who do not belong to the MSA. For example, involving the burgeoning fungal genetics community in annual meetings could help enormously. Continued geographic collaborations on annual meetings, like our joint meeting with the MSJ in Hilo last summer, will also help. Clearly it is time for a joint meeting with the Latin American Association of Mycology. **To extend our membership, the MSA urgently needs to form a proactive membership committee.**

For their insights and suggestions for the present and future of the MSA, I thank the Blue Sky Committee, **Dave Geiser**, **Steve Harris**, **Rick Kerrigan**, **Francois Lutzoni**, **Michelle Momany**, **Karen Snetselaar**, **Joey Spatafora**, and **John Taylor**. For many informative and enjoyable interactions over the past seven months, I thank MSA Council, especially Secretary **Faye Murrin**, as well as numerous MSA members.

James B. Anderson, President

2. Secretary's Midyear Report

This report presents secretarial activities conducted between July 2006 and March 1, 2006.

(1) Assisted then President David J McLaughlin at the General Council Meeting held in Hilo Hawaii, July 31st,2005. Annual reports of Society committees and representatives were published in Inoculum 56(5). Minutes of the council meeting were sent to Council for review prior to publication in Inoculum 56(6). Among the items approved at the Council meeting were 1) that the page charge fee for *Mycologia* be increased from $60 to $75 starting with volume 98; 2) that the Society discontinue production of a hard copy of the MSA member directory; 3) that the contract for indexing *Mycologia* not be renewed when the present contract expires in 4) that the Wilson Abstracting Service receive a a complimentary hard-copy subscription to *Mycologia*; 5) that MSA meeting abstracts no longer be printed as part of the program booklet; copies of the abstracts will continue to be available on-line and the option to purchase a hard-copy of the abstracts should be included in the registration; 6) that the Society revise the way it handles nominations and voting by Council for the Honorary Member and Distinguished Mycologist Awards; 7) that the Society agree to meet with the Botanical Society of America in 2009 at Snowbird, Utah; and 8) that Council express its strong support for the CD-ROM publication and its shepherding by the *Mycologia* Memoirs Committee by allocating $500 to support the hiring of a person by the authors to effect the linking of the figures with text and that the MSA facilitate distribution by putting the CD for sale on the MSA website. (Secretary's note: this publication has since been withdrawn)

(2) Assisted then President McLaughlin at the Annual Business Meeting held in Hilo, Hawaii, August 3rd 2005. (With apologies, those minutes have yet to be published in *Inoculum*)

(3) Assisted President James B Anderson in filling positions on the 2005-2006 Society Roster, including approximately 21 new appointments to MSA. This is a huge job and it was almost completed by the start of the Annual meeting. My sincerest thanks to the President for tackling this job so efficiently. Sent the new Roster to newsletter Editor Richard Baird for publication in Inoculum 56(1) 2006 and to webmaster Roy Halling for posting on the MSA website.

(4) Moderated email correspondence with Full Council and Executive Council. Council voted the approval of 1) three new Mycologia Associate Editors for the term 2006-2008: **Philippe Callac, Ian K Ross, and Scott Kroken; 2)** $6000 (in total) in support of **symposium funding** for MSA 2006 in Quebec City, 3) .$1,000 in support of colleagues

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from developing countries to attend IMC8 in Cairns, Australia, 2006; (4) a total of $4000 was approved in support of MSA International Travel Awards (to students and postdoctoral fellows who are MSA members) for IMC8 in Cairns, Australia; (5) up to $3000 in support of a joint reception with the British Mycological Society to be held in Cairns Australia at IMC8; (6) **Guidelines for MSA International Travel Awards** (appended to the end of this report)**.**

(5) Moderated, along with President Anderson, the approval and editing of blast emails sent out to Society members on behalf of the MSA. These included: a cal for **Symposia Proposals for the 2006 MSA/APS/CPS Meeting in Quebec City,** 29 July - 2 August 2006; a call for nominations and applications for MSA Awards and Fellowships for 2006, and a call for MSA **Nominations for Council**.

(6) Assisted President Anderson in organizing the midyear Executive Council meeting in Mississauga (Toronto), Ontario, scheduled for March 4th, polling Executive Council for date preferences, helping to prepare the agenda for the meeting. Many thanks to President Anderson for arranging accommodations and venue for the meeting.

(7) Issued a call to all Society Officers, Councillors, Committee Chairs and Society representatives for midyear reports and agenda items in preparation for the midyear Council meeting. Compiled all reports, along with an updated Society Roster, agenda and other items in a package for distribution electronically prior to the meeting and by hard copy at the meeting.

(8) Prepared three Email Express columns for publication in *Inoculum*. Columns included new members and emeritus candidate lists supplied monthly by Kay Rose of Allen Marketing and Management, and summaries of Council activities.

(9) Assisted in the publication in Inoculum of announcements for Call for Nominations and Call for Awards applications.

(10) Received with sadness the report of the death of **Dr. Henry Aldrich**, President of the MSA 1984-85, **Dr. John Krug** and **Dr. Keisuke Tubaki** .

(11) Responded to routine correspondence on a wide variety of issues.

Faye Murrin, Secretary

Appendix to Secretary's midyear report:

Guidelines for MSA International Travel Awards

- MSA Council may approve expenditures of up to $4000 in one fiscal year (Aug-July) for the financial support of students and post-doctoral fellows who are MSA members to attend international scientific meetings.
- Eligible meetings include those held by societies with which the MSA is formally associated; at present eligible societies include only IUMS and IMA. Under special circumstances, ALMS may also be considered as long as there is a memorandum of understanding in effect between ALMS and the MSA.
- (Societies *not* included are those identified in the MSA roster as sister/allied societies, as these are for information and site linking purposes only; nor other societies holding more specialized meetings).
- Awards are generally for $500 each.
- Meetings for which travel awards will be announced will be identified at the beginning of the fiscal year (August) and announcements will be sent out with the general awards announcements in the fall.
- Funds so allocated shall be drawn from the unrestricted endowment and/or operating funds and shall be limited to the availability of such funds in the year requested.
- Other considerations may follow those for the Mentor Travel Awards.

3. Mycologia Editorial Advisory Committee Midyear Report

(1) Thanks to the diligent efforts spearheaded by Editor-in-Chief Don Natvig, MYCOLOGIA was successfully added to PubMed. PubMed is a high profile reference resource, particularly in the biomedical realm, so this should have a positive impact on the journal.

(2) The EAC and Don Natvig have initiated discussions to increase the role of the EAC in assisting the Editor-in-Chief. In the past, the EAC has been underutilized and the EIC has been overworked. Discussions have been initiated regarding potential new roles for the EAC, particularly the nomination and selection of Associate Editors.

David Geiser

4. MSA Abstract Submission Site Report

The Abstract Submission site for the 2006 meeting is up and running on the piast server at Penn State. We have a new person maintaining it but we got it up and running with no problems, albeit a little later than we would have liked, with a due date of March 30. In 2005, we had an inopportune server failure on the submission deadline date, but the person running it assured me that this was a coincidence and not an overload issue.

David Geiser

5. Mycologia Memoirs Committee Report

Following the discussion between the chair of this committee, Keith Seifert, and the Council at the AGM in Hilo, the authors of the Monograph on the Saprolegniaceae were contacted with the council's offer to hire a student to better integrate the text, illustrations and references of this 1000 page monograph into a more user friendly, CD-ROM product. The authors refused to consider this, and after discussions among the committee members and President Anderson, we decided to reject the manuscript. The authors acknowledged this with good grace, and are pursuing other publication options.

Having fulfilled my self-imposed mandate to see the 3-year review process of this Monograph from start to (unfortunately disappointing) finish, I am hereby submitting my resignation for my chairmanship and membership of this committee. I am certain that any of the members of the existing committee will be an effective leader in any attempt to make Mycologia Memoirs more relevant to the Society.

Keith Seifer

6. MSA Local Arrangements Report (2008)

The Penn State Local Arrangements Committee consists currently of David Geiser, Gretchen Kuldau, Barb Christ, Elwin Stewart, Roger Koide, Jean Juba and Dan Royse. David Geiser, Jean Juba and Janet Patterson from Penn State Outreach worked in 2005 to put together a general plan for the meeting, which is currently scheduled to be held August 10-13, 2008.

David Geiser

7. 2006 MSA Foray

This year's MSA Foray will be hosted by the local mushroom club (CMAQ). The selected site is at Beauport, approximately 15 km from the Conference Centre. This site is recognized for its diversity of mushrooms and fungi. After the morning walk into this forest, we will go to Domaine Maizeret for lunch (inside if wet, or outside in a nice garden); facilities are available in the building. If time permits, we will visit this garden and arboretum at this site. If it is raining, we will have a large gathering room inside for fungi identification. (This is where CMAQ is holding their meeting and activities). The sites are mixed forests with young and mature forest stands. Some of the tree species present include balsam fir, spruce, hemlock, white pine, beech, maple, birch, aspen and few red oaks. Several trails are well managed and walk is easy. There will be a post-foray room at the Conference Centre. Cost to be determined.

Don Ruch, Foray Coordinator

Adenipekun, Clementina O. Department of Botany and Microbiology, University of Ibadan, Ibadan, Nigeria. oyinpek@yahoo.com. **Bioremediation of engine-oil polluted soil by *Pleurotus tuber-regium* Singer, a Nigerian white-rot fungus**.

White-rot fungi have been used in various parts of the world for bioremediation of polluted sites. *Pleurotus tuber-regium* was noted to have the ability to increase nutrient contents in soils polluted with 1-40% engine-oil concentration after six months of incubation. *Pleurotus tuber-regium* resulted in increased organic matter, carbon and available potassium of 5.19%, 2.99% and 0.97meq/100g respectively compared to 4.41%, 2.56% Carbon and 0.66meq/100g available potassium respectively in the control after 6 months of incubation. However, higher values of 0.32% Nitrogen, 11.42ppm Phosphorus and 6.94 pH were obtained in the control compared to 0.16% Nitrogen, 9.32ppm Phosphorus and 5.93 pH in soils incubated with the fungus. The fungus brought about an increase in copper content in polluted soils to 10% engine-oil concentration followed by a decrease at 20% and 40% engine oil concentrations. Bioaccumulation of zinc was recorded at 20% engine-oil concentration and Nickel at 10% engine oil concentration was recorded. This is of importance for bioremediation of engine-oil polluted soils. **Poster MP86**

Allen, Michael F. Center for Conservation Biology and Department of Plant Pathology, University of California, Riverside, CA 92521, USA. michael.allen@ucr.edu. **Developing and testing technologies to study in situ fungal dynamics in the field**.

Fungal growth dynamics in soil has been largely studied in the laboratory, microcosms, and greenhouses. The expansion in sensor technologies and computer camera systems provides new opportunities to study growth and physiological dynamics in the field in real time. But, most of the sensors are designed for single, periodic observations. We are developing remote, networked sensor units measuring CO_2, temperature, moisture, and nitrate that are organized around minirhizotron tubes at the James Reserve in southern California. We have undertaken trial campaigns to monitor daily growth using minirhizotron cameras simultaneously with on-going sensor measurements. These trial runs have shown some surprising dynamics. AM fungal hyphae can be seen growing from infected root tips at soil water potentials below -5MPa. This growth pattern probably results from linkages between deep water sources and diurnal water fluxes between roots and fungi. Soil respiration pulses on hourly and daily intervals. While respiration may correlate loosely with temperature and moisture at large scales, at hourly and sub-meter scales, rapid growth and maintenance C responds to temporal and spatial events, flushes and pulses of roots, mycorrhizae, and saprobes. **Contr. Talk: Tues AM1 Fungal ecology methods and patterns.**

*Amores-Sánchez, Hector R. Ortiz-Pérez, Zulma, Rivera-Figueroa, Francisco and Cantrell, Sharon A. Science & Technology, Universidad del Turabo, P. O. Box 3030, Gurabo, P. R. 00778, USA. scantrel@suagm.edu. **Cultural and Molecular characterization of the halophilic black yeast *Hortaea werneckii* from a hypersaline environment in Puerto Rico**.

Hortaea werneckii is a black yeast species that inhabits the soil, particularly in tropical and subtropical regions. Also, this species can be found in saline environments from tropical and temperate regions where it can tolerate high salt concentrations. In a recent survey of fungi from a hypersaline environment in the southwest coast of Puerto Rico, two isolates were obtained from water and microbial mat. The objective of this study was to observe the growth of *H. werneckii* in different media (MEB, CzDB, PDB, and SDB), and temperatures (20ºC, 25ºC, 32ºC). Also, the halotolerance test was performed using MEB amended with 10%, 15%, 20% and 25% NaCl. The growth was measured using a spectrophotometer. A phylogenetic tree based on the ITS1-5.8S-ITS2 region of the rDNA was constructed and illustrate the relationship of these isolates. In each medium the colonies presented a different color from pale green to an olive black. The growth rate varies depending on the temperature, reaching maximum growth in one week at 32ºC while at 20ºC two weeks. Its optimal growth was in the range of 10 to 15% NaCl in the Malt extract broth at 32ºC. **Poster MP140**

*Anaya, Ana Luisa[1], Maria C. González[2], Aurora Saucedo-García[1], Martha Lydia Macías-Rubalcava[1], Jordi Muria[1]. [1]Instituto de Ecología, Universidad Nacional Autónoma de México, Circuito Exterior, Ciudad Universitaria. México, 04510, D.F.; [2]Instituto de Biología, Universidad Nacional Autónoma de México, Circuito Exterior, Ciudad Universitaria, México, 04510, D.F. alanaya@miranda.ecologia.unam.mx. **Antagonic potential of endophytic fungi from tropical plants at the Ecological Reserve El Eden, Quintana Roo, México**.

Endophytic fungi live inside healthy tissues of plants without cause any apparent damage to them. Nowadays, endophytic fungi are considered as ubiquitous as mycorrhizae fungi. In the present study we present some results of a research on the endophytic fungi of some tropical trees at the Ecological Reserve El Eden, Quintana Roo, Mexico. The study of the antagonic potential of these fungi could lead us to those that produce bioactive secondary metabolites with a potential use as drugs or agrochemicals. From a total of 1920 small leafcuts of nine plant species, we obtained, following conventional methodology, 202 strains that correspond to 75 morph-species of the phylum Ascomycota. Taxonomic identification of endophytic fungi was performed using molecular methodology. Until now, among the fungi isolated, we found a novel genus and two species. To evaluate the antagonic potential of isolated endophytic fungi, we performed bioassays between endophytic fungi and phytopathogenic fungi, and we determined the percent of inhibition of radial growth and calculated the antagonism index. The bio-directed fractionation study of some selected endophytic fungi showed that they produced phytotoxic and fungitoxic secondary metabolites. These results confirm the hypothesis that antagonic potential of endophytic fungi could be partially explain by the production of bioactive compounds. Antagonic endophytic fungi could be used as a potential source of novel agrochemicals and drugs, and also as some pests' bio-control. **Poster MP83**

*Andrew W. Wilson, David S. Hibbett, Clark University Biology, 950 Main St. Worcester, MA 01610, USA. anwilson@clarku.edu. **Molecular evolution and ecology of the basidiomycete genus *Calostoma* Sclerodermatineae, Boletales**.

The genus *Calostoma* is an enigmatic group of Basidiomycetes. It is a member of the Sclerodermatineae, a suborder of the Boletales, which includes gasteroid genera with a wide array of morphologies. A recent study of the Sclerodermatineae used 28S rDNA sequences and identified a relationship between genera such as *Calostoma,* the earthstar like *Astraeus,* and the boletoid *Gyroporus.* Some reports suggested that *Calostoma* is saprotrophic. This report is inconsistent with its hypothesized relationship to the Boletales. The goals of this study are: 1) Investigate the ecological role of *Calostoma* using a combination of isotopic and molecular tools. 2) Evaluate the evolutionary relationships between *Calostoma* and its Sclerodermatineae relatives. 1) Molecular analyses of two *Calostoma* species *C. sarasinii* from Malaysia and *C. cinnabarinum* from Eastern USA will use fungal and basidiomycete-specific primers for nrITS and will identify matching below ground ectomycorrhizal sequences. Isotopic profiles of C and N will be performed on *Calostoma,* mycorrhizal and saprotrophic fungal species. These profiles will be used to infer the *Calostoma* species nutritional mode. 2) The evolution of *Calostoma* and character evolution within the Sclerodermatineae will be evaluated using a combination of 28S, RPB1, and RPB2 genes. This study will use a broader sampling of taxa compared to previous analyses. **Poster MP68**

*Andrew, Marion[1], Peever, Tobin L.[1] and Pryor, Barry M.[2]. [1]Department of Plant Pathology, Washington State University, Pullman WA 99164, USA. [2]Department of Plant Sciences, University of Arizona, Tucson AZ 85721, USA. mandrew@wsu.edu. **Molecular systematics of small-spored *Alternaria* species**.

Alternaria species are important animal and plant pathogens, and there is a need for predictive association of species names with biology to aid identification. 150 isolates of small-spored *Alternaria* spp. from five host/geographic associations were classified morphologically and phylogenies were estimated from an endopolygalacturonase gene and 3 anonymous loci. Strict congruence between morphological classification and phylogenetic lineage was generally not observed. Exceptions were the *A. arborescens* and *A. tangelonis* morphospecies that formed discrete clades with all four loci. The *A. arborescens* morphospecies, represented by 36 isolates, was phylogenetically and morphologically distinct from all other isolates. The *A. tangelonis* morphospecies, which clustered with 5 other isolates exclusively from citrus, was also genetically distinct. Phylogenetic analyses revealed 4 to 10 well-supported clades with each locus, but it is currently unclear if clades should be considered evolutionary lineages within *A. alternata* or species. **Contr. Talk: Sunday pm1 Ascomycete systematics.**

*Arnold, A. Elizabeth[1], Lee, Ming-Min[1], Shimabukuro, Mary[2], Hoffman, Michele[1], and Lutzoni, Francois[3]. [1]Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA; [2]Dine College, Tsaile, AZ 86556, USA; [3]Department of Biology, Duke University, Durham, NC 27708, USA. arnold@ag.arizona.edu. **High diversity of endophytic fungi associated with *Pinus* species: evidence from three forests**.

Continued on following page

Fungal endophytes are thought to represent a significant portion of global fungal diversity. However, the scale of endophyte diversity is not known, reflecting a lack of comparative studies of closely related plants in geographically disparate sites. We surveyed leaf-inhabiting endophytes associated with healthy foliage of *Pinus* spp. in three forests: *P. ponderosa* in southern Arizona, *P. taeda* in central North Carolina, and *P. banksiana* in southern Québec, Canada. A total of 550 non-sporulating isolates were identified using data from the nuclear ribosomal internal transcribed spacerITS rDNA). We recovered at least 71 putative species of endophytic fungi, of which 61% were found only once. Among nonsingleton species, >70% occurred in only one study site. Lowest diversity was recorded in Arizona dry forest dominated by *P. ponderosa*, while the highest diversity was found in North Carolina mesic forest with a mixed canopy. Only one species *Lophodermium* sp. was shared among all sites. The most common endophyte species differed in each site, but various *Lophodermium* species were always among the most common endophytes. Endophyte communities in North Carolina and Québec were more similar to one another than to the endophyte assemblage recovered in Arizona, which contained a variety of novel endophyte taxa. Our results indicate the importance of sampling multiple sites to capture endophyte diversity for a given host lineage, raise the question of host specificity among endophytes of these related but distinct hosts, and provide an estimate of the sampling effort needed to achieve statistical completeness in these different forest types. **Poster MP82**

*Aveskamp, Maikel M.[1], de Gruyter, J.Hans[2], and Crous, Pedro W. . [1]Centraalbureau voor Schimmelcultures, P.O. Box 85167, 3508 AD Utrecht, The Netherlands, [2]Plantenziektenkundige Dienst, P.O. Box 9102, 6700 HC Wageningen, The Netherlands. aveskamp@cbs.knaw.nl. **A phylogenetic study on the sections within the genus *Phoma*.**

The anamorph genus *Phoma* counts more than 220 taxa, and is presently subdivided into nine sections: *Phoma, Heterospora, Paraphoma, Peyronellaea, Phyllostictoides, Sclerophomella, Plenodomus, Macrospora* and *Pilosa.* Although this division into sections is helpful for morphological identification, it is uncertain whether this division can be called natural in an evolutionary perspective, as the subdivision is solely based on morphological characters. The genus and species concepts of *Phoma* are under continuous discussion, and mainly the reclassification of the former genus *Plenodomus* Preuss. into the genus *Phoma* is questioned. A phylogenetic study was performed to judge the validity of the subdivision, using over 180 strains present in the collections of the CBS and the PD, including the type strains of the various sections. ITS and partial 28S rDNA-sequences were obtained and compared to sequences deposited in GenBank. Several sections in the classification system were found to be artificial, including the sections *Phoma, Sclerophomella* and *Macrospora.* Strong support was found for a large group of *P. exigua* -like strains belonging to the section *Phyllostictoides,* and for a clade resembling the section *Plenodomus.* The latter clade showed less similarity with the other strains tested, and the recently proposed re-establishment of the genus *Plenodomus* is supported. **Poster MP138**

*Avis, Peter G.[1], Dickie, Ian[2], Mueller, Greg M.[1]. [1]Department of Botany, 1400 S. Lake Shore Drive, Chicago IL, USA. [2]Landcare Research, PO Box 69, Lincoln 8152, New Zealand. pavis@fieldmuseum.org. **A "dirty" business: Testing the limitations of terminal restriction fragment length polymorphism (TRFLP) analysis of soil fungi**.

Terminal restriction fragment length polymorphism (TRFLP) is a popular method for the study of fungal communities. Like most methods, TRFLP has limitations that can lead to inaccurate characterizations of fungal communities. To gauge these limitations in our study of ectomycorrhizal fungi, we investigated the impact of spore contamination, intra-collection ribosomal DNA internal transcribed spacer ITS region variation, and conserved restriction enzyme recognition loci on the results produced by TRFLP. In this presentation we will demonstrate three specific limitations: 1) the potential for non-target structures such as spores to contribute DNA to target sample extractions; 2) how multiple fragments, i.e. extra peaks, per PCR primer-restriction enzyme combination caused by restriction enzyme inefficiency and intra-collection ribosomal DNA ITS variation influence results; and 3) that restriction enzyme digestion in conserved vs. variable gene regions leads to different estimates of community diversity. We suggest that studies employing TRFLP should integrate these results with those from other methods so that fungi can be identified most effectively and not to rely solely on TRFLP profiles as a short cut to fungal community description. **Contr. Talk: Tues AM1 Fungal ecology methods and patterns.**

*Báez-Félix, Claribel, Ortiz-Pérez, Zulma and Cantrell, Sharon A. Science and Technology, Universidad del Turabo, P. O. Box 3030, Gurabo, PR 00778, USA. scantrel@suagm.edu. ***Cladosporium* from water and microbial mat in a hypersaline environment of Puerto Rico**.

This study analyzes the characterization of species of the genus *Cladosporium* isolated from microbial mats and water samples from an extreme hypersaline environment. These fungi were collected from the ecological system named "Las Salinas de Cabo Rojo" located on the southwest coast of Puerto Rico characterized by high solar radiation, low precipitation and salinities up to 600 psu. For the isolation of fungi from water, 40ml of water was filtered through a 0.45µm membrane and placed in two media MA prepared using water from the same pond and MEA. For the isolation of fungi from the microbial mats the serial dilution technique was used and the selected media were MA and MEA. Pure cultures were isolated in MEA, PDA and SDA. The halotolerance test was performed in MEA with 10%, 15%, 20% or 25% NaCl. After 10 days at 27C, the diameter and the growth morphology was annotated in the different media. Four species have been identified *C. cladosporioides, C. tenuissimum, C. sphaerospermum,* and *C. oxysporum.* The optimal growth for the four species of *Cladosporium* was observed in MEA with 10% NaCl concentration. Therefore, these species can be considered halophilic. A phylogenetic tree based on the ITS1-5.8S-ITS2 region was constructed and illustrate the relationship of these isolates halophilic isolates from Cabo Rojo with none halophilic isolates found in GenBank. **Poster MP142**

*Bai, Shasha. and Kretzer, Annette. Environmental and Forest Biology, State University of New York-College of Environmental Science and Forestry, Syracuse NY 13210 USA. sbai@syr.edu. **Bacterial communities associated with tuberculate mycorrhizae**.

The functioning of bacteria in the mycorrhizosphere is receiving increasing interest. Earlier studies of mycorrhizosphere bacteria were limited by the use of cultivation techniques. Although 16S rDNA analysis has been successful in identifying new bacterial groups in many ecosystems, dominant amplification of root plastid DNA from mycorrhizae can prevent examination of bacterial sequences with general bacterial primers. There is also a lack in understanding the specificity of bacterial communities partitioned between different mycorrhizal species. We are studying the bacteria associated with three tuberculate mycorrhizae TM: *Suillus spraguei* of White Pine, *Rhizopogon vinicolor* and *R. vesiculosus* of Douglas-fir. Tuberculate mycorrhizae constitute ideal models to study mycorrhizosphere bacteria because the rinds can form natural barriers between the enclosed mycorrhizae and the bulk soil. Using the PCR-based approach with a newly designed primer, we sequenced 73 different bacterial clones from *S. spraguei* TM. Bacteria identified so far include alpha-, beta-, gamma-proteobacteria, and acidobacteria. In conclusion, our newly developed primer has shown strong discrimination against both mitochondria and chloroplast DNA while amplifying a wide range of bacteria. This is the first characterization of bacteria from TM using a culture-independent, PCR-based approach. **Poster MP69**

*Bianciotto Valeria, Lumini Erica, Anca Iulia, Ghignone, Stefano and Bonfante, Paola Istituto Protezione Piante (IPP) del Consiglio Nazionale delle Ricerche (CNR) and Dipartimento di Biologia Vegetale dell'Università di Torino - Viale Mattioli 25- 10125 Torino Italy di Torino - Viale Mattioli 25- 10125 Torino Italy. **Arbuscular mycorrhizal fungi: a specialized niche for endosymbiotic bacteria.**

AM fungi, which are obligate plant symbionts, represent a specialized niche for rod-shaped bacteria. In *Gigaspora margarita* BEG 34 a homogenous bacterial population, belonging to the new bacterial taxon *Candidatus* Glomeribacter gigasporarum, is hosted inside the fungal spore and is vertically transmitted through fungal spore generations. A detailed analysis on many isolates belonging to Gigasporaceae and originating from diverse geographical areas consistently revealed the presence of endobacteria phylogenetically related to *Ca*. G. gigasporarum. Analysis of ribosomal genes demonstrated a congruence between the bacterial phylogenetic trees and those of the fungal hosts, suggesting the presence of a coevolution mechanism. In the mean time, a cellular and molecular investigation of the bacterial cell cycle as well as the expression of the *FtsZ* gene revealed a relationship between the bacterial divisions and the symbiotic status of the fungus. A protocol based on monosporal inocula caused a dilution of *Ca*. G. gigasporarum population eventually leading to bacteria-cured spores. The cured spores were not affected in their mycorrhizal capacities but show differences in their cytoplasm and cell wall organization. Our investigation demonstrates that mycorrhizal roots represent a tripartite association resulting from the interaction of plant, fungal and bacterial genomes. **Symposium: Tues 1:30-5:00 Bacterial Symbionts of Fungi**

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Bonito, Gregory[1], Vilgalys, Rytas[1], Isikhuemhen, Omoanghe[2], Trappe, James[3]. [1]Duke University, Durham NC, [2]North Carolina Agricultural and Technical State University, Greensboro NC, [3]Pacific Northwest Forest and Range Experiment Station Forestry Sciences Laboratory, Corvallis OR USA. gmb2@duke.edu. **Phylogenetic relationships of North American truffles in the genus *Tube*r**.

Convergent evolution of hypogeous fungi due to development of the hypogeous habit and dependence on mycophagy for spore dispersal presents unique challenges to morphological systematics. However, the advent molecular methods has created new opportunities to examine genetic diversity and test morphological hypotheses of truffle relationships in an independent manner. In this study, we examine molecular-based diversity of the ectomycorrhizal genus *Tuber* in North America. DNA was extracted from a broad collection of herbarium specimens originating from across the North American continent, as well as from representative European and Asian taxa. Phylogenetic analyses based upon multiple loci (e.g. ribosomal LSU, RPB2, ITS, EFa1) were used to ascertain phylogenetic relationships between North American truffle species and species-complexes, including the Oregon white truffle *Tuber gibbosum.* Results are discussed as they relate to the evolution and geography of these species and their hosts. **Poster MP130**

*Campbell, Jinx[1], Ferrer, Astrid[2], Raja, Huzefa A.[2], Sivichai, Somsak[3], Shearer, Carol A.[2]. [1]Department of Coastal Sciences, University of Southern Mississippi, Ocean Springs, MS 39564, USA. [2]Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA. [3]BIOTEC, National Center for Genetic Engineering and Biotechnology, Pathumthani 12120 Thailand. jinx.campbell@usm.edu. **Jahnulales revisited: relationships based on 18S and 28S rDNA**.

The order Jahnulales was erected to accommodate three genera: *Jahnula* 14 species, *Aliquandostipite* two species and *Patescospora* one species. Molecular studies on the 18S rDNA have previously indicated that *Jahnula siamensiae* and *Patescospora separans* actually have closer affinities to *Aliquandostipite.* Therefore, to better understand the relationships of species within Jahnulales, molecular phylogenetic analyses were performed using the combined 18S and 28S rDNA sequences on ten species of *Jahnula,* two species of *Aliquandostipite,* one species of *Patescospora,* and two anamorphs, *Brachiosphaera tropicalis* and *Xylomyces chlamydosporis,* that are occasionally found growing on wood in conjunction with *Jahnula* species and that produce very wide hyphae in culture similar to species of the Jahnulales. The type species of *Jahnula, J. aquatica,* is on a clade with *J. granulosa,* separate from the other species of *Jahnula.* Nine other species of *Jahnula* are placed in a monophyletic clade, which also includes the two anamorphs. The *Aliquandostipite* species are on a monophyletic clade with the inclusion of *Jahnula siamensiae. Patescospora separans* is a sister taxon to this clade. On the basis of molecular phylogeny only *Jahnula aquatica* and *J. granulosa* belong in *Jahnula. Jahnula siamensiae* belongs in *Aliquandostipite* and the remaining species included in the analyses should be accommodated in a new genus. **Contr. Talk: Tuesday PM 1 Ascomycete systematics.**

*Campbell, Jinx [1], Shearer, Carol A.[2], and Marvanova, Ludmila[3]. [1]Department of Coastal Sciences, University of Southern Mississippi, Ocean Springs, MS 39564, USA. [2]Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA. [3]Masaryk University, Faculty of Science, Tvrdeho 14, Brno, Czech Republic. jinx.campbell@usm.edu. **Evolutionary relationships among aquatic anamorphs and teleomorphs II: *Tricladium* and *Varicosporium***.

Tricladium, with twenty one species, is the largest genus of aquatic hyphomycetes. It encompasses species with dematiaceous as well as mucedinaceous colonies. Conidiophores range from simple and identical with conidiogenous cells, to well developed and profusely branched. Conidiogenesis is thalloblastic; conidiogenous cells proliferate percurrently or sympodially. Conidia, although typically with two alternate primary lateral branches only, may have up to four laterals, sometimes with secondaries on the proximal primaries; branch insertion is unconstricted or constricted, sometimes unilaterally or only slightly. Molecular analyses on the 28S rDNA of ten species of *Tricladium* place these species within Helotiales. There are two well supported clades: one of taxa with pale colonies and hyaline conidiogenous structures *Tricladium attenuatum, T. biappendiculatum, T. patulum* and the second of taxa with dematiaceous colonies *T. terrestre, T. castaneicola, T. splendens*. The remaining species appear scattered between these two clades. Together with the previously revealed affinities, there are now 26 taxa of aquatic hyphomycetes related to Helotiales. **Poster MP126**

*Castlebury, Lisa A.[1] and Mengistu, Alemu[2]. [1]USDA ARS Sytematic Botany and Mycology Laboratory, Beltsville, MD 20705, USA., [2]USDA ARS Crop Genetics and Production Research Unit, Jacksonville, TN 38301, USA. lisa@nt.ars-grin.gov. **Phylogenetic distinction of *Diaporthe/Phomopsis* isolates from soybeans**.

Species of *Phomopsis* and *Diaporthe* have traditionally been described on the basis of host. The value of morphological characters in distinguishing species has been limited due to the reduced features of the conidiomata. Additionally, many strains exist as endophytes and plant pathogenic strains may not always fruit. Molecular approaches to species problems in *Phomopsis* have traditionally focused on sequence analysis of the ITS rDNA, but it has not been particularly informative for answering species level questions across this genus. Using intron regions in the translation elongation factor-1 alpha and actin genes, in combination with the ITS, six closely related, well-supported groups among *Diaporthe/Phomopsis* isolates from soybeans and other hosts were found. Although three groups correspond to named taxa *P. longicolla, Diaporthe meloni,* and the *D. phaseolorum* complex due to the absence of morphological distinction and biological information, the application of appropriate names to the unidentified genetically distinct taxa is problematic. Furthermore, the biological significance of these genetically distinct groups is unclear. Additional work on host specificity, pathogenicity, and morphology will be required to solve species questions in this genus. **Poster MP132**

Celio, Gail J. Padamsee, Mahajabeen, Dentinger, Bryn T.M. McLaughlin, David J. Dept. of Plant Biology, Univ. of Minnesota, Saint Paul, MN 55108 USA. celio001@umn.edu. **The search for subcellular characters for the AFTOL structural and biochemical database traits of *Auriscalpium vulgare***.

Along with the collection of published data for the Assembling the Fungal Tree of Life AFTOL Structural and Biochemical Database, taxa of poorly represented clades are also being studied microscopically for entry into the Database. Toothed hymenophores from sporocarps of *Auriscalpium vulgare* Russulales, Basidiomycota, were examined using freeze substitution and transmission electron microscopy. Previously unreported characters of the septal pore apparatus SPA are observed: a zone of organelle exclusion surrounding the SPA, and perforate bell-shaped septal pore caps that may extend along the septum. Meiosis in basidia involves globular spindle pole bodies that are set within loose polar fenestrae of the nuclear envelope during metaphase I. The nuclear envelope remains intact and initial results indicate that it undergoes median constriction during telophase I. Cystidia contain vesicles with electron-opaque peripheral deposits and internal tubular structures, or uniform granular material. Character states were coded for entry into the Database. Comparisons to related taxa are difficult due to incomplete data sets. **Contr. Talk: Sunday PM 2 Basidiomycete systematics**

*Ceresini, Paulo C. and McDonald, Bruce A. Institute of Integrative Biology - LFW B28, Universitäetsstrasse 2, Zurich, Switzerland. paulo.ceresini@agrl.ethz.ch. **Gene flow and reproductive mode in *Rhizoctonia* from native Amazonian soils and adjacent agricultural soils**.

Rhizoctonia solani is a species complex composed of genetically distinct groups of fungi with very diverse life histories. Although a clearer understanding of the biology and ecology of *R. solani* is emerging, basic questions about the nature of populations and individuals remain unrevealed for most of *R. solani* anastomosis groups (AGs). The perfect stage of the fungus *Thanatephorus cucumeris* is frequently associated with leaf blight diseases. Two leaf pathogens sampled from the Amazon will illustrate mechanisms affecting populations, divergence in Rhizoctonia: the AG-1 IA, a Fabaceae and Poaceae-infecting pathogen; and the AG-2-2, the rubber tree foliar blight pathogen. Long distance migration characterized populations of the rubber tree foliar blight pathogen AG-2-2 in Brazil. High levels of migration and gene flow also characterized the rice and maize-infecting populations from Panama, Colombia and Venezuela, while subdivision was observed between these and the Fabaceae-infecting population from Brazil. Based on evidences of recombination, AG-1 IA is more likely to be a sexual pathogen on all of its hosts. Supported by phylogenetic reconstruction we postulate that two allopatric groups compose the AG-1 IA complex: the Fabaceae-infecting, probably originated in the Amazon, and the Poacea-infecting, with external origin but widespread by agriculture. **Symposium: Wed 8:30-1200 Population and Species Divergence in Fungi**

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*Charlton, Nikki D.[1], Carbone, Ignazio[1], Tavantzis, Stellos M.[2], and Cubeta, Marc A.[1]. [1]Dept. of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7616, USA, [2]Dept. of Biological Sciences, University of Maine, Orono, ME 04469-5722, USA. ndcharlt@unity.ncsu.edu. **Analysis of genetic diversity and evolutionary history of the M2 dsRNA of *Rhizoctonia solani* AG-3**.

The M2 double-stranded RNA dsRNA virus occurs in high frequency in field populations of the soil fungus *Rhizoctonia solani* anastomosis group 3AG-3. The M2 dsRNA has been hypothesized to regulate two metabolic pathways associated with the parasitic and saprophytic activity of the fungus. Three regions of the M2 dsRNA obtained from a representative sample of isolates of *R. solani* AG-3 from potato stems and tubers were sequenced to examine their genetic diversity and to reconstruct their genealogical history. Phylogenetic analysis of each region of the M2 dsRNA suggests the occurrence of at least two genetically divergent lineages with unique evolutionary histories of mutation and recombination. Genealogies and reticulated graphs are being used to understand the combined mutation and recombinational histories for each region of the dsRNA virus. Coalescent analysis for nonrecombining regions of the virus will be used to infer the oldest viral haplotypes and root the ancestral recombination graph. Information generated from phylogenetic analyses is currently being used to design and conduct virus transmission experiments to determine whether the M2 dsRNA can be transmitted to genetically different individuals of *R. solani* AG-3 and how acquisition of different dsRNA lineages (or genotypes) influences the phenotype of the fungus. **Contr. Talk: Tues AM2 Fungal Pathogens: population structure and distributions**

Chen, Mo-Mei. University Herbarium, 1001 Valley Life Sciences Bldg., University of California, Berkeley CA 94720, USA. mmchen@nature.berkeley.edu. **The species of edible and medicinal mushrooms in China**.

More than 1,800 years ago, during the East Han Dynasty in China, people began to use wild fungi for their nutritional and curative properties. At present, 50 species of marketable mushrooms are cultivated for nutrition, food and medicine. An additional 256 species are used for specific pharmaceutical needs. According to biogeographical and systematic studies (Chen, 2004), Chinese edible mushrooms occur in 7 geographical regions, with 800 edible and medicinal species belonging 12 families 19 genera of Ascomycetes and 45 families 130 genera of Basidiomycetes. Examples of potentially cultivatable fungi are *Auricularia reticulate*, *Auricularia polyricha*, *Cordyceps militaris*, *Cordyceps cicadae*, *Craterellus aureus*, *Lentinus javanicus*, *Lentinus subnudus*, *Lepiota sordida*, *Lepiota personata*, *Pleurotus nebrodensis*, *Poria cocos, Pseudohydnum gelatinosum, Tremella aurantialba, Boletus edulis, Fistulina hepatica* and *Hericium coralloides*. With the increase in population and demands on global natural resources, cultivation should be encouraged. As the wealth of diverse mushroom species become better known in the world, people will come to enjoy the naturally healthy nutritional and medicinal properties of these fungal treasures. **Poster MP146**

*Cifuentes, Joaquin B. and Villarruel-Ordaz Jose Luis, Dept. of Comparative Biology, FC-UNAM, Mexico DF 04510. jcb@hp.fciencias.unam.mx. **Macrofungi diversity patterns in a suburban forest in the Valley of Mexico City**.

The Rio Magdalena basin, Contreras County, in the Valley of Mexico City is an important forest conservation area with Conifer and Mixed Forest and one of few remaining in the metropolitan area; it is also the last river left in the City and where rain water is still collected. The area was explored weekly to collect macrofungi from July to October in 2004 and 2005. 305 specimens were collected belonging to 222 different species. The best represented taxa are orders Agaricales, Cortinariales, Pezizales, families Cortinariaceae, Tricholomataceae and genera *Inocybe, Mycena, Russula.* The diversity patterns as proportion of orders, families and genera are compared with those observed in a similar but air unpolluted and rather well preserved area, the monarch butterfly reserve in Sierra Chincua, Michoacan State, where Agaricales, Tricholomataceae and *Clitocybe* were the best represented taxa. Also Mexican Herbaria were searched for macrofungi historical records in the area in order to address changes in the fungal community composition. **Poster MP162**

*Cline, Erica T. [1], Edmonds, Robert L.[2], [1]Systematic Botany and Mycology, USDA ARS Beltsville MD 20705, [2]College of Forest Resources, University of Washington, Seattle WA 98195-2100, USA. ecline@nt.ars-grin.gov. **Do residual trees help seedlings? Exploring the "Nurse-Tree" effect on mycorrhizal colonization**.

