This beautiful piece of abstract art (above) is actually a negative of a photograph of fungal hyphae and (empty) asci of the marine fungus _Loratospora aestuarii_. The original is on the right. The photograph and artwork are by my summer undergraduate student, Jessica Childs, and graduate student, Allison Walker.

—Jinx Campbell

jinx.campbell@usm.edu
From the President’s Corner . . .

Just got back from a week up in the Sierra Nevada at Dennis Desjardin’s spring mushroom camp at Yuba Pass. The weather was crisp and sunny and the shrooming pretty good. There were some morels and boletes and lots of the common snow bank species. Brian Perry, Andy Wilson, and Matthew Keirle gave dynamite presentations on their doctoral research and twenty students learned how to identify mushrooms.

I hope you have your reservations made for the Annual Meetings at Penn State University. I’ll never forget the plethora of mushrooms in the forests around University Park when the meetings were held there in 1982 and Roger Goos and I walked the forests together. David Geiser and Barrie Overton have planned two pre-conference trips this year with equal promise. Now all we need are some good rains before the meetings. If you missed the deadline for registration, don’t worry, the late registration is minimal and the more mycologists the merrier.

Here’s another reminder to bring some mycological treasures for the annual auction at Wednesday night’s festivities. You should have received a blast about the photo contest from Fred Spiegel, so bring out your best photos and show off your artistic talents. We’re going to make a big deal of the winners this year. Oh yes, also bring lots of money for the bidding.

The Council decided last year to announce the members receiving distinctions before the annual meetings so that a summary of their activities and contributions can be included in the meeting program and so these individuals can be duly honored. Expect a blast about a month before the meetings of the awardees for the Distinguished Mycologist Award, the Weston Award, and the Alexopoulos Award.

I’m happy to announce that Meredith Blackwell will take over as Chair of the Memorials Publications Committee from Don Pfister. We know these two individuals are the primary holders of the history of our society and of mycology through the ages. Our thanks go to Don for his good work over the years and we look forward to memorials in Mycologia that honor those distinguished mycologists that have passed away.

Hope to see you all at Penn State in August.

—Don Hemmes
President

MSA BUSINESS

MSA Secretary’s Email Express

MSA Council has completed four email polls since my last report, approving the following:

- MSA Full Council poll 2008-03: Council unanimously approved four nominees for MSA Honorary Fellow as presented by the Honorary Awards Committee, Chaired by David McLaughlin. Honorary Fellows will be announced at the MSA Annual Meeting (Penn State, Aug 10-13).
- MSA Full Council poll 2008-04: MSA council unanimously approved the proposal of a By-laws amendment that would better describe the current constitution and duties of the Research Awards Committee. This amendment will be put to the vote of the membership in the annual Spring Ballot for 2008.
- MSA Full Council poll 2008-05: MSA council approved the proposal of a By-laws amendment that would create a new committee on Fungal Conservation. This proposed amendment will be put to the membership during the Spring 2008 Ballot.
- MSA Full Council poll 2008-06: MSA council approved the recommendation made by President Hemmes to appoint Jeff Stone as Editor-in-Chief of Mycologia, commencing January of 2009.

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

- Canada: Jeri L Parrent, Marcie Jill Renee Plishka
- China: Wei Jiang-Chun
- Finland: Masoomeh Ghobad-Nejhad
- Japan: Tomohiko Kiyuna, Yukio Sato
- United Kingdom: Michael Broughton Pilkington

- United States: Maritza Abril, Kahli Burke, Tanya Elizabeth Cheeke-icoz, Marie Clark, Daniel J Clune,
John Dighton, Jeff Garnas, John-Erich Haight, Michele Ann Mansfield, S. Coleman McCleneaghan, Brandon K. Olson, Dustin H Purcell, Pele Eye Rich, Richard A. Roeper, Megan Romberg, Christine L.S. Stone, Valerie Tournas, Gwendolyn Clare Williams, Katelyn Tilley Willyerd

Emeritus candidates: I have received two applications for emeritus status by long standing members Hansjorg Prillinger (Austria) and Richard A. Roeper (Richmond, IN). Emeritus status is conferred upon retired or retiring members who have at least 15 years good standing with the Society.

Deaths: I am saddened to report the recent death of long time MSA member Howard Clinton Whisler in September 2007, a world expert on “lower” fungi.

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

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

MID-YEAR REPORTS

President’s Mid-year Report

One of my goals this year is to increase as many of our mentor travel funds to the $10,000 level as possible, so that a minimum of 5% interest a year would generate a $500 award for each fund annually. So far we have received $3,000 in anonymous gifts that I have been asked to assign to the various mentor funds as I see fit. I have been collaborating with Betsy Arnold, Chair of the Endowment Committee, in making these allocations. Hopefully we will see more contributions by the annual meetings.

As announced in Inoculum, Tom Volk has contributed $10,000 in honor of medical mycologist John Rippon to establish a mentor research fund. Tom donated an additional $500 to make sure the first award could be presented this year. Tom, Endowment Chair Betsy Arnold, Secretary Cathie Aime, Awards Coordinator Faye Murrin, Research Awards Chair Terry Hill, and Webmaster Kathie Hodge all worked together to set the criteria and deadlines for the award, to send a blast to the membership announcing the award, and to list the award on the MSA website.

In addition to all this good news, my wife Helen and I are happy to donate $10,000 toward a mentor travel fund in honor of Bob Gilbertson. We queried those involved in awarding travel and research funds as to which type of grant was most needed and the responses were about a tie, some favoring travel grants, some favoring research grants. We found the need for travel grants the most compelling, so with the Council’s approval we will work on the criteria for awarding this grant each year and announce the new fund at the annual meetings in August.

A second goal is to monitor our membership to see what we can do to maintain and increase our numbers. I have conferred with Maren Klich, Chair of the Membership Committee, and am happy to see that her committee is very active with each member given a specific task in contacting members who have not renewed their membership and looking at ways to advertise our society in an attractive way. I agree with many of the comments I have received that we need to continue to find ways to make our society attractive to all areas of mycology. I’m happy to see that Jo Taylor’s Program Committee has a symposium on methods of looking at fungal cells with the most modern technology and I contacted a number of our young cell biologist mycologists who have all indicated they will be coming to the annual meetings. Hopefully, the Rippon Research Award will get medical mycologists back in the fold.

Three items I would like to discuss at the mid-year meetings are (1) the minimum amounts required to establish a mentor travel or research fund, (2) do we want to merge any of the mentor travel funds to get them closer to the $10,000 level, and (3) do we want to award plaques to the Honorary Award recipients (retroactive?).

Respectfully submitted, Don Hemmes

Vice President’s Mid-year Report

The following candidates have agreed to stand for the MSA 2008 Spring Ballot:

Vice President: Mary Berbee, Professor, Dept. of Botany, University of British Columbia since 1993. Research interests in systematics, early evolutionary history of fungi. MSA Distinction Committee; member, Executive Committee of the International Mycological Association; Associate Editor, American Journal of Botany; Thomas D. Bruns, Professor Plant and Microbial Biology, University of California, Berkeley since 1989. Research interests in fungal ecology and evolution. Has served the society as a councilor, and as a member of the program, awards, and annual lecture committees.

Counselor Cell Biology: Robby Roberson, Ph.D. Professor of Cell Biology and Co-Director of School of Life Sciences Bioimaging Facility, Arizona State University since 1989. Research interests include hyphal growth and morphogenesis, phylogenetics, and biofuels. Associate Editor of Mycologia; Awards Committee; Genetics and Cell Biology Counsel; N. Louise Glass, Ph.D. Professor in Plant and Microbial Biology since

Continued on following page
1999. Research interests include fungal cell biology, genetics and genomics, specializing on the genus Neurospora. Past Editor-in-Chief, Fungal Genetics and Biology, currently Associate Editor, Eukaryotic Cell and Microbiology and member of the Editorial Board of Annual Review of Microbiology. Karling Lecturer, MSA meeting in 2005; organized Transcriptional Profiling symposium, MSA meeting 2007.

Councilor Genetics and Molecular Biology: Georgiana May, Ph.D. UC Berkeley, 1987, Associate Professor, Department of Ecology, Evolution and Behavior, University of Minnesota. Research focus: Evolution of fungal interactions with other organisms. MSA activities: Genetics Counselor, Awards or Distinctions Committee (twice), organized Population Genetics symposium or workshop at MSA and Asilomar Fungal Genetics meeting; Scott Kroken, Ph.D. Assistant Professor at University of Arizona, Division of Plant Pathology and Microbiology since 2004. Research interests in molecular evolution, secondary metabolism, evolution of plant pathogenic fungi in natural and agricultural settings, and the genetic bases for host specificity. Associate Editor for Mycologia, 2006-2008.

Councilor Systematics and Evolution: Teresa Pawlowska, Assistant Professor, Cornell University, Department of Plant Pathology & Plant-Microbe Biology. Research interests in evolutionary biology and ecology of Glomeromycota; Jean-Marc Moncalvo, Ph.D. Curator of Mycology at the Royal Ontario Museum and Associate Professor at the University of Toronto. Research interests include biological diversity, systematics, and biogeography of fungi particularly in the Agaricomycotina; use of DNA-based methods from environmental samples. Currently serving the MSA as a member of the Student Awards Committee. Associate Editor for the journal Fungal Diversity.

Councilor Ecology and Pathology: Jane E. Smith, Ph.D., Research Botanist with the USDA-Pacific Northwest Research Station (since 1987). Research interests include: Impacts of fire and disturbance on soil fungi and bacteria, Microbial interactions with non-native invasive plants, Biological and functional diversity of forest fungi, and Influence of old-growth legacy on forest fungal diversity. Member of MSA (since 1996), and member of the editorial board for Applied Soil Ecology (since 2005); D. Lee Taylor, Ph.D. Assistant Professor of Biology at the University of Alaska - Fairbanks since 2002. Research interests in fungal diversity and function in soil. Organizer of “Detection and Identification of Fungi in the Environment Using Molecular Methods” Symposium, MSA Annual Meeting, Hilo Hawaii, 2005; Planning MSA Annual Meeting scheduled for Fairbanks 2011.

Respectfully submitted, Rytas Vilgalys

Secretary’s Mid-year Report

This report presents secretarial activities conducted between August 2007 and March 2008.

(1) Assisted President Don Hemmes in filling positions on the 2007-2008 Society Roster, including approximately 40 new appointments. Sent the new Roster to newsletter Editor Jinx Campbell for publication in Inoculum and to Webmaster Kathie Hodge for posting on the MSA website. Update the Roster on a monthly basis, as needed, sending updates to Inoculum Editor and Webmaster.

(2) Updated MSA 2007-2008 Officer List and sent to Webmaster, Inoculum Editor, and Mycologia Editor-in-Chief Don Natvig for posting/publication. Sent welcome emails, Officer List, and polling guidelines to MSA Full Council.

(3) Prepared and emailed welcome letters to all MSA 2007-2008 appointments, of which there are currently more than 100, including Standing Committees, Rotating Committees and special assignments; distributed Committee details, MOP instructions, and welcomed/introduced new committee members.

(4) Prepared Minutes for 2008 Annual Council meeting and 2008 Business meeting, and sent to Council for approval. Edited Annual Reports and sent to Inoculum editor Jinx Campbell, along with edited minutes, for publication in the MSA newsletter.


(6) Moderated email correspondence with Full Council and Executive Council including seven email polls. Council voted the approval of: (1) two new Mycologia Associate Editors for the term 2008-2010: Lori Winton and Frances Trail; (2) a one-time allocation of <$1,000 to cover expenses incurred by MSA Webmaster Kathie Hodge to move the MSA website and set up a new interface; (3) a one-time disbursement of <$2,500 to Inoculum Editor Jinx Campbell to cover expenses for digitizing all back issues of Inoculum and making them available online at the MSA website; (4) the nomination of Nicholas Talbott to give the 2008 Karling Lecture at the MSA Annual Meeting at Penn State, from Karling Chair Meritxell Riquelme; (5) approved the establishment of a new Graduate Research Award in the name of John W. Rippon for research in Medical Mycology, established by a generous donation from Tom Volk and to be presented for the first time at the 2008 Annual MSA meeting at Penn State; and (6) approved the allocation of an additional $1500 to supplement the symposium budget for the 2008 Annual Meeting at Penn State, allowing Program Chair Jo Taylor to provide support for three top-notch symposia this year.

(7) Moderated, along with President Hemmes, the approval and editing of blast emails sent out to Society members on behalf of the MSA. These included: (1) a call for Symposia proposals for the 2008 MSA meeting in Pennsylvania, originating from Program Chair Jo Taylor; (2) a call for MSA Awards nominations and applications, originating from Awards Coordinator Faye Murrin; (3) a reminder for MSA Awards nominations and applications, including announcement of new MSA Research Award to honour John W. Rippon; (4) a call and a reminder for nominations for council, originating from Vice President Rytas Vilgalys; and (5) in-
citation for endorsement of an open letter to Science concerning inaccurate fungal identification in GenBank, originating from MSA member Karen Hughes.

(8) Assisted President Hemmes in organizing the midyear Executive Council meeting in Berkeley, scheduled for March 29th, by polling Executive Council and guests for date preferences, arranging accommodations and meeting room with the venue, helping to prepare the agenda for the meeting, and other arrangements. deepest thanks are due to Past President John Taylor and Tom Bruns for hosting this year’s Executive Council meeting in Berkeley and for making local arrangements.

(9) Issued a call to all Society Officers, Councillors, Committee Chairs and Society representatives, Inoculum Editor, Webmaster, Allen Press Representative, and Annual Meeting Coordinators, for midyear reports and agenda items in preparation for the midyear Council meeting. In total, received seven reports and several agenda items for discussion. Compiled reports and motions along with an updated Society Roster, agenda, and minutes from previous two Council meetings in a package for distribution electronically prior to the meeting and by hard copy at the meeting.

(10) Prepared four 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.

(11) Responded to routine correspondence on a wide variety of issues and prepared miscellaneous reports as requested. In total, responded to more than 800 emails relating to MSA business.

Appendix to Secretary’s Mid-year Report

1. ELECTRONIC BALLOTING. At the 2007 Council Meeting, Baton Rouge, Council approved a motion to draft an amendment to the Constitution and Bylaws to update Society voting procedures. Current language in the Constitution and Bylaws does not adequately describe the use of electronic media for Society mailings, nominations, and balloting. (See pg. 50.)

Proposed Changes to Constitution

Proposed Changes to By-Laws

Original Language:

ARTICLE III. ELECTION OF OFFICERS AND COUNCIL MEMBERS

(A) The Vice-President, as election manager, shall mail to each member of the Society at least four months prior to the annual meeting a request for the nomination of officers and council members.

(D) The Vice-President shall provide to the Secretary the final ballot with information about the candidates. At least two months before the annual meeting the final ballots shall be mailed by the Secretary to all members. The ballots shall be returned to the Vice-President who will oversee their counting. A majority of those voting shall elect. A tie vote for any office shall be resolved by Council. Those elected will be notified by the Vice-President so that they may attend the Council Meeting as observers prior to their assumption of office.

Proposed Language (deletions stricken, additions in bold):

ARTICLE III. ELECTION OF OFFICERS AND COUNCIL MEMBERS

(A) The Vice-President, as election manager, shall oversee the sending of a request for the nomination of officers and council members by mail and/or email to each member of the Society at least four months prior to the annual meeting—a request for the nomination of officers and council members.

(D) The Vice-President shall prepare to provide to the Secretary the final ballot with information about the candidates. At least two months before the annual meeting the final ballots shall be mailed distributed by mail and/or electronic ballot by the Secretary to all members. The ballots shall be returned to the Vice-President who will oversee their counting. A majority of those voting shall elect. A tie vote for any office shall be resolved by Council. Those elected will be notified by the Vice-President so that they may attend the Council Meeting as observers prior to their assumption of office.

2. RESEARCH AWARDS. Current language in the bylaws does not accurately describe the present composition and duties of the Research Awards Committee. The present committee currently (from the MOP):

“is a rotating committee consisting of five members serving terms staggered on a five-year cycle. (Originally these six members with two co-chairs comprised this Committee, but the larger number and presence of two Co-chairs proved to be difficult to administer. The current configuration, including the 5-year cycle, may necessitate a Society By-Laws change if found to be preferable. LLN 10/1/02) At least one Committee member must

Continued on following page
belong to the Martin-Baker lineage and one to the Smith lineage."

Proposed Changes to By-Laws (See pg. 57)

Original Language:
ARTICLE IV. EDITORS, COMMITTEES, AND REPRESENTATIVES
(E)(6)(c) Research Awards. 6 members, each serving a three year term. The committee distributes the funds from the H.V. and A.H. Smith, Martin-Baker and Clark Rogerson Research Endowments and other appropriate research awards based on the merits of applicants’ proposals. The number and monetary value of the awards may vary from year to year.

Proposed Language (deletions stricken, additions in bold):
ARTICLE IV. EDITORS, COMMITTEES, AND REPRESENTATIVES
(E)(6)(c) Research Awards. 5 members, each serving a three year term. The committee distributes the funds from the H.V. and A.H. Smith, Martin-Baker, and Clark Rogerson, Forrest Ecology, and John W. Rippon Research Endowments and other appropriate research awards based on the merits of applicants’ proposals. The number and monetary value of the awards may vary from year to year.

Respectfully submitted, Cathie Aime

Mid-year Report from the Past President

MOTION: Moved by Past President Mueller that the Society form a committee that will focus on Fungal Conservation. The Fungal Conservation Committee will be a Rotating Committee that will interact with other MSA committees (e.g., Biodiversity and Ecology Committees and Liaison with Amateur Mycological Clubs & Societies) as well as international organizations such as the European Council for the Conservation of Fungi to foster dialogue on fungal conservation and stimulate the generation and compilation of data appropriate for land managers and the conservation community.

BACKGROUND: Fungi play vital roles in all environments and should be included in management plans and conservation initiatives. However, fungi are often times left out of these discussions because of (a) a paucity of easily accessible appropriate data and (2) no concerted effort by the mycological community to champion and focus efforts on fungal conservation in North America. The European Council for the Conservation of Fungi have actively been pushing for the inclusion of fungi in conservation efforts in Europe. A MSA Fungal Conservation Committee is needed to serve this role in North America.

Proposed Bylaws Amendment

Article IV(E) — proposed language if accepted (deletions stricken, additions underlined and in bold):

(E) There shall be Rotating Committees for General Service — Nominations, Program, the Karling Lecture, and Liaison with Amateur Mycological Clubs and Societies; Rotating Committees with Specific Expertise — Environmental Health and Medical Mycology, Phytopathology, Ecology, Biodiversity, Culture Collections, Genetics and Cell Biology, and Fungal Conservation, and Rotating Committees for Awards — Student Awards, Mentor Travel Awards, Research Awards, MSA Distinctions, Honorary Membership. The Chair of a Rotating Committee is that member serving his/her final year on the committee. The most recent past-chair of a rotating committee retains ex officio, non-voting status on the committee for one year to assure smooth transitions in committee leadership.

Article IV(E)(5) proposed language if accepted (deletions stricken, additions underlined and in bold):

(5) Committees providing Subject Area (“Special”) Expertise: Environmental Health and Medical Mycology; Phytopathology; Ecology; Biodiversity; Culture Collections; Genetics and Cell Biology; Fungal Conservation. Four members on each committee, each member serving a 4-year term. These committees provide liaison with other biological societies, brief articles to the Newsletter, advice to the Society and government agencies on matters of public policy, and answers to inquiries. They may also organize symposia and other sessions at annual meetings.

Respectfully submitted, Greg Mueller

Treasurer’s Mid-year Report

General financial situation: The balance sheet at the end of fiscal year (FY) 2007 (31 July 2007) shows total assets of $790,400, an apparent increase of more than $187,000 over the previous year. This is due to the majority of the meeting income being received and tracked as income in FY07. Immediately in FY08, (in August and thru October 2007) we paid out $55,000 in 2007 meeting expenses and $20,000 in grants and awards. These are meeting costs that occur in FY07 but tracked as expenses in FY08. Factoring in these variables, we had a net income of about $120,000 in 2006-2007. The increase is due to a profit on the annual meeting, an increase in subscription costs, good publication income (i.e. page charges), strong endowment contributions and investment income.

Continued on following page
Comparison of Income vs expense

Income vs Expenses

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* 2007 adjusted to include payments made in FY08
Meeting finances:
For the 2007 meeting in Baton Rouge MSA showed a net profit of $34,489.83. This follows two years of net losses on the meetings where we met with other groups. Next year despite the meeting being organized by the MSA, we do not expect to make any profit. We hope to eliminate any net loss by adequately anticipating expenses.

August 1, 2007 - March 21, 2008 FY08 to date
Meeting Income
Registration 2007 meeting 5,114.00
Total Meeting Income $5,114.00
Meeting Expense
2007 Annual Meeting 55,218.17
Total Meetings $55,218.17

August 1, 2006 - July 31, 2007 FY07
Meeting Income
Registration 2007 meeting 85,176.00
Total Meeting Income $85,941.00
Meeting Expense
2006 annual meeting 2,785.40
2007 Annual Meeting 1,347.00
Total Meetings $4,132.40

Publication finances:
Publication cost for FY07 was very close to that of FY06. In FY07 production costs for 7 issues were paid for; in FY06 production costs for 6 issues were paid for. (I don’t have the figures for number of pages that were published.) For FY08 to date we have paid production costs for 4 issues (similar to this time last year) and to date have paid total publication expenses of $146,263. The fluctuation in the publication costs over the last five years is due primarily to uneven issue/page number production of Mycologia. The proportional costs of Management and Inoculum are much smaller and more constant.

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Membership:
At the end of fiscal 2007, membership numbers were slightly up and subscription numbers were slightly down. For FY07, membership dollars dropped quite a bit but subscription dollars increased substantially and were quite strong. We had good increases in student memberships but decreased the numbers of national and international members.

Membership and subscription numbers for mid-year fiscal 2008 are quite a bit below where we were last year at this time. The trend has been that by the end of the fiscal year the numbers of each recover to close to what they were the previous year. But the long term trend is still downward. For FY08 to date, membership dollars are also quite a bit below last year’s, but subscription dollars have already surpassed the total for FY07. The increase in subscription rates is allowing us to stay ahead financially.

Respectfully submitted, Sabine Huhndorf

Continued on following page
Finance Committee Mid-year Report

The total market value of the MSA investment portfolio as of March 27, 2008 was $720,534. Assets included in the total are the Endowment Account with a value of $507,155 and Operating Account with a value of $213,379. One year ago, the values of the two accounts were $484,863 and $179,700, respectively. It should be noted with some satisfaction that the Endowment fund has now passed the $500,000 mark, thanks to the generosity of MSA members and the dedication of past and present Endowment Committees.

The strategy of the finance committee has been to invest MSA assets in conservative fixed income securities (USTreasury Notes and FDIC insured CDs) in combination with conservatively managed mutual funds to generate both current income and capital appreciation. In recent years, certificates of deposit have offered more attractive returns than US Treasury notes. Consequently, as some of our older long-term Treasury notes have matured, the principal has been reinvested in six- or twelve-month CDs, rather than five-year Treasuries.

The continuing challenge is to maximize income from MSA investments sufficient to sustain MSA Endowment supported programs at their current levels. This challenge is becoming increasingly difficult as interest rates decline in the current year. Interest rates available for T notes and CDs have declined by about 2 full percentage points in the past 6 months, and even lower rates of interest appear likely over the next year. As T notes and CDs mature, we have to exchange securities paying around 5.5% for ones that yield about 3.5%. So although the Endowment is growing, the available income for MSA programs is decreasing as we are forced to lock into much lower interest rates over the near term. A strategy to help offset this has been to invest in conservatively managed mutual funds for a balance of current income and capital appreciation. Because of the risk exposure of even conservative mutual funds, the amount of the MSA portfolio invested in this way is necessarily limited.

Currently the total MSA portfolio managed by Wachovia Securities includes $379,974 in cash and fixed income securities, or about 53% of total assets. This includes $90,000 in US Treasury notes (average yield 4.6%), $215,000 in six- to twelve-month CDs (average yield 4.23%), and $340,398 or about 47% of total assets, in three mutual funds, comprising $127,287 (17.7% of total) in Capital Income Builder Fund, and $86,938 (12% of total) in Fundamental Investors Fund. The Income Fund of America currently pays a dividend of 4.3%, Capital Income Builder currently pays a dividend of 3.4%, and Fundamental Investors pays a dividend of 1.2%. All three funds have also appreciated in value during the time we have owned them, but have decreased in value slightly in the past year. By investing in conservatively managed mutual funds, the goal of the Finance Committee has been to offset low interest rates on fixed income securities with combined equity growth and dividends. As the value of the mutual funds has increased, we have periodically sold shares to lock in capital gains and to maintain the amount of MSA assets invested in mutual funds at less than 50% of the total portfolio. There is currently $71,931 available as a cash reserve for operating expenses and awards from the endowment.

Respectfully submitted, Jeff Stone

Continued on following page
Endowment Committee Mid-year Report

This fiscal year, which commenced August 1, 2007, has seen significant growth in the MSA Endowment. Our current endowment total is $491,053, representing an increase from $428,674 since March 2007 (i.e., a one-year increase of $62,379), and growth totaling $33,971 in the first seven months of FY 2008.

Our Mentor Travel Funds have benefited greatly from the generosity of our society, with $6872 in donations received during the first part of FY2008. Eleven Mentor Travel Awards were given in 2007, representing an increase of 3 awards over the previous year; in 2008, we anticipate 12 awards. These awards are instrumental in supporting student participation in our annual meetings and are a terrific way to honor our mentors and mycological forbears. Please consider donating to our Mentor Travel funds – and thank you to all who have done so!

In addition, our research and lecture funds have grown considerably. Special thanks are due to Tom Volk, who made an exceptionally generous donation of $10,500 to establish the John W. Rippon Research Award. I also extend our sincere thanks for the generous donations provided by numerous members and friends of our society to particular award funds.

As of March 2008, our total for the Restricted Endowment (sum of our Mentor Travel funds and Research and Lecture Funds) is $280,403, reflecting an increase of $19,582 since the start of FY2008.

In addition to significant growth in the Restricted Endowment, our society’s Uncommitted Endowment has had a strong start to FY2008, growing from $196,261 at the close of FY2007 to a current total of $210,650 (a seven-month increase of $14,389). This growth reflects our membership’s very active participation in the 2007 auction, which – with T-shirt sales — generated almost $10,000, as well as the generous donations of many members and friends. Special thanks are due to our outstanding auctioneers from the 2007 meeting in Baton Rouge (led by David Geiser), and to Meredith Blackwell and the local organizing committee for their tremendous help in making the evening a success. Thanks to Cara Gibson for her T-shirt design, to Karen Snetselaar for her hard work in rounding up auction payments, and to those who donated a spectacularly rich array of mycological items to the auction effort. We will soon begin to mobilize for the 2008 auction and hope to have a similarly exciting and successful event at our upcoming meeting in University Park.

On behalf of the Endowment Committee, I extend sincere thanks to all who have donated to these funds, and to all who have supported our efforts to keep the MSA Endowment healthy and actively growing.

Respectfully submitted, Betsy Arnold

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<th>Mentor Travel Funds</th>
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*August 1, 2007-March 1, 2008 only
**Mycologia Managing Editor’s Mid-year Report**

**Production schedule.** Mycologia is nearly back to its normal production schedule. Issue 99(6), was released Feb. 1, 2008. Issue one for Volume 100 is in press and should be released in late March, 2008. Last year the first issue of Volume 99 was not released until June. Don Natvig, Jerry Hebert, Mitch Donohue, and Keith Parsons at Allen Press have been working very diligently to get Mycologia back on schedule.

Volume 99 comprised 100 articles and a total of 962 pages, which is somewhat fewer pages than the preceding three years. Volume 98 had 1106 pages, Volume 97 had 1381 pages and Vol. 96 had 1430. The target number of pages per issue is 200, or 1200 pages per Volume. Volumes 98 and 99 were both somewhat less at 188 and 164 pages, respectively. Now that Mycologia is back on its regular production schedule, efforts should focus on increasing the number of pages per issue to a target of 200. Print publication costs for Volume 98 were $142,918, or about $128 per manuscript page, costs for Volume 99 were $115,084, of about $120 per manuscript page.

Manuscript submissions have continued at about the same rate since 2005. 210 new manuscripts were submitted in 2005, and 193 in both 2006 and 2007. 38 papers have been submitted so far for 2008, which is a little less than for the same months in previous years.

**JSTOR.** JSTOR completed the scanning of all back issues of Mycologia and added Mycologia to its Biological Sciences II collection in March, 2007. Fully searchable electronic text of all articles published in Mycologia, including the Journal of Mycology (from 1885), can now be accessed through the JSTOR website [http://jstor.org] through institutional libraries that are JSTOR members. Mycologia content will be continually added to the JSTOR collection with a moving wall of three years. Currently Volumes 94 - 96 are available through both HighWire and JSTOR.

JSTOR shares its revenue from participating libraries with its hosted journals based on the total number of pages archived for the journal. The MSA received its first revenue sharing payment from JSTOR for $5,876.48 in February, 2008. This represents revenue sharing of $3,876.48, plus $2,000 for having a moving wall of less than five years. The MSA will continue to receive annual income from JSTOR as a participating publisher.

MSA members who do not have institutional access to JSTOR through their library can access Mycologia back content via the Mycologia main page at HighWire Press. The Mycologia main page at HighWire has been updated to authenticate MSA members to enable them access the JSTOR content. Instructions are given on the login page for members to activate their individual Mycologia subscription or retrieve username and password.

**Print back issues.** The availability of all Mycologia back content as digital files on JSTOR makes archiving of print back issues at Allen Press unnecessary. Last year it was agreed that after Jan 2008, all Mycologia issues older than ten years would no longer be warehoused at Allen Press. This will result in some savings to the society, as we are charged for storage of the inventory of back issues. Allen Press has been instructed to recycle all back issues of Mycologia older than 10 years. The MSA member website hosted by Allen Press will be updated to reflect the availability of back issues for sale.

**Page charges.** Mycologia has come to increasingly rely on voluntary payment of page charges to cover its publication costs. Although payment of page charges is “voluntary”, about half

[Continued on following page]
the pages published in Mycologia are supported by page charges. This trend has remained relatively constant for Volumes 98 and 99. Issue 6 of Volume 98 (the Deep Hypha issue) is not included in the Volume 98 summary because full page charges were paid by the Deep Hypha NSF grant. Costs for print publication for Volumes 98 and 99 averaged about $120 per manuscript page. The current page charge fee of $70 per page is roughly 58% of the actual print publication cost (the additional cost of online publication was not considered). This probably represents a reasonable compromise between making the journal available to authors regardless of ability to pay full page charges and the economic necessities of recovering page charges to offset publication costs.

**Subscription rates.** Beginning with Volume 98 (2006), subscription rates have been increased by about 15% annually to reach a target of $325/350 by Volume 101. This is projected to bring the income from institutional subscriptions for Mycologia to balance the costs of production. Subscription rates for Volume 100 were increased by 15% in accordance with this plan.

**NYBG list.** Under the terms of the 1999 agreement between the MSA and the New York Botanical Garden, by which the MSA took over ownership of Mycologia, the MSA agreed to provide 93 gratis subscriptions to the NYBG library exchange program for ten years. This provision of the separation agreement will expire in 2009. We will be negotiating terms for converting subscriptions in the exchange program with the NYBG to paid institutional subscriptions in the coming year.

**Color costs.** Costs associated with publishing color figures in Mycologia are coming under control. The Mycologia editorial office and Keith Parsons at Allen Press are catching most unintentional color illustrations early in the manuscript submission process, and working with authors to reduce the unnecessary use of color in illustrations. This has greatly helped reduce publication costs associated with color illustrations. We also have been working with Allen Press to ensure that color figures are approved for publication only if authors agree to pay the color publication fee ($800/color plate) or request the fee waiver under the MSA policy of providing one free color illustration per year to MSA members. Additional options available to save on color costs are to offer authors the option of publishing figures in grayscale in print and online in color, at no charge.

An additional useful tool that is now available through Allen Press is their “VeriFig” utility, which checks illustrations for file compatibility and resolution. Figure remarks at the proof stage are expensive, and if figures of low resolution are not identified until the proof stage, urgent emails and inconvenience to authors are necessary to prevent delays in production. The VeriFig tool is now being used for quality control checking of figures at the manuscript revision stage and is helping to indentify figure problems at an early stage.

**HighWire Press.** A “cover-to-cover” feature was installed on the Mycologia HighWire site, beginning with Volume 99. This provides links to non-article Mycologia content, such as the cover illustrations, as high resolution pdf files.

Mycologia met its $1500 reserve for pay per view articles downloaded from HighWire Press in January 2008. As a result, the MSA will now share (50/50) with HighWire the revenue from pay per view downloads. HighWire will provide quarterly payments. This would be a good time to reevaluate the charges for pay per view access to Mycologia online articles. There were about 60 ppv transactions for 2007.

**Respectfully submitted, Jeff Stone**

**Mid-year Report of the Inoculum Editor**

I have now been Editor of *Inoculum* for just over a year. I have started to make some changes to the format and overall look of *Inoculum*, which I hope everyone likes. I would like to thank my Production Manager, Robyn Hearn, and his team at MSU for all their hard work. *Inoculum* is published in odd numbered months (January, March, May, July, September, November). The deadline for submitting is the 15th of even numbered months: February, April, June, August, October, except December, which is the 10th.

Each issue of *Inoculum* for 2007 averaged 31 pages. In edition 58(3) a new section entitled “Take a Break” was introduced. This includes a regular Crossword feature, submitted each month by Juliet Pendray who is a member of the Vancouver Mycological Society in Canada, and a Cookery Corner, with menus submitted by many MSA mushroom cooks. From edition 58(4) the title “Inoculum” on the first page went color. In 2007 it was sky blue. In 2008 from edition 59(1) it is sea green. From issue 59(2) there is an expanded list of contents. This list is hyperlinked so you can click on the article you want to read and jump straight to it. No more scrolling through looking for a specific page! Clicking on the title of the article then returns you to the first page. Also all web sites are hyperlinked so you can click on them directly from *Inoculum* and be taken through cyberspace to the webpage directly. Additionally, email addresses were hyperlinked so one click on those will open up a new mail message window with the recipient’s address.

Currently I have an intern, a junior at Ocean Springs High School, who is archiving all editions of *Inoculum* from its first edition in 1950 up to 2001 when *Inoculum* went on line. These back issues will be converted to PDF and made available online for all MSA members to have access to our rich mycological history.

**Respectfully submitted, Jinx Campbell**

**Mid-year Report from 2010**

**Local Organizing committee**

We have begun working on our plans to host the 2010 MSA meeting here in Lexington Kentucky. It is both an advantage and a disadvantage that Lexington will be the host for the World Equestrian Games in October of 2010 (there is a brochure in the cover of the folder supplied to Council for the MidYear Meeting). The advantage is that Lexington is getting all spruced up for the big event, especially downtown, the airport, and the Kentucky Horse Park. This means it should look really nice around here by June of 2010. The disadvantage is that there might be a lot of people coming through Lexington during that summer, and so meeting and hotel space might fill up fast. We have been assured over and over again that all construction will be completed by then. One possible fly in the ointment is a very recent proposal to build a new 40-story complex (http://www.kentucky.com/
454/story/338477.html). The project has not been approved yet, and in fact may not be approved, since it seems to be quite controversial. If it is approved, we hope and anticipate that it will be finished by the time our meeting takes place, since the goal of the developer is to have it done and tenants in place before the Equestrian Games. It is possible that some popular downtown nightspots will move to other locations, but presumably these will still be within walking distance of the Radisson. The proposed site for the new building is about six-eight blocks down from the Radisson on Main Street.

JOINT MEETING: Our goal (with council approval) is to have the meeting be a joint one with the 7th International Symposium on Fungal Endophytes of Grasses. Previous ISFEG symposia were held in New Orleans (1990), Palmerston North, New Zealand (1993), Athens, Georgia (1997), Paderborn, Germany (2000), Fayetteville, Arkansas (2004) and Christchurch, New Zealand (2007). Typical attendance is approximately 125 people, including plant scientists, animal scientists, entomologists and mycologists from all over the world. As the name implies, there is a very heavy emphasis on the fungal symbionts, and because of their key ecological and agronomic roles, everyone who attends is (or intends to become) knowledgeable about the fungal endophytes. The connection with MSA is a natural one, and we expect the majority of participants in the 7th ISFEG will interact closely with the MSA members in attendance, and go to many of the MSA sessions (including the Karling lecture). We think there will be excellent synergy generated from a joint meeting of the two groups.