Retention forestry places seedlings in proximity to residual trees, exposing seedlings to additional sources of ectomycorrhizal fungus (EMF) inoculum. To investigate this, Douglas-fir *Pseudotsuga menziesii* Mirb. Franco seedlings were planted near (<6 m) and far (>16 m) from 44- to 72-year-old residual Douglas-fir trees in western Washington, USA. From 1998 through 2000, EMF taxa of seedlings and residual trees were identified using morphology and sequence analysis of internal transcribed spacer and large subunit ribosomal DNA. Seedlings near residual trees had significantly higher EMF abundance (percent active EMF root tips) and root to shoot biomass ratios. Seedlings near trees on average had 4.1 EMF taxa per seedling and 42 total taxa compared to 3.5 taxa per seedling and 33 total taxa for seedlings far from trees. Residual tree EMF communities were more similar to those of seedlings planted nearby than to those of seedlings planted >16 m from trees. Proximity to residual trees may increase seedling EMF colonization and influence the EMF community after harvesting. **Contr. Talk: Tues AM1 Fungal ecology methods and patterns.**

*Collopy, Patrick D.[1], Colot, H.V.[1], Curilla, S.[1], Ringelberg, C.[1], Litvinkova, L.[2], Altamirano, L.[2], Park, G.[2], Jones, J.[2], Borkovich, K.A.[2], and Dunlap, J.[1]. [1]Department of Genetics, Dartmouth Medical School, Hanover, NH, USA, [2]Department of Plant Pathology, University of California, Riverside, CA, USA. patrick.d.collopy@dartmouth.edu. **A high-throughput procedure for disruption of *Neurospora* genes**.

Gene disruptions have been made in predicted open reading frames (or genes) in the annotated *Neurospora* genome using a high throughput procedure as part of an NIH-funded Program Project (P01). Knockout cassettes were assembled by yeast recombinational cloning techniques in a high-throughput fashion with a pipetting robot. Confirmation of *Neurospora* gene replacements are confirmed using a program we have developed that allows automated identification of the appropriate restriction enzyme to use during Southern analysis (http://borkovichlims.ucr.edu/southern/). Additionally, we have developed and implemented a Laboratory Information Management SystemLIMS; (http://www.borkovichlims.ucr.edu/php/sLIMS.php) for our gene knockouts in process. All plates and tubes used during the knockout procedure are labeled with barcodes and managed systematically. Completed *Neurospora* knockout mutant strains have been submitted to the Fungal Genetics Stock Center and are available to the public. An updated list of submitted strains is available at the *Neurospora* genome project website (http://www.dartmouth.edu/%7Eneurosporagenome/knockouts_completed.html). Use of these tools and our current progress in creating knockout mutants will be presented. **Poster MP95**

*Collopy, Patrick D.[1+], Amey, Richard[2], Challen, Mike[3], Mills, Peter R.[3], Bailey, Andy[1], and Foster, Gary D.[1]. [1]School of Biological Sciences, University of Bristol, Bristol, UK; [2]School of Biosciences, University of the West of England, Bristol, UK; [3]Horticulture Research International, Wellesbourne, Warwick, UK; [+]Current address: Department of Genetics, Dartmouth University, Hanover, N.H. USA. patrick.d.collopy@dartmouth.edu. **Investigations into the fungal-fungal interaction between *Verticillium fungicola* and *Agaricus bisporus***.

The cultivated button mushroom, *Agaricus bisporus,* is susceptible to a number of pathogenic threats including bacteria, viruses, mites, insects and fungi. Currently, the most significant threat to the mushroom industry is the mycoparasite, *Verticillium fungicola.* Infection by *V. fungicola* can drastically reduce the yield and value of mushroom crops. The severity of this disease is dependent on the developmental stage of *A. bisporus* at the time of infection. An aim of our research has been to develop molecular tools for *V. fungicola* that will allow us to study the interaction between this pathogen and *A. bisporus.* These tools have included transformation methods, marker gene techniques as well as gene-knockout technologies. This has involved the use of Agrobacterium and T-DNA to introduce disruption constructs into *V. fungicola* as part of a molecular investigation into this fungal-fungal interaction. We have developed an efficient transformation system for *V. fungicola* that we have now adapted to give high levels of targeted mutagenesis. This technique has successfully generated targeted mutants of a beta-1-6 glucanase homologue from *Trichoderma harzianum* and a Mitogen Activated Protein Kinase homologue *PMK1* from *Magnaporthe grisea* identified using degenerate PCR primers. **Contr. Talk: Monday PM Fungal molecular and cell biology**

*Crouch, Jo Anne, Bruce B. Clarke and Bradley I. Hillman, Department of Plant Biology and Pathology, Rutgers University, New Brunswick, NJ, USA. jcrouch@eden.rutgers.edu. **Evolutionary relationships of fungal species in the genus *Colletotrichum* from diverse grass communities**.

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The genus *Colletotrichum* contains five described and several undescribed falcate-spored fungal species that are associated with grasses in both cultivated and natural grass communities. Most of these taxa are destructive pathogens and inhabit a very limited range of warm-season grass hosts, with the exception of *C. cereale,* a recently described fungal species that lives in association with an extremely broad range of cool-season grass host plants. *C. cereale* emerged in the 1990s as a destructive pathogen in turfgrass systems, however, this fungus also inhabits a wide range of cereals and grasses at non-lethal levels. Here we present an overview of our study of the variability, divergence and evolutionary relationships exhibited by this important group of organisms. Multi-locus phylogenetics combined with morphological analysis reveals previously unknown species boundaries, unique phylogenetic lineages and reconstructs the evolutionary trajectory within the group. Within the species *C. cereale,* a set of novel microsatellite markers, multi-locus nucleotide sequence data and three species of transposons altered by repeat-induced point mutation uncover ancestral haplotypes, complex population structures, and provide evidence for sexual recombination during the evolution of this clonal fungus across natural grasslands and agroecosystems. **Contr. Talk: Tues PM 2 Fungal systematics.**

*Crous, Pedro W.[1], Seifert, Keith A.[2], Samson, Rob A.[1], Hawksworth, David L.[3], [1]Centraalbureau voor Schimmelcultures, Utrecht, Netherlands; [2]Biodiversity, Mycology & Botany Environment Theme, Agriculture and Agri-Food Canada, Ottawa, Ontario KIA 0C6 Canada; [3]The yellow House, Calle Aguila 12, Colonia La Mataelpino, ES-28492 Madrid, Spain. crous@cbs.knaw.nl. **Introducing the Fungal Planet: a global initiative to describe a 1000 new species of fungi**.

With this initiative, we aim to make a contribution towards highlighting the world's incredible fungal diversity, and underlying the importance of funding fungal biodiversity research. A major aim is to link fungi to their environment, i.e. the ecosystems where they occur. High quality digital colour photographs capturing the spirit of each collection site is thus a prerequisite requirement for publication of each species description. Each description will consist of two pages, namely a technical page, and a colour illustration page. Additional information including phylogenetic trees can be included, if necessary, in supplementary pdf files available on-line. Species descriptions will be printed monthly in sets, and distributed to approximately 10-20 libraries immediately each month for validation under the ICBN. Species descriptions will then be available, free of charge, on the web at http://www.fungalplanet.org. When 200 descriptions are completed, they will be gathered into a book available for sale from CBS, with the five books completed over a targeted five year period. This initiative will be linked to MycoBank (http://www.MycoBank.org), so mycologists will also receive alerts if species have been described in genera of interest to them. **Poster M117**

*Crous, Pedro W.[1], Slippers, Bernard[2], Wingfield, Michael J.[2], Rheeder, John[3], Marasas, Walter F.O.[3], Phillips, Alan J.L.[4], Alves, Artur[5], Burgess, Treena[6]. [1]CBS, Utrecht, the Netherlands; [2]FABI, Univ. Pretoria, South Africa; [3]PROMEC, MRC, Tygerberg, South Africa; [4]Centro Microbiol. Univ. Nova de Lisboa, Portugal; [5]Centro de Biologia Celular, Univ. de Aveiro, Portugal; [6]School Biol. Sci. & Biotech, Murdoch University, Perth, Australia. crous@cbs.knaw.nl. **Defining phylogenetic lineages in the Botryosphaeriaceae**.

Botryosphaeria is a species-rich genus with a cosmopolitan distribution, commonly associated with die-back and cankers on woody plants. As many as 18 anamorph genera have been associated with *Botryosphaeria,* most of which have been reduced to synonymy under *Diplodia* conidia mostly ovoid, pigmented, thick-walled), or *Fusicoccum* conidia mostly fusoid, hyaline, thin-walled). There are, however, numerous conidial anamorphs with morphological characteristics that are intermediate between *Diplodia* and *Fusicoccum.* There ere are also several records of species outside the Botryosphaeriaceae that have anamorphs apparently typical of *Botryosphaeria* s.str. Recent DNA sequence based studies have linked *Botryosphaeria* to species with pigmented, septate ascospores, and *Dothiorella,* or *Fusicoccum* anamorphs with *Dichomera* synanamorphs. In this study we used DNA sequence data of the 28S rDNA to resolve apparent lineages within the Botryosphaeriaceae. Phylogenetic analysis of these DNA data show the existence of 12 distinct clades. Two of these lineages namely *Diplodia*-like anamorphs occurring on maize *Stenocarpella*, Diaporthales, as well as an unresolved clade including species of *Camarosporium/Microdiplodia* clustered outside the Botryosphaeriaceae. We thus recognise 10 discrete lineages in the Botryosphaeriaceae, nine of which have been provided with names. The unresolved clade most likely includes additional genera, which will be defined as new material becomes available for study. **Contr. Talk: Tues PM 2 Fungal systematics.**

*Czymmek, Kirk J. Delaware Biotechnology Institute, 15 Innovation Way, University of Delaware, Newark, DE 19711, USA. kirk@udel.edu. **Exploring fungal growth with confocal and multiphoton microscopy**.

The potential for exploring fungal activity using optical microscopy has never been greater. Numerous technological advances in equipment and fluorescent molecular tags have dramatically extended our ability to probe a variety of fungal structures in both fixed and living cells. Specifically, optical sectioning techniques such as confocal and multiphoton microscopy have led the way in this fluorescence revolution. The value of confocal and multiphoton microscopy is derived from their ability to non-invasively extract high contrast, high-resolution optical sections in the dimensions of space and time. As such, information regarding targeted subcellular entities, tissues or even interactions with the local environment can be readily garnered *in vivo.* The theoretical and practical application of these optical imaging technologies will be provided in the context of mycological research. Special emphasis will be placed on two-, three- and four-dimensional imaging of fungal entities and include contemporary methods for acquiring relevant quantitative and qualitative information from microscopic data. **Symposium: Sunday 1:30-5:00 Fungal Movement: Contemporary Experimental Analysis**

Daba, Ayman[1], Winter, *Melanie D.[1], Palmer, Jonathan M[1], Taylor, Bernadette[2], Dunek, Craig[1], and Volk, Thomas J.[1]. Departments of [1]Biology and [2]Microbiology, University of Wisconsin-La Crosse, La Crosse WI 54601 USA. adaba1@yahoo.com. **Can *Amanita muscaria* fight cancer? More questions than answers**.

Cancer continues to be the scourge of humanity, being a leading cause of early death. The current major therapies for cancer are surgery, radiation, and chemotherapy. All three impose a burden on the body and weaken immunofunction. Moreover, advanced cancer does not respond well to therapy. There is an urgent need for new anticancer agents with fewer negative side effects. The old proverb says "Food and Medicine Result from the Same Root; Mushrooms Prove this to be True." Several studies have indicated that mushroom extracts could be used to treat different types of diseases including various cancers, heart diseases, bacterial and viral infections, as well as some inflammatory and metabolic diseases. We tested Fly Agaric mushroom *Amanita muscaria* in treatment of cancer. Fruit bodies were collected, identified using morphology and PCR sequencing. The active components isolated by hot water extraction and alcohol precipitation. Structural analysis of the active components using infrared and NMR spectroscopy indicated that the active compound is a polysaccharide consisting mainly of highly branched 1->3, 1->6 glucan. Lymphopoliferative activity was tested at 10-200 µg/ml polysaccharide. The study will ultimately determine if *A. muscaria* mushroom extract can exert a selective cytotoxic effect against cancer cell lines such as leukemia and liver cancer. **Poster MP105**

*Davey, Marie L. and Currah, Randolph S. Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9. mdavey@ualberta.ca. **A new species of *Cladophialophora* (Hyphomycetes) from boreal moss gametophytes**.

During a survey of bryophilous fungi from boreal and montane habitats in central Alberta, a hitherto undescribed species of *Cladophialophora* was recovered from *Polytrichum juniperinum, Aulacomnium palustre,* and *Sphagnum fuscum.* On PDA, colonies grew slowly, attaining a diameter of 25mm after 30 days, were dark grey, velvety, radially sulcate and convolute and cracked at the center. Micronematous conidiophores gave rise to branched chains of small 1-2 mm x 8-22 mm cylindric to fusiform conidia with truncate swollen scars at each end. Phylogenies built on the internal transcribed spacer (ITS) and ribosomal small subunit (SSU) regions indicate isolates form a monophyletic clade within the family Herpotrichiellaceae (Chaetothyriales) that is composed of two geographically based groups, each with 99% within-group sequence similarity and 97 to 98% between-group sequence similarity. A teleomorph has not been found but would likely be similar to species of *Capronia. In vitro* inoculation of the isolates onto axenically grown *P. juniperinum* and *A. palustre* produced no discernible host symptoms, and host penetration could not be detected using light microscopy. The production of gelatinases and polyphenol oxidases by the fungus and the role of other *Cladophialophora* species as latent endophytes and saprobes suggests a potential role for the fungus as a saprophyte degrading the polyphenol-rich cell walls of mosses. **Contr. Talk: Tuesday PM 1 Ascomycete systematics.**

Continued on following page

*Davis, R. Michael[1], Li, Rongchun[2], and Miller, Steven L.[3]. [1]Dept. of Plant Pathology, Univ. of California, Davis, CA 95616, USA, [2]School of Agric. Sci. & Biotech. Yunnan Agric. Univ. Kunming, Yunnan 650201, China, and [3]Botany Dept. Univ. of Wyoming, Laramie, WY 82071, USA. rmdavis@ucdavis.edu. **A phylogeny of *Russula* species from northern California**.

Phylogenetic relationships among species of *Russula* collected in northern California coastal forests were inferred from nucleotide sequences of ITS and large-subunit rDNA, ATP6, and RPB2 genes. A data set of 61 genotypes representing at least 48 morphologically distinct species was analyzed by maximum-parsimony and bayesian-likelihood methods. Eight major and well-supported clades were recognized. The identity of all species was difficult to determine since more than one genotype often represented a single morphotype. For example, species recognized as *R. xerampelina* consisted of three genotypes and *R. olivacea* and *R. queletii* each consisted of two genotypes. Several species previously unreported in California, viz. *R. exalbicans, R. curtipes,* and *R. firmula,* were documented. At least two new species were tentatively identified. Based on a cursory comparison of available ITS sequences, sequences of California *Russula* species sometimes diverge significantly from sequences of European collections. **Poster MP157**

DeBellis, Tonia[1], Kernaghan, Gavin[2], Widden, and Paul[1]. [1]Concordia University, Department of Biology, Groupe de recherche en écologie forestière interuniversitaire (GREFi), 7100 Sherbrooke Street West, Montreal, QC, Canada, H3G 1M8, [2]Université Laval, Département de biologie, Sainte-Foy, QC, Canada, G1K 7P4. gavin.kernaghan@bio.ulaval.ca. **Plant-microfungal community interactions in the boreal-mixed wood forest**.

We studied the relationships between assemblages of soil microfungi and plant communities in the southern boreal mixed-wood forests of Quebec. A soil washing technique was used to isolate microfungi from sites supporting a range of boreal tree and understory plant species. Isolates were identified morphologically and by sequencing of the internally transcribed spacer region (ITS). Multivariate analysis redundancy analysis followed by variance partitioning revealed that the majority of variation in microfungal communities is explained by understory plant species composition, as opposed to soil chemistry or overstory tree species. **Poster MP74** .

*Dentinger, Bryn T. M. and McLaughlin, David J. Deptartment of Plant Biology, University of Minnesota, St. Paul, MN 55108, USA. dent0015@umn.edu. **The elusive little pig: Unraveling the taxonomy and evolution of porcini**.

Porcini *Boletus* section *Boletus* form a cosmopolitan group of ca. 30 species of fleshy boletes that typify the Boletales. Despite their broad geographic distribution and critical position in the classification of the Boletales, the phylogeny is poorly known. Phenotypic plasticity and intergrading morphospecies confound existing taxonomic treatments and impede species identification. In this study, the evolutionary history of porcini taxa collected mostly in eastern and western North America was reconstructed using phylogenetic analysis of nuclear ribosomal internal transcribed spacer region (nucITS) sequences. Identification of new collections revealed that some species descriptions are inadequate and could not be used to reliably differentiate taxa. Therefore, an attempt was made to acquire nucITS sequence "signatures" from holotype specimens representing over 100 years of collecting (1887-1999). DNA extraction methods were optimized for recovering DNA from modern and historical specimens. Commercial kits commonly used in the extraction of plant and animal DNA were found to be inefficient at recovering DNA from boletes. Efficacy of extraction with recent material was usually successful but appeared random with collections more than a few years old. **Contr. Talk: Sunday PM 2 Basidiomycete systematics**

Dettman, Jeremy, James Anderson, and Linda Kohn, Mississauga, Ontario, Canada, jdettman@utm.utoronto.ca. **The effects of divergent selection on the compatibility among experimental populations of *Neurospora***.

Reproductive isolation may develop between populations by genetic drift alone, or as a by-product of adaptation to divergent environmental conditions (ecological speciation). Interspecific hybridization may produce novel combinations of alleles which may facilitate speciation by creating new opportunities for adaptive evolution (hybrid speciation). To date, most studies of population divergence have been retrospective, with historical events inferred from contemporary patterns of genetic variation, reproductive isolation, and geographic distribution. By experimentally evolving fungi under conditions that are theoretically most likely to induce changes in inter-population compatibility, we may be able to observe replicated divergence events and examine the dynamics and mechanisms of population divergence. Populations of *Neurospora crassa,* and *N. crassa* x *N. intermedia* hybrids, were serially propagated with alternating rounds of asexual growth and sexual reproduction. To promote divergent adaptation, replicate populations were evolved under two different suboptimal growth conditions (high salinity and low temperature). Assays for adaptation and inter-population compatibility were performed throughout and at the end of the evolution regime. Did the populations adapt to the novel environments, either by a direct or correlated response to selection? Were populations evolved in divergent environments more likely to show reduced inter-population compatibility than populations evolved in the same environment? Were these effects dependent upon the genetic composition of the founding populations (non-hybrid versus hybrid) or the assay environment?, **Symposium Wed 8:30-1200 Population and Species Divergence in Fungi**

*Dewsbury, Damon R.[1], Margaritescu, Simona[2], Stephenson, Steven L.[3], Moncalvo, Jean-Marc[1,2]. [1]Botany Department, University of Toronto, Toronto, Canada, [2]Royal Ontario Museum, Toronto, Canada; [3]Department of Biological Sciences, University of Arkansas, Fayetteville, AR, U.S.A. damondewsy@yahoo.com. **Developing molecular systematics for the Myxomycota**.

The Myxomycetes (plasmodial slime molds) produce the most noticeable fruiting bodies within the Eumycetozoans. Approximately 850 species are recognized based on macromorphology, spore ornamentation, microscopic sterile tissue (capillitium and pseudocapillitium) features, and the presence of lime crystals. Many of the morphologically defined species appear to be cosmopolitan. It is possible that distinct genetic groups representing cryptic species are hidden among these broadly defined species. However, DNA systematics has been slow to develop for these organisms. Ribosomal rRNA genes have been broadly and successfully used in fungal systematics but these genes have many large introns in Myxomycetes, making PCR amplification problematic. EF1-alpha sequences have recently been shown to provide a good phylogenetic signal, but cannot fully resolve relationships among the Myxomycetes at all taxonomic levels, and non-orthologous copies have been found. Here we infer the possibility of using sequences from the mitochondrial gene cytochrome-oxidase (*COI*). This gene has recently been suggested as a possible universal marker for molecular identification, or "DNA barcode", of species across different kingdoms of life. We will present preliminary data comparing the usefulness of both EF1-alpha and COI sequences for Myxomycetes taxonomy and phylogenetics. **Poster MP121**

*Didukh, Maryna, Ya.[1,3], Vilgalys, Rytas[2], Wasser, Solomon, P.[1,3], Isikhuemhen, Omoanghe, S.[4], Nevo, Eviatar[3], and Moncalvo, Jean-Marc[5]. [1]Dept. of Mycology, M.G. Kholodny Institute of Botany, NASU, Kiev, Ukraine. [2]Dept. of Biology, Duke University, 139 Biological Sciences Building, Durham, USA. [3]International Center for Cryptogamic Plants and Fungi, Institute of Evolution, University of Haifa, Mount Carmel 31905, Israel. Maryna.Didukh@gmail.com. **DNA barcoding species in *Agaricus* section *Duploannulati*: comparison between ITS and COI data**.

The position of several endemic *A. nevoi*, *A. padanus*, rare *A. rollanii* and previously not studied *A. gennadii* var. *microsporus* taxa in genus *Agaricus* sect. *Duploannulati* and the limits of the section were investigated by analysis of sequence data from the nrITS. The results supported the recognition of two subsections - *Chitonioides* and *Duploannulati.* Based on the ITS data, *A. rollanii, A. pequinii* and *A. gennadii* proved to be well-delimited lineages placed in subsect. *Chitonioides. A. nevoi* and *A. padanus* did not receive any significant statistical support, whereas variety of *A. gennadii* - var. *microsporus* formed a clade of its own. The dubious placement and lack of resolution of these three taxa seem to result from low variation in ITS sequence amongst recently diverged taxa. Consequently, another molecular marker capable to provide a sufficient resolution and robustness is required in order to resolve the questions concerning identity of *A. nevoi, A. padanus,* and *A. gennadii* var. *microsporus.* A C-terminal fragment of the mitochondrial gene for cytochrome oxidase subunit I *COI* was shown to be efficient in elucidation of cryptic and closely related species in animals and has been suggested as a possible molecular marker for species identification DNA barcode in other groups of organisms as well. Currently, we are investigating applicability of *COI* for DNA barcoding in *Agaricus* species as compared to ITS and will present our preliminary data. **Contr Talk Sunday PM Basidiomycete Systematics**

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Dornelo-Silva, Denise and *Dianese, José C. Departamento de Fitopatologia, Universidade de Brasília, 7-910-900 Brasília, DF, Brazil. jcarmine@unb.br. **Five new *Stenella* species from the Brazilian Cerrado**.

Cercosporoid fungi are being reported lately from the Cerrado region of Central Brazil mostly as a result of a continuous survey of the plant-associated mycota by local mycologists. A study of the exsiccates deposited in the Mycological Collection of Herbarium UB, revealed a set of five new *Stenella* species, three of them thriving on members of the *Erythroxylaceae* [two on *Erythroxylum campestre* - UB mycol. col. 7508 and UB mycol. col. 7364; one on *E. suberosum* - UB mycol. col. 9153], one on a *Vochysiaseae Callisthene fasciculata* - UB mycol. col. 16309, and another on Orchidaceae *Cyrtopodium eugenii* - UB col. micol 15854. All new species were typical stenellas showing verrucose superficial mycelium copious, branched, septate, light brown to brown; conidia also verrucose, subcylindrical, elongate, septate, scared at the base, formed on sympodially proliferated primaryoriginate from a stroma, when present, or secondary superficial conidiophores always bearing scared geniculate conidiogenous cells. Morphometrical details further demonstrated that these Neotropical specimens belong in new *Stenella* species which are being prepared for publication following the the Int. Code of Bot. Nomenclature. They are especially important also because they are all first records of the genus for three different host families. **Poster MP128**

Dumais, Jacques. Dept. of Organismic and Evolutionary Biology, Harvard University. Cambridge, MA, 02138, USA. jdumais@oeb.harvard.edu. **The mechanics of tip growth in fungi and beyond**.

Many features of tip growth are shared across a wide range of organisms and seem therefore to transcend important differences in wall composition and subcellular architecture. Based on this observation, we suggest a generic model of tip growth and show how it can account for many aspects of cell morphogenesis in fungi, oomycetes, and plants. One of the most difficult issues remains to formulate a model for cell surface expansion that includes both the addition of new wall material and its stretching into a functional shape. We will discuss different ways to unite these two processes and show experimental evidence that supports the idea that wall deposition and wall stretching contribute to complementary aspects of cell surface expansion. **Symposium: Sunday 1:30-5:00 Fungal Movement: Contemporary Experimental Analysis**

*Dunek, Craig P. and Volk. Thomas J. Dept. of Biology, University of Wisconsin-La Crosse, La Crosse WI 54601, dunek.crai@students.uwlax.edu. **Preliminary isolation and characterization of novel antifungal chemicals from fungal fruiting bodies**.

The worldwide increase of immune suppressed individuals in the past twenty years has lead to a dramatic increase in fungal infections. Fungal pathogens are not easily treated, and a majority of the drugs available for treatment are toxic to humans. The aim of this study was to employ natural products chemistry to discover new antifungal drugs from fungal fruiting bodies. The suspected drug target is the microtubules, which are chemically different in Ascomycota and Basidiomycota. Testing Ascomycota pathogens with extracts from Basidiomycota and Basidiomycota pathogens with extracts from Ascomycota, has led to discovery of secondary metabolites that are inhibitory to the fungal pathogens. Using disc diffusion assays, crude extracts were tested against three tester strains of human pathogens: *Candida albicans (*ascomycete), *Cryptococcus neoformans* (basidiomycete), and *Emmonsia crescens* an ascomycete, as a surrogate for the more dangerous *Histoplasma* and *Blastomyces*. Some of the extracts have shown fungistatic or fungicidal activity against some of the tester strains, which represent both Basidiomycota and Ascomycota, as well as the two morphological forms, hypha and yeast. The advent of new techniques and new potential sources for new antifungal drugs will help to increase the arsenal of medications available to treat fungal infections. **Poster MP109**

*Edwards, Joan[1] and *Whitaker, Dwight L.[2]. [1]Biology Department, Williams College, Williamstown, MA 01267 USA. [2]Department of Physics, Williams College, Williamstown, MA 01267, USA. joan.edwards@williams.edu. **Convergence: explosive spore and seed dispersal in plants**.

Plants and fungi are in separate branches of the eukaryotic phylogenetic tree, yet both often power rapid motions by the sudden release of stored mechanical energy. We use high-speed video (1,000 to 30,000fps) to study ultrarapid movements in plants. To date, we have identified a number of distinct mechanisms for spore and seed dispersal: catapultse.g. the stamens of *Cornus canadensis* and *Urtica dioica*, airgunse.g. the capsules of *Sphagnum* spp., snapbuckling e.g. petals of *Cornus canadensisot*-like mechanism (e.g. seed capsules of *Impatiens* spp.). Using high-speed video analysis and measured structural propertiese.g. cell structure, elastic properties, and mass, we develop quantitative physical models to describe each behavior. The models allow us to pinpoint traits required for rapid motion, which enables us to develop a detailed understanding of how these traits evolved from closely related species. We use this information in conjunction with comparative studies and field observations to determine the adaptive significance of rapid motion in plants. **Symposium: Sunday 1:30-5:00 Fungal Movement: Contemporary Experimental Analysis.**

*Enos, Seth L.[1], Longcore, Joyce E.[1], and Bailey, J. Craig[2]. [1]Department of Biological Sciences, University of Maine, Orono, ME 04469, [2]Department of Biological Sciences, University of North Carolina at Wilmington, Wilmington, NC 28403, USA. longcore@maine.edu. **A new species challenges taxonomy of Leptomitales**.

The Leptomitales (Oomycota; Stramenopila) is a small order consisting of two or three families and a handful of genera. Members of the Leptomitaceae and Apodachlyellaceae are easily recognizable as belonging to this order because they have hyphal thalli that are constricted at intervals and that contain cellulin granules. In these two families four of the five genera are monospecific; consequently genera are narrowly defined. We isolated an oomycete with hyphae constricted at intervals, specialized antheridial cells, undifferentiated zoosporangia and a single oospore per oogonium, a combination of characters not found in any of the current genera in either family. To determine genus placement we isolated strains of *Plerogone* (Leptomitaceae) and *Apodachlyella* (Apodachlyellaceae) and compared the mitochondrial COII gene sequences with those of the new isolate and related species in GenBank. Our preliminary, unrooted cladogram indicated that the new isolate is not closely related to *Plerogone,* with which it shares zoosporangium type, nor *Apodachlylella,* with which it shares specialized antheridial cells. Rather the new species requires a new genus and, in the COII tree, is outside of the core Leptomitales. **Poster MP118**

Ferrer, Astrid and Carol A. Shearer, Dep. of Plant Biology, University of Illinois, Urbana, IL 61801, aferrer@life.uiuc.edu. **Three new species of *Luttrellia* from temperate and tropical freshwater habitats**.

The genus *Luttrellia* Shearer was established to accommodate a single species *L. estuarina.* During our study of freshwater euascomycetes along a latitudinal gradient, we encountered three new species of *Luttrellia* (Sordariomycetes, Halosphaeriales) from Costa Rica, Ecuador, Panama, and the USA. The characteristic features of the new species are globose to subglobose, membranous, black, ostiolate ascomata; wide, septate, hyaline catenophyses; four-eight-spored, unitunicate asci; hyaline, septate, thick-walled ascospores surrounded by a gelatinous sheaths. We amend the genus *Luttrellia* to include species with four and eight-spored asci and ascospores with or without a gelatinous sheath. The absence of ascospore appendages or a gelatinous sheath was used as a morphological characteristic at the genus level for *Luttrellia.* We now note that additional collections of *L. estuarina,* the type of the genus, in fact have a narrow gelatinous sheath around the ascospores. Distribution maps and illustrations are presented. **Poster MP139**

*Fischer, A.[1], Moncalvo J.M.[2], Malcolm, J.[3], Klironomos, J.[1]. [1]Dept. of Integrated Biology, University of Guelph, Guelph, ON NIG 2W1 Canada. [2]Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, Toronto, ON M5S 2C6 Canada. [3]Dept. of Forestry, University of Toronto, Toronto, ON M5S 3B3 Canada. fischera@uoguelph.ca. **Measuring fungal diversity associated with decaying spruce wood**.

Woody debris is a key component maintaining biological diversity in forest ecosystems. Fungi play many essential roles in these systems by releasing nutrients from dead wood, directly providing food and indirectly providing shelter for many organisms. A better knowledge of fungi associated with woody debris is therefore an important step for management and conservation of forest resources. To investigate fungal diversity in decaying wood, samples were collected from 60 spruce logs in 3 logged and 3 unlogged sites in a boreal forest in northern Ontario. Half of these logs were in an early stage of decay (decay class 1) and half in a late stage of decay (decay class 4). Three wood cores were collected from each log and pooled together. Fungal DNA was extracted from these samples, and the 5'-end of nLSU-rRNA gene was PCR amplified, cloned, and sequenced. We investigate the impact of using different values for operational taxonomic units (OTUs), in the range of 85-100% sequence similarity, for comparing fungal diversity between sites and decay class logs. We also evaluate and compare fungal diversity among the different sites and logs by using

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phylogenetic methods that do not require the definition of arbitrary taxonomic groups (OTUs). Results suggest that diversity between decay classes, based on a 99% sequence similarity, is significantly different. **Contr. Talk: Tues AM1 Fungal ecology methods and patterns.**

Fournier, Elisabeth*[1], Gautier, Angélique[1], Walker, Anne Sophie[2], Karchani, Selma[3] and Giraud, Tatiana[4]. [1]INRA Unité PMDV, Route de Saint-Cyr, 78000 Versailles, France. [2] INRA Unité UPMC, Route de Saint-Cyr, 78000 Versailles, France. [3]LMBA, Faculté des Sciences de Tunis, 2092 EL-Manar II, Tunis, Tunisia. [4]CNRS- ESE, Bâtiment 360, Université Paris Sud,, efournie@versailles.inra.fr. **Genetic structure of the species complex *Botrytis cinerea*.**

The species *Botrytis cinerea,* the Ascomycete responsible for grey mold, has long been considered as a unique morphological species attacking more than 200 host plants. Based on the confrontation of 4 independent neutral gene genealogies, we have shown that this morphological species is in fact a species complex composed of at least 2 sibling species, both polyphagous, called *Botrytis cinerea* Groups I and II. In order to determine the phylogenetic position of *B. cinerea* Group I within the *Botrytis* genus, we sequenced two other neutral genes recently used for the revision of the Botrytis phylogeny, on a panel of *B. cinerea* isolates from both groups. These data also allow to discuss the speciation process leading to the divergence between Groups I and II. We further studied the genetic structuration within *B. cinerea* Group II natural populations as a function of host plants, fungicide treatments, symptom on grapevine, or presence of transposable elements in the genome, with 8 microsatellite markers. Results confirmed the very high genetic variability within populations, agreeing with a sexual mode of reproduction, and a low geographic structure. Interestingly, a week genetic structure existed in sympatry between populations coming from the two host plants, indicating that gene flow may be reduced between *B. cinerea* Group II populations living on different host plants. The effects of the other factors will also be discussed. **Symposium: Wed 8:30-1200 Population and Species Divergence in Fungi**

*FREY-KLETT Pascale, DEVEAU Aurelie and GARBAYE Jean, INRA, IFR 110, UMR INRA-UHP Tree-Microorganisms Interactions, 54280 Champenoux, France. klett@nancy.inra.fr. **New aspects of the interactions between bacteria and ectomycorrhizal fungi**.

The tree-soil interface in boreal and temperate forest ecosystems consists in a diverse community of ectomycorrhizal short roots closely associated with bacteria. This multitrophic ectomycorrhizal complex plays a central role in gross production and nutrient cycling. So far, its functioning has been poorly documented. However, recent studies have stressed the importance of physical, metabolic and functional interactions between bacteria and ectomycorrhizal mycelia. Many mycorrhizosphere bacteria live in contact with ectomycorrhizal fungi, forming biofilms on the hyphal surface or even colonizing the intracellular compartment. Surprisingly, whereas bacterial endosymbioses are diverse and widespread in the plant and animal kingdoms, they have very rarely been reported for fungi, except within the Glomeromycota phylum. The occurrence, diversity and ecology of such intracellular bacteria will be illustrated here in the case of the ectomycorrhizal fungus *Laccaria bicolor,* commercially used in France to enhance the growth of Douglas fir plantations. In the case of the so-called Mycorrhiza Helper MHBs, which promote the establishment of the ectomycorrhizal symbiosis, different mechanisms underlying this effect have been proposed. Recent advances in the metabolic and molecular analyses of the interactions between helper bacteria and ectomycorrhizal fungi will be presented. **Symposium: Tues 1:30-5:00 Bacterial Symbionts of Fungi**

Gazis Olivas, Romina Orietta, 2800 S. University Drive, Fort Worth TX 76129, USA. r.gazis@tcu.edu. **Pleasing fungus beetles (Erotylidae) from the Peruvian Amazon**.

Mycophagous beetles (Erotylidae) make up a very important part of the mycophagous fauna in the tropics but their natural history remains practically unknown. Erotilids are largely responsible for recycling nutrients, which are absorbed by fungi during decomposition of organic matter. Fieldwork was conducted at the Biological Station "Los Amigos", located within the Amazon basin in the southeast of Peru, for a period of six months. Forty morphospecies were collected, and thirty-two were classified to the species level. They belonged to two subfamilies, Tritominae and Erotylinae. Genera included *Erotylina, Erotylus, Ellipticus, Mycotretus, Pselaphacus, Megischyrus, Aegithus, Gibbifer, Scaphidomorphus, and Iphiclus.* The Polyporaceae were the most common host for the beetles. Among the different decaying fungi, *Favolus brasiliensis, Pleurotus d'jamor,* and *Ganoderma lucidum* were often found associated with the guest organisms. The data obtained from this project showed the importance of macromycetes to be not only recycling agents but also to be as a food source and refuge for other components of the ecosystem. The latter leads us to the ultimate goal of the project: to identify "hot biodiversity spots" in pristine regions that can serve as targets for conservation management. **Poster MP76**

Gazis Olivas, Romina Orietta, 2800 S. University Drive. Fort Worth TX 76129, USA. r.gazis@tcu.edu. **Macromycetes diversity from the Peruvian Amazon - Preliminary Inventory from the Biological Station "Los Amigos" Madre de Dios, Peru**.

The Amazon is one of the most bio-diverse sites in the planet; however there are some groups of organisms, such as fungi, whose importance has been underestimated. Macromycetes play a myriad of roles within the forest community as recyclers of nutrients derived from the breakdown of plants, allowing the reuse of scarce biotic and abiotic resources. Inventories help to evaluate "hot spots of biodiversity" giving biologists a basis for preserving pristine areas. A total of 6 months of fieldwork was conducted, during which the macromycetes community was monitored and evaluated according to weather changes. Three habitats were sampled: high terrace primary forest, high terrace secondary forest, and flooded primary forest. A total of 250 morphspecies were collected, from which 55 have already been classified to species level. The most common family belonging to the Basidiomycetes was Tricholomataceae with 90 species; and Xylariaceae with 50 species from the Ascomycetes. *Marasmius and Xylaria* were most diverse genera and *Pleutorus, Favolus, Polyporus* and *Ganoderma* were the most common and abundant. More field work is needed to accurately evaluate the complete macromycetes community; however from this project we can be assured that the study area holds a great fungal diversity that should be preserved. **Poster MP149**

*Geiser, D.M. Tran-Dinh, N. Hocking, A. Juba, J.H. O,Donnell, K. Zhang, N. Summerbell, R.C. Dean, D.H. and Samson, R.A. Dept. of Plant Pathology, Penn State Univ., University Park, PA 16802, USA; Food Science Australia CSIRO, North Ryde NSW Australia 2113; NCAUR/ARS/USDA, Peoria, IL 61604, USA; Centraalbureau voor Schimmelcultures, Utrecht, Netherlands 3508; Dept. of Biochemistry, Ohio State University, Columbus, OH, 43210, USA., dgeiser@psu.edu. **Common environmental *Fusarium* clones associated with human infections, food contamination, and industrial machinery**.