Lexington has long been a focus of research in all aspects of grass endophytes and their significance, and recently an endophyte genome was sequenced by Dr. Schardl’s group at U.K., with funding from both NSF and USDA. This accomplishment has further increased interest in the system by researchers worldwide, and bodes well for attendance at the 7th ISFEG, particularly if held in Lexington.

Traditionally, the ISFEG meeting includes 3 days of talks, poster presentations, a field trip, and a banquet. Talks are in single session, to facilitate interaction among the scientists of different disciplines. We would schedule ISFEG talks concurrently with MSA sessions, with the exception of the Karling lecture, which we anticipate both groups attending together. Posters are usually displayed for the duration of the meeting, but for a joint meeting we’d try to rotate them each day along with the MSA posters. The field trip highlights implications of endophytes in pastures and turf, and practices to utilize endophytes to best effects for biological protection of the grasses. The banquet generally will include some form of entertainment, preferably with a regional flavor, but relatively inexpensive. We anticipate that we will have a joint banquet for both organizations at the Kentucky Horse Park on the last day of the meeting (see below), and a joint social on the first night. We haven’t arranged it yet, but anticipate that we will probably have a separate field trip relevant to grassland management for the ISFEG on the same day as the MSA foray.

Keynote speakers for the ISFEG meeting usually have their registration and travel expenses (or a portion thereof) paid through donated funds. Also, proceedings are published in a book, usually for the open market (the 6th ISFEG Proceedings is 520 pp.). Donors to the last meeting were the Noble Foundation (U.S.), Pennington Seeds (U.S.), Grasslanz (New Zealand), AgResearch (New Zealand), PGG Wrightson Seeds (New Zealand) and Agri-nostics (U.S.). The ISFEG will handle solicitation of donations for these expenses for the joint meeting with MSA. The donations will be kept in a separate account and utilized only for the purposes mentioned above. None of the funds for ISFEG speakers, or for publication of the proceedings book, would come from MSA or from meeting registration fees. ISFEG attendees, otherwise, will pay the same registration and room costs as MSA members, and these fees will go toward general expenses associated with the meeting (catering, banquet, etc).

GETTING HERE: One big advantage of Lexington as a meeting site is its central location. It is pretty easy to get here by car (we’re supposedly within a day’s drive of 75 percent of the U.S. population, ftp://ftp.lfucg.com/Admin Svcs/PDR/PDRInfo.ppt), or by air. We hope that the relatively low cost of getting to Lexington (for many people) will make up for what might be a bit higher registration and room cost than has perhaps been typical for MSA in the past (see below). Bluegrass Airport (http://www.bluegrassairport.com) is only ten minutes from downtown. The Radisson (our proposed meeting venue) operates a free courtesy shuttle, and we should also be able to get additional vehicles from the university, driven by student volunteers, to handle especially busy arrival times (e.g. the larger connecting flights from Chicago or Atlanta). It is also possible to fly to Louisville or Cincinnati and rent a car to drive to Lexington: we are about 1 hour from each of those cities. Flights in and out of Louisville are often especially inexpensive. We could set up something on the meeting webpage for people to sign up to carpool from those cities, if there is enough interest. Information on transportation options into Lexington can be found in the “Transportation/Tour Services” section of the folder we have sent.

MEETING VENUE: After considering several possible venues, including the University of Kentucky campus, we think that the Radisson Plaza in downtown Lexington (http://www.radisson.com/lexingtonky ) is the best choice. The Radisson has hosted meetings of similar size for colleagues here at U.K. who told us that they did an excellent job for them. The hotel has offered a reasonable room rate ($119.00 for a regular room) that could be split among up to four occupants. The details of the room rate and required room commitment are included in the contract that is in the “Meetings and Conventions” part of this folder. The Radisson has excellent meeting space that will be made available to us as long as we purchase a catering plan (worth at least $18,000) from the hotel and fill our required room allotment. The space includes a really attractive large ballroom that can be subdivided into up to four smaller meeting spaces (each of which should easily hold 100 or more people, theatre-style), several nice smaller meeting rooms, and an atrium balcony that would be excellent for poster display space (with spillover space in the “Boone” room off the atrium) and for a registration/ information desk and book sales counters. There is a map of the space in the “Meetings and Conventions” section. The Radisson will organize a website for room registration that can be linked to the one we will produce for meeting registration.

Continued on following page
An adjacent parking garage provides convenient parking free of charge to hotel patrons.

The hotel is very conveniently located in downtown Lexington, close to many restaurants, nightlife, libraries, museums, art galleries, coffee shops, and other attractions (see the “Attractions” section of the folder). Restaurants in the area range from fast-food choices in the Civic Center food court to 5-star restaurants in the historic Gratz Park area. There is a farmers market, which often features local musicians, downtown on Thursday mornings. On Monday evenings, the Kentucky Theatre hosts the nationally broadcast radio show “Woofsongs Old Time Radio Hour” (http://www.woofsongs.com/orth.html) which features bluegrass and country artists. The historic Lexington Opera House hosts many outstanding musical and artistic events, including Broadway shows (http://www.lexingtonopera house.com/). The Rupp Arena, in the Convention Center complex across the street from the Radisson also hosts many big-name concerts and events (http://www.rupparena.com/). Tickets for shows at any of these venues can be purchased in advance online. The Radisson is across the street from the Lexington Civic Center (http://www.lexingtoncenter.com/shops/) and the Victorian Square Center (http://www.victorian square shoppes.com/location_parking.html), both of which contain many unique shops and restaurants. There are also art galleries, and a wonderful Children’s Theatre and Children’s Museum (http://www.explorium.com/) in Victorian Square.

The hotel is within relatively easy walking distance (8 blocks) of the U.K. north campus, where the student center and bookstore are located. If it seems necessary, we can reserve rooms in dormitories on north campus: these would be available for around $30 per night (including rental of linens), and are typical “dorm style” housing, two to a room with a shared bathroom for each floor (U.K. summer conference housing website: http://www.uky.edu/Housing/summer_conferences/). A meal plan can be purchased from the dormitory cafeteria for people staying there. We haven’t made any arrangements for dorm housing yet because 1) we were afraid we might not fill the required room allotment at the Radisson if we offer this alternative; 2) the rooms at the Radisson will be similar in cost, if there are four students per room, and they are a lot nicer (nicer furnishings, TV, phone, wireless, and private bath); and 3) it will be a lot more convenient for students to be at the conference hotel, though the walk from campus is reasonable for a young, fit person. If it seems that we will need additional space closer to the conference date, it should still be an option to book these dorm rooms since they don’t usually fill up that quickly.

There are many other hotels in Lexington that people could choose, ranging from really nice (expensive) bed and breakfast options in the historic downtown neighborhoods to inexpensive chains including Days Inn and Super 8. People choosing to stay at another hotel might have some trouble finding parking downtown, although Radisson will sell daily parking passes for their garage to meeting attendees; currently these cost $3 per day. We don’t plan to advertise these other options to prospective attendees, because we do have some concerns about filling our room quota if too many people stay off-site. We hope that most people will choose to stay at the Radisson because it’s nice, relatively inexpensive, and it will be the most convenient.

**CATERING:** We assume that we would get most of the catering done by the Radisson, they can do morning and afternoon coffee/tea breaks as well as business breakfast, council meeting, and socials, cash bars, etc. A list of the 2008 standard offerings and their cost is in the “Meetings and Conventions” section of the folder. We’ve been told to expect these costs to increase somewhat by 2010. We met with the hotel catering staff and we gave them a “shoot for the moon” sort of menu, which worked out to $63,634, or about $160.00 per attendee (assuming 400 people). An Excel file breakdown is included on a CD in the folder jacket. The contract from the Radisson offers us a catering discount of 15% off the 2010 prices. The Excel file does not incorporate that discount.

We can work with the Radisson to pare down the catering cost by reducing some of the offerings, probably focusing particularly on hot hors-d’oeuvres at the socials (their cold hors d’oeuvres are much more reasonable in cost, but the hot ones really sounded so delicious!). Does the council have any advice about the variety and quantity of “finger foods” we should offer at the social? Is the idea to provide a snack, or a meal? Our plan is to make the business breakfast optional so that the endophyte group doesn’t have to pay to go to the MSA business breakfast if they don’t want to. It would probably cost about $20-25 to sign up for the business breakfast, does this seem reasonable? It’s going to be a VERY nice breakfast buffet, featuring cheese grits, umm-umm.

**SOCIAL:** We can have it in the Radisson on Monday evening (June 29), and have an assortment of hot and cold hors d’oeuvres, cash bar and a free drink card or two, maybe a fiddle player for inexpensive regional entertainment. We could hold the auction there.

**FORAY:** For the foray we plan to bus participants to Bernheim forest (http://www.bernheim.org/index.html). One or two tour buses would leave from the Radisson early on Sunday morning (June 28), and return in the late afternoon. Most of the local state, federal, and private lands we contacted were unwilling to host a large group of mycologists collecting samples. However, Bernheim jumped at the chance, as long as we agreed to share with them a list of the species that were identified. If you visit their webpage, you can see they have lists of many of the plants and animals found there, but no fungi. The other advantage of Bernheim is that they have some nice grassland ecosystems for the endophyte bunch, so some may go to see that. They are an educational private facility, with excellent space available for lunch and laying out of specimens (though not laboratory space: we would probably be able to bring some microscopes along with us from the U.K. collection). They have a very interesting demonstration of “mycoremediation”, in which fungi are used to remove oil runoff from hard surfaces. This might be of interest to the group. The bus trip to Bernheim would take a bit more than an hour, so we hope that is not too long? It is through some very pretty “bluegrass” country, and we might be able to get someone to come along and tell us about the area as we go (U.K. professors of geology or geography, e.g.). We need to check comparative costs for bus companies, but assume we can do the foray for about

**Continued on following page**
There are a lot of different featured breeds and some very famous race and movie horses (the horse that played “Seabiscuit” in the recent movie is there). There is a brochure and some more information in the folder. Touring the horse park does involve a lot of walking: wheelchairs are available on a limited basis in the visitor center, and most of the park is wheelchair-accessible.

The banquet itself would begin around 5:30 and would feature Kentucky-inspired fare, buffet style, a cash bar (we’re hoping for complementary Kentucky wine and beer with dinner), and entertainment in the form of a troupe of Kentucky “cloggers”. The venue is to be a large semi-permanent tent (air-conditioned) on-site next to the polo grounds, and there will be some polo matches to watch from the banquet site that evening. We thought we could do the MSA awards ceremony there. We could book a Bluegrass band and stay late for dancing if we’d like to, but we weren’t sure if that would be better than just bussing everyone back for the “Thursday night” scene in downtown Lexington instead. Naturally a band and dancing would add to the overall cost of the banquet. Without a band, the cost of the banquet should be around $45-$50 per person, including admission to the park and all attractions there (except the Parade of Breeds), the buffet, and clogging entertainment.

**SPONSORSHIP:** We will approach U.K. as the meeting gets closer for support, particularly related to printing, web design services, audiovisual equipment and posterboards, etc. We assume that U.K. will be willing to help us with many of these either for free or for a very nominal fee, but it has been difficult to get firm commitments this far in advance. There are several sources of internal money we can apply for from U.K. to try to help with costs. We also intend to approach Alltech, local wineries, and other potentially interested local industries to see if they would be willing to sponsor a social, or a symposium, or provide some other form of support (free wine!?!).

We hope that our planning so far meets with council’s approval, and we hope for some feedback to help us to make this meeting one that MSA membership will really enjoy.

Respectfully submitted, Lisa Vaillancourt

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**MSA MINUTES**

**Minutes of the MSA 2008 Executive Council Meeting**

**Saturday, March 29th**

338 Koshland Hall, Berkeley, Calif.

Call to order and Approval of Minutes

1. The 2008 mid-year Executive Council Meeting was called to order by President Don Hemmes at 8:10 am in room 338 of Koshland Hall, Berkeley, California. All MSA Executive members were present: President Don Hemmes, President-Elect Roy Halling, Vice President Rytas Vilgalys, Past President Greg Mueller, Treasurer Sabine Hahn-dorf, and Secretary Cathie Aime. Mycologia Editor-in-Chief Donald Natvig and Mycologia Managing Editor, Jeffrey Stone, were also present as invited participants. Secretary Aime 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 2007 Executive and General Council meetings.

MOTION: (approved unanimously) moved by Secretary Aime and seconded by Past President Mueller that the minutes of the MSA 2007 Executive Council meeting be approved as published in Inoculum 59(3).

**Officers’ Reports (excluding financial matters)**

2. President Hemmes presented his report [Inoculum 59(4)]. The majority of the President’s efforts have been focused on preparations for the 2008 and future MSA annual meetings, ways to increase and maintain Society membership, and especially on increasing the Society’s endowment. He presented an update on the 2008 Penn State meeting, gratefully acknowledging the hard work of the local organizer, David Geiser and Foray Coordinator Don Bueh. Because of contractual arrangements with the conference center at Penn State, MSA will not make a profit from the 2008 meeting, but neither will the Society lose money, and plans for the meeting look well underway. President Hemmes then presented an update on the activities of the new Membership Committee, chaired by Maren Klich, which has been very successful in his efforts to increase the Society’s endowment funds. For instance several of the travel awards have been increased, and the goal is to get as many as possible over the $10,000 mark for future sustainability. Additionally, the President has donated $10,000 to establish a new Student Mentor Travel Award in honor of Bob Gilbertson. This year we will be able to give 12 travel awards to students attending the annual meeting. Council proceeded to discuss whether limits should be placed on how much should be donated to establish a new award, on whether some travel awards that cannot be increased to the $10,000 level should be combined, and on the relative merits of establishing new travel awards versus new research awards.

Action to be taken (by President Hemmes): There should be a statement on the Society website regarding our not-for-profit status. President Hemmes will work with Endowment Chair Betsy Arnold, Past-Treasurer Karen Snetselaar, Treas-

Continued on following page
MOTION: (approved unanimously) moved by President Hemmes and seconded by Secretary Aime that individuals nominated for Honorary Membership in the Society be presented with a plaque. These will also be presented retroactively going back to 2005.

3. Vice President Vilgalys presented his report [Inoculum 59(4)] on the spring ballot. He thanked the Nominations Committee, Chaired by Carol Shearer, for their timely submission of a slate of candidates. All nominees have been contacted and agreed to stand.

4. Secretary Aime presented her report [Inoculum 59(4)], beginning by thanking John Taylor and Tom Bruins for hosting Council at Berkeley for the Mid-year meeting this year and for facilitating local arrangements.

MOTION: (approved unanimously) moved by President Hemmes and seconded by Past President Mueller that the wording of proposed changes to the bylaws concerning electronic balloting (see Secretary’s Appendix, Inoculum 59(4)) be accepted.

MOTION: (approved unanimously) moved by President Hemmes and seconded by President Elect Halling that the bylaws be amended to reflect changes to the Research Awards Committee and that the wording of proposed changes (see Secretary’s Appendix, Inoculum 59(4)) be accepted.

Action to be taken (by Secretary Aime): Several suggested MSA members will be contacted for their input regarding other suggested changes to the composition of the Research Awards Committee.

Financial Reports

5. Treasurer Huhndorf presented her report [Inoculum 59(4)]. Overall, the Society made approximately $123,000 last year. Although the total number of members increased, overall income from membership decreased, due to the fact that we lost some full members but increased student membership. Subscriptions slightly declined, but because of the increase in subscription rate, overall the income from these increased.

Much of the income for the past year was due to the annual meeting held in Baton Rouge, which generated a lot of money. Treasurer Huhndorf reminded Council, however, that we are not expected to make any money on the next couple of meetings. Determining costs of publications is more complicated, but the number of pages per issue has decreased and color costs are now under control so our costs for producing Mycologia have really stabilized. Treasurer Huhndorf then thanked Past-Treasurer Karen Stetselaar with whom she has been working closely to put together a budget for the current year.

6. Finance Committee Chair Jeffrey Stone presented his report [Inoculum 59(4)]. He began with the good news that, thanks to the efforts of the Endowment Committee, and the significant contributions from members such as Tom Volk and President Hemmes, the endowment has reached a significant landmark in that we have exceeded $500,000 for the first time. The endowment generates interest income that pays for the awards program. For many years we’ve had the benefit of past treasury notes that paid 8% interest. However, in recent months this has gone down to about 3.5%. So, while in the past we could have a $4-5,000 mentor fund and still afford to give an award generated on the 8% interest; this is no longer true. At present, even as the value of the endowment increases, the income generated from it is going down. Our operating account is generating approximately $6,000 per year at the moment, and we may have to supplement the endowment from this operating income.

7. President Hemmes presented the Endowment Committee report [Inoculum 59(4)] on behalf of Chair Betsy Arnold. The endowment has just received an additional $3,000 in anonymous donations that is not reflected in the report yet. President Hemmes will be assigning these to various Mentor Travel Awards in order to get as many as possible over the $10,000 mark. President Hemmes has been proactive in soliciting donations for the named Mentor and Research awards. Council then discussed various ways to raise money at the annual MSA auction.

Action to be taken (by Treasurer Huhndorf): Treasurer Huhndorf will contact the Treasurer of the North American Association to ascertain whether they will have the funds to pay the NAMA Research Award this year as soon as possible and notify Secretary Aime and Awards Coordinator Faye Merrin.

8. The report of Mycologia Editor-in-Chief Don Natvig included an update on journal statistics. For the period of July to December 2007, Mycologia received 90 manuscripts, compared to 74 received during the same period in 2006, for a rate of approximately 50 manuscripts per month.

During the last six months, Mycologia accepted 31 papers, rejected 42, and one was withdrawn. The median number of days from submission to acceptance is 114. Mycologia is running about 15 papers per issue this year. Volume 100 (1) (January/February) is finished and should be mailed soon. The March/April issue is in production. Eleven papers have been accepted and are ready to go for the May/June issue. EIC Natvig expects that Mycologia will be back on schedule with the next issue. There was some discussion of the Deep Hypha issue of Mycologia from which most of our back issue revenue can be traced. Additionally an uprising of online queries and journal accessing can also be considered as a result of increased searching on the Deep Hypha issue. Finally, EIC Natvig informed Council that ideally he would like to step down as editor in January 2009 and that the search committee (including an overview of the Allen Track online system) is already underway. Discussion of possible replacements for EIC ensued.

Action to be taken (by President Hemmes): President Hemmes will poll the Mycologia Assistant Editors for suggestions for a new EIC.

9. President-Elect Roy Halling presented a detailed audit of the Allen Track manuscript submission process. The audit was conducted from the viewpoint of author, Assistant Editor, and manuscript reviewer and detailed discussion ensued on areas of the process that could use improvement. It was agreed that difficulties with the system are fixable and that at least one MSA representative should meet with Allen Press to work out ways to streamline the submission process. A list of prioritized action points should be distilled from the audit to take to Allen Press.