In recent years, *Fusarium* isolates have been found as contaminants in processed foods and beverages, machinery associated with food processing, and with industrial fluid used in metal parts manufacture. Recent research has shown that opportunistic infections of humans caused by *Fusarium* are largely associated with two major species complexes, *F. oxysporum* and *F. solani,* and that a wide variety of commonly encountered environmental genotypes are frequent culprits. In this work, we generated multilocus DNA sequences from twenty-seven isolates derived from foods, beverages and industrial machinery, and found that all isolates were highly similar or identical to haplotypes known to be associated with human infections in both the *F. oxysporum* and *F. solani* species complexes. Some of these types are also associated with other indoor environments, with infections of plants, and with infections of other animals. We conclude that isolates contaminating foods and industrial machinery tend to be common environmental types that are adapted to a wide variety of growth conditions. **Contr. Talk: Tues AM1 Fungal ecology methods and patterns.**

*Gillett, Jennifer L. and Kimbrough, James W. PO Box 110620, Gainesville, FL 32611-0620, USA. gillett@ufl.edu. **A modified method to visualize infection sites of spores of *Beauveria bassiana,* an entomopathogen on the citrus root weevil, *Diaprepes abbreviatus*.**

Beauveria bassiana is a widespread entomopathogen which is infectious to a great variety of insects. A commercial preparation of this fungus was used to study its potential as a biocontrol agent of the citrus root weevil, *Diaprepes abbreviatus.* Laboratory reared weevils were placed in clean plastic bags with 0.05 g of powdered inoculum per bag, shaken for thirty seconds, and placed in holding cages. In order to determine the concentration, germination, and position of ingress, inoculated weevils were dipped in a collodion solution at 30 min, 6 hrs, 12 hrs, 18 hrs, and 30 hrs. Collodion peels from various areas of the exoskeleton were removed, stained with lacto-phenol cotton-blue, and observed microscopically. It was found that spores were not evenly distributed on the insect surface and their concentration decreased by 65% 3 hours post contact. At 12 hours post-inoculation, spores began to swell, and at 18 hours close to 25% were germinating except on the elytra. After 30 hours, from 45% to 75% of the

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spores germinated, depending on the body part. Most active spore germination occurred around the eyes (75%), followed by the abdomen (65%), the pronotum (60%), scales (45%), and elytra (7%). **Contr. Talk: Tues AM1 Fungal ecology methods and patterns.**

*Glaeser, Jessie A.[1], Lindner, Daniel L.[1], Banik, Mark T.[1], and Trummer, Lori[2]. [1]USDA Forest Service, Northern Research Station, Forest Products Laboratory, Center for Forest Mycology Research, Madison, WI. [2]USDA Forest Service, Forest Health Protection, Anchorage, AK, USA. jmicales@fs.fed.us. **Wood decay fungi associated with beetle-killed Lutz spruce from the Kenai Peninsula, AK. III. Culture data**.

Beetle-killed trees present a serious fire hazard in Alaska's Kenai Peninsula. A key component of understanding decomposition patterns is the identification of wood decay fungi. The isolation of fungi in culture from wood at different stages of decay is a standard procedure used in many ecological studies, but little is known about the biases and limitations of using cultural methods to sample fungal communities. Here we present cultural data that will later be compared to identifications made by sequencing fungal DNA isolated directly from wood samples and identifications of fruiting bodies. Beetle-killed Lutz spruce trees (*Picea X lutzii)* representing decay classes 2 – 4 (least to most decayed) were selected in the Dry Gulch stand of the Chugach National Forest. Snags (standing, decay class 2) and logs (fallen, decay class 2, 3, and 4) were sampled between 3 - 4 m from their base by aseptically drilling 5 holes on each side at 20 cm intervals (10 holes per log). Six chips per sample were placed in each of 4 different media. A total of 1147 cultures were ultimately isolated from 8 logs and 3 snags; 647 have been identified by DNA sequencing. The fewest unique taxa were isolated from the decay class 2 snags, but they included important decay species. The greatest number of taxa was obtained from decay class 2 logs. **Poster MP85**

*González, María C. Medina, Cristina, and Murrueta, Nayeli. Departamento de Botánica, Instituto de Biología, UNAM, Ciudad de México DF 04510 México, mcgv@ibiologia.unam.mx. **New record of *Circinella* from a hydrocarbon polluted sand beach of Tabasco, Mexico**.

During a survey of fungal biodiversity from Mexican sand beaches, an uncommon fungus of the phylum Zygomycota was isolated from the intertidal area of Playa Paraiso, State of Tabasco, located on the Gulf of Mexico coast. A study of the characteristics of this isolate on culture media demonstrated that it is a mucoraceous species belong to the genus *Circinella,* characterized by producing sporangiophores bearing circinate branches terminated by globose sporangia with persistent sporangial walls. The members of this genus have been isolated from soil, dung, fermented cacao beans, musty nuts, and recently, *Circinella lacrymispora* was described from hydrocarbon polluted soil from Argentina. In this study, several sandy soil samples were placed in sterile Ziploc bags and were processed in the laboratory within 4 h. Plates of corn meal agar (Difco) prepared with artificial seawater (Instant Ocean) were inoculated with 0.5 g of sandy soil and incubated 15 d. The fungus developed nonsepate, sympodially branched sporangiophores with fertile circinate branches bearing one or two sporangia, or a single sporangium and a sterile spine; sterile spines light in color, sporangia globose with a persistent wall and sporangiospores globose and hyaline. The characteristics of the Mexican isolate agree with the description of *C. muscae.* Few studies of zygomycetes have been performed in Mexico, and this is the first record of a mucoraceous fungus isolated from a sand beach environment of Mexico. **Poster MP136**

*González, María, C.[1], Anaya-Lang, Ana Luisa[2], Glenn, Anthony, E.[3], Saucedo-García, Aurora[2], and Hanlin, Richard T[4]. [1]Dept Botánica, Inst Biología, UNAM, México DF, 04510, México. [2]Dept Ecología Funcional, Inst Ecología, UNAM, México DF, 04510, México. [3]Toxicol & Mycot. Res Unit, Russell Research Center, USDA, ARS, Athens, GA 30605, USA. [4]Department of Plant Pathology, University of Georgia, Athens, GA 30602, USA. mcgv@ibiologia.unam.mx. **A new endophytic ascomycete from El Edén Ecological Reserve, Quintana Roo**.

During the past two years a project has been undertaken to study endophytic fungi associated with plants growing in El Eden Ecological Reserve, located in the State of Quintana Roo in the northeastern part of the Yucatan Peninsula of México. Asymptomatic, healthy leaves were collected, surface sterilized, sectioned in 0.5 mm square pieces and then plated on potato dextrose agar. Among the fungi recovered was an interesting isolate from leaves of *Callicarpa* sp. The isolate forms slow-growing, odorless colonies and does not form mitosporic or meiosporic structures. The mycelium is composed of hyaline, septate hyphae that frequently unite laterally to form groups of three or more hyphae. Colonies on V8 agar are flat and smooth, but on MEA they are raised and wrinkled. On both media the colonies are white, but on MEA a dark, brown to reddish-brown pigment forms in the agar. On the basis of sequence analysis of ITS data, this fungus belongs to the Ascomycota but does not align closely with any sequences currently in GenBank, suggesting that it represents an undescribed taxon. **Poster MP137**

*Greif, Matthew D. Gibas, Connie Fe C. and Currah, Randolph S. Dept. of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9 Canada. mgreif@ualberta.ca. **A new species of *Leptographium* from arthropods collected in an aspen-dominated woodland in western Canada**.

During a survey of fungi associated with arthropods collected in a southern boreal mixed-wood forest in Alberta we obtained multiple isolates of a unique species of *Leptographium.* An optimal growth rate at 35°C, the production of curved conidia on short-stipitate conidiophores, a secondary micronematous conidial state, and pear-shaped, bromatium-like stalked cells, together represent a distinct combination of characteristics. The isolates resemble *L. crassivaginatum* in some respects but ITS sequence comparisons indicate that our isolates cannot be assigned to this or any other sequenced species in the genus. The fact that most arthropods carrying the new species were caught in traps baited with dung suggests a coprophilous phase in its life cycle. Initial observations on the bromatium-like structures in feeding experiments with *Sancassania berlesei* shows that these structures may act as a nutritional incentive for visiting arthropods. A role for this new species of *Leptographium* as a pathogen or saprobe in one or more of the woody species in its forest habitat is suspected but unknown. **Contr. Talk: Tuesday PM 1 Ascomycete systematics.**

Greif, Matthew D. Gibas, Connie Fe C. Tsuneda, Akihiko. and *Currah, Randolph S. Dept. of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9 Canada. mgreif@ualberta.ca. ***Catinella olivacea* - an ascostromatic fungus masquerading as an inoperculate discomycete**.

In apothecioid loculoascomycetes (e.g. Patellariales) the ascostroma opens at maturity to expose clavate asci embedded in a hamathecium made up of apically free paraphysoids: these extend above the hymenial layer to form a dark-coloured epithecium. Generally, on close inspection these pseudoapothecial taxa can be readily distinguished from inoperculate discomycetes (Helotiales). Recently, however, we made multiple collections of the ascomata of *Catinella olivacea* Dermateaceae, Helotiales *fide* (Spooner & Legon) that was fruiting in cavities inside decayed, fallen logs. Pure cultures allowed us to follow development from ascospore germination to mature ascomata. Meristematic growth was evident in germlings that gave rise to dark olivaceous hyphae and in the formation of uniloculate ascostroma. Interspersed among sterile filaments were unitunicate asci with an obvious *nasse apicale*; ascospores were released through a broad bivalvate apical slit. A thick, olivaceous, acellular, gelatinous pseudoepithecial layer trapped many ascospores in a mass that persisted on the surface of the mature discoid ascoma. Together with ITS sequence comparisons, our data suggest that *C. olivacea* belongs in the Dothideomycetes. We speculate that the gelatinous pseudoepithecium and its entrapped ascospores is an adaptation for arthropod dispersal from the cavities in which the fungus fruits. **Poster MP127**

*Grunwald, Niklaus J.[1], Prospero, Simone[2], Hansen, Everett[3], Tyler, Brett[4], and Lamour, Kurt[5]. [1]Horticultural Crops Research Laboratory, USDA ARS, Corvallis, OR, USA. grunwaln@onid.orst.edu. **Population divergence in *Phytophthora ramorum***.

Phytophthora ramorum, causal agent of Sudden Oak Death on oaks and Ramorum blight on ornamentals such as rhododendron, is an emerging pathogen with significant impact on both natural oak forest ecosystems and the nursery industry. The pathogen was simultaneously discovered in Germany and California. Recent studies based on AFLP established that the US population was clonal. We screened the genome of *P. ramorum* for simple sequence repeat and single nucleotide polymorphisms loci. While trinucloeotide loci only distinguished between the EU and US clones, tetranucleotide repeats were found to be highly informative for locally evolving populations. We also developed an Affymetrix microarray with 880 SNPs. These assays were applied to the US and EU populations as well as recently discovered novel clones. SNP and SSR discovery is ongoing. All these markers indicate that both the European and North American populations are reproductively isolated and have gone through a bottleneck. There currently is no evidence for sexual recombination. Novel geno-

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types detected in the US likely originated through migration. **Symposium: Wed 8:30-1200 Population and Species Divergence in Fungi**

*Gueidan, C. and Lutzoni, F. Dept. of Biology, Duke University, Durham NC 27708, USA. cg19@duke.edu. **Molecular phylogeny of the Verrucariales (Ascomycota) and the evolution of nutritional modes in the Chaetothyriomycetidae**.

Verrucariales is an order of mostly rock-dwelling lichenized ascomycetes, found in varied habitats ranging from marine and fresh water to dry environments. Phylogenetic relationships among members of Verrucariales are mostly unknown and the morphology-based classification has never been tested with molecular data. The first goal of this project is to reconstruct a multilocus phylogeny for this order. Preliminary results suggest that the traditionally used morphological characters do not define monophyletic groups. Recent molecular phylogenetic studies showed the Verrucariales as sister to the Chaetothyriales. These two orders share a most common ancestor with members of the order Pyrenulales. Together, these three orders are recognized as forming the subclass Chaetothyriomycetidae. The order Chaetothyriales is strictly non-lichenized, whereas the orders Verrucariales and Pyrenulales contain both lichenized and non-lichenized taxa. The order Verrucariales includes non-lichenized taxa living on lichens as parasites, commensals or saprobes (lichenicolous fungi). The diversity of lifestyles within these three orders provides evidence that host-switches and changes in nutritional habits occurred frequently. The second goal of this project is to reconstruct ancestral states to test if lichenicolous lichens and fungi were transitional stages between mutualism and parasitism. **Contr. Talk: Sunday pm1 Ascomycete systematics.**

*Hallen, Heather E.[1], Guenther, John G.[1], Trail, Frances[1,2]. Departments of [1]Plant Biology and [2]Plant Pathology, Michigan State University, East Lansing, MI, 48824, USA. hallenhe@msu.edu. **Two novel calcium channel mutants in *Gibberella zeae* affect ascospore development and discharge**.

Gibberella zeae anamorph *Fusarium graminearum* infects wheat, corn and numerous other crop plants to inflict substantial economic losses worldwide. The primary inoculum is the ascospore, forcibly discharged from perithecia developed on crop debris. Consequently, ascospore discharge is of considerable interest in understanding the disease cycle of this fungus. We have been investigating the role of ion channels in ascospore discharge by performing targeted gene knockouts. Recently, we have generated two mutants which affect ascospore development and discharge. The *mid1* stretch-activated calcium channel mutant produces apparently normal perithecia and asci, but lacks ascospores. Meiosis followed by at least two mitotic nuclear divisions takes place within the ascus, but spores are not fully developed. In the *cch1* voltage gated calcium channel mutant, phenotypically normal ascospores are formed, after a 24-48 hour delaycompared to wild type), but these are never discharged. Vegetative growth is abnormal, with a zonate, fluffy, slow-growing colony. *MID1* and *CCH1* have been examined in detail in yeasts, where they are believed to form distinct subunits of a single protein. Consequently, the differing phenotypes in *G. zeae* for the two mutants are of interest. This is the first time either gene has been characterized in a filamentous fungus. **Poster MP94**

*Hallen, Heather E.[1], Guenther, John C.[1], Huebner, Marianne[2], Trail, Frances[1,3]. Departments of [1]Plant Biology, [2]Statistics and Probability, and [3]Plant Pathology, Michigan State University, East Lansing, MI 48824, USA. hallenhe@msu.edu. **Expression of ion transporter genes in *Gibberella zeae* as seen using an Affymetrix GeneChip**.

Gibberella zeae anamorph *(Fusarium graminearum)* is the causal agent of head scab of wheat and other cereal crops. An Affymetrix GeneChip has recently become available for genome-wide expression studies and we have used the chip to examine differential gene expression during sexual development *in vitro.* The presence of ions in ascus fluid and role of ion fluxes in generating the necessary turgor pressure for ascospore discharge has been documented. Consequently, we have examined the expression of all predicted ion transporters - 166 genes - in *G. zeae* during the 144 hours from induction of sexual development to mature perithecia with multiseptate ascospores. Many ion transporters are down-regulated during sexual development as opposed to during vegetative growth; these can be provisionally excluded from our search for genes involved in spore discharge. Several transporters are significantly up-regulated in sexual development; these make promising targets for gene knock-outs and functional characterization. GeneChip data, however, does not tell the whole story, as some genes, such as the *MID1* calcium channel, show no differential regulation during development, but play a vital role in spore discharge, as demonstrated by examination of a deletion mutant. **Contr. Talk: Monday PM Fungal molecular and cell biology**

Hemmes, Don E. and Desjardin, Dennis, E. Biology Department, University of Hawaii at Hilo, 200 W. Kawili St. Hilo, HI 96720 and Department of Biology, San Francisco State University,1600 Holloway Ave. San Francisco, CA 94132, USA. hemmes@hawaii.edu. **Two unidentified *Geastrum* species from Hawaii**.

Among the fifteen or more species of earthstars found in Hawaii, two of the larger species have yet to be identified. One species is locally abundant on Hawai,i Island and is readily recognized by its litchi-like exoperidium that is covered with evenly-spaced tufts of fibrils. The species appears in large clusters of 20-30 fruiting bodies in duff under coastal *Casuarina* and in coconut groves where they grow on fallen fronds and coconuts. Endoperidia average 25 mm in diameter and have an ostiole with a finely-fimbriate peristome that is surrounded by a coating of dark-colored spores. The exoperidium splits into 7-9 rays and leaves the outer exoperidium layers as a separate husk attached to the rhizomorphs. The second undescribed species also appears under coastal *Casuarina* and has exoperidia with rows of raised tufts of hairs that form a distinctive reticulated pattern on the surface of the exoperidium. The unexpanded fruiting bodies resemble those of *Geastrum morganii* in shape and size, 25 mm in diameter, with pointed apices, but the surface of the exoperidium of *G. morganii* is reddish without the reticulation pattern, whereas this undescribed species is yellowish-brown. Also, the peristome of *G. morganii* consists of a few large folds, whereas the peristome of this second undescribed species is finely plicate and seated in a distinct depression in the endoperidium. **Poster MP156**

*Henk, D. A. Pastor-Corrales, M. Aime, M.C. USDA-ARS Beltsville, MD, USA. dan@nt.ars-grin.gov. **Selection acting on infection specific genes in the common bean rust, *Uromyces appendiculatus***.

The common bean rust, *Uromyces appendiculatus,* is a destructive pathogen of *Phaseolus vulgaris.* The pathogen displays extreme host specificity in response to many unique resistance genes present in different bean cultivars. Little is known about the geographic distribution of differential responses or recombining populations in *U. appendiculatus.* In this study we use a phylogenetic approach to infer population history and detect selection on genes putatively involved in virulence. Three genes specifically expressed in infection structures have previously been characterized in a strain of *U. appendiculatus.* We compared the evolutionary history of these infection specific genes to genes not suspected to be involved in virulence using DNA sequence data from over thirty rust isolates that have also been characterized on differential plant cultivars. The genes differed from one another with respect to distribution and abundance of polymorphism but displayed a pattern correlated with virulence and host geographic origin that segregates the rust isolates into two major groups, one that infects primarily only beans of Andean origin and one that infects both Andean and Mesoamerican bean cultivars. One infection specific gene displayed evidence of positive selection with a ratio of nonsynonymous to synonymous substitutions above one. These data offer a first hint at using population genetic methods to identify genes that might act either as targets for resistance genes or as virulence factors in rust fungi, and suggest that *U. appendiculatus* isolates might be screened for virulence factors using simple molecular tests. **Contr. Talk: Tues AM2 Fungal Pathogens: population structure and distributions**

*Herrera, Jose[1], Porras-Alfaro, Andrea[2], Natvig, Donald O.[2], Sinsabaugh, Robert L.[2]. [1]Division of Science, Truman State University, Kirksville MO 63501, USA. [2]Department of Biology, The University of New Mexico, Albuquerque NM 87131, USA. jherrera@truman.edu. **Variation in the endophytic fungal community among different anatomical structures of *Bouteloua gracilis***.

Although many studies have described fungal endophytic communities within one anatomical structure of a plant, few have comprehensively studied if and how these fungal communities change within a single plant. This study examined the distribution of fungal endophytes within the roots, crown, leaves and seeds of several *B. gracilis* blue grama) plants collected from the Sevilleta National Wildlife Refuge in New Mexico, USA. Fungal diversity was assessed using culture-based techniques and molecular methods using PCR, cloning and sequencing of the internal transcribed spacer (ITS) region of the nuclear ribosomal DNA. Rates of fungal colonization on roots and seeds also were estimated using microscopy and a digital imaging system. Our results suggest that fungal communities within any one plant are very different in composition and diversity (for all structures studied). Most fungal species and sequences examined were endophytic or parasitic Ascomycetes. Microscopic work also suggests that most of the fungal biomass is made up of dark septate endophytes species and

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these are more diverse in the crown and roots compared to the leaves and seeds. Based on this and previous work on semi-arid grasslands, we suggest that many additional grass species may harbor fungal endophytes and establish complex interactions with several species of dark septate fungi. **Contr. Talk: Monday PM- Fungal Ecology - Endophytes and Saprobes**

*Hersh, Michelle H.[1], Vilgalys, Rytas[2], and Clark, James S[3]. [1]University Program in Ecology, Duke University, Durham, NC 27708, USA; [2] Department of Biology, Duke University, Durham, NC 27708, USA; [3]Nicholas School of the Environment and Earth Sciences and Department of Biology, Duke University, Durham, NC 27708, USA. mhh4@duke.edu. **The diversity of root-inhabiting fungi and oomycetes in a Southeastern mixed hardwood forest**.

Fungi and oomycetes infecting tree seedlings, especially plant pathogens, can strongly influence seedling recruitment. To address the role of pathogens in seedling dynamics, we first need to describe the diversity of fungi and oomycetes present in natural stands, particularly species with known pathogenic activity. We performed two studies to characterize fungi and oomycetes living in seedling roots in two North Carolina mixed hardwood stands. We collected seedlings of *Acer rubrum* red maple) and *Quercus alba* white oak), cultured root fragments in selective media, and identified cultures using ITS sequencing. We were able to culture many types of fungi, including *Colletotrichum, Neonectria, Pestalotiopsis,* and *Phomopsis,* but no oomycetes. Oak and maple seedlings shared few fungi, but several fungal taxa were found at both sites. In addition, we grew *A. rubrum* and *Cucumis sativus* cucumber) under controlled conditions in field-collected soils from the same sites. Oomycetes and fungi were cultured from dead or dying seedlings, and from a subsample of surviving seedlings. Both fungi and oomycetes were recovered from roots, including *Pythium, Neonectria,* and *Nectria.* These sampling efforts did not capture the total diversity of culturable fungi in this system. Based on this evidence, we suspect that seedlings are susceptible to infection from a diverse group of pathogens. **Poster MP119**

Hewitt, David A, Farlow Herbarium, Harvard University, Cambridge, MA 02138, USA. dhewitt@oeb.harvard.edu. **Effects of nutrition on ascomycete growth and development**.

Fungi grow in nutritionally heterogeneous environments, and they deal with changes in nutrient levels by adjusting growth and differentiation. Growth and differentation parameters affected by nutrient levels include: timing and amount of sporulation (meiotic and mitotic), biomass accumulation, radial colony expansion, developmental timing and amount of resistant structures (e.g. sclerotia). I am looking at how different levels of phosphate and sugar affect these parameters in ascomycetes, across a broad phylogenetic range and representing a variety of life history strategies. I am interested in how this impacts soil nutrient cycling and viability of plant pathogens. **Poster MP107**

*Hodge, Kathie T.[1], Huang, Bo[1], Humber, Richard A.[2], Klich, Maren A.[1], Faria, Marcos[3], Tigano, Myrian S.[4], Shanley, Ryan P.[3]. [1]Dept. of Plant Pathology, Cornell University, Ithaca NY 14853, USA. [2]US Plant, Soil and Nutrition Lab, USDA-ARS, Tower Rd. Ithaca NY 14853, USA. [3]Dept. of Entomology, Cornell University, Ithaca NY 14853, USA. [4]Embrapa, Parque Estacao Biologica, PqEB, 70770-901 - Brasília, DF, Brasil. kh11@cornell.edu. **Phylogenetic affiliations of insect pathogenic *Sporothrix* species**.

The mold genus *Sporothrix* includes anamorphs of the Ophiostomatales. Some insect pathogenic isolates have also been included in *Sporothrix.* They include an important biocontrol used in Brazil to control lacebugs in rubber plantations. We used molecular phylogenetic analysis to assess the relationships of a collection of *Sporothrix* -like fungi from Brazil, Hawaii, the Solomon Islands, Ghana, Russia, and the US. The results reveal that insect pathogenic isolates are not ophiostomatalean, but fall into several hypocrealean and clavicipitalean clades. We will present molecular and morphological evidence supporting phylogenetically appropriate classification of insect pathogenic isolates that have previously been referred to *Sporothrix.* **Poster MP143**

*Hoffman, Michele and Arnold, A. Elizabeth. Division of Plant Pathology & Microbiology, Department of Plant Sciences University of Arizona, Tucson, AZ 85721, USA. mhoffman@email.arizona.edu. **Fungal endophytes in native vs non-native Cupressaceae: community structure in mesic and xeric sites**.

What is the relative importance of geographic locality, host species, and biogeographic origin of hosts in shaping fungal endophyte communities? To address this question, we isolated foliar endophytes from three species of Cupressaceae: two native species within their natural ranges *Juniperus virginiana*, North Carolina; *Cupressus arizonica*, Arizona and one introduced species planted in each site *Platycladus orientalis*. From 960 tissue segments, 229 isolates were recovered, representing at least 35 species. Isolation frequency was threefold higher in the non-native than in either native species. ITS rDNA data showed that diversity was higher in native hosts than in the non-native. The non-native harbored more cosmopolitan taxa than did either native species. Diversity and host generalism were also higher in the mesic site NC vs. the xeric site AZ. Parsimony and Bayesian analyses based on LSU rDNA data showed that these cupressaceous trees can establish endophytic relationships with members of at least four classes of Pezizomycotina. Among 11 well-supported, terminal clades containing endophytes, all contained isolates from a single site; 10 contained isolates from only one host species. Our data illustrate the interactions of locality, host identity, and native/non-native status in shaping the abundance, diversity, and taxon composition of endophyte communities. **Poster MP80**

Honan, Amy H.* and Desjardin, Dennis E. 1600 Holloway, San Francisco, CA 94132, USA. ahonan@sfsu.edu. **A worldwide monograph of *Tetrapyrgos* based on morphology and ITS sequence data**.

Historically, the genus *Tetrapyrgos* comprised 16 species of saprotrophic and possibly plant pathogenic basidiomycetes. This genus is characterized by tetrahedral or jack-shaped spores, diverticulate cystidia, pileipellis and stipitipellis hyphae, and, if stipitate, a heterochroic stipe arising from a black basal disc. Of the 16 species currently recognized in *Tetrapyrgos,* six species lack the defining characteristics of *Tetrapyrgos* and are better accepted in the genus *Campanella.* Of the remaining epithets, most are represented by a single collection consisting of minimal material, and two epithets have no available type specimens. Analyses of the morphologies of the available type specimens and recent collections from Southeast Asia, South America, the Caribbean and the US reveal a character-poor genus with limited morphological differentiation. Molecular analyses of the ITS region (ITS1-5.8S-ITS2) of recently collected taxa, selected exsiccati, and sister species support the monophyly of *Tetrapyrgos,* and delimit three molecularly distinct yet morphologically indistinguishable taxa. Morphological data were combined with ITS sequence datasets to aid in delimiting species. Based on the morphological and molecular analyses, *Tetrapyrgos* comprises 12 taxa. This monograph documents the distribution, ecology, morphology and phylogeny of the known worldwide members of *Tetrapyrgos.* **Poster MP159**

*Hong, Seuk H., Kim, Changmu, and Jung, Hack S. Department of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea. minervas@snu.ac.kr. **Phylogenetic relationships of *Perenniporia, Loweporus* and *Abundisporus* based on ITS, partial 28S rDNA and IGS1 sequences**.

The genus *Perenniporia* typified by *Polyporus medulla-panis* has di- to trimitic hyphal structures with clamps on generative hyphae. Basidiospores are smooth and thick-walled, globose to ellipsoid, hyaline to yellowish, and often truncate. In addition, both vegetative hyphae and spores are dextrinoid to a varying degree, and the species of the genus cause a white rot. The genus circumscription of *Perenniporia* has been expanded and resulted in a large heterogeneous assemblage that overlaps with other genera, *Loweporus* and *Abundisporus,* making the classification difficult at present. Phylogenetic relationships of *Perenniporia, Loweporus* and *Abundisporus* were studied to compare phylogenetic trees inferred from the sequences of ITS1-5.8S-ITS2, partial 28S rDNA and IGS1. DNAs were extracted from 20 strains of *Perenniporia,* 20 strains of *Loweporus,* 11 strains of *Abundisporus* and 1 strain of *Ganoderma* and amplified through PCR. PCR products were sequenced and phylogenetically analyzed using *Ganoderma meredithiae* as an outgroup. Taxa of *Perenniporia* belonged to the *Loweporus* group (positive dextrinoid reaction) and the *Abundisporus* group (negative dextrinoid reaction) of the Polyporoid clade and proved to be polyphyletic within these groups. However, the species delimitation between *Perenniporia* and *Loweporus* was uncertain in the ITS phylogeny. On the other hand, *Abundisporus* differed from other genera by colored basidiocarps, non-dextrinoid spores and molecular data. **Poster MP155**

Hou, You-Hong and Shao-Xi Wu. Department of Medical Mycology and Dermatovenerealogy, Guangzhou TCM Hospital, 16 Zhuji Road, Guangzhou 510130, GD, P.R. China. houyh_1959@yahoo.com.cn. **Study of hydrophobicity and adhesion of the yeast *Cryptococcus neoformans* to Vero cell line in vitro**.

Objective: To observe the influence of some medicines and chemical agents on the cell surface hydrophobicity (CSH), the capsule and adherence of

Continued on following page

Cryptococcus neoformans (*C.neoformans*) to cultured Vero cells in vitro in order to explore the relationship among CSH, the outer-wall capsule and adhesion of the yeast to host cells. Methods: After a series of titers of twenty kinds of medicines and chemical components pre-treated the trial dishes of the yeast these level varieties of CSH, capsule and adhesion of the yeast are tested with the following procedures, micro bail adhering to Hexadecane (MATH), electronic microscopy scanning, radial count from isotopic labeling of 3H-Leucine to the yeast binding to host cells grown into a monolayer confluency in titer dishes. Results: The antifungals, Amphotericin B (AmB) and Fluconazole (FCZ), induced a decline levels of adhesion and capsule, while various levels of CSH appeared in both trials yeast wall ultrastructures, and especially, the medicine, Ampicillin (AMP) with little change to CSH and a typically wall ultrastructural acapsule as compared with the reversibly acapsule led by FCZ. These chemicals, PHA, ConA, Fucose (FC), Mercaptothanol (ME) and Trysin (TP), decreased CSH and adhesion without acapsule effect, but only Lectin (LC) increased both the yeast adhesion and CSH simultaneously. Conclusion: The yeast wall capsule is not related to the level of CSH and to adhesion to host cells. Obviously, there are no significant relationships among the yeast's CSH, wall ultrastructure, adhesion to organism cells, as compared with other micro-fungus. Key words: *C.neoformans*, CSH, micro-ecology. **Poster MP92**

*Houseknecht, Janice L. Weir, Alex. SUNY-ESF, 1 Forestry Dr., Syracuse, NY 13210, USA. jlhouseknecht@hotmail.com. **Diversity of saprophytic agarics in partially cut, maturing, and old growth stands in the Adirondack Park in New York**.

Saprophytic fungi are the primary decomposers of both lignin and cellulose, they function to recycle dead plant material into useable inorganic molecules, thus playing a pivotal role in the nutrient cycle of forested ecosystems. Despite widespread recognition of this role, communities of these fungi are rarely considered in forest management practices. This study examines the effects of different management practices on the diversity of saprophytic fungi in the Adirondack Mountains of New York. Management categories examined were: partially cut, maturing, and old growth. Based on previous ecological investigations, twelve study plots (50m x 20m), four per management category, were established. Each plot was visited three times between the months of August and October in two consecutive years (2002 and 2003) giving a total six visits per plot. Over the two years, a total of 8199 sporocarps, comprising 189 species within 44 genera were collected from a sample area of 12000 m^2. The most species rich genera were *Mycena* (38), *Leptonia* (20), and *Psathyrella* (19), which together accounted for 41% of the total species. In terms of individual sporocarps genera most frequently collected were *Marasmius* (234), *Mycena* (207), and *Collybia* (159), which together accounted for 47% of the total collections. Species compositions were significantly different among management categories with 64 species unique to old growth sites, 23 species unique to maturing sites, and 36 species unique to partially cut sites. Differences in species composition were not correlated with forest structure (tree basal area, litter depth, stump basal area, log volume, and log volume within decay stage), while correlations with abiotic variables (elevation, slope, aspect, and soil pH) are currently being investigated. **Contr. Talk: Monday PM- Fungal Ecology - Endophytes and Saprobes**

*Hughes, Karen W.[1], Mata, Juan L.[2], Cifuentes, Joaquin[3], Aime, M. Catherine[4], Henkel, Terry[5], Kovalenko, Alexander[6], Psurtseva, Nadezhda[6] and Petersen, Ronald H.[1]. [1]Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA; [2]Department of Biology, University of South Alabama, Mobile, AL 36688, USA; [3]Facultad de Ciencias, UNAM, Mexico City, Mexico; [4]USDA ARS Systematic Botany and Mycology Lab, Beltsville, MD 20705, USA; [5]Dept of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA; [6]Komarov Botanical Institute, St. Petersburg, Russia. khughes@utk.edu. **The Hunt for Megacollybia: One name fits all?**

The organism represented by the name *Megacollybia platyphylla* was well-known and recognized even in the later 18th century by Persoon. Once established in *Agaricus,* it was later transferred to *Collybia* and eventually found itself in *Oudemansiell* and *Tricholomopsis* before the monotypic genus, *Megacollybia,* was proposed to accommodate this species. Early on, the name was carried to North America, although the organism here bore only superficial resemblance to its European prototype. Our project used macro- and micromorphology combined with an ITS-based phylogenetic reconstruction to investigate collections from eastern and western North America, Scandinavia, western and eastern Europe, western, central and far eastern Russia, Central and northern South America. Using the western European organism as prototype, the eastern North American organism requires a new species epithet. On one hand, specimens from across the Bering Straits are closely related, but temperate east Asia also shelters an organism closely related to the northern and western European organism. North South America produces yet another species. Thus, reflected in the ITS-based phylogeny, *Megacollybia* must include at least five species. **Contr. Talk: Tues PM 2 Fungal systematics.**

*Hughes, Monica B. and Weir, Alex. Faculty of Environmental and Forest Biology, 1 Forestry Drive, State University of New York College of Environmental Science and Forestry, Syracuse, NY 13210, USA. mohughes@syr.edu. **A synopsis of the diversity, host utilization and biogeography of New Zealand Laboulbeniales**.

A total of 200 species of Laboulbeniales are known from New Zealand, a roughly ten-fold increase since the initiation of this project. Nevertheless, over 50 percent of the species have only been encountered once or twice, and separate estimates of diversity based upon species accumulation and host specificity predict at least 300-400 total species in this region. Common genera are more or less equally represented in comparison to well-studied regions of the northern hemisphere. At least five new genera have been discovered, and the perithecial development of one of them indicates a possible link between the families Ceratomycetaceae and the Laboulbeniaceae. At the species level, a few taxa are adventive or cosmopolitan. We suspect that other non-endemics may have a broader Gondwanan and/or Asiatic distribution, but the lack of well-inventoried sites elsewhere prevents sharp conclusions from being made. At least 60 percent of the species are presumed endemic. Of particular note is a diverse *Diphymyces* component, with approximately ten new species on the subfamily Cholevinae (Leiodidae, Coleoptera), which has radiated extensively in New Zealand. Overall host utilization patterns are similar to those in north temperate and tropical regions, the majority of hosts belonging to the beetle superfamilies Staphylinoidea and Caraboidea. However, Staphylinoidea appear to be more highly utilized in New Zealand than in north temperate or tropical regions. An overview of the taxonomy, host utilization patterns, biogeography, and evolution of the group will be presented as a capstone to our eight year study. Suggestions for future investigators cataloguing New Zealand Laboulbeniales will also be presented. **Contr. Talk: Tues PM 2 Fungal systematics.**

Hustad, Vincent P. and Methven, Andrew S. Department of Biological Sciences, Eastern Illinois University, Charleston, IL. 61920-3099, USA. asmethven@eiu.edu. **Coprophilous species of Coprinus in east-central Illinois**.

Although the genus *Coprinus* (Basidiomycota; Agaricales; Psathyrellaceae) is widely distributed world-wide, relatively little is known about the distribution of coprophilous species of *Coprinus* in North America. The purpose of this study was to inventory species of *Coprinus* that occur on domesticated horse *Equus caballus* dung in east-central Illinois. Samples of dung were collected beginning Spring 2005 and incubated in moist chambers to induce the production of *Coprinus basidiomata.* After maturation, basidiomata were removed from the dung, dehydrated and identified using macro- and micromorphological characteristics. A list of coprophilous species of *Coprinus* will be compiled and keys to the coprophilous species of *Coprinus* in east-central Illinois will be produced. Species descriptions and identities of *Coprinus* obtained in this study will be compared with known species from other regions in North America as well as Europe. Because coprophilous fungi are widely distributed but understudied, this research will provide important information on species richness and distribution as well as culture conditions for producing *Coprinus* basidiomata in a laboratory environment. **Poster MP154**

*Hustad, Vincent P.[1], Miller, Andrew N.[2], and Methven, Andrew S.[1]. [1]Eastern Illinois University and [2]Illinois Natural History Survey, USA. asmethven@eiu.edu. **Coprophilous fungi of the Great Smoky Mountains National Park**.

Coprophilous fungi are an important component of terrestrial ecosystems and are responsible for recycling many of the nutrients in animal feces. The purpose of this study was to inventory the coprophilous fungi that occur on elk *Cervus americanus* dung as part of the All Taxa Biodiversity Inventory currently taking place in the Great Smoky Mountains National Park GSMNP. Samples of dung were collected from the GSMNP beginning in Spring 2005 and incubated in moist chambers to induce the production of ascomata and basidiomata. Ascomata and basidiomata were removed, identified, preserved and compared with a list of known species from the GSMNP. Numerous new species records from the GSMNP have been discovered. A list of coprophilous

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species will be compiled and keys to the coprophilous fungi on elk dung will be produced. Because coprophilous fungi are widely distributed but little-studied, this research will provide important information on species richness and distribution as well as culture conditions for producing ascomata and basidiomata in a laboratory environment. **Poster MP158**

*Hyder, Naveen, Stanghellini, Michael E. and Coffey, Michael D. Dept. of Plant Pathology, University of California, Riverside CA 92521, USA; Naveenhyder@msn.com. **Role of fungus gnat larvae in the acquisition and transmission of oomycete propagules**.

Adult and larval stages of common greenhouse pests such as shore flies, fungus gnats and moth flies have been implicated as vectors of some root-infecting pathogens, especially those with above-ground life stages. Our objective was to determine if fungus gnats are involved in the acquisition and transmission of plant pathogenic oomycete propagules similar to that which has been documented for *Fusarium avenaceum* and *Pythium aphanidermatum.* Fungus gnat larvae were allowed to feed on oomycete propugules for 24 hours after which their intestinal tracts were microscopically examined for the presence of propugules. Frass excreted by the larvae on potato dextrose agar were then observed for the presence of those propagules and their subsequent ability to germinate. Chlamydospores of *Phytophthora ramorum,* hyphal swellings of *Pythium splendens, P. sylvaticum* and, *P. ultimum* were observed in the intestinal tracts as well as excreta of the larvae. Following excretion, propagules germinated within 24 hours. Additionally, chlamydospores of *P.ramorum* excreted by internally infested larvae were shown to infect and colonize detached rhododendron leaves. The role of fungus gnats and shore flies as vectors of the abovementioned oomycete species are being studied. **Poster MP91**

Inderbitzin, Patrik[1], Shoemaker, Robert A.[2], *O'Neill, Nichole R.[3], Turgeon, B. Gillian[4], and Berbee, Mary L.[1]. [1]Department of Botany, University of British Columbia, #3529-6270 University Boulevard, Vancouver, British Columbia, Canada, V6T 1Z4; [2]Agriculture and Agri-Food Canada, Biodiversity, 960 Carling Avenue, Ottawa, Ontario, Canada, K1A 06C; [3]USDA, ARS, Molecular Plant Pathology Laboratory, Belstville, MD 20705, USA; [4]Department of Plant Pathology, Cornell University, Ithaca NY 14853, USA. oneilln@ba.ars.usda.gov. **Systematics and mating systems of fungal pathogens of opium poppy: *Crivellia papaveracea* with a *Brachycladium penicillatum* asexual state and a homothallic species *B. papaveris*.**

The systematics of the fungal opium poppy pathogens formerly known as *Pleospora papaveracea,* along with allied asexual states formerly placed in *Dendryphion,* is revised based on analysis of phylogenetic relationships, comparative morphology, and analysis of mating systems. Using morphology, 18S and ITS rDNA, we established that these species belong to the *Alternaria* group rather than to *Pleospora.* We erect the new genus *Crivellia,* with *Crivellia papaveracea* as type. ITS rDNA analyses suggested with moderate support *A. brassicicola*, *A. japonica* and *Ulocladium alternariae* as *Crivellia*,s closest relatives. Combined ITS, partial GPD and EF-1 alpha analyses confirmed earlier studies showing that asexual isolates in the *Crivellia* lineage of poppy pathogens represent two closely-related species. Because *Dendryphion* was determined to be polyphyletic, the former genus *Brachycladium* was resurrected for *B. penicillatum* and for *B. papaveris*, the *Crivellia* asexual states that had been in *Dendryphion*. The mycelia from single conidium or single ascospore isolates from *C. papervaceae* either have a MAT1-1 or MAT1-2 gene and are thus heterothallic. In contrast, each single-conidium isolate of *B. papaveris* has an incomplete MAT1-2 gene fused to a MAT1-1 region and is inferred to be homothallic. We speculate that ancestral MAT fusion might have led to speciation in *Crivellia*. **Poster MP135**

*Izzo, Antonio D.[1,3], Nguyen, Diem T.[2,3], Kennedy, Peter G.[3], Stephens, Scott L.[4], and Bruns, Thomas D.[3]. [1]USDA-ARS Tree Fruit Laboratory, Wenatchee, WA, 98802; [2]Sackler School of Medicine, Tufts University, Boston, MA; [3]Dept. of Plant and Microbial Biology, University of California, Berkeley, CA, 94720; [4]Dept. of Environmental Science, Policy and Management, University of California, Berkeley, CA, 94702, USA. Izzo@tfrl.ars.usda.gov. **Belowground response of fungal and plant ectomycorrhizal root communities to fire and fire surrogate treatments**.

While a growing number of studies have investigated the ectomycorrhizal response to forest management treatments, few consider how changes in the composition of the host plant species root communities may be mediating observed responses. We examined the impact of fire and fire surrogate treatments on both the belowground host and fungal composition of the ectomycorrhizal community in a mixed-host forest. A total of 72 plots (4 treatments x 18 replicates) were analyzed in Sierra Nevada mixed-conifer forest before and after treatments. The fungal root community was characterized by terminal restriction fragment length polymorphism (T-RFLP) analysis of the ITS1 region and subsequent DNA sequence analysis of individual root tips. The host composition of the same root tips was characterized by PCR-RFLP analysis of cpDNA tRNA spacer regions. Fire and fire surrogate treatments altered host root community composition in the same way with oak roots increasing and white fir roots decreasing in each. The fungal community did not change relative to the treatments however was impacted by large host shifts that occurred regardless of host type or treatment. These results highlight the importance of considering the composition and spatiotemporal dynamics of the host root community when studying the belowground ectomycorrhizal fungal community. **Poster MP66**

James, T. Y. *Vilgalys, R. and the Assembling the Fungal Tree of Life (AFTOL) Working Group, Biology Dept. Duke University, Durham, NC 27707, USA. fungi@duke.edu. **Evolution of basal lineages in Fungi: deconstructing Chytridiomycota and Zygomycota**.

Most theories on the origin of the Fungi agree that the earliest lineages arose from a simple aquatic ancestor with a single flagellated zoospore, similar to modern unicellular chytrids. Uncertainty exists, however, about the timing and frequency of key events associated with diversification of major fungal phyla, including times of divergence, numbers of losses of flagellae, and even how many fundamental units (phyla) might exist. Phylogenetic analyses using data from six gene regions (and nearly 200 species) reveals a paraphyletic basal grade that includes several lineages including Microsporidia, chytrids (4 lineages), zygomycetes (2 lineages), and Dikarya (including Glomeromycota, Ascomycota, and Basidiomycota). During the course of early fungal evolution, flagellae were lost at least three, and possibly as many as eight times, and loss of the motile spore appears to be coincident with novel innovations of aerial dispersal and Microsporidian polar tube eversion. In spite of combined evidence from six gene regions, support for most basal nodes is weak or lacking, suggesting a radiation of basal lineages during the early evolution of Fungi. Our results also suggest that the Microsporidia may belong to the basalmost fungal lineage, which was derived from an endoparasitic chytridiomycete ancestor similar to *Rozella allomycis.* **Symposium: Monday 1:00-4:30 Diversity of Zoosporic Fungi.**

*Jewell, Kelsea[1], Clark, Erin [1], Cheshier, Ron[1], and Cage, Gary[2]. [1]BioEmergency Response and Detection, Arizona Department of Health Services, Phoenix, AZ 85007, USA; [2]Ribomed Biotechnologies, Inc. Phoenix, AZ 85006, USA. jewellk@azdhs.gov. **Microsatellite variation among clinical *Coccidioides* spp. isolates in Arizona**.

The cryptic species *Coccidioides immitis* and *C. posadasii* are saprophytic, soil-dwelling fungi endemic to the southwestern United States and parts of Mexico, Central America, and South America. Both species cause coccidioidomycosis, the symptoms of which range from influenza-like to severe, disseminated forms. This study used analysis of microsatellites - specific hypervariable tandem repeats - to define and speciate *Coccidioides* spp. populations in Arizona. Nine microsatellites (GA1, 621.2, ACJ, GA37, GAC2, K09, K01, K03, and K07) were used to type over 100 clinical *Coccidioides* spp. isolates provided by sentinel laboratories, hospitals, and clinics in Arizona. Coccidioides identification was confirmed using the AccuProbeGenProbe) culture test. DNA extraction was from heat-killed idiophase cultures, quantified with a PicoGreen assay and verified with a *Coccidioides* specific PCR reaction. Confirmed samples were PCR amplified, purified using Agencourt AMPure paramagnetic beads, denatured, and analyzed using a MegaBACE 1000 with the associated MegaBACE Genetic Profiler v. 2.0. Populations were determined using PAUP* 4.0. Both *C. immitis* and *C. posadasii* isolates have been analyzed; the *C. immitis* cases were traced back to probable exposure in California. **Poster MP111**

*Johnson, J., A.G. Sirulnik, A.R. Tuininga and J.D. Lewis. Louis Calder Biological Field Station, Fordham University, Armonk, NY 10504, USA. jajohnson@fordham.edu. **Molecular and morphological analyses of ectomycorrhizal fungal community composition across hemlock dominance and defoliation gradients**.

In forests of the northeastern US, eastern hemlock, *Tsuga canadensis*, has been experiencing defoliation and subsequent mortality from infestations of the hemlock woolly adelgid (HWA), *Adelges tsugae*, an invasive aphid-like insect. We are examining effects of hemlock defoliation and distribution on ectomyc-

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orrhizal (EM) fungal community composition from local to regional scales in forests currently being invaded by the HWA. Here we use molecular and morphotyping approaches to assess EM fungal communities in healthy hemlock, declining hemlock, and hardwood dominated stands in three watersheds. Soil cores were collected in June, July and October of 2004 and 2005. EM fungal root tips were identified by standard morphotyping techniques. DNA sequence analyses for the nuclear ribosomal DNA internal transcribed spacer (ITS) repeats were completed for the 10 most common morphotypes in each stand type to determine the identity of these morphotypes to genus or species. Richness of EM fungi was highest in the oak-dominated *Quercus* sp. and healthy hemlock-dominated stands, and least in areas of declining hemlock. Although fungal community composition varied seasonally and between years, stand-level variation in community composition was generally consistent over time. These results suggest that hemlock distribution and defoliation are key factors driving spatial patterns in EM fungal community composition in forests being invaded by the HWA. **Contr. Talk: Monday AM1 Fungal Ecology- Mycorrhizae.**

*Joneson, Suzanne, François Lutzoni, and Daniele Armaleo. Duke University, Biology Department, Box 90338, Durham NC, 27708, USA. suzanne.joneson@duke.edu. **The genetics of early lichen symbiosis between the mycobiont *Cladonia grayi,* and the photobiont *Asterochloris* sp**.

Lichens are the symbiotic association of fungi (mycobionts) with green algae and/or cyanobacteria (photobionts). Although recognized as the growth of multiple organisms for over a century, the molecular mechanisms of lichenization remain enigmatic. How do symbionts find each other, establish compatibility, and maintain long-term symbiotic relationships? The genetics of early contact and development between symbionts are the focus of this research. Using aposymbiotic and symbiotic cultures of the mycobiont *Cladonia grayi* G. Merr. *ex* Sandst. and the photobiont *Asterochloris* sp. grown in the lab, Suppressive Subtractive Hybridization was used to identify fungal and algal genes whose expression levels were significantly increased in response to lichen symbiosis. Homologues of genes up-regulated in *C. grayi* and *Asterochloris* sp. were identified by searching a database of all known fungal and chlorobiont proteins using the BlastX and Fasta algorithms. This dataset represents the first global survey of gene sequences involved in lichen symbiosis, and a summary of these genes and their Gene Ontology function will be presented. The results of this study will allow us to compare gene regulation between developmental stages of lichen symbiosis, as well as identify candidate genes of early lichen development. **Poster MP98**

*Kaur, Ramandeep, Singh, Rama SIngh, Alabouvette, Claude. Department of Entomology and Nematology, University of Florida, Gainesville, FL, USA; Department of Plant Pathology, Punjab Agricultural University, Ludhiana, PB, INDIA; INRA-CMSE, UMR BBCE_IPM, Dijon Cedex, France. ramanz15@ufl.edu. **Antagonism by selected isolates of fluorescent *Pseudomonas* against *Fusarium oxysporum* f.sp. *ciceri* causing chickpea wilt in India**.

The antagonistic activity against *in vitro* growth of *Fusarium oxysporum* f.sp. *ciceri* was determined for 90 isolates florescent *Pseudomonas* obtained from the rhizosphere and rhizosphere of healthy, partially wilted and completely wilted chickpea plants. Approximately 91% of 90 bacterial isolates from the chickpea rhizosphere inhibited *in vitro* growth of *F. oxysporum* f.sp. *ciceri* in dual cultures. Based on zone of inhibition, isolates were categorized into four categories, i.e. highly, moderately, least and non-antagonists. Maximum number of highly antagonistic isolates was obtained from rhizosphere (6) and rhizoplane (8) of healthy chickpea plants, whereas, maximum number of non-antagonistic isolates were obtained from completely wilted chickpea plants. Isolate H-Pf5 showed maximum zone of inhibition (7mm) in dual culture with *F. oxysporum* f.sp. *ciceri* and was selected for green house and field bioassays along with isolate C7R12 originally isolated from wilt suppressive soils in France. Cell free culture filtrate of both the selected isolates inhibited 88-89.5% conidial germination as compared to 100% conidial germination in control. Antagonists were applied in field as seed treatment while in green house it was applied as seed and soil treatments. Under green house conditions the seed treatment with isolate H-Pf5 and C7R12 showed 72.9- 73.9 per cent seed germination and 47.2-52.1% disease incidence after 120 days of sowing while in control 48.7 % seed germination and 100 % disease was observed after same interval. The isolate H-Pf5 of fluorescent *Pseudomonas,* selected from rhizosphere of chickpea plant significantly enhanced seed germination, reduced disease incidence and promoted plant growth of chickpea as compared to control. **Poster MP113**

Keirle, Matthew. The Committee on Evolutionary Biology, University of Chicago, Chicago, IL 60637, USA. mkeirle@uchicago.edu. **Sectional concepts in the genera *Coprinopsis* and *Coprinellus* - conflict between morphology and nuclear ribosomal sequence data**.

Previously, nLSU sequence data were used to establish monophyly for the genera *Coprinopsis, Coprinellus,* and *Parasola* within the family Psathyrellaceae (Hopple and Vilgalys, 1999), but failed to recover the traditional sections within these coprinoid genera. This project investigates the utility of the more variable ITS region in recovering the coprinoid sections historically recognized in large part by aspects of veil morphology. This analysis however produced a very similar result to that of Hopple and Vilgalys in that the traditional sections within *Coprinopsis* and *Coprinellus* were not recovered. However in both of the molecular phylogenetic reconstructions, all branches that represent non-sectional groupings lack support. It appears that the nLSU data does not provide sufficient phylogenetic resolution and that the ITS marker evolves perhaps too quickly as indicated by the difficulty in aligning sequences and a loss of signal due to potential errors in homology decision-making based on ambiguous alignments and saturation. *Coprinopsis* and *Coprinellus* sections are typically quite clearly delimited by morphology and it is not readily apparent why there is no support for those sections in these molecular data sets. **Poster MP151**

Kennedy, Allison and Campbell, Jinx. Department of Coastal Sciences, University of Southern Mississippi, Ocean Springs, MS 39564, USA. allison.kennedy@usm.edu. **Fungal associates of captive Atlantic bottlenose dolphins *Tursiops truncatus***.

Captive dolphins are particularly prone to fungal infections. Most are opportunistic fungi rather than pathogenic and appear as a result of stress, environmental compromise or other infectious disease. During Hurricane Katrina eight captive Atlantic bottlenose dolphins were accidentally released into the open waters of the Gulf of Mexico. Following their rescue and recapture four weeks later, the dolphins were examined for fungal infections in their respiratory tracts, blood, feces, and cutaneous lesions sustained during their escape from captivity. Tank water filtrate was also examined. *Aspergillus fumigatus, Aspergillus* sp. *Candida albicans, Candida* sp. *Fusarium* sp. *Mucor* sp. and *Rhizopus* sp. were found in the blowhole samples. Two dolphins had cutaneous lesions and samples taken from these were shown to be infected with *Candida albicans, Aspergillus carbonarius, Fusarium* sp. and *Rhizopus* sp. The feces and water filtrate samples were infected with *Candida albicans, Aspergillus carbonarius* and *Rhizopus* sp. and *Aspergillus fumigatus* was additionally identified from the feces. Prior to the storm two dolphins had fungal infections, compared with all eight dolphins six weeks post recapture. These results suggest that a low host resistance in these debilitated animals, caused by stress and environmental compromise, was the underlying cause of these opportunistic fungal infections. **Poster MP150**

*Kennedy, Allison and Campbell, Jinx. Dept. of Coastal Sciences, University of Southern Mississippi Gulf Coast Research Laboratory, Ocean Springs MS 39564, USA. allison.kennedy@usm.edu. **Assessment of fungal diversity of gulf coast salt marshes, with implications for coastal restoration**.

Coastal salt marshes are declining worldwide. In the northern Gulf of Mexico, salt marshes provide nursery habitats for commercially important fish and invertebrates; as well, they buffer shorelines against erosion and hurricane damage while improving water quality. Coastal restoration projects are underway in southern Mississippi and Alabama, but the current success rate is only 50%. This study assessed the role of saprophytic marine fungi as indicators of coastal salt marsh ecosystem function. Restored salt marshes were compared with reference natural saltmarshes using the following parameters: fungal species richness, abundance and belowground biomass. Fungal species on decaying *Spartina alterniflora* and *Juncus roemerianus* were inventoried using morphological and molecular techniques (ITS sequencing, T-RFLP analysis), and site-specific fungal community fingerprints were generated. Belowground fungal biomass was measured using the index biochemical ergosterol. By comparing data from natural and restored salt marshes, a set of functional metrics is being developed to reflect marsh restoration success. These metrics will be used as a template for future planned restoration activities along the northern Gulf coast. **Poster MP75**

*Kerekes, Jennifer F. and Desjardin, Dennis E. Department of Biology, San Francisco State University, San Francisco, CA 94132, USA. kerekesj@sfsu.edu. **A monograph of the genus *Crinipellis* from Southeast Asia based on morphology and nrITS data**.

Continued on following page

The genus *Crinipellis* Basidiomycota, euagarics) is distinguished morphologically from the allied genera *Marasmius* and *Chaetocalathus* by stipitate basidiomes with pileipelli composed of thick-walled, dextrinoid, hair-like hyphae. Fourteen epithets in *Crinipellis* have been reported from Southeast Asia. Based on macro-and micro-morphological data of recently collected specimens from Thailand, Malaysia and Indonesia, numerous types specimens and herbarium exsiccati, we recognize twelve morphological species, including one new species. This is supported by ITS molecular data and analysis of recently collected specimens. Spore size and substrate along with cheilocystidia and pileipellus hair characteristics are taxonomically significant micro-morphological characters in this genus. First reports of these species occurring in Thailand, Malaysia and Indonesia, in addition to geographic distribution and phylogenetic relationships, are also noted. Analysis of the ITS (ITS1-5.8S-ITS2) sequence data indicate that the genus *Crinipellis* forms a monophytletic group sister to *Chaetocalathus* using *Marasmius* s.s as an outgroup. **Poster MP152**

*Kerrigan, Richard W. and Callac, Philippe. Sylvan Research, Kittanning, PA 16201, USA, and INRA, MYCSA, BP 81, 33883 Villenave d,Ornon cedex, France. rwk@sylvaninc.com. **New taxa in *Agaricus* section *Duploannulati* from North America**.

In 2003, Challen et al. reported on seven taxa of *Agaricus* section *Duploannulati* from the temperate northern hemisphere. One of these, *A. subperonatus,* remains inadequately known or is considered an older name for *A. cappellianus = A. vaporarius* by some authors. Here we report an additional 6 new taxa from North America. One species from eastern Mexico and one species from coastal California, both associated with *Cupressus,* are related to *A. cupressicola,* a European species. Another species from *Cupressus* habitat in California is related to *A. bitorquis* and *A. cappellianus.* A new low-elevation species is segregated from *A. subfloccosus* and a subalpine subspecies from the Rocky Mountains is segregated from *A. devoniensis.* Still another new species, from the Sonoran Desert of California, attaches to the most basal node in *Duploannulati* in ITS1+2 sequence-derived phylogenies. Three of these taxa, as with an additional related taxon from France, are known only from single collections, thus appear to be extremely rare. Another is known from only three collections. None are common. This implies that obtaining a realistic inventory of extant biodiversity in this group will be a long and difficult process. Taken together, these records double the number of species and subspecies-level taxa in section *Duploannulati.* **Contr. Talk: Sunday PM 2 Basidiomycete systematics**

Klich, Maren A, USDA/ARS/SRRC New Orleans LA, C/O USDA/ARS/PSNL Tower Road, Ithca NY 14853, USA. mklich@srrc.ars.usda.gov. **Identification of the yellow-spored aspergilli**.

Yellow-spored aspergilli have traditionally been considered to belong to *Aspergillus* section *Circumdati.* A number of these species have been moved to other sections of the genus based on characters other than spore color, causing some confusion among researchers needing to identify these fungi. Eight yellow-spored *Aspergillus* species have been described in the past two years. These include: *A. rambelli,* which produces aflatoxin; *A. cretensis, A. flocculosus, A. pseudoelegans, A. roseglobulosus, A. steynii,* and *A. westerdijkiae,* all of which produce ochratoxin; and *A. neobridgeri.* In this study the yellow-spored aspergilli will be analyzed using morphological features and an identification system for them will be presented. **Poster MP133**

Kolter, Roberto Microbiology and Molecular Genetics, Harvard Medical School, Boston, MA 02115 USA. rkolter@hms.harvard.edu. **Molecular Analyses of the *Pseudomonas aeruginosa-Candida albicans* Model Microbial Community**

The bacterium *Pseudomonas aeruginosa* adheres to and forms a biofilm on filaments of the dimorphic fungus *Candida albicans. C. albicans* viability and morphology are significantly affected by the presence of *P. aeruginosa*. In environments that would normally favor filamentous growth, yeast cells are formed at the same time that filamentous cells are killed by the bacteria. Yet, the yeast cells survive Thus, this model microbial community starts as an parasitic symbiosis but later appears to become mutualistic. The effects that *P. aeruginosa* has on the morphology of *C. albicans* represents one of the ways by which bacteria can influence the behaviour of fungal cells. **Symposium: Tues 1:30-5:00 Bacterial Symbionts of Fungi**

Landolt, John C.[1], *Stephenson, Steven L.[2] and Cavender, James C.[3]. [1]Dept. of Biology, Shepherd University, Shepherdstown, WV 25443; [2]Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701; and [3]Dept. of Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA. slsteph@uark.edu. **Distribution and ecology of dictyostelids in the Great Smoky Mountains National Park**.

The Great Smoky Mountains National Park encompasses an area of 2080 square kilometers in eastern Tennessee and western North Carolina between 35 degrees 28 minutes and 35 degrees 47 minutes N latitude. Elevations range from approximately 270 to 2000 m above sea level, and the topography and vegetation are as diverse as any region of eastern North America. During the period of 1998 to 2004, soil/litter samples for isolation of dictyostelid cellular slime molds were collected throughout the Park. Collecting sites included examples of all major forest types along with the more common types of non-forest vegetation. More than 2300 clones of dictyostelids were recovered from 412 samples. These clones included representatives of 20 described species together with at least 10 species new to science. This total is higher than those reported for other temperate regions of the world. In general, both numbers of species and numbers of clones/g of sample material decreased with increasing elevation, and several species displayed a distinct preference for either the low or high end of the elevation gradient. The relatively high number of new species recovered from samples collected at high elevations is an important new finding for dictyostelid ecology and distribution. **Poster MP89**

*Lee, Soo Chan and Shaw, Brian D. Program for the Biology of Filamentous Fungi, Department of Plant Pathology and Microbiology, 2132 TAMU, Texas A&M University, College Station, TX77843, USA. sclee@tamu.edu. **N-myristoylation of ADP-ribosylation factors in *Aspergillus nidulans***.

A DP-*R* ibosylation *F* actors (ARFs) are small GTPase proteins with several biological activities including vesicle formation and trafficking and, in yeast, bud site selection. In filamentous fungi, numerous vesicles are found at the growing tips and in the Spitzenkorper where they are thought to be active in secretion of cellular components, endocytosis, and maintenance of tip growth. The exact roles of the ARFs in filamentous fungi have not been established. The *Aspergillus nidulans* developmental gene, *swoF* encodes N-myristoylation transferase. The *swoF* mutant displayed abnormal tip swellings resulting from loss of polarity. Disruption of N-myristoylation results in a polarity defective mutant phenotype. Computational analysis of the *A. nidulans* proteome suggests that the ARF proteins are myristoylated. We named these genes *arfA, arfB,* and *arfC.* ArfA::GFP localizes to cellular compartment which may be Golgi or Endoplasmic Reticulum and ArfB::GFP localizes to septa. But in *swoF* mutants, ArfA::GFP and ArfB::GFP showed non-specific localization. In addition, in wild type cells, mutant ArfAG2A::GFP and ArfBG2A::GFP, each with a G2A amino acid substitution that disrupts myristoylation mislocalized. This observation suggests that N-myristoylation determines subcellular localizations for ArfA, and ArfB. The ArfC::GFP localization study is ongoing. Progress toward deletion of each ARF gene will be discussed. An in vivo myristoylation assay will be discussed. **Contr. Talk: Monday PM Fungal molecular and cell biology**

*Letcher, Peter M. Powell, Martha J. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487, USA. letch006@bama.ua.edu. **Chytrids - morphology and the demise of old hypotheses**.

Among Chytridiomycota, thallus morphology and zoospore ultrastructure have been used classically for taxonomic delineation. With the advent of molecular-based phylogenetics, when structural characters are mapped on gene trees greater understanding of evolution of structural characters in lineages is gained, transforming our view of systematic relationships. Four examples of how morphological characters have evolved repeated times in distinct lineages are analyzed: 1) Monocentric and polycentric thalli; 2) Operculate and inoperculate discharge; 3) Organelles within organellar assemblages; and 4) Structural components of the flagellar apparatus. These analyses show that loss of a morphological character may occur repeated times in different lineages, especially in highly divergent organisms. Consequently, "absence" of a feature should not necessarily be considered the "same" character state in different lineages. These examples highlight that care must be exercised in considering homologies between structural characters. When morphological characters are considered within a well-supported monophyletic molecular-based lineage, structural character states can be confidently mapped to understand character evolution. **Symposium: Monday 1:00-4:30 Diversity of Zoosporic Fungi**

*Letcher, Peter M. Powell, Martha J. Churchill, Perry F. Chambers, James G. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487, USA. letch006@bama.ua.edu. **Ultrastructural and molecular delineation of a new order, the Rhizophydiales (Chytridiomycota)**.

Continued on following page

In the order Chytridiales, *Rhizophydium* is a morphologically defined genus based upon the production of a monocentric, inoperculate, epibiotic sporangium, an endobiotic rhizoidal axis which branches, and an epibiotic resting spore. Despite its simple morphology, over 200 species of *Rhizophydium* have been described. Recent phylogenetic analyses using nuclear large subunit ribosomal RNA (28S rRNA) gene sequences of a geographically diverse sampling of *Rhizophydium* cultures revealed that the classical genus *Rhizophydium* is genetically more variable than previously understood and actually represents multiple genera. In the present study, we use zoospore ultrastructural characters and 28S rRNA and 5.8S ribosomal gene sequences of 96 isolates to circumscribe the monophyletic *Rhizophydium* clade as a new order, Rhizophydiales. Correspondingly, zoospores of members of the Rhizophydiales exhibit a unique suite of ultrastructural character states that further define the order and distinguish it from the order Chytridiales. Molecular analyses reveal several strongly supported clades within the Rhizophydiales. Three of those clades encompass a broad range of isolates and are defined as new families Rhizophydiaceae, Terramycetaceae, and Kappamycetaceae. To resolve close relationships within Terramycetaceae, combined 28S and ITS1-5.8S-ITS2 sequences were analyzed and details of zoospore ultrastructural character states determined, with two new genera, *Terramyces* and *Boothiomyces,* described. This work provides a framework for additional taxonomic revisions within the new order Rhizophydiales and compares genetic variation useful in defining genera, species, and populations within this lineage of chytrids. A broader sampling of representatives is needed before taxonomic decisions can be made for remaining clades within the Rhizophydiales. **Poster MP120**

*Levesque, C. Andre and *Tambong, James T. Biodiversity, Environmental Health Program, Agriculture and Agri-Food Canada, Ottawa, ON Canada. levesqueca@agr.gc.ca. **A functional genomics approach to study the ecology of *Pythium* and *Phytophthora*.**

Once the complete genome sequence for a species is available, the next investigative phase is often based on a functional genomics approach, whereby gene function and up/down regulation are assessed. Similarly, as comprehensive phylogenetic databases including all known taxa in a microbial group become available, studying the interactions between species and changes in their relative abundance in environment samples (i.e. their "up or down regulation") becomes easier. DNA microarrays have been developed to study functional genomics. We have developed *Pythium* and *Phytophthora* DNA arrays that can be used to compare species profiles in soil or rhizosphere under different treatments. In functional genomics, the relative intensities of positive microspots on a microarray provide a semi-quantitative assessment of up and down regulation of genes between treatments. We demonstrate that the intensity of microspots on an ITS-based DNA array can provide semi-quantitative assessment of species abundance among *Pythium* species within a treatment or between treatments for given species. In functional genomics, microarray results are validated with other techniques such as RT Q-PCR to confirm the regulation of the most critical genes. For species that were most affected by different treatments in this study, we used Q-PCR to confirm results obtained by DNA array hybridization. Together, these techniques were ultimately used to assess the effect of soil compaction and crop rotation on populations of different *Pythium* species. **Symposium: Monday 1:00-4:30 Diversity of Zoosporic Fungi**

Li, De-Wei. 153 Cook Hill Road, Windsor CT 06095, USA. dewei.li@po.state.ct.us. **The effects of human activities and air disturbance on airborne fungi in a water damaged building**.

A study was conducted to determine the effects of routine human activities on airborne fungi and the effects of air disturbance on release and resuspension of fungi in an office building with fungal infestation caused by water damage in New Haven, Connecticut. The results showed that the predominant fungi associated with the water damage were *Cladosporium sphaerospermum, Aspergillus ochraceus, Ochroconis* sp. *Penicllium* spp. and *Aspergillum* spp. in a descending order. Human activities highly significantly elevated airborne fungal populations. The total concentration of airborne fungi elevated from 13346 to 34548 spores /m^3 and *Cladosporium sphaerusorum* from 3429 to 8761 conidia /m^3 with the presence of human activities, respectively. Air disturbance generated by a 30 cm oscillating fan showed the significant effects on airborne fungal populations of most fungi in the building. The air disturbance increased the airborne fungal spores from 3430 to 21221 conidia /m^3 for *Cladosporium* and from 13262 to 53935 spores /m^3 for the total concentrations, respectively. Sampling locations did not show the significant differences in airborne fungi populations, except *Ochroconis sp.* **Poster MP112**

*Li, Chunjie[1,2], Nan, Zhibiao[1], Schardl, L.Christopher[2]. [1]College of Pastoral Agriculture Science and Technology, Lanzhou University; Lanzhou 730020, China; [2]Plant Pathology Department, University of Kentucky, Lexington, KY 40546, USA. ChunjieLi@uky.edu. **Levels and temporal variation of ergot alkaloids in endophyte-infected drunken horse grass, *Achnatherum inebrians*, in China**.

Ergot alkaloids levels and their temporal variation of *Neotyphodium* endophyte-infected (E+) and endophyte-free (E-) drunken horse grass, *Achnatherum inebrians*, were determined by HPLC analysis of extracts from seeds, seedlings, and mature plants from the wild and from the greenhouse. Ergonovine and ergine were only detectable in E+ plants. However, ergocryptine, ergocornine, ergocristine and ergotamine were not detected in either E+ and E- plants. Levels of ergonovine were significantly higher than ergine levels in all parts of E+ *A. inebrians* plants. In wild plants, concentrations of both ergonovine and ergine decreased over the plant growing season. Levels of both alkaloids in leaf blades and ears were significantly ($p<0.05$) higher than those in stems. Concentrations of ergonovine and ergine, respectively, ranged from 267¯C1082 and 130¯C393 mg/kg seeds of E+ *A. inebrians* collected from 10 different locations. Under greenhouse conditions, concentrations of either ergonovine or ergine in leaf sheathes were significantly ($p<0.05$) higher than those in leaf blades in 3-month-old seedlings, but when plants were older than 5 months, their concentrations were higher in leaf sheathes than in leaf blades. Mean levels of ergonovine in leaf blades and leaf sheathes, respectively, were 50 and 290 mg/kg in 3-month-old seedlings, increasing to 1215 and 629 mg/kg in 5-month-old plants, then decreasing to 731 and 327 mg/kg in 15-month-old plants. Ergine in leaf blades and leaf sheathes, respectively, averaged 17 and 104 mg/kg in 3-month-old seedlings, 998 and 366 mg/kg in 5-month-old plants, and 438 and 125 mg/kg in 15-month-old plants. Even in senescent dried tillers, ergonovine and ergine contents were 97 mg/kg and 61 mg/kg, respectively. **Poster MP81**

*Lickey, Edgar B. Hughes, Karen W. and Petersen, Ronald H. Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA. elickey@utk.edu. **2006 update of the fungal TWIG of the Great Smoky Mountains National Park's ATBI**.

We present an update on efforts to catalog the basidiomycete taxa, particularly the mushroom-forming fungi, of the Great Smoky Mountains National Park (GSMNP) for the All Taxa Biodiversity Inventory. The goals of this project are to; 1) collect, identify, and voucher specimens with the help of visiting mycologists and volunteers, 2) extract DNA, amplify and sequence the nrITS region for barcoding, and deposit these sequences on GenBank, and 3) create species web pages for general public use. At present (7 April 2006), approximately 2000 specimens comprising about 770 species have been collected. As many as 45% are new park records, and several may represent species new to science. DNA has being extracted from about 1000 specimens and the nuclear ribosomal ITS region has been amplified and sequenced for about 600 of those. A surprising amount of genetic heterogeneity has been found, possibly due to population migration patterns in response to glacial cycles. *Artomyces pyxidatus* will be presented as an example to illustrate this hypothesis. **Poster MP144**

*Lim, Young W., Chedgy, Russell, Amirthalingam, Sabarish and Breuil, Colette. Department of Wood Science, University of British Columbia, Vancouver, B.C. Canada. ywlim@interchange.ubc.ca. **Screening for decay and pioneer fungi that are tolerant to Western red cedar extractives**.

Western red cedar (WRC), *Thuja plicata* Don, a softwood species that is native to the northwestern North America, is naturally durable because its heartwood extractives are strongly anti-microbial. Despite this, cedar products can still fail in service due to colonization initiated by extractive-tolerant fungal species, as well as to depletion of extractives caused by weathering. When WRC-feeder strips were placed on MEA plates, extractives leached into and accumulated in the media. Five compounds leached out of the feeder strips: plicatic acid, gamma-thujaplicin, beta-thujaplicin, beta-thujaplicinol and thujic acid. gamma- and beta-thujaplicin appeared to be the most important inhibitors of fungal growth; although high concentrations of plicatic acid and thujic acid were leached into the media, they did not inhibit fungal growth. *Pachnocybe ferruginea* and *Acanthophysium lividocaeruleum* were extractive-tolerant, and may be important in the initial stages of degradation of WRC products. **Poster MP71**

*Lim, Young Woon[1], Sturrock, Rona[2], Leal, Isabel[2], Pellow, Kevin[2] and Breuil, Colette[1], [1]Dep. of Wood Science, University of British Columbia, 2424 Main Mall, Vancouver, B.C. Canada and [2]Canadian Forest Service, Pacific Forestry

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Centre, Victoria, B.C. Canada. ywlim@interchange.ubc.ca. **ITS polymorphisms distinguish *Phellinus sulphurascens* homokaryons and heterokaryons**.

Phellinus sulphurascens Pilat causes laminated root rot in Douglas-fir in western North America (WNA) and in other conifers in Asia. Accurate somatic incompatibility tests for mapping population structures have been difficult to conduct for *P. sulphurascens* because no single, unambiguous criterion has allowed differentiation of homokaryotic and heterokaryotic isolates. In a population study of *P. sulphurascens* in WNA, two types of ITS sequences were found in the basidiospores and vegetative isolates. All single spore isolates had either type 1 or type 2, and never both types together. However, some vegetative isolates had both ITS types. The segregation pattern in nine spore families suggested that each ITS type was in a different nucleus, and a Mendelian segregation pattern indicated that each basidiospore inherited only one ITS type. In four single spore isolates from Russia and eight heterokaryon isolates from Japan, nine different types of ITS were detected. ITS polymorphism and pairing of Asian homo- and heterokaryon isolates with WNA vegetative isolates permitted differentiation of WNA homokaryotic and heterokaryotic isolates. **Contr. Talk: Tues PM 2 Fungal systematics.**

*Lodge, D. Jean[1] and Gonzalez, Grizelle[2]. [1]International Institute of Tropical Forestry, PO Box 1377, Luquillo, PR 00773-1377 and [2]Jardín Botanico Sur, 1201 Calle Ceiba, San Juan, PR 00926-1119, USA. djlodge@caribe.net. **Effect of white-rot fungi and arthropods on early-stage tropical leaf decomposition**.

A natural mixture of freshly fallen leaves (10 g fresh wt. = 4.0 g dry wt.) was placed on forest floor white rot-litter basidiomycete mats and adjacent (<50 cm away) forest floor lacking mats (12 pairs) and decomposed for three months in the Luquillo Mountains of Puerto Rico. Weighed leaves were placed between two 1-mm mesh screens, and surrounded by a plastic rim to reduce lateral movements of mycelia. At harvest, arthropods were extracted using Tullgren funnels before oven drying. Percentage white-rot was 40% higher in the white-rot treatment (60% +/-10.7 vs 19.6% +/- 12.1). Percent mass loss after 3 months was 8.4% faster in the white-rot treatment, and was significantly different from the non-mat treatment (paired t-test, P=0.0028). The best overall regression model for predicting rates of early decomposition (adjusted R^2 0.37, P = 0.0006) included % white-rot, total number of isopods, and total number of invertebrates. Total isopods and % white-rot were positively correlated, while total number of invertebrates was negatively correlated with rates of decomposition. Thus, white-rot basidiomycete fungi significantly accelerated the rate of leaf decomposition. These results suggest that differences in abundances of both basidiomycete fungi and litter arthropods contribute to the high variance in rates of leaf decomposition in tropical wet forest. **Poster MP73**

*Lodge, D. Jean[1], Matheny, P. Brandon[2], Cantrell, Sharon A.[3], Moncalvo, Jean-Marc[4], Vilgalys, Rytas[5] and Redhead, Scott[6]. [1]Int. Inst. of Tropical Forestry, USDA-FS, Luquillo, PR 00773-1377; [2]Biology, Clark Univ. 950 Main St. Worcester, MA 01610; [3]Biology, Univ. Turabo, PO Box 3030, Gurabo, PR 00778; [4]Cntr. Biodiv. & Conserv. Biology, Royal Ontario Museum & Botany, Univ. Toronto, Toronto, Ontario, M5S 2C6, Canada; [5]Biology, Box 90338, Duke Univ. Durham, NC 27708-0338, [6]Syst. Mycology & Botany, E. Cereal & Oilseed Research, Ag. & Agri-Food Canada, Ottawa, Ontario K1A0C6, Canada. djlodge@caribe.net, dlodge@fs.fed.us. **Delineating the Hygrophoraceae: character myths vs. gene trees**.

Members of the Hygrophoraceae have traditionally been recognized to form a natural group based on the presence of thick waxy lamellae and basidia 5-7 times longer than the spores. However, some taxa outside the Hygrophoraceae also exhibit waxy lamellae, such as *Neohygrophorus* and *Camarophyllopsis* - genera now excluded from the Hygrophoraceae based on molecular phylogenies. While most Hygrophoraceae have thick lamellae, an undescribed *Lepiota* -like species from Ecuador does not. Also, exceptions exist within the Hygrophoraceae where long basidia are not found, e.g. *Hygrocybe rosea* and *H. roseoflavida* with spore:basidia ratios of 3-4. In addition, while spores of most Hygrophoraceae are smooth, conical spines occur on spores of *Hygroaster* as well as in *Hygrocybe anomala* and *H. insipida,* often with spiny- and smooth-spored forms occurring together. Spore amyloidy has been heavily considered in traditional systematics, thus, only some authorse.g. Singer and Hesler & Smith) have included the genus *Neohygrophorus,* with amyloid spores, waxy lamellae and elongate basidia in the Hygrophoraceae. Molecular phylogenetic analyses indicate that while *Neohygrophorus* should be excluded from the Hygrophoraceae, *Pseudoarmillariella ectypoides,* which also has amyloid spores and waxy lamellae, but spore:basidia ratios <5, belongs in the Hygrophoraceae. Thus, while traditional morphological characters are useful in identifying most members of the Hygrophoraceae, none are infallible. Finally, while species of Hygrophoraceae generally occur on soil or humus, some, such as *Hygrocybe mexicana, H. pseudoadonis,* and *H. rosea* grow exclusively on mossy tree trunks or logs, while other are ectomycorrhizal (*Hygrophorus*). There is thus not a synapomorphy for the Hygrophoraceae. **Poster MP161**

*Lodhi, A. Mubeen[1,2], Shahzad, Saleem[2], Ghaffar, Abdul[2], and Levesque, C. Andre[1]. [1]Biodiversity (Mycology and Botany), Agriculture and Agri-Food Canada, Ottawa, Ontario K1A 0C6, Canada. [2]Department of Botany, University of Karachi, Pakistan. **Oomycete species of Pakistan - a morphological and molecular study**.

During a taxonomic study of Oomycetes from Sindh province of Pakistan, close to 300 isolates were obtained from the following sources: cultivated and uncultivated fields; roots; ponds; and irrigation canals and ditches. Different baiting methods as well as direct plating on different agar media were used for isolation. Approximately 200 isolates belonged to different *Pythium* species; most of which have not been reported in Pakistan. The most common species found were *P. aphanidermatum, P. deliense, P. catenulatum, P. oligandrum, P. acanthicum, P. ostracodes, P. orthogonon, P. multisporum,* and *P. plurisporium*. The other isolates belonged to the genera *Phytophthora, Pythiogeton, Achlya, Isoachlya, Saprolegnia,* and *Dictyuchus*. Based on morphology and rDNA sequence analyses (ITS and partial LSU), some of the isolates represent new species. Phylogenetic analyses and morphological descriptions of these new species, including comparisons with related species, were performed. Many morphologically different isolates of *Pythiogeton* were obtained from cultivated fields and water samples, making this one of the largest collections of *Pythiogeton* species. All isolates were able to grow on corn meal agar. Phylogenetic placement of these isolates shows that they are within the genus *Pythium*, therefore, the definition of the genus *Pythiogeton* needs to be revisited with these new data. **Contr. Talk: Monday AM2 Fungal Systematics**

*Long, Melissa, Thon, Michael, and Shaw, Brian D. Program for the Biology of Filamentous Fungi, Department of Plant Pathology and Microbiology, Texas A&M University, College Station, Texas, 77843, USA. mmlong@ag.tamu.edu. **The *Aspergillus nidulans* guanine exchange factor, GefA, localizes to hyphal tips**.