Action to be taken (by EIC Natvig): EIC Natvig, in consultation with President Halling and ME Stone, will put together a list of items to bring to Allen Press, ideally by June.

The meeting broke for lunch from 12:00 – 1:00.

10. Mycologia Managing Editor Jeffrey Stone presented his report [Inoculum 59(4)], emphasizing three areas: Allen Press Management contract renewal; Highwire Press contract renewal and additional features; JSTOR revenue sharing rider. The good news is that the journal is nearly back on schedule and the submission rate is holding fairly steady. We received our first check, for $5876, from JSTOR based on the number of pages we have deposited with them and the number of individual accesses to Mycologia articles. This will now be a recurring source of income for Mycologia. Additionally, JSTOR is starting a new revenue sharing fund which makes it into the 3rd tier and would be eligible. Next under discussion was an update of our Highwire relationship. Mycologia is now part of the cover to cover feature which allows the user to access the cover art and other inside content that is not part of the actual article. Mycologia has met its initial reserve so, from now on Highwire will share any paid per view charge 50/50 with Mycologia. Currently we are charging $7 per view. Council discussed whether we should consider raising this price (other journals charge up to $30 per view). However, Mycologia received 60 paid per view last year, so it was decided to leave the charge at $7 per download. ME Stone presented a chart illustrating how many people were accessing Mycologia online. People are now downloading and accessing more articles online, especially since March of last year (which is about the time that the Deep Hypha issue came out). The Highwire contract renewal was then discussed, as were new suggested features such as Cross Ref and Cite Track. ME Stone recommended Cross Ref, which will provide a hyperlink that will take the reader back to the original Mycologia paper and costs about $65,000 each year. This will take us through March 21, 2011. It was also noted by ME Stone that the NYBG agreement is going to expire in 2009 although he has not heard anything more from them about terms for renewal. Finally, the Allen Press Management contract, which is currently up for renewal, was discussed. This is a three year contract that will come to about $27,000 a year. This includes all of our services, business office support, membership directory, email renewals, renewal campaign, etc. After voting all contracts were signed by President Hemmes.

Action to be taken (by ME Stone): Highwire can provide statistics such as the top 10 most read Mycologia articles and Vice President Vilgalys suggested that these should be made available to members on the website.

Action to be taken (by Treasurer Huhndorf): Treasurer Huhndorf will investigate the actual yearly billing of Allen Press, which appears slightly different in our bookkeeping system.

MOTION: (approved unanimously) moved by Vice President Vilgalys and seconded by Past President Mueller that we sign the license agreement for the JSTOR Amendment to continued on following page.
Upcoming meetings
11. President Hemmes noted that plans for MSA 2008 at Pennsylvania State University, State College Pennsylvania seem to be progressing well.

12. President-Elect Halling reported that he has been consulting with representatives of the Botanical Society of America and MSA member Marc C. beta who will be Program Chair for the MSA/BSA 2009 meeting at Snowbird, Utah regarding joint symposia. Council decided to provide funding for 2-3 joint symposia at $1000 each, and 1-2 MSA symposia at $1500 each. BSA would like MSA to send a representative to their annual meeting this year in Vancouver and it was decided that President-Elect Halling will contact MSA member Mary Berbee to see if she will represent MSA at this meeting. The BSA will be sending a representative to our 2008 annual meeting at Penn State. Vice President Vilgalys suggested a joint foray be coordinated as well.

13. President Hemmes reported that MSA 2010 to be held at the University of Kentucky, Lexington, Kentucky is in exceptionally good hands. Local Coordinator Lisa Vaillancourt sent a full report [Inoculum 59(4)] and comprehensive notebook regarding meeting preparations that was gratefully received by Council.

14. Vice President Vilgalys presented options for potential MSA 2012 venues. Vice President Vilgalys would like to hold the 2012 meeting as a joint meeting with the Mycological Society of Mexico. Potential sites could be the Yucatan, or Oaxaca. Another, surprisingly affordable idea would be to hold the meeting on a Cruise Ship sailing from New Orleans to the Yucatan and back. Preliminary quotes from Carnival are promising. A cruise ship would offer plenty of interaction time with colleagues in the evenings.

Council had some questions regarding the cruise ship option, such as how poster sessions would be accomplished, whether there would be any hidden fees for registration/nametags, etc, what the quotes would be if we went with early June rather than the peak early August season, and how much flexibility would we have?

Action to be taken (by Secretary Aime): Secretary Aime will consult with MSA member Allison Walker to obtain additional quotes and information from Carnival in time for the Annual Council Meeting in Penn State.

Any other business
15. Past President Mueller read from his report [Inoculum 59(4)] regarding the establishment of a Fungal Conservation Committee.

MOTION: (approved unanimously) moved by Past President Mueller and seconded by Vice President Vilgalys that the Society form a committee that will focus on Fungal Conservation. The Fungal Conservation Committee will be a Rotating Committee that will interact with other MSA committees (e.g., Biodiversity and Ecology Committees and Liaison with Amateur Mycological Clubs & Societies) as well as international organizations such as the European Council For the Conservation of Fungi to foster dialogue on fungal conservation and stimulate the generation and compilation of data appropriate for land managers and the conservation community.

The meeting was adjourned by President Hemmes at 3:00.

**MSA 2008 ABSTRACTS**

Adams, Gerard C.1*, Cutal, Mursel1, Trummer, Lori2 and Worrall, James.3 1Department of Plant Pathology, Michigan State University, East Lansing, MI 48824, USA, 2USDA Forest Service, Forest Health Protection, Alaska Region, Anchorage, AK 99503, USA, 3USDA Forest Service, Forest Health Management, Rocky Mountain Region, Gunnison, Colorado 81230, USA. gadams@msu.edu. Phytophthora and Pythium species new to North America, California or Colorado, from beneath Alnus spp. For the last several years, widespread, severe dieback and mortality of thleaf alder, Alnus incana subsp. tenfolia has been observed and studied in Alaska and in the southern Rocky Mountains. Evidence has strongly indicated that the damage is associated with Cytospora canker, caused by Valsa melanodiscus, and unusual host predisposition to the disease. Factors influencing host predisposition may be climate change but are yet unresolved. Because of concern about the possibility of cryptic invasion by the European Phytophthora alni, together with growing efforts to survey for Phytophthora ramorum, a survey for Phytophthora species (Ph.) in Alaska and Colorado was conducted in 2007. Rhododendron leaves were used as bait to trap plant pathogenic Peronosporomycetidae from soils and roots beneath alders and streams adjacent to alders. A standard medium PARPH selective for Phytophthora and containing Hymexazol® to inhibit Pythium species (Py.) was used in isolations. Unique species discovered in Alaska included; Ph. alni subsp. uniformis, “Ph. hungarica”, Py. boreale, Py. macrosporum, Py. pachycaule, and Py. sterilum. Unique species in Colorado included; “Ph. hungarica”, Ph. mirabilis, Ph. siskiyouensis, Py. dictinum, Py. dissotomum, Py. flevense, Py. indigoferae, Py. montanum, Py. pachycaule, and Py. sterilum. Hungarian workers have submitted sequence of “Ph. hungarica” to NCBI GenBank as a new species in press. Several undescribed species of Phytophthora and Pythium were isolated repeatedly from samples of Alaska and Colorado, as were many common species. Approximately 650 isolates were sequenced during the survey. Visible evidence of root rot was not apparent in any of the excavated roots from 70 plots. However, we will be further examining alders for evidence of Phytophthora in 2008. Poster

Alexander, Mark T.* and Baird, Richard E. Plant Pathology, P.O. Box 9655, 206 Dorman Hall, Mississippi State, MS 39762, USA. MAlexander@plantpath.msstate.edu. Baseline data on fungi associated with old growth eastern hemlock and impact of Hemlock Woolly Adelgid on rhizospheric fungal communities in the Great Smoky Mountains National Park. At the current rate of spread, the exotic Hemlock Woolly Adelgid (HWA) will infest and devastate the entire southern range of eastern hemlock within the next 2 decades. The imminent loss of this cornerstone tree species will have an unknown impact on the associated belowground fungal community in the southern Appalachians. This project seeks to establish baseline data on the total rhizospheric microflora associated with healthy, mature eastern hemlock. Diversity, richness, and abundance of fungal populations was characterized by incorporating traditional cultural isolation with DNA sequence analysis. Root segments from 40 eastern hemlock trees were plated on 4 types of selective growth media. A 5 mg composite root sample from each tree was used for genomic DNA extraction and PCR amplification using the fungal-specific primers ITS1F and ITS4. Fifty clones were obtained from each sample and RFLP analysis was used to group genotypes for sequencing. In addition, monthly macrofungi collections within the research plots contributed to the species diversity data. Putatively ectomyorrhizal fungi have been isolated in pure culture and cryogenically preserved in a fungal repository. After confirmation by ectomychorrhizal synthesis, these hemlock symbionts will be made available for use in future reforestation efforts. Poster

Amend, Anthony1*, Yi, Cui2 and Zhendong, Fang.1 1University of Hawaii, Department of Botany, 3190 Mailie Way, Honolulu, HI 96822, USA, 2University of Michigan, Ann Arbor, MI, USA. 1Shangrila Alpine Botanical Garden, Zhongdian, Yunnan, China. amend@hawaii.edu. Ain’t no mountain high enough? Himalayan topography affects gene flow in a prized edible mushroom. Tricholoma matsutake, an edible and medicinal ectomychorrhizal mushroom, has been revered in Japan for centuries for its distinguished flavor, medicinal properties and iconic significance. Previous studies have demonstrated that this Asian species shows significant isolation by distance (IBD) population structure at scales ranging from continental to ~1,500 km. At shorter distances, however, this

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Inoculum 59(4), July 2008 17
pattern attenuates. The main goal of this study was to determine what role
topography plays in *T. matsutake* population structure. Using multilocus
single-nucleotide polymorphic DNA markers, IBD patterns were tested
on populations within and among Himalayan valleys. We find that high
ridgelines prove to be effective boundaries to gene flow, even at distances
less than 64 km, whereas populations located within valleys only showed
significant differentiation at distances over 125 km. Mantel tests demon-
strated a significant positive correlation between genetic dissimilarity and
landscape distance, which accounts for topographical boundaries, how-
ever no significant correlation was found between population genetic dis-
similarity and geographic distance measured as the crow flies. AMOVA
analysis revealed significant hierarchical variance partitioning with 95% of
the genetic variance found within populations, and 5% found among
valleys. Finally, we examined fine-scale population genetic structure of
mycorrhizas in a human-disturbance chronosequence to infer how habi-
at affects reproductive strategy and dispersal. Small genet size and evi-
dence for sexual recombination at small spatial scales throughout is
indicative of prevalence of long-distance spore dispersal. This study
systematically examines the fine scale population genetic structure of *T.
matsutake* to test the effects of topography, distance and dispersal on pop-
ulation substructure. We show that the relationship between topography
and gene flow is an important, if little studied, determinant of ectomycor-
rhizal population structure in three-dimensional landscapes. Implications
for management of this economically important species are discussed.

**Contributed Presentation**

Amira El-Ganiny, Amira¹, Sanders, David A. R.² and Kaminskiy, Susan,
G. W.¹ Department of Biology, University of Saskatchewan, Saskatoon
SK S7N 5E2, Canada, ²Department of Chemistry, University of
Saskatchewan, Saskatoon SK S7N 5C9, Canada. susan.kaminsky@usask.ca.
*Aspergillus nidulans* UDP-galactopyranose mutase (*UgmA*) plays key roles in colony growth, hyphal morphogenesis, and conidiation. Fungal wall components provide useful
targets for antifungal drug development, since they are not found in hu-
mans. However, there is growing resistance to current drugs that target
fungal walls. Galactofuranose (Gal) is found in the walls of many fungi
including *Aspergillus fumigatus*, the most prevalent opportunistic fungal
pathogen in developed countries, and *A. nidulans*, a closely related, trac-
table model system. Analysis of Gal biosynthesis in prokaryotes shows that UDP-Gal (or the five-membered ring form) is generated from UDP
*galactopyranose* (UDP-Galp, the six-membered ring form) by
UDP-galactopyranose mutase (UGM) prior to cell wall incorporation. We
deleted the single-copy UGM sequence (AN3112.4, which we call
*Ugma*) from an *A. nidulans* *nud* deletion (del) strain, creating
*Ugm*del. Hayloid *Ugm*del strains were able to complete their asexu-
al cycle, showing that UGMa is not essential. However, *Ugm*del strains
had compact colonial growth. Conidiation in *Ugma* deletion strains had
50-fold reduced abundance. In addition, *Ugm*del strains had aberrant
hyphal morphology, producing wide, uneven, highly branched hyphae.
Hyphal defects were partially remedied by growth on 1 mM sucrose,
or on 10 µg/mL Calcofluor. Characterization of the deletion phenotype is
proceeding. The *Ugma*del phenotype is consistent with Gal residues
being important in cell wall structure and/or function. Thus UGM may be
a useful target for anti-fungal drug development. **Poster**

Andrew, Marion* and Kohn, Linda M. Department of Ecology and Evo-
olutionary Biology, University of Toronto, 3359 Mississauga Road, Mis-
sissauga, ON L5L 1C6, Canada. marion.andrew@utoronto.ca. **Molecu-
lar phylogeny of pathogenicity-related genes and the evolution of
nectrotrophic parasitism in the Sclerotiniaceae.** Members of the Scle-
rotiniaceae (Ascoscytomata; Leotiomycetes) represent the full spectrum
of trophic types: including obligate and facultative biotrophs, broad host-
range necrotrophs and narrow host-range facultative parasites, some of
which evidence co-evolution with their hosts. We are screening for the
presence/absence of genes involved in latency or host cell death to: i.
determine origins of necrotrophic pathogenesis and symptomless biotro-
phy, and ii. compare the genetic mechanisms differentiating trophic
types. Our initial four candidate genes code for the pathogenicity-related
proteins: acid protease 1, aspartyl protease, exopodagalacturonase 1, and
endopodagalacturonase 5. Gene genealogies were inferred from both pri-
mary and protein sequences. These were compared to a molecular phy-
logeny of the Sclerotiniaceae generated from the combined sequence of
heat shock protein 60, glyceraldehyde-3-phosphate dehydrogenase, and
calmodulin. Major conflicts between the pathogenicity-related gene phy-
logenies and the expanded Sclerotiniaceae phylogeny based on “neutral”
loci indicate that the evolutionary history of the genes differs from the
presumed evolutionary history of the organisms. Conflicts between gene
and protein trees suggest that some taxa may have selective constraints
on the gene product, and Ka/Ks analyses were performed to identify sites
of purifying/positive selection. **Contributed Presentation**

Avis, Peter G. Department of Biology, Indiana University Northwest,
Gary, IN 46408, USA. pavis@ius.edu. **An ITS-based phylogenetic hy-
pothesis for the Russula amoeno lens species complex.** The *Russula
amoeno lens* species complex is a systematically notorious but typically
abundant and ecologically important clade of mycorrhizal fungi. Mor-
phologically, this complex which includes *Russula amoeno lens, R. pecti-
natoides, R. pectinata*, and not yet described species found worldwide
exhibits a challenging to differentiate set of the reproductive structures or
mycorrhizas. Ecologically, the *Russula amoeno lens* complex can be
especially abundant. Members of this complex have been found to domi-
nate the ectomycorrhizal communities in pine and oak woodlands in Cal-
ifornia, Minnesota, Illinois and Indiana. They have also been found to be
numerous in tropical (India) and sub-tropical (Costa Rica) forest ecosys-
tems and can also be major symbionts of non-photosynthetic plants such as
myco-heterotrophic orchids. This poster will present a ribosomal
DNA internal transcribed spacer (ITS) based molecular phylogenetic hy-
pothesis for this complex from a sampling of approximately 300 collec-
tions made in the Midwestern U.S, a selection of tropical collections and
ITS sequences gathered from Genbank. **Poster**

Avis, Peter G.¹, Mueller, Gregory M.², Branco, Sara² and Tang, Yaya.²
¹Department of Biology, Indiana University Northwest, Gary, IN 46408,
USA, ²The Field Museum, Chicago, IL 60605, USA. pavis@ius.edu.
**Checking the pool: Pooled samples bias estimates of fungal species
richness and composition.** In ecological studies of fungi, pooling (i.e.
mixing) many samples of fungal tissue (e.g., mycorrhizal root tips) fol-
lowed by molecular analysis offers the potential for much greater repli-
cation and statistical power. However, little verification has been con-
ducted on how pooling samples affects community descriptions. To test
how well pooling measures fungal species richness and composition, we
combined fungi into pools of known species composition and used three
different molecular techniques to see if these simulated communities
could be accurately recovered. We used equal amounts of sporocarp tis-
sue from identified fungi to create combinations of two to 20 species per
pool. DNA from each pool was then extracted and analyzed by Auto-
mated Ribosomal Intergenic Spacer Analysis (ARISA), Terminal Re-
striction Fragment Length Polymorphisms (T-RFLP), and cloning-se-
quencing. Our results indicate that all methods failed to recover the
known species number and composition and we found little relationship
between the known combinations and the species detected by each
method. Our results suggest that pooling can bias descriptions of fungal
communities. We will explain how biases in DNA extraction, PCR, or
cloning could produce the error and suggest additional tests of pooling
are required. **Symposium Presentation**

Bainard, Luke D.³ and Kilronomos, John N. Department of Integrative
Biology, University of Guelph, Guelph, ON, N1G 2W1, Canada.
lbainard@uoguelph.ca. **Spatial community composition of arbucus-
lar mycorrhizal fungi in a temperate tree-based intercropping sys-
tem.** Tree-based intercropping (TBI) systems involve planting annual
crops in alleys between rows of permanent trees and are alternative agri-
cultural land use practices that promote increased diversity and sustain-
bility compared to conventional farming. The incorporation of trees into
an agricultural field results in interactions between the roots of the tree

Continued on following page
and crop components and may influence the composition of arbuscular mycorrhizal fungi (AMF). Sustainable land use practices such as TBI may be a way to ameliorate the negative impact agricultural practices have on AMF. The objective of this study was to investigate the influence of three different tree species (white ash, Norway spruce, hybrid poplar) with varying mycorrhizal associations on the spatial variation of AMF communities within a TBI site and compare to a conventionally managed (monoculture) field. The study took place at the University of Guelph Agroforestry Research Station (ARS) which is a long-term TBI research site that was planted with soybean during the 2007 season. The AMF communities were characterized from soil and root samples using large subunit rDNA-based terminal restriction fragment length polymorphism analysis. Results from this study provide a detailed spatial analysis of the AMF communities that associate with the tree and crop components from a TBI and conventionally managed site. Poster