Our objective is to analyze a putative polarity circuit in *A. nidulans* by gene knockout and GFP localization. In *S. cerevisiae,* a circuit consisting of Bud1, 2, and 5 positively regulates bud site selection through Cdc24 and Cdc42 which in turn regulate the polarisome. The polarisome nucleates the actin cytoskeleton to bud sites and may be analogues to the Spitzenkorper. Orthologs of Bud1 (AN4586.2 - GtpA) and Bud2 (AN3735.2 - GapA) were identified in *A. nidulans* by using BLAST algorithms to find the best bidirectional matches. This data is further supported by phylogenetic analysis. A putative *A. nidulans* ortholog of Bud5 (AN4369.2 - GefA) was also identified. However, the phylogenetic analysis of GefA did not support the hypothesis that this gene is the filamentous ortholog of Bud5. GefA does appear to group with other guanine exchange factors found only in filamentous fungi. We GFP tagged GefA and found that it localized to growing cell apices. Preliminary data shows that GefA::GFP also localizes at the sites of lateral branch emergence and in conidia to sites of possible germ tube emergence. Further analysis of gene knockouts and GFP-tagging will be discussed. **Contr. Talk: Monday PM Fungal molecular and cell biology**

*Lutzoni, Francois[1], Kauff, Frank[1], Miadlikowska, Jolanta[1], Winslow, David[2], and Brady, Rachael[2]. [1]Department of Biology, Duke University, Durham, NC 27708, [2]Department of Computer Science, Duke University, Durham, NC 27708, USA. flutzoni@duke.edu. **More characters or taxa? A case study with the Lecanoromycetes using new tree visualization tools**.

The ever-increasing size of phylogenetic datasets requires a continuous reassessment of the preferential need for additional characters or taxa. This decision is usually based on internodal support values. If support values are high this is usually interpreted as an indicator that characters at hand are sufficient and warrants the sampling of more taxa. If phylogenetic uncertainty is high, more characters are usually included in future phylogenetic studies. However, simulation and empirical studies have shown that this decisional process lacks predictability. The addition of taxa to a data matrix with the same set of characters can lead to higher support values and more characters can result in lower support values. The unavoidable increase in the amount of missing data in large-

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scale multi-locus phylogenetic studies and the variation among various methods to accurately estimate support values obscure even more this decisional process. Therefore, phylogenetic trees should display the sensitivity of support values in response to varying quantities of characters, taxa, missing data, and to methods used. We present here a novel way to visualize this information that is applicable to large phylogenetic trees by the use of new bioinformatics tools. To gain a comprehensive understanding of phylogenetic confidence, we conclude that large-scale multi-locus phylogenetic studies should report multiple estimates of support values based on various amounts of missing data, number of taxa and characters as well as different phylogenetic methods. **Contr. Talk: Monday AM2 Fungal Systematics**

*Malvarez, Gabriela[1], Carbone, Ignazio[2], Kohn, Linda M.[1]. [1]Dept. of Botany, Univ. of Toronto, Mississauga, Ontario, Canada; [2]Center for Integrated Fungal Research, North Carolina State University, Raleigh, NC 27695, USA. gmalvare@utm.utoronto.ca. **Tales of the Gold Rush: gene flow with South America in a newly discovered population of *Sclerotinia sclerotiorum* associated with California lettuce crops**.

Samples from lettuce, peanut and soybean in South America were compared with samples from lettuce from California and Ontario (total 640 isolates). From S. America and California, samples showed high diversity, lack of association of markers, and net-like coalescent genealogies of DNA sequences from two loci indicative of recombination over the entire population history. In contrast, Ontario samples, like previous samples from North America, Europe and New Zealand, were less diverse and highly clonal, with association of independent markers and little contemporary recombination. All isolates from N. and S. America were homothallic; each isolate had both MAT1-1 and MAT1-2 in southern hybridizations, consistent with results from PCR amplification. S. American and Californian samples comprise one, newly identified population, distinct from others in N. America. Coalescent genealogies indicate that the new population is older than the major clonal population in N. America. The directionality of migration (N to S, or S to N) is unknown by available methods, but the circumstantial evidence is that lettuce and other vegetable crops were introduced to California just after human migration to the Gold Rush that brought thousands of Chileans as well as most others from the eastern U.S. via the route around S. America. We propose this introduction of *S. sclerotiorum* to California. **Symposium: Wed 8:30-1200 Population and Species Divergence in Fungi**

*Massoumi Alamouti, Sepideh, Kim, Jae-Jin, Breuil, Colette. Dept. of Wood Science, University of British Columbia, Vancouver BC V6T 1Z4, Canada. alamouti@interchange.ubc.ca. **Fungal associates of the northern spruce engraver, *Ips perturbatus,* in northwestern Canada: *Leptographium fruticetum* sp. nov**.

Species of the genus *Ophiostoma* and its related anamorphs are the dominant fungal associates of bark beetles. Some associates have a more specific relationship with the beetle, while others are less specific. The spruce-infesting bark beetle, *Ips perturbatus,* occurs across Canada and infests freshly harvested logs and stressed trees. A survey in the Yukon Territory and Northern BC showed that this beetle species carries a number of fungi, which includes the known species like *O. bicolor* and several unknown species of the anamorph genera *Leptographium* and *Hyalorhinocladiella.* One *Leptographium* species was the most frequent fungi isolated from the beetle's exoskeletons (77% in the Yukon and 82% in Northern BC) and galleries. Morphologically, this fungus was similar to *L. abietinum* and *L. hughesii,* but differed in a number of characteristics, e.g. the arrangement of its conidiophores. The fungus grew optimally at 25 C on 2% malt extract agar and showed a high level of tolerance to cycloheximide. Comparison of rDNA and beta-tubulin gene sequences confirmed that the species was undescribed. We designated it as *Leptographium fruticetum* sp. nov. **Poster MP122**

*Massoumi Alamouti, Sepideh[1], Kim, Jae-Jin[1], Lim, Young Woon[1], Uzunovic, Adnan[2], Breuil, Colette[1]. [1]Dept. of Wood Science, University of British Columbia, Vancouver BC V6T 1Z4, Canada; [2] Forintek Canada Corp. 2665 East Mall, Vancouver, BC V6T 1W5, Canada. alamouti@interchange.ubc.ca. **Phylogenetic analyses of the ambrosia fungi isolated from bark and ambrosia beetles in northwestern Canada**.

Ambrosia fungi are ascomycetes belonging to the group Ophiostomatoid. During a survey in northern British Columbia and the Yukon Territory, ambrosia fungi were frequently isolated from the spruce-colonizing bark beetle *Ips perturbatus* and ambrosia beetles of the genus *Trypodendron* affecting lodgepole pine. Phylogenetic analyses of the partial nuclear ribosomal DNA region and beta-tubulin gene showed that the isolates consist of three divergent lineages representing four phylogenetic species: *Ambrosiella ferruginea* and three undescribed taxa. The three undescribed taxa were placed with species of the genus *Ambrosiella* within the order Ophiostomatales. Of the three undescribed taxa, two were isolated from *I. perturbatus.* These two along with pri>Ambrosiella species also isolated from bark beetles, were resolved as a monophyletic lineage. The members of this monophyletic lineage produced the monilioid conidiophores and confluent sporodochia, characteristic of *Ambrosiella* species. However, differences in ribosomal DNA and beta-tubulin gene sequences, ecological niche, conidial development and cycloheximide sensitivity distinguished the undescribed taxa from *Ambrosiella xylebori,* the type species of the genus *Ambrosiella* belonging to the order Microascales. Consequently, the undescribed taxa could not be assigned to the genus *Ambrosiella.* Detailed studies of conidial development are needed to clarify whether the undescribed taxa should be assigned to the genus *Dryadomyces* or a new genus should be introduced to accommodate the ambrosia fungi isolated from the phloem-feeding bark beetles. **Contr. Talk: Tuesday PM 1 Ascomycete systematics.**

*Mata, Juan L.[1] and Lewis, David[2]. [1]University of South Alabama, Mobile, AL. [2]Gulf States Mycological Society, Newton TX, USA. jmata@usouthal.edu. **Basidiomycetes of the Mobile River Basin**.

The Mobile River Basin is the largest Gulf Coast drainage east of the Mississippi River. It drains portions of 10 physiographic provinces providing a wide variety of different habitats for many biological organisms. While biodiversity in the Mobile river basin has been assessed for major biotic assemblages in plants and animals, very little has been accomplished in fungi. Mata started an initial inventory of the Basidiomcyetes, with an emphasis on Agaricales, in 2005. Even though mild temperatures predominate in the Gulf Coast yearround, most basidiomata emerge during the summer months when rainfall is copious and temperatures remain high. Lewis, has been collecting in the Gulf Coast for the last 20 years and most of his species reports are generated from annual forays with the GSMS. Data from both authors, and searches in literature, are contrasted with those from Mohr in 1901, the only comprehensive inventory of fungi for the state of Alabama, and the main reason motivating this project. **Poster MP125**

Matula, John D. and *Taylor, Josephine. Dept. of Biology, Stephen F. Austin State University, Nacogdoches TX 75962, USA. jtaylor@sfasu.edu. **Field and laboratory evaluation of resistance to *Puccinia virgata***.

Five varieties of indiangrass, *Sorghastrum nutans* L. Nash, were assessed for their level of resistance to *Puccinia virgata* under field and laboratory conditions. In the field study disease severity was estimated using a modified Cobb scale to determine the area under the disease progress curve (AUDPC) for each variety. Average rust severity was significantly different ($p = 0.0006$) among varieties, with the variety Osage exhibiting less disease than varieties Lometa, Cheyenne and Rumsey. Four week old seedlings were inoculated and maintained under greenhouse conditions in order to quantify uredospore germination, appressorium formation and colony size. Spore germination ($p = 0.01$) and appressorium formation ($p < 0.001$) were dependent on variety. Colonies were largest in Rumsey and smallest in Osage, with average colony length significantly different between these two varieties at both 4 and 8 days post-inoculation. **Poster MP115**

*McDonald, Tami R. Armaleo, Daniele, and Lutzoni, Francois. Department of Biology, Duke University, Durham, NC 27708, USA. trm5@duke.edu. **Epigenetics of lichen symbiosis**.

The molecular mechanisms by which fungi and algae establish the lichen symbiosis are largely unelucidated. However, the discovery of wide-scale DNA methylation in the lichen thallus (Armaleo and Miao, 1999) raises the possibility that chromatin remodeling could be a critical step in the formation of symbiosis. Remodeling chromatin from transcriptionally active (euchromatic) to transcriptionally repressive (heterochromatic) forms involves several steps that are highly conserved throughout eukaryotes with the exception of *Saccharomyces cerevisea.* These steps include deacetylation of histones, methylation of histone H3 at lysine 9, condensation of HP1 onto DNA, DNA methylation, and the adoption of a closed heterochromatic conformation that inhibits transcriptional machinery. The finding that DNA in lichenized fungi is heavily methylated in symbiotic tissues suggests that much of the genome is epigenetically silenced either to facilitate symbiotic interaction or as a response to symbiosis. I

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investigate the relationship of the aforementioned silencing events to DNA methylation levels in the symbiotic state with an emphasis on histone methyltransferase activity using western blotting and heterologus expression of lichen genes in closely related model fungi. **Poster MP99**

*McLenon, Terri M.[1], Schadt, Christopher W.[2], Rizvi, Leena[1], Martin, Andrew P.[4], Schmidt, Steve K.[4], Vilgalys, Rytas[5], Moncalvo, JeanMarc[3]. [1]University of Toronto, Canada; [2]Oak Ridge National Laboratory, USA; [3]Royal Ontario Museum, Canada; [4]University of Colorado, USA; [5]Duke University, USA. terri.mclenon@utoronto.ca. **Members of a novel Ascomycota clade detected from soil**.

Several recent DNA sequencing-based studies have reported many unknown fungal rDNA sequences from environmental samples. The purpose of this study was: 1) to reconcile disparate data sets of unknown fungal rDNA sequences from previously published studies; and 2) to determine the phylogenetic placement of this clade within the Ascomycota using SSU and LSU rDNA data. We developed specific primers and used a nested PCR approach to amplify and sequence ca. 3 Kb of rDNA from coniferous forest soil. BLAST searches using various portions of the newly produced 3Kb rDNA fragment as a query sequence retrieved many unclassified sequences from a broad range of habitats and geographic origins which were monophyletic in phylogenetic analyses. This is a novel clade that occupies a unique and basal position in the phylogeny, distinct from the three currently recognized subphyla of Ascomycota, the Taphrinomycotina, Saccharomycotina, and Pezizomycotina. Based on the position of this novel clade between the Taphrinomycotina and Saccharomycotina, we hypothesize that these fungi do not produce conspicuous ascomata or other macroscopic structures, and similar to many Taphrinomycotina, are obligate biotrophs or intracellular parasites. This would explain why this subphylum has been overlooked in the past. **Contr. Talk: Sunday pm1 Ascomycete systematics.**

*Meding, S. Mercer, Bledsoe, Caroline S. Horwath, William R. Zasoski, Robert J. Univ. of CA, Davis, One Shields Ave. Davis, California, 95616, USA. smmeding@ucdavis.edu. **Hyphal transfer of ^{15}N-nitrate and rubidium between 2-3 yr established blue oak seedlings in an oak woodland of the California Sierra Nevada Foothills**.

Mycorrhizal plants have the ability to form underground hyphal connections. Common mycorrhizal networks provide the potential for rapid nutrient movement between connected organisms while bypassing the soil pathway. Plots were developed at an oak woodland site in order to examine the hyphal mediated transfer of nutrients between mycorrhizal blue oak seedlings within a field setting. Two year old oak seedlings were planted and plots setup during the summer of '01. Each plot 0.37 m^2 was divided into two square 0.186 m^2 areas by a buried double layer 25 micron stainless steel mesh screen. Screen layers were separated by a 1 cm air-gap. In June of ,04, a donor oak was chosen from one side of each screened plot and leaves were labeled with 1 ml of 150 mM RbCl and 1 ml of 150 mM KNO_3 at 99 atom percent ^{15}N. Receiver oaks were harvested after 2 weeks and analyzed for the labels. Concentrations exceeding control and pre-harvest background levels were detected in receivers from both sides of the screen barriers. Movement of labels did not correlate with proximity to the donor, and label concentrations were higher in receivers with a screen barrier to donors than in receivers without screens in 1/3 the treated plots for Rb and 3/4 for ^{15}N. Results provide evidence of nutrient transfer across a 1 cm air-gap via fungal hyphae, thus bypassing a soil pathway. **Poster MP63**

*Mehl, Hillary L. and Epstein, Lynn. Department of Plant Pathology, University of California, Davis CA 95616, USA. hlmehl@ucdavis.edu. **The distribution and quantification of *Fusarium solani* f. sp. *cucurbitae* race 2, teleomorph *Nectria haematococca* mating population V, in a sewage system**.

In a phylogenetic study of *Fusarium* isolates from clinical specimens and hospital environments, the most common lineage was conspecific with *Fusarium solani* f. sp. *cucurbitae* race 2 (Fsc2), a pathogen of cucurbit fruits. Identification of environmental sources of Fsc2 is important in understanding its epidemiology as an opportunistic human pathogen. Fsc2-specific primers were designed from translation elongation factor 1-alpha sequences, and a PCR assay was used to identify Fsc2 from various sources. In a survey of cucurbit fruits, Fsc2 was rarely isolated, and the fungus was not detected in agricultural soils. However, Fsc2 was isolated consistently from sewage solids from wastewater and from shower and sink drains. Dilution plating and real-time PCR were used to quantify Fsc2 at different locations in the wastewater treatment system and in drains. Fsc2 was present at a concentration of approximately 10^3 CFU per g dry weight of sewage solids in building effluent, wastewater treatment plant influent, and treatment plant oxidation ditches, presumably as conidia. Fsc2 was associated with sewage solids, and was not detected in the clarified effluent. Fsc2 was isolated from solids in sink and shower drains at approximately 10^5 CFU per g dry weight. Both drains and wastewater may be important sources of Fsc2 inoculum in opportunistic human infections. **Contr. Talk: Tues AM2 Fungal Pathogens: population structure and distributions**

*Mejia, Luis C.[1], Castlebury, Lisa A.[2], Rossman, Amy Y.[2], White, James F. Jr.[1]. [1]Dept. of Plant Biology and Pathology, Rutgers University, 59 Dudley Road, Foran Hall, New Brunswick, NJ 08901. [2]USDA-ARS Systematic Botany and Mycology Laboratory, 10300 Baltimore Ave, Beltsville, MD 2075-2350, USA. mejial@eden.rutgers.edu. **Clarification of the nomenclature and relationships of the genera *Cryptosporella, Ophiovalsa* and *Winterella* (Gnomoniaceae).**

Fungi of the genera *Cryptosporella* Sacc, *Ophiovalsa* Petrak and *Winterella* O. Kuntze J. Reid and Booth have been reported as saprobes, endophytes and pathogens mainly from trees belonging in the Betulaceae and Ulmaceae and have recently been assigned to the family Gnomoniaceae (Diaporthales). These genera have been historically treated as closely related. Depending on the particular author and what morphological characters were emphasized, they have been considered to constitute a single genus or different genera and confusion persists today. The present study involving a selection of collections used a combination of classical morphological characters, cultural studies, and a multigene sequencing approach (ITS and RPB2) to clarify relationships. The specimens show a wide range of ascospore morphologies but formed a single clade within the Gnomoniaceae. Our results and review of the literature indicate that the fungi assigned to the three genera above represent a single genus *Cryptosporella* Sacc. with *C. hypoderm* Sacc. as the type species. **Contr. Talk: Tuesday PM 1 Ascomycete systematics.**

*Meyer, Allen F. Schmidt, Steven K. Department of Ecology and Evolutionary Biology, U Colorado Boulder, Boulder, Colorado, USA. allen.meyer@colorado.edu. **Molecular determination of zoosporic fungi in the environment**.

Soil microbes show surprisingly high activity in under-snow alpine environments, and fungi dominate these under-snow microbial communities. We have demonstrated that zoosporic fungi, particularly chytrids, are a key component of this fungal soil diversity. Using both culture-free and culture-based molecular techniques we have demonstrated the presence of multiple major zoosporic groups, including the Chytridiales ("Rhizophydium clade"), the Spizellomycetales, and the Monoblepharidales. In addition our results suggest that several novel, major, zoosporic groups are present in such environments. **Symposium: Monday 1:00-4:30 Diversity of Zoosporic Fungi.**

*Miadlikowska, Jolanta[1], Kauff, Frank[1], Hofstetter, Valerie[1], Fraker, Emily[1], Grube, Martin[2], Reeb, Valerie[1] and Lutzoni, Francois[1]. [1]Department of Biology, Duke University, Durham, NC 27708-0338, USA; [2]Institut fur Botanik, Karl-Franzens-Universitat, Holteigasse 6, A-8010 Graz, Austria. jolantam@duke.edu. **"More and better": improvement in phylogenetic systematics of the Lecanoromycetes (Pezizomycotina, Ascomycota).**

Lecanoromycetes includes the majority of lichen-forming fungi and represents phenotypically the most complex class of all fungi. We reconstructed phylogenetic relationships of the Lecanoromycetes with Bayesian and Maximum Likelihood methods based on combined multilocus (nucSSU, nucLSU, mitSSU, RPB 1 and RPB 2) data sets using a supermatrix approach. Nine of ten orders and 43 out of the 64 families currently recognized in the classification of the Lecanoromycetes were represented in the sampling. Our analyses strongly support the Acarosporomycetidae and Ostropomycetidae as monophyletic, whereas the delimitation of the largest subclass, the Lecanoromycetidae, remains uncertain. Our study shows that recent classifications include several non-monophyletic taxa at different rankse.g. Lecanorales, Lecanoraceae, Lecideaceae, Psoraceae, and Ramalinaceae), which need to be re-circumscribed. The formerly recognized family Candelariaceae (currently part of the Lecanoraceae) represents the second evolutionary split within the Lecanoromycetes, after the Acarosporomycetidae. Our phylogenies confirm that ascus morphology cannot be consistently applied to lichen classification. The inclusion of *RPB* 1 (first time for the Lecanoromycetes) and *RPB* 2 greatly improved phylogenetic resolution and internode support within the Lecanoromycetes compared to existing phylogenies. **Contr. Talk: Monday AM2 Fungal Systematics**

*Miller, Bradley[1], McCleneghan, S. Coleman and Neufeld, Howard[2]. [1]Virginia Polytechnic Institute and State University, Blacksburg VA 24061; [2]Appalachian

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State University, Boone, NC 28608, USA. bwmillergk@hotmail.com. **The successful nursery production of red spruce seedlings with indigenous ectomycorrhizal fungi of the endangered Southern Appalachian spruce-fir ecosystem**.

The endangered southern Appalachian spruce-fir forests have been negatively affected by exotic pests and excessive timber harvests. Reforestation efforts to rapidly expand this endangered ecosystem may require the nursery production of red spruce seedlings with indigenous ectomycorrhizal (ECM) fungi. Previous research has shown that exponentially increasing fertilization regimes, compared to conventional regimes, has produced nutrient loaded seedlings while increasing ECM colonization with cultured fungi. Our results show that exponential fertilization of spruce seedlings grown in native spruce forest soils increased seedling N and P concentrations even at low ECM colonization rates. Exponential fertilization at operational and low nutrient loading rates did not prohibit indigenous ECM morphotype diversity or colonization of nursery raised spruce seedling when compared to conventional fertilization. Five indigenous ECM, commonly found in elevated N environments, accounted for greater than 98 percent of ECM species after two growing season. These results show that exponential fertilization of red spruce seedlings raised in native forest soil mixtures is a viable strategy for the nursery production of seedlings to be outplanted in the endangered southern Appalachian spruce-fir forests. **Contr. Talk: Monday AM1 Fungal Ecology- Mycorrhizae.**

*Money, Nicholas P.[1], Pringle, Anne[2], Patek, Sheila N.[3], Stolze, Jessica L.[1], Fischer, Mark[4]. [1]Miami University, Oxford, OH; [2]Harvard University, Cambridge, MA; [3]University of California, Berkeley, CA; [4]College of Mount St. Joseph, Cincinnati, OH, USA. moneynp@muohio.edu. **The launch of the Ballistospore**.

Ballistospore discharge is a feature of 30,000 species of mushrooms, basidiomycete yeasts, and pathogenic rusts and smuts. A few seconds prior to the launch of a ballistospore, a drop of fluid called Buller's drop, develops at its base. This drop enlarges until it approaches the volume of the spore and then, "instantaneously", spore and drop are catapulted into the air. Until recently, the launch process eluded analysis, but spore motion has now been captured using ultra high speed video microscopy. Images obtained at camera speeds of up to 100,000 frames per second demonstrate that spore discharge occurs when the expanding Buller's drop merges with fluid on the spore surface. Although this coalescence may result from the directed collapse of Buller,s drop onto the spore, it may also involve the movement of the spore toward the drop. The release of surface tension at coalescence provides the energy and directional momentum to propel the spore and drop into the air. Analyses show that the initial acceleration of the spore exceeds 10,000 g. **Symposium: Sunday 1:30-5:00 Fungal Movement: Contemporary Experimental Analysis**

*Moreau, Pierre-Arthur[1], Peintner, Ursula[2], and Gardes, Monique[3]. [1]Laboratoire de Botanique, Université de Lille, France; [2]Institute of Microbiology, University of Innsbruck, Austria; [3]Laboratoire Evolution et Diversité Biologique, Université de Toulouse III, France. gardes@cict.fr. **Phylogeny of the ectomycorrhizal mushroom genus *Alnicola* (Basidiomycota, Cortinariaceae) based on rDNA sequences with special emphasis on host specificity and morphological characters**.

Alnicola = Naucoria, pro parte, is a mushroom genus of strictly temperate, obligately ectomycorrhizal species, traditionally included in the family Cortinariaceae. Most *Alnicola* spp. are primarily host specific on *Alnus,* although a few are mycobionts of *Salix* or other hosts. We used a combination of classical morphological, and phylogenetic methods (rDNA ITS and LSU sequences) to address the following questions: i) Is *Alnicola* monophyletic? And ii) Are characters like host specificity or microscopical structures synapomorphic for certain clades? The study included nearly all currently known European *Alnicola* sp. Our results demonstrated that, on one hand, the genus *Alnicola* is polyphyletic, with sistergroup relationships to *Hebeloma, Anamika* or the clades, Hymenogaster I, and, Hymenogaster II. On the other hand, *Alnicola* splits into three well-supported clades corresponding to the sections *Alnicola, Submelinoides* and *Salicicolae.* The strict host-specificity to *Alnus* is a derived character and has occurred at least twice. The following morphological characters are synapomorphic for defined clades: the spindle-shaped hymenial cystidia for sect. *Alnicola,* the hymeniform pileipellis for sect. *Submelinoides,* and monocaryotic/clampless hyphae for sect. *Salicicolae* and its sistergroup, Hymenogaster II. **Poster MP147**

*Moss, Angela S. Dortaj, Ida, Reddy, Nikla S. and San Francisco, Michael J. Dept. of Biological Sciences, Texas Tech University, Lubbock TX 79409, USA. michael.sanfrancisco@ttu.edu. **Factors influencing virulence in *Batrachochytrium dendrobatidis*.**

Batrachochytrium dendrobatidis causes amphibian chytridiomycosis, a disease characterized by hyperkeratosis, sloughing and erosion of the epidermis, and occasional ulcerations. The organism has been implicated in extinctions and global declines of amphibians in parts of Australia, New Zealand, Europe, and North, Central and South America. Recent studies indicate that global warming may play a role in the infectivity of this organism and its sudden emergence as an infectious disease of amphibians. We are currently investigating environmental triggers that may impact the virulence and chemotaxis of *Batrachochytrium dendrobatidis.* Our studies suggest that amphibian epidermal tissues infected with the organism undergo rapid maceration. Thick sections of infected tissues prepared for electron microscopy show complete destruction of epithelial tissues. We are also investigating mechanisms responsible for host tissue destruction. Additionally, we are assessing model organisms that may serve as alternate hosts in order to facilitate our study of the organism. **Poster MP114**

*Mullaney, Edward J.[1] Ullah, Abul H. J.[1], Locovare, Heather[1], Sethumadhavan, Kandan[1] and Lei, Xin Gen.[2]. [1]SRRC-ARS-USDA, New Orleans, LA, USA; [2]Department of Animal Science, Cornell University, Ithaca NY, USA. emul@srrc.ars.usda.gov. **Modification of the pH profile of *Aspergillus niger* phytase by site-directed mutagenesis**.

A huge quantity of phosphorus is sequestered as phytate in plant seeds and grains. The increased use of soybean and other plant meals in the feed of animals that lack a digestive phytase to hydrolyze phytates (wine, poultry and other monogastrics) has resulted in concern over the negative environmental impact of increased levels of phosphorus in manure. Over the last decade, the efficacy of fungal phytase as an animal feed additive to reduce phosphorus levels in manure has been established. The principal fungal phytase that is marketed today is the native enzyme whose gene has been cloned and overexpressed to make it commercially viable. While this enzyme performs well in this capacity, its pH profile does not permit optimal activity at the pH environment found in the digestive tract. As research has provided information on the catalytic mechanism of this enzyme, a histidine acid phosphatase, efforts have now focused on defining the role of the individual amino acids that constitute the substrate specificity site of the enzyme. These amino acids determine both the binding specificity for phytate and the pH profile of the enzyme. In *Aspergillus niger* NRRL 3135 phytase (PhyA), research has established the vital role of amino acid residues 300 and 228 in increasing the specific activity of the enzyme in the mid acidic pH range 3.0-4.0 compared with the wild type PhyA. This alteration of the pH profile better matches the pH profile of the stomach. Results of a swine feed trial confirmed the increased performance of mutant E228K by significant weight gain over the same diet supplemented with wild type PhyA.**Poster MP103**

Necla Caglarirmak[1] and Ralph H. Kurtzman, Jr.[2]. [1]Celal Bayar University, Saruhanli College, Food Technology Department, Saruhanli Manisa, Turkey; [2]445 Vassar Ave, Berkeley CA, USA. kurtzmanr@earthlink.net. **Composition of *Agaricus bisporus* harvested from three flushes**.

Analyses of the nutritional value of *Agaricus bisporus* has shown considerable variation. Agaricus and other cultivated mushrooms are harvested in successive "flushes" on individual beds. Various factors might explain the variations. We chose to investigate the possibility that each of three flushes might give different analyses due to substrate depletion, increased ramification or possibly senescence. Since approximately ten kg of substrate are lost for every kg of mushrooms, it was not surprising that the ash content was greatest in the third flush. However, most common minerals did not increase. Protein increased after the first flush, but there was significantly more protein in all flushes of the second planting than in the first. Vitamin C was much greater in the second flush and less, but also significantly greater in the third flush. While there was less niacin in the second flush than in the first and the third. We conclude that the flush does have an effect, but that many other factors make the nutritional value of mushrooms variable. **Poster MP106**

*Neves, Maria-Alice[1,2], Halling, Roy E.[1]. [1]New York Botanical Garden, ISB, Bronx, NY 10458; [2]City University of New York, New York, NY 10016, USA. mneves@nybg.org. **Phylogenetics of *Phylloporus* (Boletales) species based on molecular data**.

Phylloporus produce a lamellate rather than poroid hymenophore although other basidiome characters, spore morphology, and chemical and molecular data support placement in the Boletales. Despite several broad-scale phylogenetic studies in the Boletaceae, the phylogenetic relationships of *Phylloporus* remain unclear. Previous phylogenies of this group include only

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two species from Europe and North America. The results of Binder (1999) suggest that *Phylloporus* is the sister group to the *Xerocomus subtomentosus* group, species of which produce poroid hymenophores. While the majority of *Phylloporus* species have a pantropical distribution, no studies on this group have included the majority of known tropical species in addition to the few north temperate taxa. In this study, we present preliminary results toward clarifying infrageneric phylogenetic relationships in *Phylloporus* ; our analysis includes the largest selection of *Phylloporus* species represented in a phylogenetic study. Phylogenetic relationships of selected species of *Phylloporus, Xerocomus, Aureoboletus,* and *Chalciporus* were estimated by maximum parsimony analysis of the rDNA large subunit; *Chalciporus piperatus* was used as an outgroup. The results reveal that specimens from Costa Rica show a big phylogenetic diversity and include several undescribed species. Our study establishes preliminary hypotheses for species distribution and morphological evolution in this important ectomycorrhizal genus. **Poster MP148**

O'Brien, Heath, Jolanta Miadlikowska, Trevor Goward, Franocis Lutzoni. Department of Biology, Duke University, Durham US 27708, USA; Herbarium, Department of Botany, University of British Columbia, Vancouver BC V6T 2B1 Canada. heo3@duke.edu. **Resolving species boundries in *Peltigera* using multi-locus phylogenetics**.

Species delimitation has been a long-standing problem in the lichen forming fungal genus *Peltigera,* with many specimens exhibiting combinations of morphological features of various species. We obtained sequence data for three loci (ITS, beta-tubulin, *RPB1*) from 221 specimens collected in sympatry at four sites in British Columbia, Canada. These represented 15 described species, as well as a number of putative hybrids or undescribed species. We also obtained ITS for additional specimens of each described species collected throughout their range. Each described species formed a monophyletic group in ITS phylogenies, but we identified five additional groups with no corresponding name. Phylogenies from the additional loci were not as well resolved as those from the ITS but the haplotypes were nevertheless unique in all but two cases, apparently representing either hybrid individuals or ancestral alleles that have not had time to accumulate mutations since speciation. In any case, there is strong evidence of linkage disequilibrium for interspecific comparisons. Two of the new species, belong to the morphologically variable *Peltigera leucophlebia* group and are morphologically distinct, helping to settle earlier problems with species identification in the group. The remaining species are members of the *Peltigera canina* group, in which morphological variability is considerable, until now defying our attempts to find good diagnostic characters for our species. Nevertheless, this study demonstrates the power of multi-locus phylogenetic approaches (in combination with detailed morphological work) for clarifying the delimitation of new species. **Contr. Talk: Monday AM2 Fungal Systematics**

*O'Reilly, Bernadette, D. and Volk, Thomas, J. Department of Biology, University of Wisconsin - La Crosse, La Crosse WI 54601, USA. oreilly.bern@students.uwlax.edu. **Using Microscopy and PCR to verify the mycorrhizal association of *Morchella esculenta* with *Ulmus americana***.

Our previous research (presented at earlier MSA meetings) has shown that certain microbes are consistently isolated from morel fruiting bodies and induced significant morphological changes in *Morchella* hyphae in vitro. Previous research from our lab (unpublished) showed that *Morchella* can form a mycorrhizal association with *Ulmus americana* in the laboratory. We have expanded this work to use more sophisticated microscopy techniques. *Ulmus americana* seeds were axenically germinated on water agar and transferred after one week to individual Petri dishes containing CYM agar. The dishes were separated into three groups and inoculated with *Morchella esculenta* mycelium. One group was additionally treated with a bacterial isolate and one group with a yeast isolate. Controls were uninoculated roots. After being in a growth chamber for 14 days, the seedlings were checked microscopically for mycorrhizae synthesis and isolate interactions. Whole and sectioned roots tips were examined using vital dye Fluorescence Microscopy, Scanning Electron Microscopy and Transmission Electron Microscopy. To check for mycorrhizal associations *in vivo,* root samples from elm seedlings found near wild morel fruiting bodies were checked for *Morchella* mycorrhizae using the microscopy techniques described above, as well as PCR. Significant interactions were seen between the two or three partners in each association, although the exact nature of the interactions remains to be elucidated. **Contr. Talk: Monday AM1 Fungal Ecology- Mycorrhizae.**

*Ortiz-Santana, B.[1], Lodge, D. J.[1], and Baroni, T. J.[2]. [1]Center for Forest Mycology Research and Int. Inst. Tropical Forestry, USDA-FS, Luquillo PR 00773; [2]Department of Biological Sciences, SUNY-Cortland, Cortland, NY 13045, USA. bortizsantana@yahoo.com. **Phylogeny and biogeography of Caribbean Boletales**.

Results are presented from a four-year study of the diversity, distribution and phylogeny of Boletales from the Dominican Republic (DR) and Belize in the Caribbean Basin (CB). About 450 collections from Belize comprised ±60 species in 14 genera, including 20 new species; 28 of the 31 identified species are new records for Belize. About 200 collections from the DR comprised ±20 species in 6 genera, including 5 new taxa. Seven species represent disjunct populations in Belize, the DR and N. Am.: *Austroboletus subflavidus, Boletellus ananas* complex, *Retiboletus griseus* complex, *Strobilomyces confusus, Suillus decipiens, S. salmonicolor* and *Tylopilus ballouii.* Disjunct populations restricted to Belize and N. Am. were *Gyroporus castaneus* and *Pulveroboletus ravenelii,* while those restricted to the DR and N. Am. were *Suillus tomentosus* and possibly *S. pseudobrevipes.* A phylogenetic analysis of the disjunct populations was conducted to determine their evolutionary relationships and possible dispersal between N. Am. and the CB. Phylogenetic relationships were based on genetic distance analyses of sequences from the ITS region and the 5' part of the LSU of the nuclear ribosomal DNA. Collections of *A. subflavidus, R. griseus, S. confusus,* and *S. decipiens,* from Belize were closer to those from the DR than to ones from eastern USA, whereas *B. ananas* and *S. salmonicolor* from Belize were closer to those from eastern USA than those from the DR, suggesting different dispersal patterns. **Contr. Talk: Sunday PM 2 Basidiomycete systematics**

*Padamsee, Mahahabeen, Ceilo, Gail J., Dentinger, Bryn T. M., McLaughlin, David J. Dept. of Plant Biology, Univ. of Minnesota, St. Paul, MN 55108, USA. pada0003@umn.edu. **What can ultrastructure of cystidia tell us about fungal evolution**?.

Constructing a database of subcellular characters of cystidia for the Assembling the Fungal Tree of Life (AFTOL) Stuctural and Biochemical Database has revealed gaps in our knowledge. In 24 years there have been only 21 published studies of cystidia utilizing transmission electron microscopy. Fourteen of these studies are from taxa in the Euagaric clade but within a genus no two closely related species have been examined. Limited interpretation of character homology increases the difficulty in reaching phylogenetic conclusions. Organisms examined for the AFTOL project will be presented as models for collecting and coding of cystidial subcellular characters. Ultrastructure reveals striking variations in the endomembrane system among genera. Light microscopic cytochemistry is used as a guide to clarify subcellular characters. Initial analyses of cystidial characters illustrate the challenges and evolutionary potential of subcellular details. **Contr. Talk: Sunday PM 2 Basidiomycete systematics**

Padgett, David E. and J. Craig Bailey, Dept. of Biology and Marine Biology, Univ. of NC, Wilmington NC, USA. padgett@uncw.edu. **The Saprolegniaceae — new species concepts**.

Species of the Saprolegniaceae are difficult to identify because of the plasticity of the morphological features used to characterize them. This has resulted in significant overlap of described taxa to the extent that unknowns often can be identified only to a species cluster. Our attempt to resolve this problem focused on the genus *Saprolegnia* and was based on the proposition that the most valid criterion for circumscribing both genera and species is gene sequence comparisons. Our phylogram for 55 randomly-selected *Saprolegnia* isolates revealed 10 robustly supported clades that probably represent distinct species. Morphological identifications of individuals within each clade, however, yielded multiple names in most instances; thus confirming the need for comprehensive systematic revision of the genus. We found that all ten *Saprolegnia* clades were distinguishable from each other using unique combinations of morphological features but not without including some features that had not heretofore been used at the species level. Preliminary work on several other saprolegniaceous genera has shown morphological plasticity similar to or greater than in *Saprolegnia* and suggests that our approach to resolving species overlap may well be broadly applicable within the family. **Symposium: Monday 1:00-4:30 Diversity of Zoosporic Fungi**

*Palmer, Jonathan M.[1], Czederpiltz, Daniel L.L.[2], Volk, Thomas J.[1]. [1]Biology Department, University of Wisconsin-La Crosse, La Crosse WI 54601; [2]Center for Forest Mycology Research, USDA Forest Service, Madison WI 53726, USA. palmer.jona@students.uwlax.edu. **Morphological and molecular characterization of mycorrhizal fungi associated with a disjunct stand of American chestnut, *Castanea dentata*, in Wisconsin**.

Continued on following page

Circa 1900 a farmer from the eastern U.S. planted eleven American chestnut (*Castanea dentata*) seeds on a newly established farm near West Salem in western Wisconsin. These trees were very successful, producing a large stand of over 6000 trees. Since this area was well outside of the natural range of chestnut, these trees remained free from chestnut blight, caused by *Cryphonectria parasitica,* until 1988. Because chestnut was almost entirely eliminated from its native range by the early 1950,s, no modern studies have examined chestnut mycorrhizae. To identify putative mycorrhizal associates of chestnut, our approach was two-fold: 1) an extensive fruiting body survey was conducted for 3 seasons that yielded over 400 collections, of which approximately 110 were putatively mycorrhizal, and 2) a below-ground molecular approach was used to generate DNA sequences of the ITS region from mycorrhizae. To date, 102 root tip sequences have been generated. These sequences are phylogenetically diverse, although all are basidiomycetes or ascomycetes falling into 11 families. In addition, 73 of the 110 fruiting body collections have been sequenced. From these data we have created a website, http://www.chestnutfungi.com, which contains a BLAST searchable database of ITS sequences coupled with pictures of both root tips and fruiting bodies. **Contr. Talk: Monday AM1 Fungal Ecology- Mycorrhizae.**

*Pan, Jean J.[1,2] and May, Georgiana[1]. [1]Dept. of Ecology, Evolution, and Behavior, University of Minnesota, St. Paul, MN 55108; [2]Dept. of Biology, University of Akron, Akron, OH 44325-3908, USA. jepan@uakron.edu. **The effects of host plant variation on the endophyte community of corn, *Zea mays*.**

The primary focus of many fungal endophyte studies has been to understand how plants benefit by engaging in this symbiotic interaction. One overlooked and extremely important aspect of this symbiotic interaction is the role of the host plant in shaping the fungal endophyte community, and consequently, plant effects on fungal biodiversity. I addressed this issue by investigating whether host plants could affect fungal endophyte communities in corn, *Zea mays*. Using DNA-based approaches to identify fungi, I compared the endophyte communities on recombinant inbred lines of ctheir resistance to the host specific fungal pathogen, *Ustilago maydis* (corn smut). I found that fungal species diversity and evenness was not significantly different between corn lines. However, endophyte community composition was significantly affected by both corn line with smut infection status and corn line with field plot. I found that endophyte community composition was: 1) more similar among *U. maydis* infected plants than uninfected plants within corn lines, and 2) more similar across plots for lines susceptible to *U. maydis* infection. Results from this study indicate that host plants, host symbiotic interactions, and spatial location can all affect fungal endophyte communities. **Contr. Talk: Monday PM- Fungal Ecology - Endophytes and Saprobes**

Partida-Martinez, Lalia P., Kirstin Scherlach and Christian Hertweck. Leibniz-Institute for Natural Product Research and Infection Biology, (HKI) Beutenbergstrasse 11a. 07745 Jena, Germany. christian.hertweck@hki-jena.de. **Pathogenic fungus harbours endosymbiotic bacteria for toxin production**.