Ball, Bernie* and Lutzoni, François. Department of Biology, Duke University, Durham, NC 27708, USA. bernieb@duke.edu. Priming the Fungal Tree of Life. Reporting on the design and testing of “universal” primer sets for amplifying single-copy, nuclear protein coding regions across the fungal kingdom in support of AFToL2. The journey from orthologous alignments to the amplification of novel genes follows the road less traveled. Symposium Presentation

Baroni, Timothy J.1*, Lodge, D. Jean1 and Aime, M. Catherine.2 Department of Biological Sciences, State University of New York – College at Cortland, Cortland, NY 13045, USA. 2Center for Forest Mycology Research, Northern Research Station, USDA – Forest Service, LaFayette, PR 07773, USA. Department of Plant Pathology and Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, USA. baronit@cortland.edu. Doyle’s Delight, the highest peak in the Maya Mountains of Belize, Revisited. In August 2004, mycologists Baroni, Lodge and Lindner joined an international team of biologists to undertake the first ever helicopter-assisted expedition to study the biodiversity of Doyle’s Delight, an unexplored cloud forest and the highest peak in the Maya Mountains of Belize. Mycologists Baroni, Lodge and Aime participated in a second expedition in August 2007 with support from the National Geographic Society and the British Mycological Society. During the 2007 expedition nearly 500 collections of fungi were documented over 10 days. Approximately 20-30% of the species were collected during both expeditions, but because conditions for fruiting were more favorable in 2007, the diversity was greater. Additionally, data on microfungi in the Pucciniolectinymenia were added in 2007, including the first reports of species in the genera Tuberculina and Dietelia, and numerous new rust and host records for Belize were obtained. We found a new genus and many new species on the first Doyle’s Delight expedition (some already published). Our preliminary results from 2007 indicate we have found many more new taxa including new species of Sarccodon, Protuberia, Entoloma, Inocephalus, Cantharellus, Mycena, Hygrocybe, and two taxa that resist generic placement. A discussion and photo essay of these newest finds will be presented. Poster

Barrett, Craig F.1*, Freundenstein, John V.1 and Taylor, D. Lee.2 The Ohio State University Herbarium (OS), Museum of Biological Diversity, 1315 Kinnear Rd. Columbus, OH 43212, USA. 2Institute of Arctic Biology, University of Alaska-Fairbanks, 311 Irving Building 1, Fairbanks, AK 99775, USA. barrett.586@osu.edu. Host associations of the epiparasitic striped coralroot orchid complex. Corallorhiza striata Lindley is a mycotrophotrophic orchid species complex that shows considerable variation in size, flower shape, phenology, and color across its North American range from Mexico to Canada. The complex also contains an endangered species, C. bentleyi, native to the Appalachian Mountains of Virginia and West Virginia, USA. Members of this species complex associate with members of the basidiomycete family Thelephoraceae. However, very little is known about the patterns of association between C. striata and fungal host haplotypes across North America. We used DNA sequencing for both orchids (rbcL, rpl32-trnL) and fungi (ITS) to test the hypotheses of: 1) strict host specificity of orchid clades and haplotypes on fungal clades or haplotypes, and 2) codivergence between parasite and host phylogenies. GenBank BLAST searches indicated that all C. striata and C. bentleyi fungal associates shared high identity with ectomycorrhizal Tomentella spp. An analysis of 82 individual orchids and their associated fungi from 42 populations across North America suggested incomplete host specificity and lack of strict codivergence. Neither morphological groupings nor plastid DNA clades (orhids) could fully explain patterns of fungal host association. These data suggest that geography is of equal or greater importance in determining haplotypic associations between the orchids and their fungal hosts, and that the orchids generally demonstrate a lack of host specificity to putative species of Tomentella. More extensive sampling among and within populations should give a clearer picture of these associations. These findings have important implications for the conservation of C. striata and the endangered C. bentleyi. Contributed Presentation

Bartz, Faith E.1*, Danehower, David A.2, Tavantzis, Stellos M.2 and Cuba, Marc A.1.1 Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7616, USA. 2Department of Crop Science, North Carolina State University, Raleigh, NC 27695-7620, USA. 3Department of Biological Sciences, University of Maine, Orono, ME 04469-5722, USA. febartz@ncsu.edu. Quinic acid catabolism and production of the plant growth regulator phenylacetic acid by Rhizoctonia solani AG-3. The production of the plant growth regulator phenylacetic acid (PAA) by the soil fungus Rhizoctonia solani has been associated with its parasitism and infection process on plants. The biosynthetic pathway that leads to production of PAA shares two metabolic intermediates with the substrate inducible quinic acid (QA) carbon catabolism pathway. It is hypothesized that the induction of the QA pathway by exposure to the carbon source QA can sequester these shared intermediates and lead to a reduction in PAA production and subsequent Rhizoctonia disease development. The in vitro production of PAA and its hydroxy and methoxy derivatives was quantified by gas chromatography for 11 field isolates of R. solani anastomosis group 3. All isolates were grown in Vogel’s minimal medium amended with either 25 mM QA or no QA. A bioassay was developed to determine the effects of exposure to 25 mM QA on seedling damping off and canker diseases caused by these isolates on tomato. QA reduced production of PAA and its derivatives as well as the severity of Rhizoctonia disease, with some variability observed in the responses of different isolates. Analysis of the correlation between PAA production and disease development is currently in progress. Contributed Presentation

Bates, Scott T.1*, Nash III, Thomas H. and Garcia-Pichel, Ferran. School of Life Sciences, Arizona State University, Tempe, AZ 85278, USA. scott.bates@asu.edu. Fungi associated with biological soil crusts in the Western United States using culture-independent methods. Biological soil crusts (BSCs) are communities of microorganisms within certain ecosystems that have the potential to contribute significantly to nutrient cycling, act to stabilize the upper soil strata through the production of extracellular polysaccharides (EPS) and ramifying filament-like cells, and exert influence on the hydrologic cycle. BSCs dominated by eukaryotic lichenized fungi have been recognized for the significant contributions that they make in terms of soil stability and nutrient input in arid-semi-arid systems; however, free-living fungal components of crusts are rarely investigated. In this study, we use molecular methodologies to examine fungal communities (primarily free-living) associated with BSCs in arid-lands of the Western United States. PCR-DGGE fingerprinting and sequencing are employed to determine fungal community diversity and composition, and fungi-specific qPCR is used to measure fungal population densities as compared to those of bacteria. The methods presented in this study provide a rapid means to assess BSC community diversity and structure; as such, these molecular-based techniques address some previously cited limitations of culture-dependent research and can be readily employed in advancing the study of BSC-associated fungi. Contributed Presentation

Continued on following page
A survey of introduced and native ectomycorrhizal fungi in strip mined soils that aid in the growth and survival of American chestnut (Castanea dentata). This study evaluated germination, survival, and ectomycorrhizal (ECM) infection of American chestnut (Castanea dentata) and blight-resistant hybrid seeds sown within three areas of a reclaimed mine: forest edge, center, and adjacent to 10-year-old Pinus virginiana inoculated with Pisolithus tinctorius (Pt). Germination percentages were higher within plots adjacent to the Pt pines (48%) when compared to center plots (26%) and forest edge (21%) (P ≤ 0.002). Plots adjacent to Pt pines also had significantly higher survival rates (60%) than the other treatments (center 24% and forest edge 13%) (P ≤ 0.01). The second objective of this study compared seedling establishment between seeds that were sown with commercial Pt inoculum to seeds sown without. Interestingly, the introduced Pt inoculum did not influence the growth parameters. Further, all ECM species found on roots were not part of the introduced inoculum. Site selection influenced ECM diversity; seedlings planted with the Pt Pines (0.66) and along the forest edge (0.58) had a greater diversity index than the center plots (0.20). EMC associations resulted in significantly larger seedling biomasses (6.34 g) compared to seedlings lacking an ECM symbiont (4.01 g) (P = 0.005). This indicates that severely nutrient deficient sites harbor native ECM capable of infecting chestnut resulting in mutualistic relationships.

**Contributed Presentation**

Beiler, Kevin J. 1, 2, Durall, Daniel M. 1 and Simard, Suzanne W. 2 1Biological and Physical Geography Unit, University of British Columbia Okanagan, Kelowna, BC, Canada, V1V 1V7. 2Department of Forest Sciences, University of British Columbia, Vancouver, BC, Canada, V6T 1Z4. KJBeiler@interchange.ubc.ca. Spatial patterns and host associations of Rhizopogon vesiculosus and R. vinicolor in a mixed-age interior Douglas-fir forest. We investigated the spatial ecology of the ectomycorrhizal species Rhizopogon vesiculosus and R. vinicolor (Basidiomycota, Violesiuloid-group sensu Kretzer et al) within a mixed-aged interior Douglas-fir (Pseudotsuga menziesii var. glauca) forest. Tree and fungal individuals were distinguished based on microsatellite analysis of DNA obtained from Rhizopogon tuberculate mycorrhiza samples and from aboveground forest reference trees. Our results indicate that R. vesiculosus and R. vinicolor are continuous and contiguous in the soil through diffuse rhizomorphs and patchily-dense mycelia, are indiscernimant with respect to species of vegetation cover and soil substrate types, and colonize all Douglas-fir tree cohorts from seedlings to mature trees. R. vesiculosus genets were significantly larger and associated with significantly more trees (1-19 trees) than R. vinicolor genets (1-10 trees). We also found that these species co-occur in horizontal space but are partitioned vertically in the soil, with R. vesiculosus occurring across a significantly broader depth range than R. vinicolor. Together, these species colonized roots from 43 out of 65 trees in a 900 m² plot and an additional 14 trees with boles outside the plot, thus linking these trees in a potential mycorrhizal network that was highly interconnected and easily traversed. **Contributed Presentation**

Bench, Molly and White, Merlin. a Boise State University, Dept. of Biological Sciences, Boise, ID 83725, USA. merlinwhite@boisestate.edu. Biodiversity and seasonality of gut fungi in an ephemeral aquatic system and urban setting. The phylum Zygomycota is a diverse group of non-zoosporic fungi that traditionally has consisted of two classes, Zygomycetes and Trichomycetes. Trichomycetes, commonly called “gut fungi”, are microscopic hair-like fungi that have evolved a unique endosymbiotic relationship in the digestive tracts of various arthropods. Many species of these fungi are commonly associated as obligate symbionts of immature stages (larvae and nymphs) of insects, but others are harbored by adult arthropods as well. To date, there are no reports of gut fungi in Idaho, and our knowledge of the biodiversity of this group in the Pacific Northwest is limited, in general. Preliminary surveys are underway to assess the biodiversity and seasonality of Harpellales and other Trichomycetes in an ephemeral stream system, Cottonwood Creek Low, located in an urban setting near Military Reserve in Boise, Idaho. This long term study is a bit unusual in that temporal change in species presence, abundance and prevalence of gut fungi will be documented across multiple seasons. Additionally, Cottonwood Creek Low is an ephemeral system, presenting habitats potentially under surveyed compared to permanent, pristine lotic systems that are more commonly sampled for gut fungi during routine surveys. We report on the species of gut fungi recorded with their prevalence after the first two seasons of collecting. **Poster**

Bergemann, Sarah E. 1, 2, Bowman, Tiffany N. 3, Bruhn, J. 1 and Baumgartner Kendra. 3 1Middle Tennessee State University, Biology Department, Davis Science, Murfreesboro, TN 37132, USA. 2University of Missouri, Division of Plant Sciences, 109 Waters Hall, Columbia, MO 65211, USA. 3USDA-Agricultural Research Service, Department of Plant Pathology, University of California, One Shields Avenue, Davis, CA 95616, USA. sbergema@mtsu.edu. Interspecific hybridization among multiple phylogenetic species of Armillaria mellea in eastern US populations. In recent years, evidence has accumulated that interspecific hybrids may occur in all fungal phyla, although this phenomena is considered rare among basidiomycetes. In a recent study examining population structure within populations of Armillaria mellea sampled in the eastern United States, we found evidence of interspecific hybridization between multiple phylogenetic species. Hybridization was confirmed by cloning and sequencing nuclear (translation elongation factor 1a and glyceraldehyde-3-phosphate dehydrogenase) genes in conjunction with nuclear ribosomal internal transcribed spacer regions. In one hybrid population in Pennsylvania, we find evidence of interspecific hybridization between two divergent phylogenetic species (designated PS1 and PS2). A second hybrid collection found in east of the Appalachians appears to be the result of hybridization between PS1 and a third phylogenetic species (PS3). The complexity of the phylogeographic structure of Armillaria mellea has likely evolved due to allopatric separation, coupled with migration perhaps after the last glacial maximum, and hybridized followed by gene introgression. In addition, our results also suggest that the major areas of secondary contact occur in just east or west of the Appalachian Mountains and warrant further examination as a significant zone of secondary contact. **Contributed Presentation**

Bezerra, Andrea Carla C. 1, Cavalcanti, Laise de H. 1 and Diannese, José C. 2 1Laboratório de Myxomycetes, Departamento de Botânica, Universidade Federal de Pernambuco, 50.670-420 Recife, PE, Brazil, 2Departamento de Fitopatologia, Universidade de Brasília, 70904-970 Brasília, DF, Brazil. jcarmine@unb.br. The genus Hemitrichia (Trichiaeae, Myxomycetes) in Brazil. In Brazil eight Hemitrichia species [H. calyculata, H. clavata, H. insignis, H. leiocarpa, H. minor, H. pardinia, H. serpula and H. spinifera] were found. Although the number of specimens is still low their geographical distribution reaches the four main Brazilian biomes: Amazonian Forest, Cerrado, Caatinga, and Atlantic Forest. The local specimens will be described and a key to the Neotropical Hemitrichia species will be shown, followed by a discussion dedicated to Hemitrichia spinifera that is recorded now in the Brazilian Cerrado, for the first time outside of the type locality in Colombia. **Contributed Presentation**

Blair, Jaime E. Franklin & Marshall College, Department of Biology, Lancaster, PA, USA. Jaime.e.blair@gmail.com. Phytophthora genomics: Identifying new markers for population-level studies. Traditionally, genetic diversity within Phytophthora species has been examined using one or a few molecular tools, such as single gene sequencing, isozymes, or RFLPs. A robust phylogeny for the genus has recently been established using molecular markers derived from complete genome sequence data. Additional markers are now being identified from genomic sequences to study genetic diversity within populations and species complexes. Here I will present preliminary data on five studies which have used information from complete genomes to develop new popula-
tion - and species-specific molecular tools. Two studies investigate genetic diversity within species complexes using intron-containing coding sequences, and three studies use random genomic survey sequence (GSS) libraries. Technical challenges for generating and analyzing data from a large number of diploid and possibly polysomy isolates will also be discussed. **Poster**

Boehm, E.W. ¹•, Schoch, C.L.² and Spatafora, J.W.³ ¹Department of Biology, Kean University, Union, NJ 07083, USA, ²Department of Botany & Plant Pathology, Oregon State University, Corvallis, OR 97333, USA, eboehm@kean.edu. **On the evolution of the Hysteriaceae and Mytiliniidaceae using four nuclear genes.** We present a molecular phylogenetic analysis for two families of Dothideomycetes, the Hysteriaceae (Hysteriurn, Hysterothecium, Gloniopsis, Glonium & Farlowiella), currently classified in the Hysteriaceae, and the Mytiliniidaceae (Mytiliniidion, Lophium, & Ostreichnion), originally in the Melanomatales, more recently viewed as Pleosporomycetidae incertae sedis. Multigene phylogenies, using the nuSSU, nuLSU, TEF1 & RP2B genes, and based on 50+ representative isolates, indicate strong support for placing both families within the subclass Pleosporomycetidae. Although core groups for many genera in the Hysteriaceae have been defined, most are broadly polyphyletic, with affinities not premised on spore appearance. In contrast, despite divergent spore morphologies, Mytiliniidion & Lophium form a highly supported clade, thus defining the Mytiliniidaceae. Our data suggest that the ability to perennialize may be the driving force behind the evolution of the hysterothecium among unrelated groups, since many of these fungi occur on decorticated woody substrates prone to prolonged periods of desiccation. **Contributed Presentation**

Bowman, Tiffany N.¹•, Baumgartner, Kendra M.², Bruhn, Johann³ and Bergemann, Sarah E.¹ ¹Middle Tennessee State University, Biology Department, Davis Science, Murfreesboro, TN 37132, USA, ²USDA-Agricultural Research Service, Department of Plant Pathology,University of California, One Shields Avenue, Davis, CA 95616, USA, ³University of Missouri, Division of Plant Sciences, 109 Waters Hall, Columbia, MO 65211, USA, sbergema@mtsu.edu. **Reconstructing the evolutionary history of Armillaria mellea within the eastern North America phylogenetic species complex.** Previous molecular studies using the intergeneric spacer regions (IGS) have confirmed at least four phylogenetic species within the Armillaria mellea species complex defined by their geographic distribution in North America, Europe, and Asia. Our goal was to investigate the population structure of A. mellea in eastern North America by expanding the geographic extent and intensity of sampling among the north-, southeastern and midwest populations within the eastern North America phylogenetic species range. We have developed variable, microsatellite loci to estimate recent gene flow among populations in addition to sequencing three nuclear loci and one mitochondrial locus to reconstruct the evolutionary history of the 'eastern North American' species. Within populations, we find evidence of three phylogenetic species often co-occurring within a single population, evidence of inter-specific hybridization among phylogenetic species, and recurrent gene flow within populations. Our analyses suggest that the history of A. mellea has likely been affected by allopatric speciation, followed by hybridization in secondary contact zones coupled with gene introgression among multiple, phylogenetic species. **Poster**

Brown, Aaron D. Department of Plant Pathology, The Pennsylvania State University, University Park, PA 16802, USA, adh247@psu.edu. **Inventory of fungi within Hartley Woodlot: PSU Arboretum.** An inventory of the fungi found within the 42-acre Hartley Woodlot on the Penn State Arboretum and the completion of a web-based database describing aspects of those fungi are the main objectives of this research project. The woodlot is composed of several species of oak and pine, with the oak species constituting the majority of the tree population. An electronic database including maps of collection localities, photographs of specimens, information about the fungi, and DNA sequences will be available through the Internet. ITS sequence data provided in the database will prove useful for scientists cross-referencing ITS sequences they have generated. The list of fungal species recorded during the inventory will be useful for the future monitoring of tree health and biodiversity within the Hartley Woodlot. This inventory and its corresponding database may be instrumental in establishing The Pennsylvania State University Arboretum as an entity that satisfies the interests of both the public and scientific community. **Poster**

Brown, Matthew W.⁴, Silberman, Jeffrey D. and Spiegel, Frederick W. Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville, AR 72701, USA, mwbrown@uark.edu. **Morphological and molecular variation in three morphotypes of Acrasis.** In a recent survey study of simple slime molds from worldwide locales, several morphotypes of Acrasis have been identified by gross fruiting morphology. Acrasid cellular slime molds represent a unique assemblage of amoeboid organisms that produce erect multicellular fruiting bodies with little cellular differentiation within the fructifications. In this study we examine the morphological and molecular intergeneric variation in the genus Acrasis which has recently been placed by morphology and molecular phylogenetics into the group Heterobasidione, a taxon in the contentious eukaryotic supergroup Excavata. We have obtained five isolates of Acrasis spp. from Hawaii, New Zealand, Thailand, and Ukraine. Three of the isolates represent typical morphological characteristics of the well-characterized species, Acrasis rosea. Two isolates exhibit unique fruiting morphologies, one of which has been noted in the original description of A. rosea. In A. rosea substantial intraspecies variation occurs in fruiting morphology with most sorocarps having distinctive stalk supporting flexuous chains of spores. One isolate from Hawaii consistently produces a uniseriate column of spores without branching, which is subtended by a single bottle-shaped stalk cell. Though uniseriate fruiting bodies have been reported in A. rosea, they are always intermixed with branched sorocarps. Another Hawaiian isolate has a fruiting morphology with a uniseriate stalk from which very straight, nonflexuous branches extend, and the branches usually form at near right angles to each other. Using the small subunit ribosomal RNA genes from each isolate we examine the molecular variation among these morphotypes of Acrasis. **Poster**

Bruns, Thomas D. Dept. Plant & Microbial Biology, University of California, Berkeley, CA 94720-3102, USA, pogon@berkeley.edu. **Surveying the macrofungi of Point Reyes National Seashore: a community-wide project.** Point Reyes National Seashore is a 283 sq km national park located roughly 80 km from San Francisco, Oakland, and surrounding urban areas. It contains a mixture of Douglas-fir, bishop pine, and mixed live oak forests, shrub communities, and grasslands. Graduate students, postdocs, and faculty from four universities combined with members of four local mushroom clubs and the general public worked together to survey the macrofungi in the park. Five public forays and small group collecting by these participants over a three-year period were used to survey the macrofungi and establish voucher specimens for all species. Forays were structured into two-day events, in which the first day involved collecting by the general public, followed by course identification and sorting, and the second day involved more detailed examination of collections, and preservation of selected specimens. The ITS region and RB51 loci were later sequenced from a subset of collections and outside expertise was enlisted to aid in identification of taxonomically difficult groups such as Russula, Cortinarius, Inocybe species and corticoid taxa. The species accumulation curve derived from this effort documents a sharp rise in the number of known fungi and shows little inflection up to the current total of 503. The distribution of collection records shows that a small subset of species are very common, while approximately a third of all species are represented by single records. From examining this latter group it appears that many of these apparent rare species are only rare because of our collection biases and our limited taxonomic expertise. This result provides excellent motivation for organizing targeted taxonomic training sessions. Sequence analysis proved to be crucial in refining our application of names
in morphologically difficult groups such as Armillaria, Russula, and Inocybe. Working with members of the local mushroom societies was very rewarding as some members of these groups are highly skilled taxonomists, and many are enthusiastic participants. There is great potential to expand such survey efforts to a much broader geographic scale and to enlist many additional professional and amateur mycologists. The ultimate goal would be to assemble a base-line knowledge of macrofungi in our national parks and to train the next generation of professional and amateur mycologists. Symposium Presentation

Bunyard, Brit A. 1,*, Wang, Zheng1, Malloch, Duve1, Cladyen, Stephen3 and Voitik, Andrus.1 1FUNGLI, PO Box 8, 1925 Hwy 175, Richfield, WI 53076-0008, USA, 2Department of Ecology & Evolutionary Biology, Yale University, Osborne Memorial Labs, 165 Prospect Street, PO Box 208106, New Haven, CT 06520, USA, 3New Brunswick Museum, Natural Sciences Department, 277 Douglas Ave., Saint John, New Brunswick, E2K 1E5, Canada, 4Foray Newfoundland and Labrador, PO Box 2312, RR #1, Corner Brook, NL A2H 2N2, Canada. bbunyard@wi.rr.com. New North American records for Ascomycere turficola (Ascomycota: Helotiales), a rare European fungus. Ascomycere turficola (Boud.) Dennis, one of the most rare fungi in Europe, is newly reported from North America. This interesting ascomycete fungus was collected from boggy localities in eastern and western Newfoundland. Morphological descriptions and ecological notes for this mysterious fungus, as well as its placement within the Helotiales, are discussed. Contributed Presentation

Bushley, Kathryn E.* and Turgeon, B. Gillian. Cornell University, Department of Plant Pathology and Plant-Microbe Biology, Plant Science Rm 343, Tower Road, Ithaca, NY 14853, USA. keb45@cornell.edu. Distribution and diversity of nonribosomal peptide synthetases in fungi. Non-ribosomal peptide synthetases (NRPSs) are multimodular enzymes, found in fungi and bacteria, that make peptides (NRPs) through a thioesterase mechanism independent of ribosomes. NRPs are structurally diverse, bioactive, small molecules that can have significant impact on the lives of their producers, as well as on other organisms, through antibiotic, immunosuppressant, etc. activities. Previous studies suggest that genes encoding NRPSs are rapidly evolving and have highly discontinuous distributions even among closely related taxa. Various evolutionary processes could explain this pattern: 1) gene duplication and differential loss, 2) recombination, 3) gene conversion, 4) diversifying selection, and 5) horizontal gene transfer. We have investigated diversity and evolution of these genes across the fungi utilizing NPSs extracted from whole genome sequences, as well as from closely related species, to address which of these mechanisms might be involved in generating novel NPS genes. We have also explored the relationship between NRPSs and corresponding chemical products by tracing evolution of NRPS modular architecture and by identifying amino acid residues involved in substrate recognition. Poster

Buyck, Bart1,2* and Hofstetter, Valerie.2 1Museum National d’Histoire Naturelle, Dept. Systematique et Evolution, USM602, F-75005 Paris, France, 2Station de recherche Agroscope Changins-Wadenswil, Dept. Protection des plantes, Mycologie, 1260 Nyon 1, Suisse. buyck@mnhn.fr. A multigene phylogeny for worldwide Cantharellus. Notwithstanding the fact that Cantharellus is one of the economically most important edible forest mushroom genera in the world, the taxonomy and systematics of the genus has received only very little attention in the past. The genus has been attributed some 500 taxa, but hardly 10% of these are presently accepted as good Cantharellus species. Traditional taxonomic approaches were hindered by the great importance of field experience coupled with a very poor microscopic diversity among species, whereas the few published phylogenetic studies involving Cantharellus were mainly treating it marginally as core genus of the cantharelloide clade or were focusing on the delimitation with the closely related Crateurellus. To infer phylogenetic relationships within Cantharellus, we sampled some 45 species from 4 continents that are representative of the six subgenera recognized by Buyck and Eyssartier in 2001. Partial sequences of two ribosomal loci (mitSSU and nucLSU) and two protein-coding loci (tef-1 and RP2B) were recovered and combined analyses of these four loci were used to investigate intermolecular relationships within Cantharellus. Preliminary results suggest the recognition of at least six different clades within Cantharellus that correspond partially to those recognized previously on the basis of morphological criteria. Endemity between the various continents approaches 100% with ongoing speciation demonstrated for several species or species-complexes, even for such supposedly ubiquitous taxa as C. cibarius. In depth molecular and morphological studies on larger data-sets are needed to define many individual taxa more precisely. Contributed Presentation

Callejas-Negrete, Olga A.1,*, Mourrito-Pérez, Rosa R.1, Roberson, Robert W.2 and Bartnicki-García, Salomón.1 1Department of the Microbiology, CICESE, Ensenada, Mexico, 2Department of Cellular and Molecular Biosciences, Arizona State University, Tempe, AZ, USA. ocalleja@cisce.mx. pac-1A and pac-1B: Two homologues of human lis1 in Neurosopora crassa. The pac-1A and pac-1B genes of Neurosopora crassa have a high identity with the nuf4 gene of Aspergillus nidulans, the pac1 gene of Saccharomyces cerevisiae and the human gene lis1. The proteins encoded by these genes appear to interact with the dynein/dynactin complex at the plus end of microtubules (Mts) and are required for proper nuclear distribution and cell growth. In order to understand the cellular dynamics and functions of PAC-1A and PAC-1B in N. crassa, we used live-cell imaging methods to record and analyze growing hyphae after labeling these proteins with sGFP. We also analyzed the knockout strain of the pac-1A gene. PAC-1A-sGFP and PAC-1B-sGFP had the same behavior and distribution. Both proteins were observed with different density through the various regions of the hypha. Single fluorescent particles could be seen in the subapical region; as these particles reached the apex, they lined up forming prominent short filament-like structures. At the hyphal tip, where highly polarized growth takes place, there was a higher accumulation of PAC-1A-sGFP and PAC-1B-sGFP, although it seemed to disappear when the filament-like structures reached the apical plasma membrane. The fluorescent structures moved exclusively in anterograde fashion along the microtubular cytoskeleton pathway. In the apex, they entered the Spitzendrper (Spk) region and traversed it. The fast speed of PAC-1A and PAC-1B indicated that the fluorescent particles move independently of cytoplasmic bulk flow. In cells treated with benomyland in the cytoplasm, the fluorescent particles were observed to move exclusively in an anterograde manner. In the subapical and apical region, the fluorescent particles were observed to move exclusively in an anterograde manner. In the subapical and apical region, the fluorescent particles were observed to move exclusively in an anterograde manner. In the subapical and apical region, the fluorescent particles were observed to move exclusively in an anterograde manner. In the subapical and apical region, the fluorescent particles were observed to move exclusively in an anterograde manner. In the subapical and apical region, the fluorescent particles were observed to move exclusively in an anterograde manner. The organized displacement of PAC-1A and PAC-1B, from individual particles at the base of the hypha to the filament-like pattern at the tip, suggests that PAC-1A and PAC-1B participate in unique fashion in the dynamics of polarized growth. Poster

Campbell, Jinx and Walker, Allison. Department of Coastal Sciences, University of Southern Mississippi, Gulf Coast Research Lab, 703 East Beach Drive, Ocean Springs, MS 39564, USA. jinx.campbell@usm.edu. What’s for dinner? Fungi as feed in marine aquaculture. Aquaculture is the fastest growing segment of food production. Most popular farmed marine species are carnivorous and feed either whole fish or pellets made from meal and oil extracted from wild-caught fish. As a result, one-third of the world’s fish catch is currently used to produce fishmeal and fish oil. Thus, alternative protein sources must be found to reduce the need for wild-harvested fish. Our goal was to investigate fungal single cell protein (SCP) and microbial floe, and consider them for use in aquaculture diets. To produce SCP, five fungal species (Candida utilis, Candida kruzei, Geotrichum candidum, Pichia anomala and Gliocladium deliquesens) were grown in batch culture on brewery waste as mono- and polycultures. Microbial floe develops-
taneously in closed recirculating aquaculture systems and consists of bacteria, algae, fungi and detritus. To date we are characterizing both SCP and floc to determine the nutritional content. After assessing the suitability of SCP and floc as high protein food sources, diets will be formulated and fish feeding trials will be conducted using seaturt fingerlings (SCP) and shrimp (floc). The digestibility and palatability of each diet will be ascertained and the degree to which fungi can replace fishmeal in diets without detrimental effects on fish growth and dietary nitrogen utilization will be determined. Contributed Presentation

Cannon, Paul F.1,*, Macey, Norbert1, Hywel-Jones, Nigel L.2 and Norbu, Lungetn.1 1CABI Europe UK Centre, Egham TW20 9TQ, UK, 2BIOTEC, Pathumthani 12120, Thailand, 3Council for RNR Research of Bhutan, Ministry of Agriculture, Yusigang, Bhutan. p.cannon@cabi.org. Steps towards sustainable harvest of the caterpillar fungus Ophiocordycipes sinensis in Bhutan. Ophiocordycipes sinensis is highly prized in traditional Eastern medicine, as a tonic and to improve recovery from illness. Increasing demand has led to enormous prices (up to $12500/kilo in 2007) being paid to the yak herders who gather the fungus in Bhutan, and there is great concern that unsustainable harvesting is causing long-term damage to the fungus populations and to the fragile montane grasslands in which they grow. The fungus is parasitic on caterpillars of Thitarodes moths, but little is known of its life history or host-parasite relations. Funded by the UK Government’s Darwin Initiative, CABI is assisting the Royal Government of Bhutan to set up permanent monitoring sites, to gain a better idea of fungus biology, population sizes and seasonality. Research on the moth hosts has identified a probable new species of Thitarodes in Bhutan, and ongoing studies are investigating its feed plants and life cycle. The initial purpose is to establish sustainable harvesting regimes, but the research could ultimately lead to local small-scale farming enterprises. The research so far has led to changes in the legal collection period to improve quality without compromising sustainability, and we are now working with the yak herders to encourage local responsibility for the long-term conservation of their fungi through community-based natural resource management. Contributed Presentation

Carneiro, J.S.9 and Hintz, W. University of Victoria, 3800 Finnerty Road, Victoria, BC V8P SC2, Canada. js carnei@uvic.ca. RNA silencing in Ophiostoma novo-ulmi. Dutch elm disease (DED) is a vascular disease caused by an aggressive subtype of the pathogenic fungus Ophiostoma novo-ulmi. Two pandemics of DED have occurred during the last century, decimating the native elm species (Ulmus spp.) in North America. A potential strategy for DED control involves the use of a relatively new technology called RNA interference (RNAi) that may be used to regulate the expression of virulence genes in the pathogen. The down-regulation of specific genes will permit the identification of parasitic fitness genes in O. novo-ulmi. The pectinase endopolygalacturonase (ePG) has been implicated as a virulence factor in other pathogenic fungi and served as a target for RNA interference. Following the introduction of an RNAi expression cassette encoding a 400 bp stem-loop RNA structure targeting the ePG locus, pectinase activity was found to be down-regulated using a qualitative pectin plate assay. The amount of ePG-specific miRNA was subsequently quantified using qPCR methods showing a reduction in the RNA levels for those transformants containing the RNAi expression construct. The ultimate goal of this research is to determine whether RNAi may be used as part of a biological control strategy to reduce the impact of DED on native elm trees by altering the expression of ePG and other relevant genes that play a role in pathogenicity of this fungus. Contributed Presentation

Castillo, Dean M.* and Pawlowska, Teresa E. Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853-5904, USA. dmc79@cornell.edu. Patterns of molecular evolution in the bacterial endosymbionts of arbuscular mycorrhizal fungi. Candidatus Glomeribacter gigasporarum are endosymbiotic beta-proteobacteria that live in the cytoplasm of spores and mycelium of several species of arbuscular mycorrhizal fungi in the phylum Glomeromycota. The bacteria are believed to be vertically transmitted through spores and, like prokaryotic endosymbionts of animals, possibly experience a small effective population size, recurrent population bottlenecks as well as being effectively asexual. The population dynamics of maternally transmitted bacterial endosymbionts are well studied in several insect species, and it has been shown that most of the bacterial endosymbionts (typically gamma-proteobacteria) share similar patterns of molecular evolution. The patterns of evolution that have been described as distinguishing characteristics of these obligate endosymbionts include a small G+C-poor genome, and the accumulation of deletional mutations. These deleterious mutations, when located within highly conserved rRNA genes, have been shown to lead to the destabilization of rRNA secondary structure. To understand population dynamics of Ca. Glomeribacter gigasporarum, we compared the stability of Domain I of the 16S ribosomal subunit with closely related free-living bacteria, in the genus Burkholderia. We also compared the closely related mealybug (Pseudococcidae) endosymbiont Ca. Tremblaya princeps based on its similar genome structure to Ca. Glomeribacter gigasporarum, but divergent host affiliation. Unlike the pattern observed in insect endosymbionts, including Ca. Tremblaya princeps, we found that Ca. Glomeribacter gigasporarum exhibited an increase in ribosome stability, indicating that it might have a different lifestyle than the lifestyle of obligate endosymbionts of insects. Poster
group maximumparsimony, maximumlikelihood and genetic distance-based methods show that pistilsmutexhibits an elevated rate of nucleotide substitution, similar to mechanisms described for Magnaporthe grisea. Laser flow cytometry has revealed zoospore-derived colonies (mitotic progeny) containing different combinations of nuclear types than the heterokaryotic parental super-race strains. The differences are stable over time in each colony. Beginning with two parental strains, we identified the 1) nuclear conditions of several mitotic progeny, 2) AFLP patterns of genetic markers in mitotic progeny, and 3) virulence characteristics of mitotic progeny, compared to parental types. Variability in genetic and phenotypic markers among the mitotic progeny is reported and the apparent mechanisms responsible for the variation are discussed for individual progeny.

Poster

Chaijuckam, Patcharavipa and Davis, R. Michael, Department of Plant Pathology, University of California, Davis, CA 95616, USA, pchaijuck@ucdavis.edu. Determination of antifungal activity of plant products against Rhizoctonia oryzae-sativae for the control of aggregate sheath spot on rice. Several plant products, including plant extracts and plant essential oils, were examined for antifungal activity against Rhizoctonia oryzae-sativae, the cause of aggregate sheath spot disease on rice. Extracts from garlic, ginger, pepper and basil coupled with plant essential oils, including garlic oil, neem oil, lemongrass oil and cinnamon oil, were compared for their ability to inhibit vegetative growth of the fungus, their effect on the number of sclerotia produced by the fungus, and inhibition of germination of sclerotia. Five percent concentrations of the compounds were tested on a wide range of R. oryzae-sativae isolates. All plant essential oils and garlic extracts demonstrated antifungal activity with different degrees of intensity. In contrast, the extracts of ginger increased growth and the extracts of pepper and basil enhanced both growth and sclerotia production. The most efficacious products were lemongrass oil and cinnamon oil which completely inhibited growth, sclerotia production and sclerotia germination of the fungus. However, the LD50 of cinnamon oil at 1.61% was significantly lower than the LD50 of lemongrass oil at 2.52%. The fungus died when exposed to cinnamon oil for 55 minutes at a concentration of 0.5%. This study provided information on potentially promising options for the control of aggregate sheath spot disease.