Pathogenic fungi generally exert their destructive effects through pathogenicity factors. An important example is the macrocyclic polyketide rhizoxin, the causative agent of rice seedling blight, from the fungus *Rhizopus microsporus*. The plant disease is typically initiated by an abnormal swelling of the seedling roots caused by rhizoxin without any sign of infection by the pathogen. The phytotoxin exerts its destructive effect by binding to rice ß-tubulin, which results in inhibition of mitosis and cell cycle arrest. Owing to its remarkably strong antimitotic activity in most eukaryotic cells, including various human cancer cell lines, rhizoxin has attracted considerable interest as a potential antitumour drug. By a series of experiments we could unequivocally demonstrate that rhizoxin is not biosynthesized by the fungus itself, but by endosymbiotic bacteria of the genus *Burkholderia*. Our unexpected findings unveil a remarkably complex symbiotic-pathogenic alliance that extends the fungus' plant interaction to a third bacterial key player. In addition we were able to culture the symbiont and produce antitumoral rhizoxin derivatives. Our progress in studying the molecular basis of this rare symbiosis is presented. **Symposium: Tues 1:30-5:00 Bacterial Symbionts of Fungi**

*Picard, Kathryn T.[1], Powell, Martha J.[1], Letcher, Peter M.[1], Laursen, Gary A.[2]. [1]Dept. of Biological Sciences, The University of Alabama, [2]Dept. of Biology and Wildlife, University of Alaska, Fairbanks AK, USA. letch006@bama.ua.edu. **Diversity of chytrid fungi in disparate biomes**.

Although chytrid fungi are important nutrient recyclers and plant and animal pathogens, little is known about either their evolutionary history or biodiversity. In our attempts to understand genetic diversity in the *Rhizophydium* clade in the Phylum Chytridiomycota, we have learned much about species richness in vastly different biomes. The current focus of our research is chytrid diversity in Australian and Alaskan soils. Despite the incongruence between these habitats (Australian sclerophyll forests versus Alaskan taiga and tundra), there is considerable overlap in their biodiversity, with several individual species being found in both regions, suggesting that there may be osmopolitan chytrid species. **Poster MP141**

*Pivarski, Kara L. and Pawlowska, Teresa. Department of Plant Pathology, 334 Plant Science, Cornell University, Ithaca, NY 14853 USA. klp37@cornell.edu. **Population structure of endosymbiotic bacteria associated with arbuscular mycorrhizal fungi**.

Arbuscular mycorrhizal (AM) fungi (Glomeromycota) have been reported to contain bacterium-like organelles (BLOs). The application of molecular identification methods revealed that the BLOs are in fact endosymbiotic bacteria. In a number of different *Gigaspora* species studied so far, the endosymbiotic bacteria are closely related to *Burkholderia*. Based on in vitro observations, it is believed that the endosymbiotic bacteria, are vertically transmitted. However, no information is available about the population structure of these endosymbiotic bacteria within naturally occurring AM fungal populations. Our study intends to look at natural populations of AM fungi, particularly *Gigaspora* sp., in coastal sand dunes of the eastern U.S. in order to study the population structure of their endosymbiotic bacteria. **Poster MP70**

Plattner, Alex*[1], Jae-Jin Kim[1], Breuil, Colette[1], Hausner, Georg[2], Reid, James[2], Yamaoka, Yuichi[3]. [1]Department of Wood Science, University of British Columbia, 2424 Main Mall, Vancouver, BC, V6T-1Z4; [2]Department of Microbiology, University of Manitoba, Winnipeg, MB R3T-2N2, Canada; [3]Institute of Agriculture and Forestry, University of Tsukuba, Tsukuba JAPAN. plattner@interchange.ubc.ca. **Phylogeny of the *Ophiostoma minutum* complex**.

Ophiostoma species are the dominant fungal associates of bark beetles. They are economically important because they stain sapwood and cause tree mortality. During recent surveys of the mountain pine beetle in British Columbia, the second most frequently isolated fungus was an *O. minutum* -like species. *O. minutum* is one of several members within an unresolved species complex. Species within the complex are united by falcate ascospores. The objective of this research was to resolve the species complex. Over fifteen strains of *O. minutum* and *O. minutum* -like species from Europe, Japan and North America were examined, along with strains from other species within the complex, such as *O. rollhansenianum, O. minuta-bicolor* and *O. minimum.* Phylogenetic analysis of the beta-tubulin gene and internal transcribed spacer and large subunit regions of ribosomal DNA showed a monophyletic group of *O. minutum* species from Europe and Japan, whereas North American strains were polyphyletic. We suggest describing a new European neo-type from the monophyletic clade, since the original holotype from Europe was destroyed in World War II. The species complex was resolved down to the species level, thus resolving the polytomies that existed from previous work. **Contr. Talk: Sunday pm1 Ascomycete systematics.**

Porter, David. Dept. of Plant Biology, University of Georgia, Athens, GA 30602, USA. porter@plantbio.uga.edu. **What are zoosporic fungi and how has our view of them changed?**

The term 'zoosporic fungi' is one of those hard-to-describe terms, like pornography, that we may not be able to clearly define, but we know it when we see it. Many eukaryotic protists with absorptive heterotrophy and flagellated spores have been included in the umbrella group that we call 'zoosporic fungi'. These include the Oomycetes, Hyphochytrids, Labyrinthulids, Plasmodiophorids, Chytrids and Blastocladiales. With the advent of cladistic analysis of gene sequences, our understanding of the phylogeny of the early eukaryote radiation has become dramatically more informed than it was 20-30 years ago when phylogenetic hypotheses were supported by little more than structural homology and intimidation. In the mid 19th Century a few zoosporic fungi started to attract significant attention as major plant pathogens, but for the most part these organisms were relegated to the purgatory of curious basic research. Today we see excellent examples of how basic research in 'zoosporic fungi' has been important to applied scientists interested in pathology, conservation and bio-prospecting. **Symposium: Monday 1:00-4:30 Diversity of Zoosporic Fungi**

Pruett, Grechen. 108 Waters Hall, Division of Plant Sciences, University of Missouri, Columbia MO, USA. gebc07@mizzou.edu. **Performance of burgundy truffle oak host in multiple potting substrates**.

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The European Burgundy truffle *Tuber aestivum* syn. *Tuber uncinatum* is a valuable food commodity and may be a profitable commercial crop in the south central USA. Truffle cultivation involves germinating host trees such as white oaks and hazels in the presence of truffle spores. The spores produce hyphae that surround the root tips and form ectomycorrhizae. High levels of *Tuber* root colonization early in the tree life cycle may reduce competition from other fungi and improve future truffle production. The purpose of this two part study was to develop a host growth medium that satisfied the environmental requirements of the truffle fungus and the host while reducing colonization by other mycorrhizal fungi. The first part of the study evaluated the performance of the English oak x Swamp white oak *Quercus robur* x *Q. bicolor* host grown for 4 months in seven potting mixes. The mixes consisted of different proportions of rice hulls, ground bark, sand, vermiculite, lime, and fertilizer and were based on the RPM (patent pending) potting process developed by Forrest Keeling Nursery in Elsberry MO. Our trees performed best (greatest height, largest root system) in mixes with ground pine bark instead of hardwood bark and with low levels of lime. This combination appears to produce pH and porosity values in an acceptable range for the trees and the fungus. The second part of the study, a year long pot-trial currently in the greenhouse, evaluates truffle fungus performance in the three potting mixes deemed most appropriate for tree growth. **Poster MP62**

*Pryor, Barry M. Hong, Soon Gyu, and Runa, Farhana. Department of Plant Sciences, University of Arizona, Tucson, AZ, USA. bmpryor@u.arizona.edu. **Molecular sytematics of *Alternaria*: species-groups and species concepts.**

The genus *Alternaria* represents approximately 150-200 species of dematiacious Hyphomycetes characterized by the production of phaeodictyospores generally ovate to obclavate in shape. Systematics of the genus to date is based primarily upon morphotaxonomy, recognizing common characteristics of the spore and sporulation apparatus. Recent phylogenetics studies based upon sequences of rDNA and protein coding genes have revealed 10 distinctive subgeneric clades or species-groups, each encompassing taxa with distinct spore/sporulation characteristics. Species-groups correlate well with groupings based upon morphotaxonomic studies with a number of notable exceptions. Over 60% of all taxa are encompassed in two large clades; the alternata and porri species-groups. Other notable species-groups include the infectoria, radicina, brassicicola, sonchi, and panax groups. Species delimitation based upon sequence identity differs among groups with variation in identity ranging from 95-98%. Inclusion into specific *Alternaria* species-groups of members from the genera *Embellisia, Nimbya,* and *Ulocladium* reveal the need for revision of morphological criteria that define *Alternaria* as well as these closely related taxa. **Contr. Talk: Sunday pm1 Ascomycete systematics.**

*Raghavendra, Anil Kumar, Newcombe, George and Shipunov, Alexy. Department of Forest Resources, University of Idaho, Moscow, Idaho 83844-1133, USA. ragh0867@uidaho.edu. **Co-Introduction of fungal endophytes in spotted knapweed *Centaurea maculosa* Lam**.

Invasive exotic plants threaten plant community structure and function. These exotic plants may bring with them a cohort of symbionts, including fungal endophytes to the introduced range. Spotted knapweed *Centaurea maculosa* is an exotic, invasive plant, which was accidentally introduced into North America from Eurasia in the late nineteenth century. If endophytes had been co-introduced in seeds of *C. maculosa,* then the same fungi would be found in both the invaded (North America) and native ranges (Eurasia). In 2004, seeds were collected from eight different locations in the invaded range and the endophyte isolation frequency from these locations ranged from 0 to 85%. Similarly, endophyte isolation frequencies from nine different locations in 2005 ranged from 0 to 59%. A total of 21 morphologically distinct fungal endophytes were isolated from the seeds collected in the invaded range. Endophyte isolation frequencies from seven different locations in the native range (Europe) in 2005 ranged from 13 to 73%. A total of 16 morphologically distinct fungi were isolated from the native range. Further, fungi belonging to *Alternaria, Fusarium* and *Botrytis* were observed in both the invaded and native ranges. It was also noticed that seeds with fungal endophytes when grown in green house conditions produced seeds which were free of endophytes. **Contr. Talk: Monday PM- Fungal Ecology - Endophytes and Saprobes**

*Raja, Huzefa A. and Shearer, Carol A. Dept. of Plant Biology, University of Illinois, Urbana IL 61801, USA. raja@uiuc.edu. **Freshwater euascomycetes of Florida**.

Species identities, diversity, systematics, geographical, habitat and substrate distribution patterns of freshwater euascomycetes are poorly understood. Therefore, as part of an on-going latitudinal survey of freshwater euascomycetes in the Americas, we undertook a study across a temperate/subtropical ecotone at five different geographical sites along the Florida peninsula to address the following questions; 1) Does species richness and composition differ between lotic (streams and rivers) and lenticlakes, ponds) habitats? 2) Are lotic species more widely distributed geographically than lentic species? 3) Are species substrate specialists or generalists? 4) Does the community composition and species richness differ across the temperate/subtropical ecotone of the Florida peninsula? Research to date reveals; 1) Some geographically broadly distributed species occur in both habitat types but cies occur in either lotic or lentic habitats than in both; 2) Preliminary results suggest that lentic habitats may support more taxonomically distinctive communities than lotic habitats; 3) Species occurring on wood were also observed on herbaceous substrates, while species colonizing herbaceous substrates were seldom recorded on wood; 4) Information thus far does not support the idea that species composition and richness varies along a latitudinal gradient in the Florida peninsula. **Contr. Talk: Tuesday PM 1 Ascomycete systematics.**

Raja, Huzefa A. and Shearer, Carol A. Dept. of Plant Biology, University of Illinois, Urbana IL 61801, USA. raja@uiuc.edu. ***Jahnula* species from North and Central America, including three new species**.

We are investigating the geographical distribution patterns of meiosporic and mitosporic freshwater euascomycetes on submerged wood and herbaceous substrates in lotic and lentic habitats along a latitudinal gradient in North, Central and South America. During our investigations, several species of the freshwater euascomycete genus, *Jahnula* Kirschst. (Dothidiomycetes, Jahnulales) were isolated from decorticated softened submerged wood. Here we present three new species of Jahnula collected from North America. Four additional species, *J. aquatica,* from Illinois, and Tennessee, and *J. bipolaris, J. potamophila,* and *J. seychellensis* from Costa Rica are reported for the first time from the Western Hemisphere. Distribution maps and illustrations are presented for the seven species. Species of *Jahnula* share the following morphological character states: hyaline to dark brown membranous ascomata with wide, septate, subtending, brown, superficial hyphae; peridia of mostly large, thick-walled, angular cells; septate pseudoparaphyses; clavate-cylindrical fissitunicate asci; and one-septate, brown, multiguttulate ascospores equipped with a gelatinous sheath and/or appendages. **Poster MP131**

Rivzi, Leena[1], Skillman, Jane[1], Khasa, Damase[2], Piche, Yves[2], Fortin, Andre[2], Moncalvo, Jean-Marc[13]. [1]Department of Botany, University of Toronto, Toronto, Canada, [2]University Laval, Quebec, [3]Royal Ontario Museum, Toronto, Canada. jeanmarcm@gmail.com. **Phylogeographic relationships and taxonomy of Eastern Canadian forest mushrooms**.

Where do fungi that reconstituted Eastern Canada boreal forests following the last glaciation come from? We are investigating this question by sampling molecular phylogenetic data from ectomycorrhizal mushrooms that are widespread in the Northern Hemisphere, with particular attention to taxa of high economic value. A thriving wild mushroom harvesting industry on the Pacific coast of North America has stimulated research about the taxonomy, ecology, and management of this fungal resource. These studies resulted in the recognition of two novel chanterelles species endemic to North Western America, *Cantharellus cascadensis* and *C. formosus,* and of one novel variety, *C. cibarius* var. *roseocanus.* Phylogenetic evidence from multiple genes indicates that the latter two taxa also occur in Eastern Canada. Also, *C. cibarius* var. *roseocanus* is genetically clearly distinct from *C. cibarius* described from Europe, and warrants recognition at the species level. These results indicate a common origin of today,s eastern and western chanterelles, but their exact origin remain unknown. In contrast, DNA sequence data indicate that the matsutake in Eastern Canada is clearly distinct from that in the North America Pacific coast and genetically very close to the European and Eastern Asian matsutake. Phylogeographic data in the *Amanita caesarea* and *A. muscaria* species groups are also presented. Overall, our results indicate complex modes of fungal colonization in boreal areas following glaciation. **Poster MP145**

*Rojas, A.[1], Mikán, J.[2], Villalba, L.E.[3], and De García, M.C.[1], [1]Universidad de los Andes, Laboratorio de Micología y Fitopatología, [2]Universidad Militar Nueva Granada, [3]Archivo de Bogotá, Columbia. jorg-roj@uniandes.edu.co. **Partial purification of proteases from filamentous fungi that cause deterioration of industrial paper**.

Biodeterioration is an essential component for the recycling of organic matter in nature. However, it becomes undesirable when it affects materials with

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cultural or economic importance. Among environmental microorganisms, fungi constitute the biggest problem in microdeterioration of industrial paper stored in archives. The ability of fungi to degrade this and other substrates is mainly due to the production of a battery of enzymes such as cellulases, amylases and proteases. Here, we report the screening and initial characterization of proteolytic activities from fungi present on paper undergoing deterioration in the Archive of Bogotá (Colombia). Thirty two morphotypes of filamentous fungi were isolated and subsequently screened for proteolytic activity in two different solid medium. Fungi with the highest proteolytic activity were selected and cultivated in liquid medium with four different substrates. The resulting proteolytic activities were fractionated with ammonium sulphate, and the more active were partially biochemical characterized. Results from this research will be useful in developing preventive measures for deterioration of paper by fungi in this and other archives. **Poster MP96**

*Rojas, Carlos, Stephenson, Steven L. Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. crojas@uark.edu. **Myxomycetes of Cocos Island, Costa Rica**.

Cocos Island is a small oceanic island located approximately 500 km north of the Galapagos Archipelago in the Pacific Ocean. Although the marine biota of the island has been studied extensively, few biogeographical studies of the terrestrial biota have ever been carried out. For example, the ecology and biogeography of myxomycetes (also known as plasmodial slime molds or myxogastrids) had never been studied on Cocos Island prior to the present investigation. During a visit to Cocos Island in April 2005, six study sites along an elevational transect that extended from the northern coast of the island at Bahía Chatham to the highest peak at Cerro Yglesias were selected. At each site both field and substrate samples of ground litter, aerial litter, bark and twigs were collected. Substrates were studied using the moist chamber culture technique and approximately 20 species, all of them known from the same latitudes on mainland Costa Rica, have been recorded thus far. It seems that the lower elevation sites are richer in myxomycete species than the higher sites, which is probably related to the different plant communities and microhabitats that occur along the elevational transect. However, some species that appear to be common on Cocos Island are only occasionally encountered on the mainland, and the very presence of myxomycetes on this isolated island represents a challenge in understanding the biogeography, evolution and ecological importance of this group of organisms. Molecular analysis is needed in order to understand the genetic relatedness of these species to their counterparts on the mainland, and this process should begin in the near future. **Contr. Talk: Monday AM2 Fungal Systematics**

*Rollins, Adam W. Rojas, Carlos, and Stephenson, Steven L. Dept. of Biological Sciences, University of Arkansas, Fayetteville AR 72701, USA. arollin@uark.edu. **Myxomycetes associated with North American grasslands**.

The assemblages of myxomycetes associated with the grasslands of North America are poorly known. In fact, we are not aware of a single paper dealing specifically with the myxomycetes of grasslands. In the present study, the moist chamber culture technique was used to isolate myxomycetes from samples of aerial litter, ground litter and herbivore dung collected from study areas representing the three main types of grassland (tall grass, mixed grass and short grass) found in North America. Overall, our results indicate that members of the order Physarales are the predominant (i.e. characterized by the highest numbers of species and collections) myxomycetes associated with grasslands, with members of the order Trichiales next in importance. In general, the ground litter microhabitat appears to support a more diverse assemblage of myxomycetes than does the aerial litter microhabitat. Fewer species were recovered from dung, but the assemblage of species associated with dung apparently includes a number of examples restricted largely or even exclusively to this microhabitat. **Contr. Talk: Tues PM 2 Fungal systematics.**

*Runa, Farhana and Barry M. Pryor, University of Arizona, Tucson, AZ, USA. bmpryor@u.arizona.edu. **Phylogenetic relationships among *Ulocladium* and related *Alternaria* and *Embellisia* spp. based upon rDNA and protein coding genes**.

The genus *Ulocladium* represents phaeodictyosporic Hyphomycetes that produce conidia essentially obovoid in shape. Earlier molecular studies that included 5 *Ulocladium* species and related taxa in *Alternaria, Embellisia,* and *Nimbya* revealed conflict between morphology and phylogeny, and revealed the genus was polyphyletic with a core group that was paraphyletic. In the present study, total genomic DNA was extracted from 13 *Ulocladium* species and sequences determined for nuclear internal transcribed spacer and mitochondrial small subunit rDNA, and two protein coding genes: the translation elongation factor 1-alpha and the glyceraldehyde-3-phosphate dehydrogenase gene. Subsequent phylogenetic analyses included related *Alternaria* and *Embellisia* spp. using maximum parsimony and Bayesian methods. Results supported previous findings of polyphyletic and paraphyletic relationships. Ten species clustered into a core *Ulocladium* clade that included *A. cheiranthi* and *E. indefessa. Ulocladium alternaria* and *U. oudemansii* were distantly related and clustered in a single clade related to *A. japonica. Ulocladium obovoideum* represented a single lineage that was basal to all other *Ulocladium* species. All taxa possessed the diagnostic feature of obovoid condium shape, however, this character is homoplasious. Other unique diagnostic characters defining species are discussed. **Contr. Talk: Sunday pm1 Ascomycete systematics.**

*Sagaram, Uma Shankar. Shaw, Brian D. and Shim, Won-Bo. Dept. of Plant Pathology & Microbiology, Texas A&M University, College Station, TX77843-2132, USA. bdshaw@tamu.edu. ***Fusarium verticillioides GBB1,* a heterotrimeric G-protein beta subunit, regulates fumonisin biosynthesis, conidiation, hyphal development, and maize stalk rot virulence**.

Fumonisins produced by *F. verticillioides* pose considerable health and economic concerns. In this study, *GBB1,* a heterotrimeric G protein beta subunit, was disrupted and its role in fumonisin (B1FB1) regulation was investigated. The *GBB1* deletion mutant (BM83) showed normal growth but produced significantly lower levels of FB1 and reduced colonization of maize stalks compared to the wild type. Repression of key FB1 biosynthetic genes in BM83 provided further evidence that *GBB1* is involved in FB1 regulation. Also, results suggested that *GBB1* is involved in the regulation of conidiation via carbon-source sensing mechanism. The mutant also displayed a growth phenotype where hyphae maintained their axis of polarity in an undeviating straight line perpendicular to the point of germination in contrast to wild type hyphae that meander as they grow. Complementation of BM83 with *GBB1* restored FB1 production, virulence, and hyphal growth. Our results suggest that *GBB1* is associated with FB1 regulation, stalk rot virulence, hyphal growth, and conidiation in *F. verticillioides.* **Poster MP104**

*Samuels, Gary J.[1], Thomas, Sarah E.[2], Holmes, Keith A.[2], and Evans, Harry C.[2]. [1]United States Dept. of Agriculture-ARS, Systematic Botany and Mycology Lab. Rm. 304, B-011A,e, MD 20705, U.S.A. [2]Biological Control of Weeds & Plant Diseases, CABI Bioscience, Ascot, U.K. gary@nt.ars-grin.gov. ***Trichoderma* endophytes of sapwood**.

Trichoderma endophytes occur in sapwood of trunks of *Theobroma* spp. *Herrania* sp. *Cola* spp. *Fagus sylvatica, Scalesia pedunculata,* and in the woody liana *Ancistroderma korupensis. Trichoderma* is a genus of soil fungi; trunks of trees represent a new niche for soil fungi. *Trichoderma* endophytes are rare in leaves. Sequences of at least two genes are available for each of the approximately 100 described *Trichoderma* species, making accurate identification possible. Thus species diversity and host specificity of endophytes in one genus can be assessed. Many new species were found, including one non sporulating species. New infra specific lineages distinct from non endophytic lineages represent new genetic diversity, suggesting that endophytic strains may have been isolated. Many new species are based on single cultures or single clones from individual trees; others are based on a few cultures. Only rarely did isolates from different tree genera cluster together, but often isolates from different *Theobroma* species found in the same area clustered together. Thus, while there is evidence of host specificity, this may be a reflection of locale. *Trichoderma* endophytes are abundant in trunks of *Theobroma* trees in America but rare in *Theobroma* trees grown in Africa, suggesting that cacao germplasm moved from its center or origin may have lost an originally rich endphytic biota. **Contr. Talk: Monday PM- Fungal Ecology - Endophytes and Saprobes**

Saunders, Megan and Linda M. Kohn. Department of Biology, University of Toronto at Mississauga, 3359 Mississauga Road, North Mississauga ON Canada L5L 1C6. msaunder@utm.utoronto.ca. **Production of secondary metabolites by corn increases the frequency of colonization by *Fusarium* species**.

Among the most common stressors encountered by plant-associated fungi are the antifungal secondary metabolites produced by their host. Some of these compounds, phytoanticipins, are found constitutively in the plant. We hypothesize that production of phytoanticipins by corn will lessen fungal endophyte diversity. Corn produces benzoxazinoids (Bxs), a class of phytoanticipins that are widely toxic to microbes, insects and plants. Three varieties of corn including

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two high-Bx producing varieties and one non-Bx producing variety were planted in two locations in Ontario, Canada. Endophytic fungi were isolated from root tissue in the seedling and adult plant. We found a significant difference in the community composition of fungi isolated from non-Bx producing versus high Bx-producing corn at the seedling stage. Plants that do not produce Bxs harbor a more diverse and even distribution of fungi as compared with Bx-producing plants. Several species in the genus *Fusarium* that are commonly associated with corn are able to detoxify Bxs. Bx-producing plants contain a higher frequency of both Bx-tolerant and Bx-intolerant *Fusarium* species, a pattern that may indicate phylogenetically determined facilitation between *Fusarium* species. **Contr. Talk: Tues AM2 Fungal Pathogens: population structure and distributions**

Saunders, Megan and Linda M. Kohn. Department of Biology, University of Toronto at Mississauga, 3359 Mississauga Road, North Mississauga ON Canada L5L 1C6. msaunder@utm.utoronto.ca. **Testing the effect of secondary compound production on fungal endophyte community structure in corn**.

Corn produces benzoxazinoids (Bxs), compounds that are widely toxic to microbes, insects and plants. We tested the influence of Bx production on the community structure of fungal endophytes in corn, in both leaf and root tissue, in the seedling and adult plant. We found that in the seedling, there was a significant difference in the community composition of fungi isolated from non-Bx producing versus high Bx-producing corn in root but not in leaf tissue. In the adult plant, no correlation between community composition and Bx-production was detected in either tissue type. Several species in the genus *Fusarium* that are commonly associated with corn are able to detoxify Bxs. A second assay was conducted in the adult plant to determine the frequency of isolation of Bx-tolerant fungi. We found that in leaf tissue, isolation frequency of Bx-tolerant fungi was 3 to 8 times greater in the Bx-producing versus non Bx-producing corn. In root tissue, isolation frequency of Bx-tolerant fungi was genotype specific, but not correlated with Bx-production. In addition, we tested twelve species of fungi for BOA-tolerance, and found several unreported BOA-tolerant species. It appears that Bx production in corn significantly influences the community structure of fungal endophytes in the root tissue of the seedling, and in the leaf tissue of adult plants. **Poster MP79**

*Schilling, Jonathan S. and Jellison, Jody. Department of Biological Sciences, University of Maine, 311 Hitchner Hall, Orono, ME 04469 USA. jonathan@maine.edu. **Calcium extraction from gypsum board (sheetrock) by wood-degrading fungi**.

The common association between wood rot fungi and calcium-containing building materials, coupled with the propensity for these fungi to translocate calcium (Ca) into degrading wood, has led to the theory that Ca importation facilitates fungal wood decay. Specifically, Ca may bind excess oxalate, secreted by fungi metabolizing carbon-rich lignocellulose. We tested effects of gypsum board and calcium chloride on fungal wood decay and oxalate regulation in petri microcosms. We prepared gyp-board using lab-grade Ca sulfate and added fractions to the agar surface. Calcium chloride treatment was 2 mM in agar. All microcosms, including controls, contained 20 mL Type A low-calcium agar. Spruce blocks were decayed 12 weeks in these microcosms by brown rot fungi *Serpula lacrymans*, *Meruliporia incrassata*, and *Fomitopsis pinicola*, and by a white rot species *Irpex lacteus*. Wood weight loss was significant at harvest; however, decay rate and wood pH were unaffected by Ca source. HPLC revealed no treatment effect on soluble/acid-extractable oxalate, despite SEM-EDS confirmation of calcium oxalate crystals along hyphae. Wood cation analysis by ICP-OES and confocal microscopy using FURA RED fluorophore will reveal the extent of wood Ca enrichment and sequestration in hyphae. This work suggests that Ca accumulation during wood decay may be incidental, not mechanistic. **Poster MP72**

*Shamieh, Karimeh S. and Pawlowska, Teresa E. Dept. of Plant Pathology, Cornell University, Ithaca NY 14853, USA. ks382@cornell.edu. **Global patterns of variation in *Glomus etunicatum***.

Arbuscular mycorrhizal (AM) fungi (Glomeromycota) are ubiquitous and important members of the terrestrial soil community, creating symbiotic associations with the majority of land plants. They are also thought to be one of the oldest asexual lineages. The cells and spores of AM fungi contain hundreds of nuclei. Peculiar polymorphisms in rDNA sequences derived from individual spores have triggered a debate over the genetic organization of this group of fungi, originating the heterokaryosis hypothesis, which states that many genetically distinct nuclei may exist within the same individual. To test this hypothesis, we are exploring patterns of geographic variation in a PLSDNA polymerase-like sequence genetic marker that is variable within individual spores of *Glomus etunicatum.* We established in vitro cultures of *G. etunicatum* isolates from several locations around the globe, including Brazil, Great Britain, Australia, Kenya, and the US. Our preliminary data suggest that 1) spores from each single-spore isolate sequenced contain a set of identical PLS variants and 2) the number of PLS variants remains constant among the globally distributed isolates. These data support a homokaryotic model of genetic organization. **Poster MP61**

*Shaw, Brian D. and Upadhyay, Srijana, Program for the Biology of Filamentous Fungi, Department of Plant Pathology and Microbiology, Texas A&M University, College Station, Texas, 77803, USA. bdshaw@tamu.edu. **Live cell imaging of actin::GFP in *Aspergillus nidulans***.

A C-terminal GFP fusion with *A. nidulans* actin (under control of the inducible *alcA* promoter) was constructed using Gateway technology. Only ectopic insertions of this construct are viable. We have used live cell fluorescence and confocal imaging to examine the actin distribution. In wild type hyphae, cortical actin patches are observed at actively growing tips, in a distribution pattern much like that seen before using actin antibodies. We have been unable to resolve actin filaments with this construct. Our current work to image actin in actively growing swollen cell developmental mutants will be discussed. Additionally, we have used a transposon insertional strategy to disrupt *A. nidulans* fimbrin. Fimbrin is an actin bundling protein that stabilizes the actin cytoskeleton. The fimbrin knock out manifests in germinating conidia with simultaneous emergence of multiple germ tubes. **Contr. Talk: Monday PM Fungal molecular and cell biology**

Shevlin, Dennis E, Morrison, Janet, Shupak, Raymond, Dept. of Biology, The College of New Jersey, Ewing, NJ 08628, USA. shevlin@tcnj.edu. **A preliminary laboratory and field study of the smut *Sporisorium ellisii* on Broomsedge, *Andropogon virginicus* in the Eastern US**.

The smut *Sporisorium ellisii* is often encountered as a parasite on the common successional grass *Andropogon virginicus* (broomsedge) within its Eastern US range. Thus far, it has not been encountered in the disjunct Hawaiian and central Californian host populations. Some of the basic biology of the smut was elucidated and the impact of this parasite on its host in the field was explored. The unique rDNA ITS and LSU sequences of *S. ellisii* were identified and teliospore germination was shown to be hyphal (no basidiospores developed in various solid and broth media). Viable teliospore-derived mycelia grew and survived a few weeks on agar or in broth cultures. The initial field work was done in central New Jersey over two years in a gridded portion of a large old-field community in which broomsedge was dominant. Based on 480 1m2 plots, it was found that 10.7% and 8.9% of the plants were infected in 2004 and 2005, respectively. Infection was either partial (not all inflorescences) or complete. Completely infected plants were twice as likely to die between 2004 and 2005 as healthy and partially infected plants and only 10% of completely infected plants recovered from the disease in 2005. Partially infected plants were the largest and completely infected, the smallest. Work has begun to identify smut populations using primers for the tandem repeats found in the *Ustilago maydis* genome. **Poster MP84**

*Silliker, Margaret E. Castle, Whitney K. DiMarco, Michael J. and Williams, Calvin L. Department of Biological Sciences, DePaul University, Chicago, IL 60614, USA. msillike@depaul.edu. **Sequence analysis of the mitochondrial genome of *Didymium iridis***.

Mitochondrial DNA (mtDNA) was isolated from the Pan 2-16 strain of *Didymium iridis* on bisbenzimide CsCl gradients and digested with *Eco* RI, *Bgl* II, *Kpn* I, *Pst* I, and *Xba* I and ligated to pBSKII+, or pLit28 for cloning. The cloned fragments were hybridized to total *D. iridis* DNA to verify that the fragments hybridized to the corresponding sized mtDNA bands recognizable in total DNA digests. Though we have not completed the mt genome sequence we have sequenced over 48 kb and identified the following genes: *cox1, cox2, cox3, cytb, nad1, nad2 (partial), nad4, nad3, nad4L, nad5, nad6, nad7, atp1, atp6, atp8, atp9, rps12,* the large and small rRNAs and 5 tRNAs. Comparison of our genomic sequences with genomic and mRNA sequences from *Physarum polycephalum* suggest that the two share some RNA editing sites, but the patterns are not identical. We have also identified 6 ORFs, two of which show homology to *P. polycephalum* ORFs with homology to DNA dependent RNA polymerases found in mt-plasmids. A 7th ORF with weak homology to fungal mt-plasmid polymerases may be located on a sub-genomic molecule generated by recombination. **Poster MP93**

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*Simmons, D. Rabern[1], Longcore, Joyce E.[1], and James, Timothy Y.[2]. [1]Department of Biological Sciences, University of Maine, Orono, ME 04469, [2]Department of Biology, Duke University, Durham, NC 27708, USA. david.r.simmons@umit.maine.edu. **Genetic and zoospore ultrastructural data support a new chytrid genus**.

Chytriomyces angularis (Chytridiomycota) is a monocentric, operculate, epibiotic member of the Chytridiales that can be baited on pollen from soil. *C. angularis* occupies a long branch in published molecular phylogenies, and its zoospore ultrastructural features differ from those of the type of the genus, *C. hyalinus.* In an effort to properly classify this chytrid and to determine whether it is closely related to a morphologically similar species, *C. poculatus,* we examined the small subunit rDNA regions of two isolates of *C. poculatus,* the type isolate of *C. angularis* and three isolates that we tentatively classified as *C. angularis.* Phylogenetic analysis indicated that these species and isolates constitute a monophyletic clade; however, the putative *C. angularis* isolates differ morphologically and physiologically from the type isolate and may represent additional species. Examination of zoospore characters and additional molecular analyses will help delineate a new genus, and possibly additional species, for this group. **Poster MP124**

Simonis, Joseph L. Raja, Huzefa A. and *Shearer, Carol A. Dept. of Plant Biology, University of Illinois, Urbana IL 61801, USA. simonis@uiuc.edu. **Substrate degradation patterns of freshwater euascomycetes: extracellular enzymes and soft-rot decay**.

Seventeen meiosporic and ten mitosporic euascomycetes isolated from submerged dead plant material in a variety of freshwater habitats were qualitatively tested for production of extracellular plant-degrading enzymes. Isolates were also assayed for chitinolytic activity and soft-rot decay capabilities. All species produced amylase, beta-glucosidase, and xylanase. Eighteen species were cellulolytic, fifteen produced laccase, fourteen produced polygalacturonase, four produced tyrosinase and three produced peroxidase. After five weeks of growth, only *Porosphaerellopsis bipolaris* was positive for chitinase production. Eighteen species caused soft-rot decay. Species isolated from lotic and lentic habitats had similar results for all assays. In accord with previous studies, there were no noticeable differences between tropical and temperate or herbaceous and lignicolous species in their enzyme-production capabilities. Approximately 80% of both tropical and temperate lignicolous lotic species produced soft-rot cavities. Approximately 70% of lignicolous species and one of two substrate generalist species caused soft-rot decay, yet neither of the two herbaceous species did. Results indicate that meiosporic and mitosporic euascomycetes are capable of playing a crucial role in the breakdown of herbaceous and woody debris in lotic and lentic freshwater systems across ecoclimatic divisions. **Poster MP110**

Skillman, J. E.[1], McLenon, T.M.[1], and Moncalvo, J.M.[2]. [1]University of Toronto, Canada [2]Royal Ontario Museum, Canada. jes.skillman@gmail.com. **Comparison of the diversity of fungi at different soil depths in an old-growth forest**.

Fungi are highly diverse and abundant in soil. However, there is still little information about how taxonomic, genetic and ecological diversity is distributed in a vertical forest soil profile. To address these questions we used DNA sequences from the nuclear large ribosomal subunit gene (nLSU) to detect fungi at three depths (0-2 cm, 18-20 cm, and 38-40 cm) of a single soil core. The core was obtained from an old growth hemlock-cedar forest with gleysolic soil at Joker's Hill, Ontario. We sampled over 500 fungal sequences. Sequences were identified to the nearest clade using BLAST searches and phylogenetic analyses, and when possible their ecological function were inferred based on their cladistic affinities. Sequences with > 99% similarity were grouped in the same Operational Taxonomic Unit (OTU). OTUs were used to estimate sampling accumulation curves in each depth, and taxonomic and ecological variations at the different depths were evaluated with a Chi-square test. Results from traditional tests were compared with recently developed phylogenetic methods that can assess taxonomic and genetic diversity, sampling effort, and among-samples variation without the need for arbitrary taxonomic definitions like species or OTUs. Our results indicate that the ratio of saprophyte:ectomycorrhizal taxa decrease with depth accordingly to nutriment decrease. **Poster MP78**

*Slot, Jason C. Hibbett, David S. Department of Biology, 950 Main Street, Worcester, MA 01610, USA. jslot@clarku.edu. **Teaching the fungal tree of life to high school teachers and students with a comprehensive website and adapted peer reviewed literature**.

Information about Fungi is exploding on the internet, yet a thorough guide and quality teaching materials for fungal ecology and evolution have remained hard to find or inaccessible to novices. Teaching the Fungal Tree of Life is an expanding website that seeks to directly address the needs of secondary school teachers with an easily navigated and understood website of fungus science content, embedded with downloadable lesson plans and Adapted Peer Reviewed Literature. In this poster, we present sample web pages and teaching materials as they are now available at http://www.clarku.edu/faculty/dhibbett/TFTOL. **Poster MP116**

*Slot, Jason C., Hibbett, David S. Department of Biology, 950 Main Street, Worcester, MA 01610, USA. jslot@clarku.edu. ***Hebeloma helodes*: a model for diversification of nitrate transporter function in mycorrhizal fungi**.

The discovery of two paralogous high affinity nitrate transporter *nrt2* genes in *Hebeloma helodes* provides an opportunity to address the relationship between amino acid sequence and transporter function. Amino acid translations of the paralogous genes suggest divergence in regulation and substrate binding capacity. By analyzing the expression of each paralogous gene under different states of mycorrhization and an array of nitrogen conditions we can correlate aspects of secondary structure with gene function. Comparisons of expression patterns between species of different ecologies will allow us to address the role of nitrate transport in ecological transitions in the Cortinariaceae. **Poster MP97**

*Smith, Matthew E.[1], Rizzo, David M.[1], and Douhan, Greg[2]. [1]University of California, Davis CA; [2]University of California, Riverside CA, USA. mesmith@ucdavis.edu. **Ectomycorrhizal community structure in a xeric *Quercus* woodland as inferred from rDNA sequence analysis of pooled EM roots and sporocarps**.

Seasonally dry *Quercus* woodlands are key components of Californias wild landscapes, yet little is known about their associated ectomycorrhizal (EM) fungi. Sporocarp collections and rDNA sequence data from EM roots of *Quercus douglasii* in California yielded 163 EM species, suggesting that EM fungal communities of seasonally arid biomes are extremely diverse. We detected a large number of Ascomycota and hypogeous species, both on EM roots and as sporocarps. Because of the erratic weather conditions, we expected seasonal and annual variation among EM fungi on roots sampled in winter and spring of 2003 and 2004. However, evidence suggests that the belowground EM community was relatively stable. Hierarchical cluster analysis indicates that soil cores from within a 25 cm radius were similar in terms of EM species composition regardless of sampling date. We found no evidence of EM taxa specifically adapted to winter or spring. Furthermore, only one common EM species varied widely between the two sampling years and several rare EM species were detected within the same 25 cm radius on successive sampling dates, suggesting they persisted in or re-colonized small, localized areas. We compare and contrast these results with those from other EM studies and discuss implications for future studies of EM community ecology. **Poster MP67**

Smith, Matthew E.*[1], Rizzo, David M.[1], and Trappe, James. M.[2]. [1]University of California, Davis CA; [2]Oregon State University, Corvallis OR, USA. mesmith@ucdavis.edu. ***Genea*, *Genabea*, and *Gilkeya* gen. nov. (Ascomycota, Pyronemataceae): ascomata and ectomycorrhiza formation in a *Quercus* woodland**.