Poster

Chandra, Ambika and Huff, David R. 2 Texas A&M AgriLife Urban Solutions Center, Dallas, TX 75252, USA, 2Department Crop & Soil Sciences, Pennsylvania State University, University Park, PA 16802, USA, drh15@psu.edu. Salmacisia, a new genus of Tilletiales: Reclassification of Tilletia bulbocoeana causing induced hermaphroditism in buffalograss. For 119 yrs, the fungal parasite Tilletia bulbocoeana has been known to induce female sex organs (pistils) in male plants of buffalo grass, making them hermaphroditic. We found that T. bulbocoeana induces hermaphroditism in not only male plants by inducing the development of otherwise vestigial pistils, but also in female plants by inducing hypertrophy of otherwise vestigial stamens (male sex organs). The fungus also induces the development of additional pistillate flowers in both infected male and female plants. Due to its pistil inducing effects, we refer to T. bulbocoeana as pistil smut. Pistil smut exhibits a set of morphological and life cycle characteristics that are unique among species of order Tilletiales. Phylogenetic analyses of nLSU-rDNA sequences using maximum parsimony, maximum likelihood and genetic distance-based methods show that pistil smut exhibits an elevated rate of nucleotide substitution and is as, or more, distant from Tilletia species than the basal group Erratomyces patellii. As such, pistil smut occupies a phylogenetic position outside the current taxonomic circumscription of genus Tilletia. Therefore, a new Latin binomial combination Salmacisia bulbocoeana is proposed as a sister taxon to Tilletia in order to accurately describe the phylogenetic position of pistil smut. Contributed Presentation

Chaudhary, Preeti, Miller, Andrew N. 1 and Huhndorf, Sabine M. 2 1Section for Biodiversity, Illinois Natural History Survey, Champaign, IL 61820-6970, USA, 2Botany Department, The Field Museum of Natural History, Chicago, IL 60605, USA, amiller@ihnssuiuc.edu. A phylogenetic study of Lasiosphaeris and morphologically similar taxa. The genus Lasiosphaeris (Lasiosphaeriaceae, Sordariomycetes) represents a species complex comprised of at least seven morphologically similar taxa in three genera including Cerocaphora, Lasiosphaeria and Lasiosphaeris. Although taxa are typically distinguished based on features of the ascomata and ascospores, these characters are quite variable and frequently overlap among taxa leading to species boundaries that are not well defined. Relationships among Lasiosphaeris and the morphologically similar Lasiosphaeria and Cerocaphora species were assessed through morphological study of ascomatal characters and phylogenetic analyses of the nuclear ribosomal internal transcribed spacer (ITS) and 28S large subunit (LSU). Several well supported clades were recovered from maximum parsimony, maximum likelihood and Bayesian analyses of separate and combined data sets. Results indicate that the morphological features commonly used to delimit taxa are not phylogenetically informative. The convergence of morphology and the occurrence of clades with no apparent distinguishing features suggest that these could be cryptic species.

Poster

Chaverri, Priscila 1* and Samuels, Gary J. 2 1Howard University, Department of Biology, 415 College St NW, Washington, DC 20059, USA, 2Systematic Mycology and Microbiology Laboratory, Agricultural Research Service, US Department of Agriculture, 10300 Baltimore Ave., Beltsville, MD 20705, USA, pchaverri@howard.edu. Phylogenetic data from fast-evolving genes reveal that sapwood endophytic Trichoderma species originate in the soil. Studies show that species composition of fungal endophytes in sapwood is different than in leaves. Differences may be due to different mechanisms of horizontal transmission as well as the surrounding environment. A study found that many stem endophytes were members of genera usually thought of as soil fungi, e.g., Trichoderma. The objective of this study is to show that some sapwood endophytes originate in soil and colonize the vascular system. Phylogenetic analyses were conducted on DNA sequences from multiple fast-evolving genes obtained from Trichoderma species on wood, other fungi, soil, and endophytes of sapwood. Results show ca. 50 lineages/phylogenetic species containing endophytic Trichoderma species. Of these lineages, several contain just endophytes or endophyte/sap soil isolates. For example, within the T. harzianum species complex, there are lineages with just endophytes and soil isolates; lineages on decaying wood, bark, or other fungi form separate clades. Results support two hypotheses: 1) Trichoderma sapwood endophytes likely enter plants through roots; 2) New endophytic species likely evolved from soil fungi after adaptation to the endophytic niche. These ecological and evolutionary hypotheses could not be explained from ITS rDNA data alone. Results from this and other taxonomic studies demonstrate that ITS is too conserved to reveal Trichoderma species. Contributed Presentation

Chaves, Zuleide M., Castro, Marcelo T. and Dianese, José C. 9 Departamento de Fitopatologia, Universidade de Brasília, 70910-901 Brasília, DF, Brasil; jcarmine@unb.br. New microfungi on Mauritia flexuosa (Arecaceae) from the Cerrado. Three new microfungi were found on Mauritia flexuosa: a coelomycete, a hyphomycete, and an ascomycete. All three belong to new genera to be published soon. The coelomycete shows subepidermal to mesophytic conidiomata with cylindrical holoblastic conidiogenous cells (CCs) yielding large oblong guttulate conidia measuring up to 70 × 12 micrometers. The closest genus would be Coleophoma Hoenel that, however, shows enteroblastic phialidic CCs, branched conidiophores, and paraphyses. The hyphomycete

Continued on following page
occurs on the leaf surface; shows hemispherical sporodochia with bi- or trifurcate, septe, hyaline conidia originated from micronematous CCs. The sporodochia are connected to a setose superficial mycelium. The fungus shares some features with *Wieneriomycyes* Koordiders that, however, shows setae that are located just on the sporodochial periphery. The new ascomycete belongs in family Pseudopiorosporiacaeae, and shows superfical setose ascomata on a subicle, and showing long flexuous ascomatal setae; with bitunicate evanescent asc in a apophysate centrum; the cylindrical-clavate ascopores are 3-septate with a middle constriction. The closest genus is *Nematosistigma* H. & P. Sydow. *Poster* **Chaves, Zuleide M. 1, Fonseca, Maria E. N. 2, Boitexu, Leonardo S. 2, Junqueira, Keize P. 3 and Diencas, Jose C. 1 1Dept. Fitopathologia, Universidade de Brasilia, 70910-900 Brasilia, DF, 2Embrapa-CNPH, CP 0218, 70359-970 Brasilia, DF. jarcimine@unb.br. First record of *Kernkampella* (Uredinales) in Brazil, and its relationship to Ravenelina species. *Kernkampella* species are known to occur in India, and in Neotropicae ranging from Bolivia through Central America until Mexico. This is the first record of *K. appendiculata* on *Phyllanthus acuminatus* (Euphorbiaceae) in Brazil. *Kernkampella* and *Ravenelina* are two morphologically similar genera of rust fungi. Thus, members of both genera show a typical telial head on top of a multiyphal pedicel. The presence of a patelliform cell layer under the teliospore head is a common characteristic among *Kernkampella* species. However, some *Ravenelina* species also share the same feature. So far, the most reliable biological criterion to distinguish *Kernkampella* from *Ravenelina* is the host range of their species. *Kernkampella* spp. infect exclusively euphorbiaceous hosts whereas *Ravenelina* species are reported on Fabaceae. Sequence data of the 18S and 28S rDNA genes were used to compare *Kernkampella* sp. from *Phyllanthus acuminatus* with *Ravenelina santos-costae* found on *Calliandra dysantha* (Fabaceae), and also with rust fungus sequences available at the NCBI database. Parsimony analyses of the aligned DNA sequences showed that the Brazilian isolate of *Ravenelina* clusters together with *Baitostopora, Puccinia, and Ravenelina*. However, a considerable diversity in the rDNA gene was observed (78-84% nucleotide identity). *Kernkampella* was placed in a clade separated from *Ravenelina*. Bootstrap analysis (1,000 replicates) gave strong support to the clades. *Poster* **Cheeke-Icoz, Tanya*, Rosenstiel, Todd and Cruzan, Mitchell B. Department of Biology, Portland State University, Portland, OR 97201, USA. cheeketipdx.edu. Effects of nutrient stress on mycorrhizal colonization in transgenic *Bt* corn. Transgenic *Bt* crops are genetically engineered to express an insecticidal toxin derived from the soil bacterium *Bacillus thuringiensis* (Bt) to protect plants from certain agricultural pests. We used Bt corn as a model system to evaluate the effects of transgenic crops on arbucular mycorrhizal fungi (AMF) in the soil ecosystem. AMF are symbiotic soil organisms that are dependant on a plant host for nutrition and reproduction, and this mutualistic relationship is especially important to the host plants when grown in low nutrient or drought conditions. To determine whether reductions of AMF in transgenic Bt corn are observed across different soil and environmental conditions, we compared the level of AMF colonization in Bt and non-Bt corn in three different fertilizer treatments (No, Low, and High) and with three different inoculation levels (0, 40, or 80 spores) of *Glomus mosseae*. Fertilizer treatments were applied weekly and after 60 days plants were harvested and AMF structures (hypheae, arbuscules, and vesicles) in the root system were stained and quantified. Chlorophylls a and b were extracted from leaf tissue to determine the extent of nutrient stress in plants. Results from this experiment revealed a trend of reduced AMF colonization in Bt plants across all fertilizer treatments, but this effect was most significant under severe nutrient stress. In the ‘No’ fertilizer treatment Bt plants were 13.4% colonized while non-Bt plants were 35% colonized by AMF (p=0.0058), in the ‘Low’ fertilizer conditions Bt plants were 3.2% colonized while non-Bt plants were 21.4% colonized, and in the ‘High’ fertilizer treatment very little AMF colonization was observed in either plant type to do to the high availability of added nutrients. Percent AMF colonization was positively correlated with root biomass (p = 0.0118) and spore levels (0.0180), and negatively correlat-ed with increasing fertilizer levels. The reduction in AMF colonization may represent a potential disadvantage for Bt crops under poor nutrient conditions, but it may also represent a breakdown in the AMF-plant root symbiosis of Bt plants that is exacerbated by certain plant stress conditions. The long-term implications of Bt crop production on the soil ecosystem have yet to be established, however reductions in AMF could have significant ecological implications in the future as more Bt crops are developed and the potential for outcrossing increases. *Contributed Presentation* **Chung, Dawoon* and Shaw, Brian D. Department of Plant Pathology and Microbiology, Program for the Biology of filamentous fungi, Texas A&M University, College Station, TX 77843, USA. dwchung@tamu.edu. A putative eisosomal protein, SurA, is involved in conidiation in *A. nidulans*. Eisosomes are immobile protein complexes at the plasma membrane, which mark sites of endocytosis in *Saccharomyces cerevisiae*. Sur7, Pll1 and Lsp1 are components of eisosomes. Sur7 is also a multicycop suppressor of mutations in rvs167 that encodes an actin binding protein. Deletion of sur7 altered sphingolipid metabolism and ascospor production in yeast. In other projects in our laboratory, we have described a novel role for endocytosis in hyphal growth of filamentous fungi, and discovered that the *Neurospora crassa* orthologs of Sur7 and Pll1 are significantly regulated during conidiation. Therefore, this study was undertaken to determine the role of eisosome mediated endocytosis in development in *Aspergillus nidulans*. Sequence analysis showed that *A. nidulans* had one putative ortholog of Sur7. We generated a deletion mutant of surA by double-joint PCR, and the mutant displayed reduced production of conidia. Analysis of hyphal growth and endocytosis in the surA mutant is underway. In additional, localization of GFP-tagged SurA showed that it localized to immobile patches at the cell cortex and also to septa. Our results suggest that endocytic eisosomal components are associated with conidiation in *A. nidulans*. *Poster* **Chung, Dawoon*, Upadhyay, Srijana, Ebbole, Daniel J., Wilkinson, Heather H. and Shaw, Brian D. Department of Plant Pathology and Microbiology, Program for the Biology of Filamentous Fungi, Texas A&M University, College Station, TX 77843, USA. dwchung@tamu.edu. Assessing conservation of function in conidiation regulators of *Aspergillus nidulans* and *Neurospora crassa*. Conidiation is a crucial process for fungal survival, and dissemination. To study functional conservation of general regulators of conidiation in filamentous fungi, we conducted a comparative analysis of two model filamentous fungi, *Aspergillus nidulans* and *Neurospora crassa*. Two well characterized transcription factor mutants from *A. nidulans*, abaA and stk, were transformed with the predicted orthologous genes from *N. crassa*. The predicted abaA ortholog in *N. crassa* (NCU02612) has low sequence identity (only 34% across a 90 amino acid stretch), but is likely the ortholog of *A. nidulans* abaA based on conservation of microsynteny. In contrast, *N. crassa* ama-1 (NCU01414) is considered the ortholog of *A. nidulans* amaA with higher sequence identity (49% identity across the entire protein). Expression of the *N. crassa* amaA ortholog, using its endogenous promoter, or via an alcA promoter fusion, in the *A. nidulans* abaA mutant did not complement the developmental phenotypes. Overexpression of *N. crassa* amaA (ama-1) via alcA promoter induction partially complemented the conidiophore morphology defect of the *A. nidulans* amaA mutant. Localization of GFP fusion proteins demonstrated that *A. nidulans* AbaA and StaA localized in nuclei. Complementation of the function of *A. nidulans* conidiation regulators with the *N. crassa* orthologs was dependent on degree of sequence conservation. *Contributed Presentation* **Cifuentes, Joaquín* and Cappello, Silvia. 1 Facultad de Ciencias UNAM, Mexico, 2Division of Ciencias Biologicas UIAT, Mexico. jcbl@hp.fcienicas.unam.mx. Macrofungi biodiversity patterns in Calakmul Reserve, Mexico. Calakmul Biosphere Reserve is located south of the Campeche State, Yucatan Peninsula, Mexico and it is the biggest one in the country. Nearly 2000 plant species have been record-
ed from several tropical forests in the area. From 2001 to 2006, field trips were carried out every year ten days. More than 1200 macrofungal specimens were collected, fully annotated and photographed, housed at FCME and duplicates in ENCB and UJAT. More than 400 different morpho-species have been recognized, of them 153 are taxonomically identified so far. From all different species collected a richness analysis is presented after proportions of taxonomic groups and compared mainly with those reported by Guzman (2003) and Douanla-Meli (2007). Results show that in the Calakmul Reserve are present more species than cited by those authors. Agaricoid and aphyllophoroid taxa are present in a similar proportion, both groups comprising more than 80% of all macrofungi, others being gasteroid and Pezizomycotina taxa. The recorded plant/macrofungi ratio appears close to the 5:1 considered by Mueller et al. (2006) for the tropics. **Poster**

Clune, Daniel J.*, VanKuren, Nicholas W. and Pawlowska, Teresa E. Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853, USA, djc74@cornell.edu. **Visualizing inter-individual interactions in Glomus etunicatum.** The nature of hyphal interactions in confrontations between mycelia of different individuals of arbuscular mycorrhizal fungi (phylum Glomeromycota) has implications for our understanding of both the ecology and the evolutionary biology of these fungi. The way common mycorrhizal networks might form will be at least in part determined by whether mycelia of initially separate individuals can fuse. If anastomoses between individuals are rare, even between hyphae of individuals within a clonal lineage, then the potential formation of widespread common mycorrhizal networks will be a slower process than if fusions between individuals are possible. If hyphal fusions are possible between individuals that differ genetically within the same species then this might represent one way in which diversity can be maintained. This also might allow for recombination in this asexual clade. We are developing a system that will allow us to visualize interactions between hyphae of genetically characterized isolates of *Glomus etunicatum*, distinguishing hyphal fusion and establishment of cytoplasmic continuity. We will present results of our observations on several isolates, and discuss their implications for our understanding of mycorrhizal biology. **Poster**

Crabtree, Christopher D.*, Keller, Harold W. and Ely, Joseph S. Department of Biology and Earth Sciences, University of Central Missouri, Warrensburg, MO 64093, USA, cdcrabtre@hotmail.com. **Ectomycorrhizal and saprobe macrofungi associated with five natural communities of Ha Ha Tonka State Park, Camden County, Missouri.** Different floristic communities have unique assemblages of both ectomycorrhizal and saprobe macrofungi. Vegetation and macrofungi were monitored in five natural communities between May 2006 and October 2007 at Ha Ha Tonka State Park, Missouri. Communities included glades, open woodlands, closed-canopy forests, flatwoods, and karst sinks. A total of 249 macrofungal taxa were collected and identified during this study. A stratified random sampling technique was used in each community with 0.01 ha circle plots for macrofungi and overstory sampling and a 1m squared quadrate for vascular plant sampling. Non-metric multidimensional scaling (NMS), multi-response permutation procedures (MRPP), and indicator species analysis (ISA) were used to analyze associations of macrofungi and vegetation, test the hypothesis of no association among macrofungal taxa with herbaceous plant communities, and to list macrofungal species that were indicators of each community type. Certain macrofungi were associated with particular communities. Indicator species were found for forests, flatwoods, and karst sinks. Flatwood communities contained three species of *Elaphomyces*, one extends the range of a proposed species, another may be a new species to science. Financially supported in part by the Missouri Department of Natural Resources Award #226001-02 and the NSF-DEB #0343447. **Contributed Presentation**

Couch, Jo Anne*, Clarke, Bruce B. and Hillman, Bradley I. Rutgers University, 59 Dudley Road, New Brunswick, NJ 08901, USA. crouch@aesop.rutgers.edu. **Does movement of Colletotrichum cereale from natural grasses and cereal crops promote turfgrass anthracnose disease?** Anthracnose disease caused by *Colletotrichum cereale* is one of the most destructive maladies of golf course turfgrasses. The fungus has also been identified from numerous natural grasses and cereal crops, although disease symptoms are rarely observed. In this research we investigated the role of ecosystem (turf, cereal crop or prairie) and the impact of natural grass/cereal strains on turf anthracnose. Genotypic signatures from 4 nuclear genes and 22 microsatellite markers were used to analyze an extensive sample from North America, Europe and Japan. 11 major populations were identified, structured according to ecosystem type: 3 turfgrass groups, 7 prairie/cereal groups and one diverse group comprised of both turf and non-turf isolates. The turfgrass populations were further defined according to host species: two groups almost entirely limited to Poa annua, the third to Agrostis stolonifera. In cereal/prairie populations, a similar pattern was observed, dividing wheat and oat isolates into discrete groups. Extreme differentiation between locally-adapted populations suggests asymptomatic grasses are unlikely reservoirs of infectious disease particles that could serve to fuel disease in turf. But gene flow between the generalist founder population and specialized genotypes provides a mechanism for genetic exchange between otherwise isolated populations. These findings demonstrate that while disease occurrence and spread is currently localized to the turfgrass environment, introgression between *C. cereale* ecotypes can lead to the expansion of anthracnose disease into new ecosystems. **Contributed Presentation**