Genea and *Genabea* are considered ectomycorrhizal symbionts of plants, but because of their hypogeous habit, dark coloration, and small size, little is known about these genera. Ascomata of six morphological species of *Genea* and one of *Genabea* were collected at a single site in *Quercus* woodlands of Northern California. While most ascomata collections were easily referred to known species, those putatively identified as *Genea harknessii* and *Genea arenaria* were problematic. *Genea harknessii* collections appeared homogenous based on morphology but ITS variation suggested cryptic species diversity. Specimens of *G. arenaria* approximated the original species description except for abundant clumps of septate setae on the peridial warts. To verify the identity of this species, we reexamined the holotype and analyzed morphology and ITS sequences of *G. arenaria* ascomata from a wide geographic area. To authenticate the ectomycorrhizal status of *Genea* and *Genabea,* we collected healthy EM of *Quercus* spp. and compared their ITS sequencesmata. We confirmed EM colonization by nine distinct ITS types of *Genea* and *Genabea.* Two new species, *Genea bihymeniata* sp. nov. and *Genea cazaresii* sp. nov. were discovered during study of herbarium specimens. A phylogenetic analysis of 28s rDNA from *Genea* and *Genabea* indicated three distinct lineages: *Genea, Genabea,* and a

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third represented by *Genea intermedia.* For the latter we propose *Gilkeya* gen. nov. to accommodate the single known species, *Gilkeya compacta* comb. nov. A dichotomous key to all known *Genea, Genabea,* and *Gilkeya* spp. from Western North America is presented. **Poster MP65**

*Snetselaar, Karen, Yerrum, Smitha, and McCann, Michael. Biology Dept St Joseph's University, Philadelphia, PA 19131, USA. ksnetsel@sju.edu. **3-D characterization of a dimorphic fungus using conventional fluorescence microscopy**.

The dimorphic fungus *Ustilago maydis* produces buds and filaments that are a few microns thick. This means that a Z-series of 6-10 sections, each 0.5 microns thick, will include a group of cells from top to bottom. We found that a conventional (widefield) fluorescence microscope outfitted with a motorized Z-axis stage controller, monochrome digital camera, and image analysis software including deconvolution and 2-D projection algorithms was effective for characterizing these fungal cells. Several types of filaments were studied, including mating filaments and the constitutively produced filaments made by a mutant lacking adenylate cyclase *uac1*. Strains transformed with GFP-tubulin were labeled with DAPI and rhodamine-conjugated WGA. This combination of fluorochromes permitted simultaneous imaging of nuclei, microtubules, and cell walls. The pattern of nuclear division and timing of septum formation was similar in budding cells and the *uac1* filaments, but septal morphology differed. The membrane fluorochrome FM4-64 allowed us to observe the secretory patterns characterizing septum formation. Mother and daughter buds both participated in septum formation, forming a double wall, while septa in *uac1* filaments were single. Septa in mating and infection filaments shared characteristics of budding cells and *uac1* filaments. **Contr. Talk: Monday PM Fungal molecular and cell biology**

*Sogonov, Mikhail V.[1], Castlebury, Lisa A.[2], Rossman, Amy Y.[2], White, James F. jr. [1]. [1]Dept. of Plant Biology and Pathology, Rutgers University, New Brunswick NJ 08901, USA, [2]Systematic Botany and Mycology Laboratory, Beltsville MD 20705, USA. msogonov@nt.ars-grin.gov. **The Gnomoniaceae on the Juglandaceae**.

The Gnomoniaceae is a common but inconspicuous diaporthalean family of fungi associated with plants. Most occur as symptomless endophytes of hardwood trees, although some can be pathogenic. Host associations in this group usually vary from species- to family-level host specificity. Eight species in the Gnomoniaceae are considered specific to hosts in the Juglandaceae, a family of hardwood trees with economic value as wood and nut crops. Of these, *Sirococcus clavigignenti-juglandacearum, Gnomonia leptostyla* and *G. dispora* cause butternut *Juglans cinerea* canker, walnut *J. regia* anthracnose and pecan *Carya pecan* leaf blotch respectively. Two additional species typically occurring on other hosts have been also been reported from hosts in the Juglandaceae. From 2004-2006, 31 specimens of gnomoniaceous fungi on hosts in the Juglandaceae from the eastern U.S. and Canada were collected and examined. In addition to the previously described *G. caryae, G. pecanae* and *Plagiostoma micromegalum,* five apparently undescribed species supported by morphology and ITS sequence data were collected. The results of this work indicate that the diversity of gnomoniaceous fungi associated with the Juglandaceae in North America has been underestimated, in part because fungi in the Gnomoniaceae have not been well studied outside of Europe. **Poster MP129**

*Stchigel, Alberto M.[1], Miller, Andrew N.[2], and Guarro, Josep[1]. [1]Unitat de Microbiologia, Facultat de Medicina i Ciencies de la Salut, Universitat Rovira i Virgili, C/Sant Llorenc 21, 43201 Reus, Spain; [2]Illinois Natural History Survey, Center for Biodiversity, 1816 South Oak Street, Champaign, Illinois 61820, USA. amiller@inhs.uiuc.edu. **Reappraisal of *Chaetomium ampullare* Chivers and *Coniochaeta emodensis* Udagawa & Y. Hori from soil**.

In a first attempt to gain knowledge of the soil mycobiota of the Great Smoky Mountains National Park (a UNESCO Reserve located in the eastern USA), soil samples were collected throughout the Park in sterilized plastic bags. Using a cellulose bait technique, two rarely collected fungi were isolated in pure culture: *Chaetomium ampullare* Chivers and *Coniochaeta emodensis* Udagawa & Y. Hori. *Chaetomium ampullare* is characterized by pyriform, ostiolate ascomata covered by long, stiff, setae, 8-spored, clavate asci, and 1-celled, brown, limoniform and bilaterally flattened ascospores; anamorph was not produced. *Coniochaeta emodensis* produces subglobose, ostiolate ascomata which are nearly glabrous, 8-spored, cylindrical asci, and 1-celled, opaque, olive-brown to dark brown ascospores that are usually inequilateral-ellipsoidal to concavo-convex. Our strain did not produce the *Geniculosporium* -like anamorph, but the reverse of the colonies growing on potato-carrot agar produced the typical dark olive-green color, similar to that of the holotype. Living strains derived from the holotypes are not available in any culture collection and later isolations have not been reported. Thus, our isolations are noteworthy since they represent the first report of these species for the America,s, and also provide new material for further molecular studies. **Poster MP134**

*Stefani, F.O.P[1], Moncalvo, J-M.[2], Hamelin, R.C.[3]. [1]Centre de Recherche en Biologie Forestière, Université Laval, Sainte-Foy, QC, Canada, G1K7P4. [2]Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, 100 Queen's Park, Toronto, ON, Canada, M5S2C6. [3]Natural Resources Canada, Canadian Forest Service, Sainte-Foy, Quebec, Canada; fstefani@cfl.forestry.ca. **Effect of Novel Living forest Organisms on ectomycorrhizal diversity**.

In response to the increased need for timber and fibre, areas planted with novel living organisms (NLO) such as hybrid or transgenic trees have grown in recent years. Addressing the impact of these NLOs on forest-associated microoganisms and establishing a biodiversity baseline are important prior to their widespread cultivation. We measured and compared ectomycorrhizal diversity in 3 untransformed and 3 GUS-transformed *Populus tremula* x *alba* in a plantation and in poplars in natural stands. We sampled 4 soil cores around each target tree. Soil DNA was extracted and rDNA ITS regions were amplified using fungal specific primer sets. PCR products were cloned and 24 PCR clones per sample were analysed by PCR-RFLP-sequencing and identified by sequence similarity with fungal sequences in GenBank database. We identified 1152 soil fungal ITS sequences (700 kb) from untransformed and GUS transformed poplars. *Cortinarius* sp. and *Inocybe* sp. were the two main ectomycorrhizal species colonizing the organic layer, whereas the mineral layer was exclusively colonized by *Acremonium strictum.* Differences between clone libraries from untransformed and transgenic poplars were investigated. The paucity of fungal diversity at the NLO site was an unexpected feature of our investigation. We are currently testing hypotheses to explain this observation. **Contr. Talk: Monday AM1 Fungal Ecology- Mycorrhizae**

Stephenson, Steven L. Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. slsteph@uark.edu. **Global patterns of myxomycete biodiversity**.

The myxomycetesalso called plasmodial slime molds or myxogastrids) are the largest and best known of the eumycetozoans. Members of the group have been known from their fruiting bodies since at least the middle of the seventeenth century. There are approximately 875 recognized species of myxomycetes, many of which have been described in the past half century. The majority of species are probably cosmopolitan, but a few species seem to be confined to the tropics or subtropics and some others have been collected only in temperate regions of the world. Myxomycetes appear to be particularly abundant in temperate forests, but at least some species apparently occur in any terrestrial ecosystem with plants (and thus plant detritus) present. Field-based studies carried out in many different regions of the world over the past two decades have generated a considerable body of information that has provided evidence for a number of ecological patterns not reported previously for myxomycetes while also continuing to substantiate patterns or general observations that have long been suspected. However, although our knowledge of the biogeography, ecology and global distribution of myxomycetes has increased considerably, there is still a need for additional research. **Poster Monday M 88**

*Stolze, Jessica L.[1], *Fischer, Mark[2], Yafetto, Levi[1], Davis, Diana J.[2], Money, Nicholas P.[1]. [1]Miami University, Oxford, OH, [2]College of Mount St. Joseph, Cincinnati, OH, USA. stolzejl@muohio.edu. **The Launch of Ascospores: Observations and Mathematical Analysis**.

Explosive spore discharge is a feature of thousands of ascomycete species. The basic process is straightforward: ascus sap is pressurized by osmosis and this pressure is used to propel the spores into the air. The details of the mechanism vary greatly, however, between ascomycete species, and are poorly understood. As part of an ongoing study of ascus function in *Ascobolus immersus,* we have captured the exit of spores from its large asci, and their subsequent flight, using ultra high-speed digital video microscopy. Ascospores are shot from asci of this species at initial velocities ranging from 8 to 11 meters per second. The spores are expelled within 40 microseconds of the rupture of the ascus apex and achieve an initial acceleration of 25,000 *g.* In an earlier study, we measured ascus turgor pressure and developed a mathematical model for the motion of discharged spores. The new video data are consistent with this work

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but also offer novel insights into this remarkable biomechanical process. **Symposium: Sunday 1:30-5:00 Fungal Movement: Contemporary Experimental Analysis**

Tabor, Michael, University of Arizona, Tucson AZ, USA. tabor@math.arizona.edu. **Modeling fungal penetration**.

Two topics in the mathematical modeling of fungal structure and movement will presented that are connected by their common use of exact elastic shell theory: i) Models for hyphae that incorporate growth, and show how a growing hyphal filament develops a "self-similar" profile. ii) Models for appressorial design in *Magnaporthe grisea* that show how the walls of the appressorium act as a "smart" material in order to maintain the appressorial shape under enormous increases in turgor pressure. Additional results concerning estimates of the adhesive forces that attach the appressorium to a host surface, and of the forces involved in the penetration of the host surface will also be presented. **Symposium: Sunday 1:30-5:00 Fungal Movement: Contemporary Experimental Analysis**

*Toda, Takeshi[1], Qu, Ping[2], Yamashita, Koji[3], Cubeta, Marc A.[1], and Hyakumachi, Mitsuro[3]. [1]Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7919, [2]United Graduate School of Agricultural Science, Gifu University, Japan, [3]Faculty of Applied Biological Science, Gifu University, Gifu 501-1193, Japan. ttoda@ncsu.edu. **Investigation of sexuality and mating behavior on *Thanatephorus cucumeris* AG 1-IC**.

Three field isolates of *Thanatephorus cucumeris* AG 1-I Canamorph=*Rhizoctonia solani* and their 10 basidiospore progenies were examined for heterokaryon formation and hyphal growth. Single basidiospore isolates (SBIs) from the same (intra-specific) and different (inter-specific) parents were paired in all possible combinations on potato dextrose agar amended with 1 % charcoal. Subsequent pairings between parental and SBIs were also conducted. The hyphal interaction zone between paired isolates was examined for heterokaryon formation using morphological (production of a tuft of mycelium) and amplified fragment length polymorphism (AFLP) criteria. SBIs of each parental field isolate could be placed into two mating types and segregated in an approximately 1:1 ratio. Fifteen AFLP phenotypes were observed from SBIs of three parental field isolates. The information of tuft mycelium and AFLP analysis provided evidence for heterokaryon formation in intra- and inter-specific pairings of SBIs. Hyphal growth of parental field isolates and most synthesized heterokaryotic isolates was greater than that of the SBIs. Pairings between heterokaryotic field isolates and single basidiospore isolates also produced a tuft of mycelium which was confirmed as new heterokaryon based on AFLP criteria. This new data suggests that heterokaryon may also form as a result of di-mon mating. **Contr. Talk: Tues AM2 Fungal Pathogens: population structure and distributions**

*Traquair, James A. White, G.J.[1], and Singh, B.L. Southern Crop protection and Food Research Centre, Agriculture and Agri-Food Canada, 1391 Sandford Street, London ON N5V 4T3, Canada and [1]Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson AZ 85721, USA. traquairj@agr.gc.ca. **Antagonism of *Botrytis cinerea* by *Aureobasidium pullulans* and a cellulolytic, *Phoma* -like fungus**.

Botrytis cinerea Pers.:Fr is a cosmopolitan pathogen of a wide range of different perennial crops including American ginseng. It survives non-cropping periods as vegetative mycelium and sclerotia in infested crop debris and spreads from plant to plant by means of airborne conidia. Chemical fungicides are available for control but there is a growing interest in the development and commercialization of biological controls. Two fungi were found frequently as epiphytes on crop debris (overwintering stems) of American ginseng and the straw and wood-chip mulches used in ginseng gardens. *Aureobasidium pullulans* (deBary) G. Arnaud and *Phoma* -like fungus (Leptosphaeriaceae) were found to degrade cellulose, to inhibit the growth of *Botrytis* mycelium in dual cultures and to suppress sclerotial germination and mycelial growth on water agar. Diffusion zones in paired cultures and mycelial inhibition (temporary) upon exposure to cell-free culture filtrates were indications of antibiotic mechanisms of antagonism. Competition by cellulolytic, debris- and mulch-borne fungi is a promising approach to inoculum reduction and biological control of grey mold and blight in perennial crop situations. **Poster MP87**

*Vega, Fernando E.[1], Posada, Francisco[1], Aime, Mary Catherine[2], Peterson, Stephen W.[3], and Rehner, Stephen A.[1]. [1]Insect Biocontrol Laboratory, [2]Systematic Botany and Mycology Laboratory, USDA, ARS, Beltsville, Maryland 20705, USA; [3] Microbial Genomics and Bioprocessing Research Unit, USDA, ARS, NCAUR, Peoria, IL 61604, USA. vegaf@ba.ars.usda.gov. **Coffee endophytes**.

A survey for fungal endophytes in various coffee *Coffea arabica* L. tissues was conducted in Colombia, Hawaii, Mexico, and Puerto Rico. Tissues were sterilized in 0.5% sodium hypochlorite for 2 min, 70% ethanol for 2 min, and washed in sterile distilled water prior to plating in yeast malt agar (YMA). All fungal growth was subcultured on individual plates containing YMA. Isolates were then grown in potato dextrose broth, harvested, lyophilized, and stored at -80 C for subsequent DNA extraction. The internal transcribed spacer region of the nuclear rDNA repeat was sequenced for each isolate. Over 700 isolates were sequenced: 281 from Colombia, 240 from Hawaii, 119 from Mexico, and 68 from Puerto Rico; these comprise more than 170 distinct unique sequences. The most common genera were *Colletotrichum, Fusarium, Penicillium,* and *Xylaria.* Various genera containing fungal entomopathogens were also isolated, including *Acremonium, Beauveria, Cladosporium, Clonostachys,* and *Paecilomyces.* The role of fungal endophytes in coffee tissues remains enigmatic and deserves further study. **Contr. Talk: Monday PM- Fungal Ecology - Endophytes and Saprobes**

*Vernier, Kimberly[1], Hustad, Vincent P.[1], Methven, Andrew S.[1], Meiners, Scott J.[1], Gaines, Karen F.[1], and Miller, Andrew N.[2]. [1]Eastern Illinois University and [2]Illinois Natural History Survey, USA. asmethven@eiu.edu. **Macrofungi associated with tree windfall in old growth prairie groves**.

This study is investigating macrofungi associated with tree windfall in Brownfield and Trelease Woods, Champaign Co. Illinois. These woods are remnants of a larger, contiguous, pre-settlement prairie grove now encircled by houses, fragmented forests, prairie and agricultural land. Although initially a virgin, deciduous upland forest dominated by oak, ash and maple with a high, closed canopy and fairly open (Brownfield Woods) to moderately dense (Trelease Woods) understory, sugar maple is rapidly becoming the dominant tree species. Beginning with a windstorm in November 1994, fallen trees in both woods have been tagged with an ID number, date of windfall, dbh and location relative to a network of marked grids. Wood-inhabiting macrofungi are being surveyed from 180-200 fallen trees and terrestrial macrofungi are being surveyed along twenty, 100 m long transects. Objectives include: i) Does macrofungi species composition change on woody substrates of different species, dbh, decay class and bark condition? ii) Does macrofungi production vary within and between years?; iii) Does macrofungi species composition and species richness change within and between years?; iv) Do tree windfalls perturb macrofungi species composition and richness patterns?; and, v) Are parameters that influence macrofungi species composition spatially autocorrelated?, **Poster MP77**

*Voth, Peter D.[1], Linah Mairura[2], Ben E. Lockhart[3], and Georgiana May[2]. [1]Plant Biological Sciences Graduate Program, [2]Department of Ecology, Evolution, and Behavior, [3]Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108, USA. voth0016@umn.edu. **Population structure of *Ustilago maydis virus H1* across the Americas**.

Ustilago maydis virus H1 (Umv-H1) is a mycovirus that infects *Ustilago maydis,* a fungal pathogen of maize. As *Zea mays* was domesticated, it carried with it many associated symbionts and the subsequent range expansion and cultivation of maize should have dramatically affected maize symbionts' evolutionary history over time and geographic space. Transmission of Umv-H1 takes place only through cytoplasmic fusion during mating of *U. maydis* individuals, thus, the population dynamics of *U. maydis* and maize are expected to strongly affect the population structure of the viral symbiont. We investigated the impact of changes in *U. maydis'* evolutionary history on that of Umv-H1. The high viral mutation rate allows us to examine the evolution and divergence of Umv-H1 lineages as a result of the recent changes in U. maydis population structure. We determined the phylogeographic history and genetic structure of Umv-H1 populations in the Americas using analyses of viral nucleotide sequence. We, also, assessed infection and recombination frequencies, genetic diversity, rates of neutral evolution, and selection acting on regions of the viral genome. The results suggest the USA, Mexico, and South America represent distinct populations; viral populations do not show isolation by distance; and the dates of founding events for fungal host populations coincide with the domestication of maize. **Symposium: Wed 8:30-1200 Population and Species Divergence in Fungi**

*Wakefield, Scott W, Letcher, Peter M. Powell, Martha J. Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487, USA. wakef002@bama.ua.edu. **Ultrastructural and molecular analyses of the soil chytrid fungi, Spizellomycetales (Chytridiomycota)**.

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The Phylum Chytridiomycota is commonly considered as aquatic fungi because of reproduction with zoospores. However, despite adaptations to dispersal in water, chytrids are common in soil and parasitize a range of terrestrial organisms, and members of the order Spizellomycetales are the most predominately terrestrial. Barr established the order Spizellomycetales based on zoospore ultrastructural characters that were distinctive from those of other members of the Chytridiales. However, recent molecular analyses demonstrate that Spizellomycetales as currently defined is not monophlytic, highlighting the need for more extensive molecular and ultrastructural analyses of this order. As a beginning to the revision of the order Spizellomycetales, we used over 60 cultures isolated from a broad geographical range in molecular and ultrastructural analyses. These isolates included cultures used as types for erecting five of the 10 genera in the Spizellomycetales. Maximum parsimony, maximum likelihood and Bayesian methods of phylogenetic inferences were used and combined sequences of ribosomal (nuclear large subunit and ITS1-5.8S-ITS2) and protein coding (RPB1, RPB2) genes. New phylogenetically informative zoospore ultrastructural characters are also explored. Zoospore ultrastructural character differences correlate with the genetic divergence discovered in the Spizellomycetales. Results support the monophyly of genera analyzed thus far, but also demonstrate that new genera and new orders will have to be erected to accommodate the genetic diversity found within the Spizellomycetales. **Poster MP123**

*Wang, Xin. White, David. Wamatu, J. and Chen, Weidong. USDA-ARS, Washington State University, Pullman, WA 99164, USA. w-chen@wsu.edu. **Identifying pathogenesis-related genes of *Sclerotinia sclerotiorum* by using *Agrobacterium* - mediated transformation**.

S. sclerotiorum causes white mold disease on >400 plant species including lentil. To better understand the genetic mechanisms of pathogenesis of *S. sclerotiorum, Agrobacterium* -mediated transformation was used to identify and characterize pathogenicity-related genes using hygromycin resistance gene *hph* as a selection marker. Among 127 transformants screened, 6 showed significantly reduced pathogenicity on lentils both in greenhouse pathogenicity tests and in detached stem assays. Some of the transformants with reduced pathogenicity produced less oxalic acid compared to the wild type strain, which is a proven pathogenicity factor. Southern hybridization using *hph* as a probe confirmed these transformants contained single insertions at random locations. Disrupted regions of the fungal genome of several less pathogenic transformants were identified by inverse-PCR and TAIL-PCR. Possible ORFs of these disrupted genome regions have revealed high homology (>80%) with conserved domains of a number of enzymes. Further analysis using targeted transformation and complementation will be performed to confirm the role of these genes in pathogenesis of *S. sclerotiorum.* **Poster MP102**

White, David and Chen, Weidong, USDA-ARS, Washington State University, Pullma, WA 99164, USA. w-chen@wsu.edu. **Construction of the first phage library of chickpea blight pathogen *Ascochyta rabiei*.**

During studies on pathogenic determinants of *Ascochyta rabiei,* the causal agent of chickpea blight, we developed a library of insertional mutants of *A. rabiei* using *Agrobacterium* - mediated transformation. Non-pathogenic mutants were identified after screening more than 1000 transformants using pathogenicity bioassays. Because the genome sequence of *A. rabiei* is unavailable, a genomic library is needed in order to isolate the genes disrupted in the non-pathogenic mutants. This study was to generate a phage library of *A. rabiei* suitable for isolation of potential pathogenicity determinants. Genomic DNA fragments between 7,000 and 10,000 bps of ApoI digest from a pathotype II strain were ligated to EcoRI-digested Lambda ZAPII vector arms, packaged using Gigapack III extracts, and amplified in E. coli strain XL1-Blue. Ten randomly selected plaques were used to determine the average size of DNA insert. A phage library consisting of approximately 1.7 x 10^6 recombinants was constructed, with average insertion size of 6.5 Kb. A single round of amplification of the library was performed to produce a final titer of 1 x 10^{11} pfu/ml. Recombinant DNA can be rescued from the phage in the form of a plasmid. This represents the first phage library of *A. rabiei.* **Poster MP101**

Winsett, Katherine E., Silberman, Jeffrey D., Stephenson, Steven L. Department of Biological Sciences, Science Engineering 632, University of Arkansas, Fayetteville, AR 72701 USA. kwinset@uark.edu. **Internal Transcribed Spacers 1 and 2 as molecular markers for the study of genetic variation in populations of myxomycetes**.

The internal transcribed spacers (ITS) are commonly used as molecular markers for measuring genetic variation in and among populations and closely related taxa. Results for molecular characterization of genetic variation in myxomycete (plasmodial slime molds) taxa is only recently available. ITS 1 and 2 were used to measure intraspecific genetic variation in the myxomycete *Didymium squamulosum* (Physarales, Didymiaceae), a cosmopolitan myxomycete found as both sexual and apomictic strains in nature. This region was found to be highly variable in this species for both nucleotide sequence and sequence length. It is not known if the ITS sequences are similarly variable in other species of myxomycetes. The entire region (ITS1, ITS2 and 5.8S) was amplified for species representing major genera in the myxomycetes. The sequences for the isolates were compared for intraspecific and interspecific variation in base sequence and length. Patterns of conservation occur in isolates of the same species, but despite the usefulness of this marker for study of populations in other groups, ITS is not recommended for study of intraspecific variation in any of the species of myxomycetes examined**. Contr. Talk: Monday AM2 Fungal Systematics**

Winsett, Katherine E.[1], Edwards, Sally[1], Lindley, Lora[1], Mcelderry, Melissa[1], Nelson, Rodney K.[2], Stephenson, Steven L.[1]. [1] Department of Biological Sciences, Science Engineering 632, University of Arkansas, Fayetteville, AR 72701[2]Department of Biology, University of Arkansas - Fort Smith, Fort Smith, AR 72913 USA. kwinset@uark.edu . **Mycetozoans of the National Parks**.

Our knowledge of the mycetozoans (true slime molds) of the United States is incomplete for many regions and habitat types. In order to fill in some of these gaps, surveys are being carried out in a number of National Parks across the country. The true slime molds (dictyostelid cellular slime molds, myxomycetes or acellular slime molds and protostelids) are bacteriovores with an amoeboid vegetative state that occurs in three major habitats (soil, plant litter and woody substrates) and in many specific microhabitats within these habitats. Spores are very small and generally wind-dispersed, meaning that mycetozoans have the potential for long-distance dispersal, and many species are considered cosmopolitan. However, distribution patterns and habitat specificity appears to exist for many species, and genetic variation is found in geographically separated individuals of a cosmopolitan species. National Parks are protected areas that encompass much of the ecological variation found within the United States. As such, they provide ideal situations in which to survey the slime molds in order to develop a more detailed picture of the biodiversity for these organisms in North America. Over the past year, nine parks were visited, and an effort was made to sample all habitats found within each park. Soil, bark and litter samples were collected and processed in the lab for myxomycetes, dictyostelids and protostelids. **Poster MP90**

*Winter, Melanie D. and Volk, Thomas J. University of Wisconsin-La Crosse, WI, USA. winter.mela@students.uwlax.edu. **Preliminary investigation of gene regulation in a heterokaryon of *Neurospora crassa*.**

Filamentous ascomycetes are economically important organisms, being the most significant fungal cause of food spoilage and crop diseases, as well as important industrial organisms. Despite their significance, very little is known about the regulation of their remarkably plastic genomes. Previous studies on their multinucleate state have indicated that their nuclei can complement each other but that an increase in the number of nuclei does not lead to an increase in protein production. Does one nucleus become dominant? Is the regulation pre- or post-transcriptional? For this study, we created a his+/his- heterokaryon of *Neurospora crassa* with a tyrosinase reporter gene. By growing the heterokaryon in media with different concentrations of histidine, we were able to get different proportions of the *his+/his-* nuclei. Through the use of Nothern blots and protein assays, we were then able to compare the number and types of nuclei present to the amount of mRNA and protein produced. By comparing these data, we were able to tentatively determine the mechanism of gene regulation in a heterokaryon. **Poster MP100**

*Wolfe, Benjamin E. and Pringle, Anne. Harvard University, Organismic and Evolutionary Biology, Cambridge, MA 02138, USA. bwolfe@oeb.harvard.edu. **Distribution and host-specificity of *Amanita phalloides* in North America**.

Amanita phalloides (the death cap mushroom) has been introduced into North America from Europe where this ectomycorrhizal species is native. We annotated historical records using molecular data and combined these data with recent collections to map the historical and current distribution of *A. phalloides* on the East and West Coasts of North America. We also used herbarium records and assessment of ectomycorrhizal root tips from the field to determine what species of trees serve as hosts for this species. *A. phalloides* is much more abun-

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dant on the West Coast versus the East Coast with populations in 24 counties, ranging from Vancouver, British Columbia to Los Angeles County, California. We are only aware of 9 extant populations on the East Coast, with many of these occurring in New Jersey. On the West Coast of North America A. phalloides is frequently found growing in association with *Quercus* spp. as it does in its native range, but on the East Coast we only find *A. phalloides* in disturbed environments such as forest plantations and urban parks, often in association with *Pinus* spp. We are currently seeking information from other mycologists in both regions to further clarify the distribution of *A. phalloides* in North America so we can develop tools to better understand the ecology of this introduced species. **Poster MP64**

*Worrall, James J.[1] and Adams, Gerard C.[2]. [1]USDA Forest Service, Rocky Mountain Region, Forest Health Management, Gunnison CO 81230, USA; [2] Department of Plant Pathology, Michigan State University, East Lansing, MI 48824, USA. jworrall@fs.fed.us. ***Cytospora* canker of *Alnus* in the Southern Rocky Mountains**.

Previously we documented extensive dieback and mortality of thinleaf alder *Alnus incana* ssp. *tenuifolia* associated with *Cytospora* canker in the Southern Rocky Mountains, with about one-third of stems dead and one-third with dieback. Although other fungi fruit on diseased and dead alder, *Valsa melanodiscus* anamorph *Cytospora umbrina* is consistently present, even in young cankers, and appears to be the proximal cause. Although we cannot yet rule out the possibility that steady-state dynamics of alder populations lead to the observed proportions of healthy, diseased and dead stems, evidence indicates that heavy mortality began in the early 1990's and possibly earlier. Although this group of pathogens usually attacks stressed hosts, several observations suggest aggressive behavior: a) the pathogen often grows and kills host tissue during the active growing season; b) cankers extend up to a meter in several months; and c) cankered trees usually are girdled and killed. Isolations indicate occasionally heavy colonization on or in vegetative buds, which may be an important infection court. Isolations have revealed no evidence of latent/endophytic infections. **Contr. Talk: Tues AM2 Fungal Pathogens: population structure and distributions.**

*Wright, Shannon H.A. Lim, SeaRa, Berch, Shannon, and Berbee, Mary L. Dept. of Botany, University of British Columbia, Vancouver BC V6T 1Z4 Canada. shannon.wright.asi@shaw.ca. **Long-term effect of fertilization on ectomycorrhizal diversity of western hemlock *Tsuga heterophylla***.

Nitrogen fertilization typically reduces ectomycorrhizal diversity within the first two years of its application. Less is known about the long-term influence of fertilization. We compared ectomycorrhizal diversity and community composition among three fertilization treatments in plots of 18-year-old western hemlock from western Canada. Of 9 plots, 3 were unfertilized controls. Six plots were fertilized in 1987 and 1997; three with 300 kg/ha urea; and three with the urea plus 100 kg/ha P. Four sets of 100 mycorrhizal root tips were sampled per plot and used for random clone libraries of amplified ITS regions. Fungal species were identified from sequenced clones using parsimony analysis. Assuming that clones with > 97% identity were conspecific, 86 species were detected among 1004 clones. Overall fungal diversity was high and not significantly different across treatments. The most abundant species were *Craterellus tubeaformis, Cenococcum geophilum, Piloderma fallax,* and *Lactarius pseudomucidus.* Species composition differed significantly in urea + P plots compared to control plots or plots that received urea alone. This research contributes new knowledge about the diversity of hemlock's ectomycorrhizal fungi and shows that N + P fertilization used in forestry management resulted in a long-lasting change in the ectomycorrhizae fungal community composition. **Contr. Talk: Monday AM1 Fungal Ecology- Mycorrhizae.**

*Yafetto, Levi[1], Money, Nicholas P.[1], Davis, Diana J.[2]. [1]Miami University, Oxford, OH,[2]College of Mount St. Joseph, Cincinnati, OH, USA. levi_yafetto@yahoo.co.uk. **Solving the chemical composition of ascus sap**.

Explosive discharge of spores is a feature of thousands of ascomycete species. The basic process is straightforward: ascus sap is pressurized by osmosis and this pressure is used to propel the spores into the air. But until recently, there was very little information on the compounds responsible for generating pressure within the ascus. In this poster presentation, we document the identity and concentration of inorganic ions and the organic osmolytes in ascus sap of *Ascobolus immersus.* Quantitative ICP-MS showed that inorganic ions generate two-thirds of the total ascus pressure of 0.3 MPa3 atmospheres). Quantitative GC/MS identified glycerol and mannitol as the dominant organic osmolytes that generate the balance of the ascus pressure. In terms of their wider significance, these experiments are important because they offer a clear strategy for analyzing the chemical composition of highly-diluted fluid samples. **Poster MP108**

*Yan, Zhun., Xu, Jianping. Department of Biology, McMaster University, 1280 Main Street, West Hamilton, On, L8S 4K1 Canada. yzhun@hotmail.com. **Patterns of cytoplasmic inheritance in fungi**.

Mitochondria exist in virtually all eukaryotes. Because of their vital metabolic function, small genomes and distinct patterns of inheritance, mitochondrial genes and genomes have attracted much attention in the last several decades. Here, we review our current understanding of the patterns and mechanisms for mitochondrial inheritance in fungi. Unlike the relatively uniform pattern of uniparental mitochondrial inheritance in plants and animals, fungal mitochondrial genomes exhibit diverse patterns of inheritance. Using the bipolar basidiomycete yeast *Cryptococcus neoformans*, we recently demonstrated that mitochondria are inherited almost exclusively from the MATa parent. Two specific genes located within the mating type locus, the *SXI1alpha* gene in MATalpha locus and the *SXI2a* gene in MATa locus were identified controlling mitochondrial inheritance in *C. neoformans*. Mutation of these two genes resulted in biparental inheritance. The possible reasons for the prevalence of uniparental inheritance will be discussed. **Symposium: Tues 1:30-5:00 Bacterial Symbionts of Fungi**

*Zhou, Shuang and Anagnost, Susan E. Faculty of Construction Management and Wood Products Engineering, State University of New York, College of Environmental Science and Forestry, SUNY-ESF, Syracuse, NY 13210, USA. szhou@syr.edu. **An integrated approach to identify basidiomycete cultures**.

The identification of basidiomycete cultures is difficult. The difficulties stem from the lack of basidiomata of which the morphology is the foundation of taxonomy of basidiomycetes. The species code system was designed to identify basidiomycete cultures. The species code for each taxon was based on the collective morphological characters of many cultures derived from identified basidiomata of this species. Not every culture forms all those characters described in the code; by lacking one or more characters, the unknown culture could not be identified with certainty. Additionally, the hyphal characters of the cultures that this system heavily relied on are not distinct. A molecular identification method utilizing the BLAST search of the ITS rDNA sequences provides an alternative method in identification. The weaknesses of this method are the misidentified sequences in the GenBank and lacking of the knowledge of intraspecific and interspecific variations. A combined approach of morphology including mating tests and molecular data can provide efficient and reliable identifications. The essentialness of morphological studies to overcome the weakness of molecular identification and the resolving power of ITS rDNA sequences to a group of cultures with similar morphology will also be discussed. **Contr. Talk: Sunday PM 2 Basidiomycete systematics and Poster MP153**

Search for Eumycetozoans in South America

The noisy green parakeets with a red tail (*Enicognathus leptorhynchus*) were not the only migrants to fly in to the *Araucaria* forests of Central Chile this year. The three authors, investigators from the Real Jardin Botánico Madrid, Spain, and the Universidad Autónoma de Tlaxcala, Mexico (Fig. 1), spent the period from March 17 to April 10 completing the second stage of a three part north-south transect of Chile in search of eumycetozoans (slime molds). The survey is one component of a global inventory project ("PBI: Global Biodiversity of Eumycetozoans") based at the University of Arkansas (slimemold.uark.edu/) and funded by a grant from the National Science Foundation.

Sampling was carried out in six of the major regions of Chile, from La Serena at latitude 29º S to latitude 39º S in Araucania, and included pristine or protected areas of the major types of Chilean autochthonous vegetation. The survey involved driving 4,300 km by road, with visits to the national parks and reserves of this portion of Chile. Conditions were unusually dry and cold for the fall, but based on the number of field collections, it appears that Central Chile is very rich in myxomycetes, the largest and most diverse group of eumycetozoans. More than 100 species were represented among the more than 500 collections. Some of the most common species found were *Badhamia melanospora* (Fig. 2)*, Physarum newtonii, Physarum bitectum, Trichia varia* and *Fuligo septica*, but the normally common *Arcyria cinerea* was again conspicuous by its scarcity, as was the case last year in Argentina (Inoculum 56(2): 6-7). Some particularly interesting finds were several fruitings of snowline myxomycetes, including *Trichia alpina, Physarum albescens* (Fig. 3), *Lamproderma* spp. and *Diderma* spp., still present and even abundant in places, in good condition at the end of the summer, and in the absence of snow for many months.

Figure 1. The collecting team in front of the Lonquimay Volcano and flanked by Araucaria araucana.

Figure 2. A fruiting of Badhamia melanospora.

In addition to the field collections, more than 150 samples of different substrates were obtained for subsequent laboratory culture of all three groups of eumycetozoans (protostelids, dictyostelids and myxomycetes). The expedition was one of stark contrasts. The vegetation (consisting mainly of members of the *Cactaceae*) at the northern end of the transect, where the desert fans out into the canyons of the mountains, receives only the cool damp hand of the dense marine fog, whereas torrential rains occur on the Lanin Volcano in Villarica National Park to the south. Elevations of collecting sites varied from sea level at the Pacific coast to 3,000 m among the Andean peaks, over a distance of only 80 km. The dry forests dominated by *Acacia caven* and the dense southern beech (*Nothofagus* spp.) forests higher up are replaced by alpine scrub and then snow on the slopes of the line of volcanoes that occur along the border of Chile and Argentina. The hills along the coast are clothed with the Chilean national tree, the majestic and enormous *Araucaria araucana*, or dominated by the stately palm *Jubea chilensis* and surrounded by southern beech forests or examples of Mediterranean vegetation with sclerophyllous evergreen trees. In the more northern portions of the general study area, around La Serena, endemic columnar cacti with lethal spines are the dominant plants, and *Puya spp*. a very productive substrate, provide conditions similar to the *Agaves* of North America. This wide variety in the plants present gives rise to a large number of microhabi-

Continued on following page

tats suitable for eumycetozoans, and this situation is reflected in the occurrence of succulenticolous species and snowline species as well as typical lignicolous and foliicolous species of myxomycetes. Even amid the driest dust of the Elqui Valley, tussocks of grass and decayed cacti remains yielded collections. These native forests and rugged mountain relief, in addition to providing inspiration to the poets Pablo Neruda and Gabriella Mistral, represent some of the most stunning natural landscapes on earth and generate a sense of wonder in all who have the extraordinary opportunity to contemplate them firsthand.

—Diana Wrigley de Basanta, Carlos Lado, and Arturo Estrada-Torres
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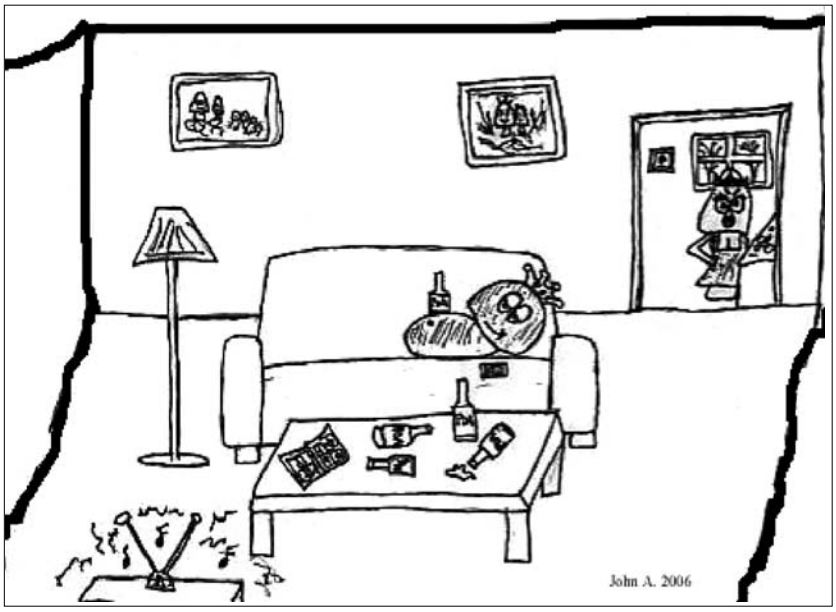
Figure 3. A fruiting of Physarum albescens.

Center of Forest Mycology Research under New Managment

The USDA-Forest Service, Center of Forest Mycology Research at the Forest Products Laboratory (FPL) in Madison, WI will become part of the Northeast Research Station, headquartered in Newton Square, PA as of July 24, 2006. The change is primarily administrative since we will be physically staying at the Forest Products Laboratory. We do not anticipate any major immediate change in our mission - the biosystematics of wood-inhabiting fungi with major emphases on the roles of decay fungi in fire prevention and restoration and on invasive species. Our web page, including a searchable database of our culture collection, can still be found at www.fpl.fs.fed.us/rwu4501/ index.html. Dr. D. Jean Lodge had been transferred from CFMR to the Institute of Tropical Forestry previous to this realignment. If you have any questions about CFMR research, please contact **Dr. Jessie Micales Glaeser**, Project Leader, at jmicales@fs.fed.us or 608-231-9215.



A Day in the Life of King and Queen Bolete

"If you think I'm going to slave in this kitchen all day while you lay on your lazy stipe drinking potato dextrose agar, you are sorely mistaken, mister!"

A Big Thank-You to Our Sustaining Members

I would like to take time to issue a big thank-you to our Sustaining Members, listed elsewhere in this *Inoculum*. The Sustaining Members are an important part of MSA. By supporting our program with added membership dollars, they provide necessary funds to the society, especially important in these difficult times. In return, they receive acknowledgement in issues of *Mycologia* and *Inoculum.* If you belong to a company with an interest in mycology, please consider a Sustaining Membership. Contact Jessie Micales Glaeser, Sustaining Membership Committee, 608-231-9215 or jmicales@fs.fed.us for more information. Information is also available on the MSA web page.

—Jessie Micales Glaeser, Chair
Sustaining Members Committee

"Fungal Bonsai Technique" for Growing Osmophilic Fungi

Several fungi are slow growing on commonly used culture medium on Petri plates. These include the Osmophilic fungi, which are ubiquitous in the natural environment, and can frequently be found in food stuffs with high sugar and salt concentration and in dry environments. Because of their slow growth and selective environmental requirements they are not easily isolated.

Wallemia is a slow growing osmophilic environmental fungus. An experiment was conducted to grow this fungus on Malt Extract Agar (MEA) medium using the '*Fungal Bonsai Technique*, Rabbani (2004)' and simultaneously with the commonly used Perti plate method. This fungus, which is widely known to be slow growing, germinated and began sporulation after only 36 hours (Figure 1). Fully sporulation of dematiaceous micro colonies was seen with long chain of conidia after 48 Hours (Figures 2-4). On the Petri plate there was no visible growth even after seven days.

The fast growth of this fungus by *Bonsai Technique* is due primarily to the range of osmotic conditions available to the fungus on the slide, which presents a gradually decreasing moisture level and increasing salt / sugar concentration in the substrate. Spores deposited along the area of substrate bed that has suitable moisture and sugar /salt concentrations start germinating and sporulating within a few hours. Because the entire growth cycle occurs on microscopic slide, continuous examination and easy identification of the fungus is achieved.

Reference: Rabbani GM (2004) **Fungal Bonsai**: *Inoculum* 5(55) ; Pp 5-6.

Ghulam M. Rabbani and Donald R. Cortes
Stat Analysis Corporation,
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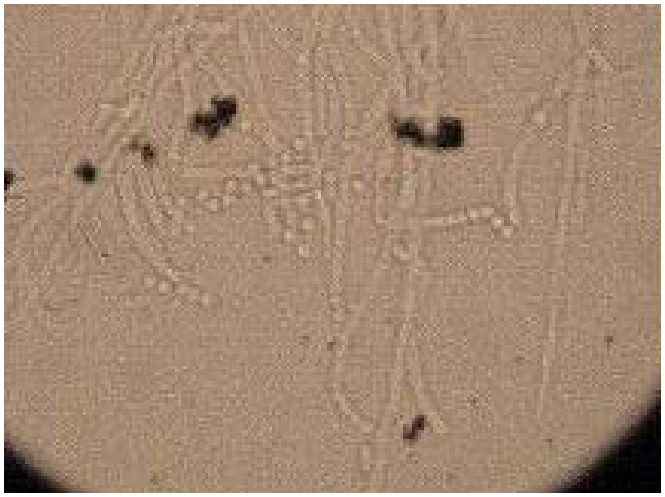


Figure 1. *Wallemia* growth after 36 hours.

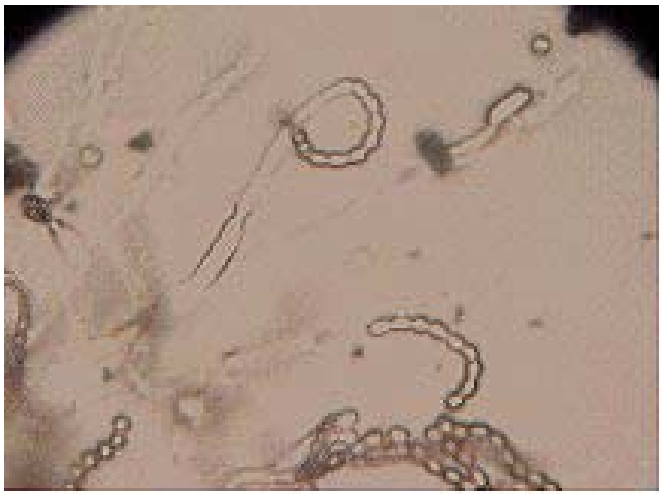


Figure 2. *Wallemia* growth after 48 hours.

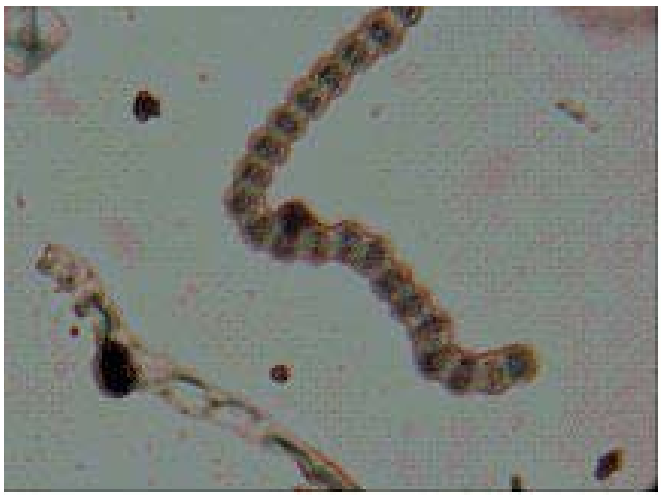


Figure 3. Mature conidia growth after 48 hours.

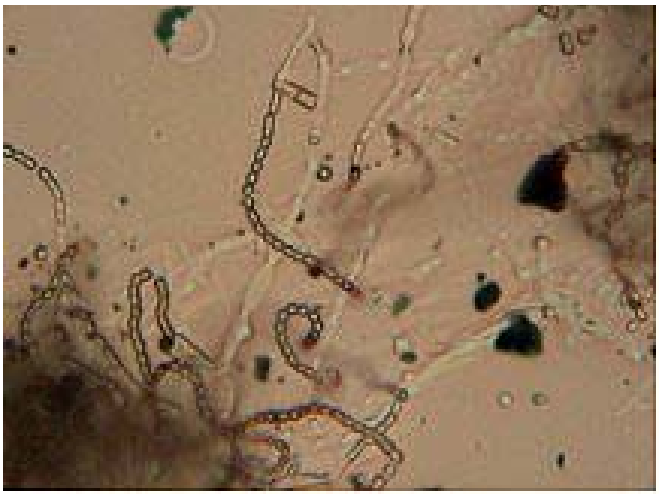
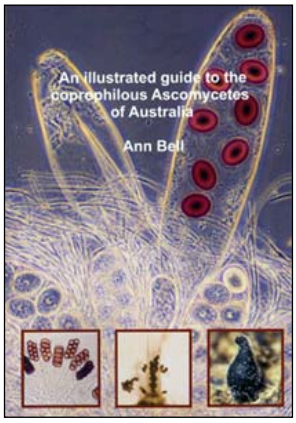


Figure 4. Sporulating conidiaphores.

MYCOLOGIST'S BOOKSHELF

Five books are reviewed below. Three new books and two CD publications have been received since the last Mycologist's Bookshelf. Several previously published books are listed with a note at the end indicating their availability for review. If a review is needed and you would like to review it, just send an email. I will send you the book, you write the review, and then you can keep the book. All requests for books to review should be sent to Dr. Amy Rossman at arossman@nt.ars-grin.gov.

An Illustrated Guide to the Coprophilous Ascomyces of Australia



An Illustrated Guide to the Coprophilous Ascomycetes of Australia. 2005. Ann Bell. Centraalbureau voor Schimmelcultures, Fungal Biodiversity Center, Utrecht, The Netherlands. www.cbs.knaw.nl. 172 pp. Price: €55.00.

Ann Bell's book on the dung fungi of New Zealand, published in 1983, set a standard that was difficult to match, but she has done more than match it with this new volume on the coprophilous Ascomycetes of Australia. And, because so many dung fungi are cosmopolitan, this book, like the New Zealand one, is useful the world over. Bell's study of the Australian species was based initially on the extensive studies and large collections of these fungi by the multifaceted Maj. Harry Dade, who took them on with characteristic energy in his retirement years. But Bell did not stop with Dade's material. She supplemented it with many additional collections from all over Australia.

The 8 x 12 inch, 172 page, spiral-bound book opens with a concise but engaging biography of Dade, with emphasis on his work with coprophilous fungi as recorded in his extensive notes and correspondence with collaborators. Methods and materials follow, then descriptions of the various groups of Ascomycota that inhabit this omnipresent substrate (or, substrates, as some taxa appear to be rather selective about which animals' dung they enjoy). Keys are presented for all taxa. An appendix presents 10 new species, described in keeping with the International Code of Botanical Nomenclature, and another appendix gives recipes for reagents used in the work.

The keys are not all ordinary keys. Bell's skills as an illustrator have been applied to make it easy on those of us who have not specialized in these fungi: she provides handy picture keys. No agonizing about what the terminology means or leafing through glossaries. No vacillating between choices in a dichotomous key. You look at the specimen in hand and compare it with the illustrations in Figure 1, the picture key which shows representative Discomycetes, Plectomycetes and Pyrenomycetes. If, for example, you have a Pyrenomycete, you are directed to the picture key to genera in Figure 7. Now you check spore characteristics to see which illustration matches the spores of your specimen. Having done that, you have determined the genus. Suppose the spores match those illustrated for the genus *Cercophora*: the picture key directs you to the pages dealing with that genus. There you find a brief discussion of the more salient features of the genus (although not a formal description) and a dichotomous key to the species included in the book. The first dichotomy asks you to determine if the perithecial wall is cephalothecoid. Excuse me? Now I need a glossary, but there is none! Not to worry: the key invites you to examine Figure 87, where all is made clear. Every species is illustrated with emphasis on key characters.

And the illustrations, oh, the illustrations! The brightly colored cover of the book is a feast of splendid photomicrographs of asci and spores. When you open the book and flip past the title page, you encounter Harry Dade's water-color, "Dungscape," which shows dozens of species in all their diversity of form and color…the substrate is tastefully subdued. The next two pages are full color plates of attractive and informative photos by D.P. Mahoney, Ann Bell's husband who, I presume, did the cover photos as well. Of the book's 172 pages, more than 100 pages are devoted to illustrations. Color is used where it has diagnostic importance.

This "illustrated guide…" is what it claims to be: not a monograph, not an exhaustive treatise, but a guide. I have dabbled in dung off and on over the years, gathering up some deer, bear, mountain goat, kangaroo or bandicoot dung, popping it in a plastic tub on a damp paper towel, and setting it aside for a week or two to see what fungi emerge. It is quite fun, especially if one has dealt mostly with mycorrhizal fungi, which refuse to fruit except in circumstances of their own choosing. Now I am involved with fungal diversity studies in a variety of habitats in Australia, and I can include the coprophilous Ascomycetes with reasonable expectation of identifying them. When I'm back home in Oregon, I'll be keen to see how well this guide will work there. If not to species, I should at least be able to identify genera with relatively little pain, and the extensive list of references Bell provides will guide me to monographs that may include more North American species of dung fungi.

The Centraalbureau voor Schimmelcultures deserves congratulation for the book's high quality of paper and printing. It is dismaying to report, therefore, that the last several pages easily came partly loose from the rather strange spiral binding just in the course of opening and re-opening the book as I reviewed it. This shouldn't happen in a book of this quality and price.

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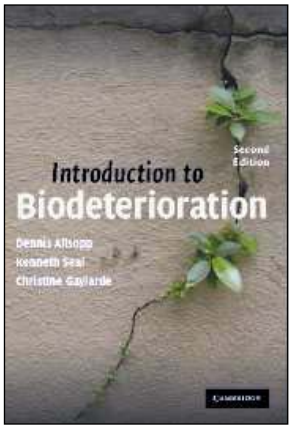
MYCOLOGIST'S BOOKSHELF

Introduction to Biodeterioration, Second Edition

Introduction to Biodeterioration, Second Edition. 2004. D. Allsopp, K. Seal & C.. Gaylarde. Cambridge University Press, New York, NY, uk.cambridge.org/, 237 pp. Price: $75.00 hardback, $34.99 paperback.



Introduction to Biodeterioration is a succinct little book with the goal of introducing the general reader to various disciplines associated with biodeterioration, i.e."undesirable changes in the properties of materials caused by the vital activities of organisms." It assumes a basic understanding of biological and chemical principles but is written for the general student at an introductory level. The topics are not developed in excessive detail, but the authors provide a broad overview of many different subjects. This book could even be useful for specialists who are interested in expanding their knowledge of biodeterioration. The book begins with some general definitions of biodeterioration and biodegradation, differentiating among biological, physical, and chemical decay processes. The chapters are arranged initially by substrate, starting with "natural materials" in Chapter 2, "refined and processed materials" in Chapter 3, and "built materials" in Chapter 4.

Natural materials discussed in Chapter 2 include cellulose-based items, such as paper and wood, but also includes an interesting discussion of food and grain storage problems due to microorganisms, insects, mites, and vertebrates. Problems with the storage of materials of animal origin, including wool, leather, fur, feathers, and museum specimens are also considered. Chapter 2 concludes with the degradation of stone by microorganisms and invertebrates.

Chapter 3, detailing the biodeterioration of refined and processed materials, is the largest and most diverse chapter of the book. It begins with a lengthy discussion of the chemistry and deterioration of fuels and lubicants and then moves to plastics and natural and synthetic rubber. This section of the book is well illustrated with chemical formulas to show how the components of plastics and rubbers degrade. Somewhat more interesting to me was the discussion of biodeterioration of paint, glass, and cosmetics. It is rather alarming to see how many species of bacteria and fungi are associated with common household items, such as soap, toothpaste, and baby oil! The chapter concludes with a discussion of the biodeterioration of metals and magnetic media, the latter a new entry in this edition that will become rapidly outdated as the technology develops and changes.

Moving back to more familiar ground, Chapter 4 presents a discussion of the biodeterioration of "built objects," including houses and transportation structures. The section on wood decay fungi was focused primarily on problems found in the U.K., especially "dry rot" associated with *Serpula lachrymans*. The discussion on "wet rot", i.e. the overwhelming majority of decay problems in the U.S., was quite abbreviated and was focused primarily on decay caused by *Coniophora puteana* and *Fibioporia* species, the latter of which is not a major decay agent in the U.S. There is a short discussion of problems associated with mold fungi, including a brief but dated discussion of the possible health effects of mold exposure – a topic of much concern in both the U.S. and Europe. Damage to buildings by insects, birds, rodents, algae, lichens and higher plants is discussed extensively. The chapter concludes by considering special problems affecting transportation structures, including higher plants growing in roadways and railways; bird strikes, pest transmission and fuel problems associated with aircraft; and hull fouling, cargo deterioration, and fuel and lubicant problems found in ships. The chapter ends with an interesting discussion of problems specific to museums.

The book starts to wind down with a chapter on "Investigative Biodeterioration," which includes techniques on identifying biodeterioration problems and standardized laboratory research protocols. It concludes with a chapter on the principles of "Control," stressing the importance of prevention. Specific control measures are also discussed throughout Chapters 2 – 4.

The book is nicely expanded from the first edition, which I found so useful 20 years ago. I was even surprised to find a table listing species of algae that grow on wood – a question I had received by e-mail earlier in the week for which I had not found a suitable answer in other references. Except for the section on wood decay, most of the topics have been nicely expanded. References and recommended readings are now at the end of each chapter instead of all listed together at the end of the book. I recommend this book to anyone wishing to expand their knowledge of microbiology (and bugs and mice) into additional areas of biodeterioration research.

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MYCOLOGIST'S BOOKSHELF

Systematic Botany of Flowering Plants . . .

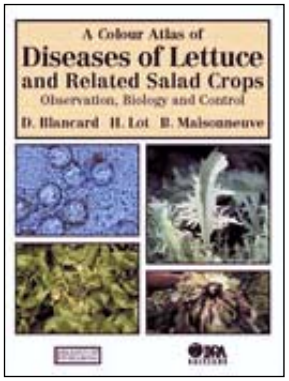
Systematic Botany of Flowering Plants. A New Phylogenetic Approach to Angiosperms of the Temperate and Tropical Regions. 2004. R.-E. Spichiger, V. Savolainen, M. Figeat, & D. Jeanmonod. Science Publishers, Inc. Enfield, NH 03748, www.scipub.net. ISBN 1-57808-315-X (Hardback), ISBN 1-57808-373-7 (Paperback). 413 pp plus CD. Price: $58.00.

Plants serve as hosts to a myriad of fungi and the identification of these hosts is often essential as for rust fungi or very useful as for saprobic ascomycetes. This book will be of interest to mycologists who need to increase their skills in plant host identification as well as those who find themselves teaching plant systematics. The first 100 pages present a succinct overview of the history and phylogeny of flowering plant classification. One chapter on species and speciation defines biological species, populations and various modes of speciation while the chapter on floras and vegetations explains the dominate vegetation types throughout geological history and briefly describes each vegetation type from tundra to forests of tropical mountains with color plants to illustrate them. The two chapters on the evolution and classification of plants includes seeds with keys to the major angiosperm lineages and keys to families in selected orders based on the most recent molecular research.

The bulk of the book consists of a synopsis of each of 113 families along with a plate of essential characteristics. The synopsis includes the number of accepted genera, the major genera, the number of species, and distribution along with a description of the family, placement in various classification schemes, and useful plants in each family. The illustrations are high quality line drawings of plant habit, floral diagrams, entire and cross-sections of flowers, and attached leaves along with the occasional photograph of plant parts. At the end is a very complete glossary and a key to identification of tropical families based on vegetative characters. If this latter key works, it could be extremely useful for mycologists and even botanists working in the tropics. Among the characters used in these keys are tree architecture, branching patterns, presence of exudates, myrmecophily, leaf characteristics, and venation patterns. The book is accompanied by a CD with color illustrations of up to eight plants for each family, although the illustrations on the CD are not adequately labelled. Given its compact size and the CD, I could see this as a welcome addition to a fungal collecting expedition in the topics as well as to the reference library of most mycologists.

— Amy Y. Rossman
Book Review Editor

A Colour Atlas of Diseases of Lettuce and Related Salad Crops . . .



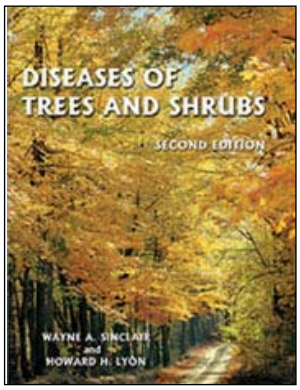
A Colour Atlas of Diseases of Lettuce and Related Salad Crops: Observation, Biology and Control. 2006. first published 2003. D. Blancard, H. Lot, & B. Maisonneauve. Translated from French. Published by Academic Press. Available from APS Press, 3340 Pilot Knob Road, St. Paul, MN 55121, aps@scisoc.org, ISBN 978-0-12-372557-8. 376 p. Price: $169.00.

This book by a group of French plant pathologists is the second in a series that are comparable to the crop-related APS disease compendia. Initially published in 2003 and here translated into English, this volume is more comprehensive and more expensive than the APS disease compendium. Similar to the volume on cucurbits in the series, this hard bound book includes numerous color illustrations with a plate on almost every page and goes into details on every cause of damage to these crops. Both biotic and abiotic causes are included. The book is organized into two major sections: the first section is on diagnosing the disease problem and the second on the characteristics of the disease-causing agents and methods of protecting the crop. The first section is then divided into a section on diseases affecting leaves and head that is further subdivided and color-coded into growth, coloration, spots, and wilting. Similarly the second section on diseases of leaves in contact with the soil and underground parts is subdivided into leaves in contact with soil and crown, roots, and taproot and stem. In the second major section on pathogenic agents and methods of protection the fungi play a dominant role although a number of bacteria, viruses, and nematodes are also important agents of disease. Several pages are devoted to each causal species including details for protection. Here the treatment may be specific to France especially in the recommendation of fungicides. The fungi are well illustrated with several pages devoted to such major pathogens as *Bremia lactucae*, cause of downy mildew of lettuce, and *Erysiphe cichoracearum*, cause of lettuce powdery mildew or white mould, and minor pathogens listed in a table format still with numerous details. Unlike the APS compendia this book does not provide reference to additional literature. Except for that minor criticism, this reference provides a powerful resource to the plant disease diagnostician and those mycologists who help the public with their disease problems.

— Amy Rossman
Book Review Editor

MYCOLOGIST'S BOOKSHELF

Diseases of Trees and Shrubs, Second Edition



Diseases of Trees and Shrubs, Second Edition. 2005. W.A. Sinclair & H.H. Lyon. Cornell University Press, P.O. Box Box 6525, Ithaca, NY 14851, www.cupserv.org, ISBN-13: 978-0-8014-4371-8. 660 pp. plus CD. Price: $85.00.

What a book! Wayne Sinclair's second edition of his already fantastic book of tree diseases is incredible—incredibly comprehensive, incredibly accurate, and incredibly useful. Similar in its large format to the first edition, there is a page of text on one side and a full-color plate of symptoms and the causal agent on the other. This new edition has been updated and improved. Whether one needs picture diagnostics or accurate information and additional literature on a tree disease, this book provides the answer.

The order of presentation is logical starting with diseases on foliage caused by ascomycetes and their asexual states, progressing through ascomycetes on woody tissues, merging into other kinds of fungi on woody tissues. The bulk of tree diseases are caused by fungi but other kinds of organisms are included. The latter part of the book provides details of diseases caused by bacteria, viruses, nematodes and parasitic plants such as mistletoe.

The amount of information packed into each page of text is amazing. The page starts with an overview of the disease based on the common name, scientific name of the causal agent, host range and geographic distribution. And that's just in the first paragraph! The section on signs and symptoms notes variability based on geographic region and time of year such as, for oak wilt "In southern USA the symptoms and progress of the disease differ from the description above," followed by the differences. The section on disease cycle reviews the biology of the disease indicating insects that may contribute to pathogen transmission. At the end of each section on a disease is listed the recent literature by number. With 4537 references listed at the end of the book, you can bet that this resource is comprehensive. The index is detailed with listing for host genus followed by all diseases on that host, disease common name, and causal agents by scientific name and common name.

Always a supporter of accurate systematic knowledge, Sinclair has updated this book to include changes that have resulted from progress in systematic knowledge about the causal organisms. In the index he lists the common name of the host but refers the user to the generic scientific name. One of the remarkable features of this book is the glorious color photographs. These pictures are worth more than a thousand words! This book is a goldmine for anyone needing information on trees diseases at an affordable. My deepest appreciation to Wayne Sinclair and Howard Lyon for this outstanding contribution.

— Amy Y. Rossman
Book Review Editor

Recently Received Books

- **A Colour Atlas of Diseases of Lettuce and Related Salad Crops: Observation, Biology and Control.** 2006. First published 2003. D. Blancard, H. Lot, & B. Maisonneauve. Translated from French. Published by Academic Press. Available from APS Press, 3340 Pilot Knob Road, St. Paul, MN 55121, aps@scisoc.org, ISBN 978-0-12-372557-8. 376 p. Price: $169.00. *Reviewed in this issue*.
- **Aflatoxin and Food Safety**. 2005. H.K. Abbas (ed). CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, **orders@crcpress.com**. ISBN 10: 0-8247-2303-1 (Hardcover). 587 pp. Price: $178.95**.** ***Review needed***.
- **British Fungus Flora 9 / Russulaceae: *Lactarius***. 2005. R.W. Rayner, assisted by R. Watling and E. Turnbull. Print and Publications Section, Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 5LR, United Kingdom, **pps@rbge.org.uk**. ISBN 1 872291 34 1 (Softcover). 203 pp. Price: British pounds 12.50 (excluding postage). *Review in progress*.
- **Fungal Flora of Taiwan, 1st Edition**. 2005. S.S. Tzean, W.H. Hsieh, T.T. Chang, S.H. Wu (eds). National Science Council, Department of Plant Pathology and Microbiology, National Taiwan University. One CD. For availability, contact the author.
- **MycoAlbum CD Introductory Mycology Laboratory Review**. 2006. G. Barron. For availability, contact the author: www.uoguelph.ca/~gbarron/. Over 1,000 illustrations. 2 CDs. US $25 plus shipping and handling for professional biologists, US $15 plus S & H for students. An Instructor's Version US $35 plus S & H includes an image folder with over 600 downloadable images at 800 x 600 pixels for power point presentations. *Review in progress***.**

MYCOLOGIST'S BOOKSHELF

Previously Listed Books

- **Biodiversity of Fungi: Inventory and Monitoring Methods**. 2004. G.S. Mueller, G.F. Bills, & M.S. Foster (eds). Elsevier Academic Press, Burlington, MA, www.elsevier.com, ISBN 0-12-509551-1. 777 pp. Price: $99.95. *Reviewed in this issue*.
- **Common Mushrooms of the Talamanca Mountain, Costa Rica.** 2005. R.E. Halling & G.M. Mueller. The New York Botanical Garden, 200th St. & Kazimiroff Blvd., Bronx, New York 10458-5126 USA, www.nybg.org/bcsi/spub, ISBN 0-89327-460-7. 195 pp. Price: $19.95. *Review in progress*.
- **Diseases of Trees and Shrubs, Second Edition.** 2005. W.A. Sinclair & H.H. Lyon. Cornell University Press, P.O. Box Box 6525, Ithaca, NY 14851, www.cupserv.org, ISBN-13: 978-0-8014-4371-8. 660 pp. plus CD. Price: $85.00. *Reviewed in this issue*.
- **Evolutionary Genetics of Fungi.** 2005. J. Xu (ed) Horizon Scientific Press, 270 Madison Ave. New York, NY 10016, email: spoornam@taylorandfrancis.com. ISBN 1-904933-15-7. 345 pp. Price: $173.00. *Reviewed in this issue*.
- **Flora Agaricina Neerlandica. Volume 6.** 2005. M.E. Noordeloos, Th. W. Kuyper, & E.C. Vellinga. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, orders@crcpress.com. ISBN 9-0541-0496-1, 310 pp. Price: $59.95. *Requested from publisher*.
- **Forest Canopies (Second Edition).** 2004. M.E. Lowman & H.B. Rinker. Elsevier Academic Press, Burlington, MA 01803 , www.elsevier.com, ISBN: 0-12-457553-6. 517 pp. Price: $79.95. *Review in progress*.
- **The Fungal Community: Its Organization and Role in the Ecosystem, Third Edition.** 2005. J. Dighton, J.F. White, Jr. & P. Oudemans. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, USA, email: orders@crcpress.com. ISBN 0-8247-2355-4, 936 pp. Price: $139.95. *Requested from publisher*.
- **Fungi: Experimental Methods in Biology.** 2005. R. Maheshwari. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, orders@crcpress.com. ISBN 1-57444-468-9. 350 pp. Price: $149.95. *Review in progress*.
- ***Fusarium* Mycotoxins: Chemistry, Genetics and Biology.** 2006. A.E. Desjardins. APS Press, 3340 Pilot Knob Road, St. Paul, MN 55121, aps@scisoc.org, www.shopapspress.org. ISBN: 09-89054-335-6. 268 pp. Price: $89.00. ***Review needed.***
- **The Genus *Gymnopilus* (Fungi, Agaricales) in the Czech Republic with Respect to Collections from Other European Countries.** 2005. J. Holec. Acta Musei Nationalis Pragae, Series B., Historia Naturalis 61: 1-52. Available from the author (jan.holic@nm.cz) or Myris Trade Company (myris.myris.cz).
- **Growing Gourmet and Medicinal Mushrooms, Third Edition.** 2000. P. Stamets. Ten Speed Press, Box 7123, Berkeley, CA 94797, www.tenspeed.com. ISBN-10: 1-58008-175-4, 574 pp. Price: $45.00. *Review in progress*
- **Handbook of Industrial Mycology.** 2005. Z. An. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, orders@crcpress.com. ISBN 0-8247-5655-X, 784 p. Price: $169.95. *Requested from publisher*.
- ***Hypocreales* of the Southeastern United States: An Identification Guide.** 2006. G.J. Samuels, A.Y. Rossman, P. Chaverri, B.E. Overton & K. Poldmaa. CBS Biodiversity Series 4. Centraalbureau voor Schimmelcultures, P.O. Box 85167, Utrecht, The Netherlands. www.cbs.knaw.nl/publications/ index.htm. ISBN-10: 90-70351-59-5, 144 pp including 102 color plates. Price: €70.00.***Review needed***.
- **The Identification of Fungi: An Illustrated Introduction with Keys, Glossary, and Guide to Literature.** 2006. F. Dugan. APS Press, 3340 Pilot Knob Road, St. Paul, MN 55121, aps@scisoc.org, www.shopapspress.org. ISBN 0-89054-336-4, 182 pp. Price: $65.00. *Review in progress*.
- **An Illustrated Guide to the Coprophilous Ascomycetes of Australia.** 2005. Ann Bell. CBS Biodiversity Series 3. Centraalbureau voor Schimmelcultures, P.O. Box 85167, Utrecht, The Netherlands. www.cbs.knaw.nl/publications/index.htm. ISBN: 90-70351-580, 172 pp. including 32 black & white plates and 66 color plates. Price: €55.00. *Reviewed in this issue*.
- **Insect-Fungal Associations: Ecology and Evolution.** 2005. F.E. Vega & M. Blackwell (eds). Oxford University, Oxford, United Kingdom, www.oup.com/us, ISBN 0-19-516652-3, 333 pp. Price: $49.50 (hardbound). *Review in progress*.
- **Introduction to Biodeterioration, Second Edition**. 2004. D. Allsopp, K. Seal & C.. Gaylarde. Cambridge University Press, New York, NY, uk.cambridge.org/, 237 pp. Price: $75.00 hardback, $34.99 paperback. *Reviewed in this issue*.
- **The Missing Lineages. Phylogeny and Ecology of Endophytic and Other Enigmatic Root-associated Fungi.** 2005. Centraalbureau voor Schimmelcultures, P.O. Box 85167, Utrecht, The Netherlands. www.cbs.knaw.nl/publications/index.htm. Studies in Mycology 53: 1-262. Price: €55.00.*Review in progress*.
- **Monograph of the Genus *Hemileia* (Uredinales).** 2005. A. Ritschel. Bibliotheca Mycologica 200: 1-132. www.schweizerbart.de/pubs/series/bibliotheca-mycologica-59.html. ISBN 3-443-59102-7. Price: €55.00.*Review in progress*.
- **Mushrooms: Cultivation, Nutritional Value, Medicinal Effect, and Environmental Impact, second Edition.** 2004. S.-T. Chang & P.G. Miles. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, orders@crcpress.com. ISBN 0-8493-1043-1. 480 p. Price: $159.95. *Requested from publisher*
- **Mycelium Running. How Mushrooms Can Help Save the World.** 2005. P. Stamets. Ten Speed Press, Box 7123, Berkeley, CA 94797, **www.tenspeed.com**. ISBN-13: 978-1-58008579-3 (Paperback). 339 pp. Price: $35.00. *Review in progress*.
- ***Mycobacterium* Molecular Microbiology.** 2005. T. Parish (ed.). Horizon Scientific Press, 270 Madison Ave. New York, NY 10016, spoornam@taylorandfrancis.com. ISBN: 1-904933-14-9, 351 pp. Price: $173.00. ***Review needed.***
- **Phylogenetic Relationships and Morphology of *Cytospora* Species and Related Teleomorphs (*Ascomycota, Diaporthales, Valsaceae*) from *Eucalyptus*.** 2005. G.C. Adams, M.J. Wingfield, R. Common & J. Roux. Centraalbureau voor Schimmelcultures, P.O. Box 85167, Utrecht, The Netherlands. **www.cbs.knaw.nl/publications/index.htm**. Studies in Mycology 52: 1-147. Price: €55.00. *Reviewed in Jun-July issue*.
- **Revised Synopsis of the Hyaloscyphaceae.** 2004. A. Raitviir. Estonian Agricultural University Insitute of Zoology and Botany. Scripta mycologia 20. ISBN 9985-9293-3-0. 133 p. Available from the author (ain@zbi.ee) or from Edizione Candusso di Candusso Massimo (maxcandusso@libero.it).
- **Systematic Botany of Flowering Plants. A New Phylogenetic Approach to Angiosperms of the Temperate and Tropical Regions.** 2004. R.-E. Spichiger, V. Savolainen, M. Figeat, & D. Jeanmonod. Science Publishers, Inc. Enfield, NH 03748, **www.scipub.net**. ISBN 1-57808-315-X (Hardback), ISBN 1-57808-373-7 (Paperback). 413 pp plus CD. Price: $58.00. *Reviewed in this issue*.

MYCOLOGICAL CLASSIFIEDS

New Scientific Journal *Pacific Northwest Fungi* Now Online

First discussed at a meeting of the region's mycologists nearly four years ago, the new journal is part of the Pacific Northwest Fungi Project, an ongoing effort to develop a complete inventory of the lichenized and non-lichenized fungi of the region.

Pacific Northwest Fungi is designed specifically for the World Wide Web and benefits from the speed, broad distribution, and low costs inherent in internet publishing. The journal publishes papers on all aspects of fungal natural history, ranging from ecology and biogeography to taxonomy, morphology and phylogeny. Article categories include Notes, Brief Reports, Full-Length Research Articles, and Reviews.

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- Any reader with access to a computer and an internet search engine can find and download articles.
- The journal publishes color photographs.
- There are no page charges.

The journal welcomes submissions. Please see the journal website **www.pnwfungi.org** for information on submitting manuscripts for review.

—Dean Glawe
daglawe@earthlink.net

Foray Planned for Southern Nigeria

Dr. J. A. Okhuoya, Department of Botany, University of Benin, Benin City, Nigeria will be holding a foray from 9-23rd October 2006 in Nigeria. This will involve collecting of fungi from ecological niches with tropical rainforest conditions in the Midwest region of Southern Nigeria. Arrangements are in place for foreign scientists to participate and collect fungi of interest while helping the local mycologists and students with hands-on training in fungal identification and classification. Dr. Omon Isikhuemhen (NC A&T State University, Greensboro, NC) and Dr. Catherine Aime (USDA-ARS, Beltsville, MD) will be participating. There is space for two more scientists. If you are interested, please contact Dr. Isikhuemhen at omon@ncat.edu or 336 334 7259 for further information.

New Myconet Website Online

Sabine Huhndorf and Thorsten Lumbsch took over Myconet from Ove Eriksson. They will continue to try to have an updated classification of Ascomycota and regularly publish Notes on new publications regarding the systematics of Ascomycota at generic and all higher levels. Please feel free to submit notes and also they would be very thankful if you could keep them updated by sending pdf files or reprints of your papers and hints to papers that they may have missed. Their email addresses are: tlumbsch@fieldmuseum.org and shuhndorf@fieldmuseum.org. The new Myconet website can be found at: **www.fieldmuseum.org/myconet/** Any comments on the new website are welcome.

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CALENDAR OF EVENTS

Event dates and descriptions **(bold)** precede event locations *(italic)*, contacts (plain font), and Email/Websites (**bold**, no brackets). Those wishing to list upcoming mycological courses, workshops, conventions, symposia, and forays in the Calendar should submit material formatted as shown below and include complete postal/electronic addresses.

2006 (August 21-26)
8th International Mycological Congress
Cairns, Australia
Wieland Meyer, Chair
Ceri Pearce, Vice-Chair
www.sapmea.asn.au/imc8

2006 (July 29 - August 2)
MSA/CPS/APS Meeting
Québec City, Québec, Canada
Centre des Congrès de Québec

NOTE TO MEMBERS:

If you have events to announce, please notify *Inoculum* editor Richard Baird so they can be listed in the *Calendar of Events*.

rbaird@plantpath.msstate.edu

Change of Address

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Note: Members may also submit directory corrections via the form included in the MSA directory via the MSA Home Page: www.msafungi.org

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

MYCOLOGY ON-LINE

Below is an alphabetical list of websites featured in *Inoculum* during the past 12 months. Those wishing to add sites to this directory or to edit addresses should email <rbaird@plantpath.msstate.edu>. **Unless otherwise notified,** listings will be automatically deleted after one year (at the editors discretion). * = New or Updated info (most recent *Inoculum* Volume-Number citation)

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

Australasian Mycological Society Website
for Introductory Fungal Biology (53-4)
bugs.bio.usyd.edu.au/mycology/default.htm

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

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

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

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

Cordyceps Website
www.mushtech.org

Corticiod Nomenclatural Database (56-2)
phyloinformatics.org

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

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

Cybertruffle's Fungal Valhalla (56-2)
www.cybertruffle.org.uk/valhalla/index.htm

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

Distribution Maps of Georgian Fungi (56-2)
www.cybertruffle.org.uk/gruzmaps/index.htm

Distribution Maps of Ukrainian Fungi (56-2)
www.cybertruffle.org.uk/ukramaps/index.htm

Electronic Library for Mycology (56-2)
www.cybertruffle.org.uk/cyberliber/index.htm

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

Funga Veracruzana (53-6)
www.uv.mx/institutos/forest/hongos/fungavera/index.html

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

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

Interactive Key, Descriptions & Illustrations
for *Hypomyces* (52-6)
nt.ars-grin.gov/taxadescriptions/hypomyces/

Interactive Key to *Hypocreales* of Southeastern
United States (57-2)
nt.ars-rin.gov/taxadescriptions/keys/HypocrealesSEIndex.cfm

ISHAM: the International Society
for Human and Animal Mycology
www.isham.org

Libri Fungorum Mycological Publications (57-4)
194.203.77.76/LibriFungorum/Index.htm

Mycologia On-Line (53-3, page 18)
www.mycologia.org

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

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

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

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

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

Plant-associated Fungi of Brazil (54-2)
nt.ars-grin.gov
(Select Search Fungal Databases, option 3, Host-Fungus Distributions)

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 Website
members.cox.net/ mushroomsinart/

Searchable database of culture collection
of wood decay fungi (56-6, page 22)
www.fpl.fs.fed.us/rwu4501/index.html

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

Systematics of the Saprolegniaceae (53-4)
www.ilumina-dlib.org

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

U.S. National Fungus Collections (BPI)
Complete Mushroom Specimen Database (57-1, page 21)
www.ars.usda.gov/ba/psi/sbml

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

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

inoculum

The Newsletter of the Mycological Society of America

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