Cubeta, Marc A.1*, Dean, Ralph A.1, Bayman, Paul2, Jabaji, Suha3, Neate, Stephen4, Nolte, Philip5, Tavantzis, Stellos M.6, Toda, Takeshi7, Vilgalys, Rytas8, Fedorova, Natalie9 and Nierman, William C.1 1Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7616, USA, 2Department of Biology, University of Puerto Rico, San Juan, PR 00931-3360, USA, 3Department of Agricultural and Environmental Sciences, McGill University, Quebec H9x 3V9, Canada, 4Department of Plant Pathology, North Dakota State University, Fargo, ND 58105-5012, USA, 5Idaho Center for Potato Research and Extension, University of Idaho, Idaho Falls, ID 83402-1575, USA, 6Department of Biological Sciences, University of Maine, Orono, ME 04469-5722, USA, 7Department Biological Resource Science, Akita Prefectural University, Akita 010-0195, Japan, 8Department of Biology, Duke University, Durham, NC 27708, USA, 9.Craig Venter Institute, Rockville, MD 20850, USA. marc_cubeta@ncsu.edu. **Whole genome sequencing of the soil fungus Rhizoctonia solani AG-3.** A collaborative research project is currently being conducted to obtain a high quality complete genome sequence of the soil fungus *Rhizoctonia solani* anastomosis group 3 (AG-3) isolate Rhs1AP. Sanger and 454 pyrosequencing methods are being used to provide 6X and 10X coverage of the genome, respectively, followed by automated directed sequencing into the remaining gaps. Our experimental approach involves a multiple library strategy with different insert sizes to obtain maximal genome coverage and linkage of contigs, followed by assembly and annotation. Genome assembly will be validated by use of an optical restriction map. Sequencing of full-length and assembly of normalized cDNAs will also be employed to augment annotation and provide authentic gene models to the annotation process. The complete DNA sequence of the fungus will reveal genes associated with its ability to cause plant disease and complement current genome sequencing projects on potato and tomato to increase our understanding of host parasite interactions. In addition to understanding the genetic basis of phenotypic traits of economic and ecological importance, the taxonomic placement of *R. solani* (teleomorph=*Thanatephorus cucumeris*) as a basal lineage of the Homobasidiomycetes will provide a basis for comparative studies to increase our understanding of the evolution of basidiomycete fungi. **Contributed Presentation**

Cui, Y.1*, Stevens, M.I.H.1, Fischer, M.W.F.1 and Money, N.P.1 1Department of Botany, Miami University, Oxford, OH 45056, USA, 2Department of Chemistry and Physical Sciences, College of Mount St.
Joseph, Cincinnati, OH 45233, USA. cuiy2@muohio.edu. Adaptations to the ballistospore discharge mechanism among Agaricomycetes. Most Agaricomycetes share the same basic mechanism of spore discharge referred to as the “surface tension catapult.” Within the basidione, spores must be propelled over limited distances to avoid impaction on the opposing surfaces of gills, spines, or tubes. We report data obtained by mathematical modeling that pinpoint factors that affect the discharge distance. Our models suggest that the size of Buller’s drop, irrespective of spore size and mass, is the primary determinant of discharge distance. Poster

DaRin, Matthew P.1, Anagnost, Susan E.2, Newhouse, Andrew2* and Dickinson, Richard K.1 1Bluepoint Environmental LLC, 706 N Salina Street, Suite 204, Syracuse, NY 13208, USA, 2Department of Construction Management and Wood Products Engineering, SUNY College of Environmental Science & Forestry, 1 Forestry Drive, Syracuse, NY 13210, USA. mdarin@bpe-llc.com. Application and demonstration of macroarray analytical techniques for the detection of fungal bioaerosols in buildings. Macroarray membrane technology is being developed to identify multiple species of airborne fungi with a single test. This procedure employs custom-designed, species-specific oligonucleotides (oligos) that are fixed to a nylon membrane, which is exposed to labeled PCR products from the target fungal organisms. When a PCR product matches an oligo on the membrane, it binds and can be detected via a chemiluminescent signal. Thus any species in a sample that matches an oligo can be detected and identified. To date, species-specific oligos have been developed for 13 species, and are being tested for specificity and reproducibility. Once final oligos have been selected and hybridization conditions have been optimized, membranes will be tested against spore mixtures from multiple taxa. The macroarray analytical technique is being evaluated for its commercial application in identifying fungal bioaerosols in commercial and residential buildings. The expectation is that this technique will provide a more rigorous procedure for identifying airborne fungi in indoor environments than the other commonly used analytical techniques. Poster

Duvey, Marie L.*, Tsuneda, A. and Currah, R.S. Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9. mdavey@ualberta.ca. A new plesiosporalean pathogen of mosses. During a survey of bryophylic fungi from boreal and montane habitats in Alberta, five isolates of a hitherto unknown pathogenic member of the Plesporales were recovered from Aulacomnium palustre, Hylocomium splendens, and Polystichum juniperinum gametophytes. Phylogenetic analysis of the ITS region places this new species in the Plesporales, nested within the Phoma-Ascochyta-Didymella clade that is sister to the Phaeosphaeriaceae. The fungus produces minute (<100 µm), unilocular, setose pseudectoria and brown, fusiform, 1-septate ascospores. The anamorph is morphologically similar to Phoma herbarum, but has somewhat smaller (1-2 x 2.5-5.5 µm compared to 1.5-2.5 x 3-8 µm) conidia. Penetration of both natural hosts and the model host Funaria hygrometrica is done directly or via appressoria, and the host responds by forming layered, darkly pigmented deposits at penetration sites, similar to the papillae formed by vascular plants in response to fungal infection. Infected hosts gradually become chlorotic as hyphae grow both inter- and intra-cellularly. Pycnidia and pseudothecial stromata are initiated as tightly packed masses of dematiaceous hyphae within a single host cell. Mature pycnidia and pseudothecia are erumpent. Spore dissemination is probably by wind and water. Contributed Presentation

dela Cruz, Thomas Edison E. Department of Biological Sciences, College of Science and Research Center for the Natural Sciences, University of Santo Tomas, Espana 1015 Manila, Philippines. tedelacruz@mln.ust.edu.ph. Marine fungi from seagrasses, seaweeds and seawater as sources of secondary metabolites and as biosorption agents. Marine fungi are an ecologically and physiologically defined group. They are actively involved in nutrient cycling in marine habitats. Thus, this research study aims to isolate marine fungi from seagrasses, seaweeds and seawater, and test their inhibitory activities against test mi-
croorganisms as well as their ability to bioabsorb toxic heavy metals. Decaying seagrasses and seaweeds from different sites were cut into 10 mm explants and plated on Potato Carrot Agar supplemented with 33 g/L marine salts. Seawater was also collected and spread-plated on Malt Extract Agar with 33 g/L marine salts. Following incubation at room temperature, fungal strains were isolated and purified by subsequent subculture. The isolated marine fungi were characterized morphoculturally and identified. Their ability to grow in the presence of marine salts was also assessed. Selected marine fungal strains were grown on culture medium for the production of secondary metabolites. Results showed the isolates to be active against at least one of the test microorganisms, e.g. Vibrio fisheri, Aeromonas hydrophila, Staphylococcus aureus, Mycobacterium phlei, and Fusarium oxysporum. Strains of the marine Dendryphiella species were also tested for the biosorption of mercury from liquid culture medium. Results showed 88 – 92 % biosorption of mercury by the D. salina strains. Poster

Deng, Jian Xin and Yu, Seung Hun.* Department of Applied Biology, Chungnam National University, Daejeon 305-764, Korea(S). shunyu@cu.ac.kr. Genetic diversity among Alternaria panax isolates from Korean ginseng and six araliaceae plants in Korea. The fungus Alternaria panax Whetzel causes leaf and stem blight of Korean ginseng (Panax ginseng). It also causes leaf spots on various araliaceae plants. Genetic diversity among 35 isolates from Korean ginseng and six other araliaceae plants in Korea was determined using sequence analyses of ITS region of rDNA, beta-tubulin gene and analysis of amplified fragment length polymorphisms (AFLPs). All of the isolates were divided into two groups based on beta-tubulin gene sequence and AFLPs analysis. Sequences of the beta-tubulin gene of the group B isolates were identical to those of the isolates of A. panax from American ginseng (Panax quinquefolius) deposited in GenBank, while those of the group A isolates have a nucleotide difference from GenBank isolates. There was no correlation between host plant and genetic group of the isolates. The ITS4 and ITS5 gene sequences of the 35 isolates of A. panax were identical with each other, indicating that rDNA analysis revealed no intra-specific variation. Poster

Dentinger, Bryn T. M.1,2, Didukh, Maryna1 and Moncalvo, Jean-Marc.1 1Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, ON, Canada, 2Department of Natural History, Royal Ontario Museum, Toronto, ON, Canada. bryn.masondentinger@utoronto.ca. Comparing COI and ITS for DNA barcoding in mushrooms. The object of DNA barcoding is to provide a DNA-based marker to aid in species identification. Based on data in animals, a ca 650 bp portion of the mitochondrial cytochrome oxidase I gene (COI) was proposed as a universal barcode marker. In fungi, however, the ITS region, rather than COI, has been used successfully for fungal identifications for over a decade. We examined the utility of COI and ITS for species-level identification using a broad taxonomic sampling of ~650 eastern North American mushroom collections (Agaricomycotina). The production of COI sequences from about two-thirds of the collections was impeded by the presence of large introns of variable length and position complicating primer design, while a single primer pair for ITS was successful for >95% of the samples. In general, ITS had greater intra- and inter-specific variation than COI, although both COI and ITS typically recovered the same numbers of terminal clades. For some taxonomic groups, e.g., Boletus edulis and allies, the COI gene lacked introns, enabling us to directly compare COI and ITS with a comprehensive dataset of closely related taxa. Intra-specific variation in COI was <1% while ITS variation was greater, though in one case COI was more variable than ITS. More critically, inter-specific variation in COI (0.2 – 3.77%) was generally much lower than ITS (1.93 – 21.76%). Taken together, the greater variation of ITS both within and between terminal clades (species), and its ease of amplification across all taxonomic groups, makes it a preferred marker over COI as a DNA barcode in mushrooms for a quick first-order estimate of species-level identification. Contributed Presentation

Inoculum 59(4), July 2008 27

Continued on following page
Dentinger, Bryn T. M.1,2*, Roy, Bitty A.1, Jenkins, Thomas S.3, Policha, Tobias1 and Manobanda, Rocao.4 1Center for Ecology and Evolutionary Biology, University of Oregon, Eugene, OR, USA, 2Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, ON, Canada, 3Department of Biology, San Francisco State University, San Francisco, CA, USA, 4Herbario Nacional del Ecuador, Quito, Ecuador. bryn.masondenntinger@utoronto.ca. Testing the hypothesis of mushroom mimicry for Dracula felix orchids. Dracula orchids appear to mimic mushrooms using visual and olfactory cues. However, there are no studies that have tested the orchid’s adaptive resemblance to mushrooms, which is needed to establish true mimicry. Therefore, we documented the pollination ecology and tested the mimicry hypothesis for one species, Dracula felix, in a cloud forest on the western side of Ecuador. Many species of mushrooms co-occurred with D. felix at this site that are similar in shape and size to the flowers. Through observation, we recorded an abundance of small flies visiting both mushrooms and D. felix flowers. The flies treated the flowers the same way they did mushrooms: they guarded them, loitered about the labellum, and mated within the flowers. We also observed flies carrying orchid pollinia landing on and emerging from flowers, and even from swarms about populations of mushrooms. Second, we performed a mushroom augmentation experiment to determine whether visitation was increased in the presence of mushrooms. There was a significant treatment effect for fungus fly visitation and we observed individual flies moving between mushrooms and flowers. We performed a second experiment to determine how important fragrance and visual cues are to fly attraction. There was a significant treatment effect: significantly more fungus flies visited flowers than the bag controls, but there was not a significant difference in visitation between the unbagged and bagged flowers, suggesting that fragrance cues are critical. For the first time, our observational and experimental data support the fungal mimicry hypothesis for these enigmatic orchids. Contributed Presentation

Dewsbury, Damon R.1,2 and Moncalvo, Jean-Marc.1,2 1Department of Ecology and Evolutionary Biology, University of Toronto, ON, MSS 3B2, Canada, 2Department of Natural History, Royal Ontario Museum, ON, MSS 2C6, Canada. damondewsy@yahoo.com. A multigene phylogeny of eastern North American morels and its implications for species level taxonomy. Taxonomy within the Morchellaceae has been historically problematic and the morels of eastern North America are no exception. Although Charles Horton Peck and Lewis [Ludwig] David von Schweinitz described Morchella species from eastern North America towards the end of the nineteenth century, more morpho-species are known but yet to be described. The taxonomy of the genus is further complicated by DNA studies, such as those from Europe, which have discovered cryptic species within traditional recognized species. The focus of this study is the delineation of Morchella species which occur in eastern North America as well as their taxonomic revision. DNA sequences from collections made in four Maryland national parks as well as southern Ontario are compared to available morel sequence data from other origins. A multigene phylogeny and ITS barcodes are used to define relationships within the genus and to distinguish species. We currently recognize at least six species in Eastern North America. Contributed Presentation

Djeddour, Djami H.1, Evans, Harry C.1, Cannon, Paul F.1,3,4 and Kurose, Daissuke.2 1CABI Europe UK, Bakeham Lane, Egham TW20 9TY, UK, 2Laboratory of Plant Pathology, Faculty of Agriculture, Kyushu University, Fukuoka 812-8581, Japan. p.cannon@cabi.org. Potential of the leafspot fungus Mycosphaerella polygoni-cuspidati for classical biological control of the invasive weed Fallopia japonica (Japanese knotweed). One of the 100 worst invasive species in the world, Japanese knotweed (Fallopia japonica) has become a serious environmental and economic weed across the world. Recorded from 40 US States (invasive in 12), and 8 Canadian Provinces (invasive in all), this highly adaptable, rapidly regenerating and persistent rhizomatous plant has proved increasing difficulty to control mechanically and chemically and is continuing to spread. In the UK, a pioneering research project began in 2003 with the potential to make Japanese knotweed the first target of a full classical weed biocontrol program in Europe. A novel weed management approach for Europe, it is a strategy that has long been recognised as one of the most sustainable means of controlling invasive weeds worldwide. Surveys across its native range in Japan revealed a large number of specialist natural enemies. Several promising fungal pathogens were investigated. Of these, a highly damaging and host specific Mycosphaerella species was found to be one of the most suitable agents and was therefore comprehensively screened for selectivity. The systematics, life-cycle and pathogenicity of this recently re-described leaf spot fungus are detailed and prospects are addressed for biocontrol of this high profile weed in Europe and across the Atlantic. Poster

Dwayne, Vinson P.1,2, Sundue, Michael1 and Samuels, Gary J.1 1The New York Botanical Garden, Bronx, NY 10458, USA, 2USDA-ARS Systematic Mycology and Microbiology Lab, Beltsville, MD 20705, USA. vdwayne@nybg.org. Evaluating host specificity of epibiotic Acrospermum on neotropical polygrammoid ferns. Acrospermum is a genus of sапротrophic and biotrophic bitunicate ascomycetes distributed mostly throughout the Americas. Acrospermum maxonii is found on polygrammoid ferns primarily in the genus Terpsichore. Closer examination reveals that Acrospermum specimens on Terpsichore species occurring above 3000 meters on the eastern slope of the Andes are morphologically distinct from those occurring elsewhere. The morphological, host and geographic differences suggest the existence of two species within what has been known as Acrospermum maxonii. Here we discuss both the geographical and host distribution of Acrospermum maxonii and a closely related novel taxon in the context of the host phylogeny to test hypotheses of host specificity and coevolution. Poster

Dubal, Kinnari Jayendra-prasad. St. Xavier’s College, Navrangpura Road, Ahmedabad City, 380009, Gujarat State, India. kinaridubal@yahoo.com. Medicinally important plants, Ocimum species, of the family Labiatae. Ocimum species of the family Labiatae were selected because of their typical characteristics, including a verticillaster in florescence, bilabiata corolla, leaves and other parts with oil glands containing essential oils, alkanoïds, flavonoids, etc. The following plants were selected for the study: 1. Ocimum basilicum, 2. Ocimum americanum, 3. Ocimum microanthum, 4. Ocimum gratissimum, and 5. Ocimum kilimandscharicum. The data consists of plant description, common name, part of the plant used, chemical constituents, its uses and efficacy, toxicity and also ecological distribution. Many plants are studied nowadays in order to determine the medicinal value of their active components. Synthetic drugs do prevent and cure many diseases to a certain extent, but they have many contra-indications harmful to the human body, whereas active components derived from plants are generally free from side effects. Poster

Edwards, James L. Encyclopedia of Life, National Museum of Natural History, Smithsonian Institution, P.O. Box 37012, MRC 106, Washington, DC 20013-7012, USA. edwardsjl@si.edu. Fungi and The Encyclopedia of Life. The Encyclopedia of Life (EOL) is a free, Internet-based compendium of information about the world’s plants, animals, fungi and microorganisms. At its heart are web pages for each of the approximately 1.8 million validly known species. Building upon its collaborations with the Catalogue of Life, Tree of Life Web, FishBase, AmphibiaWeb, and a host of other partners, as of May 2008 the alpha version of the EOL portal is serving a little more than a million species pages and several thousand supraspecific pages. However, many of these pages are in essence placeholders, waiting to be filled with authentic content. EOL has been working with relevant scientific organizations to develop plans for how the communities they represent will assemble the information for the species pages. EOL looks to this workshop as the catalyst for the mycological community to self-organize and determine how it wishes to populate the fungal pages in EOL. Symposium Presentation

Continued on following page
Epps, Mary Jane1,2* and Arnold, A. Elizabeth.1 1Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721, USA, 2Department of Plant Sciences, University of Arizona, Tucson, AZ 85719, USA. mycota@gmail.com. Patterns of community structure and host visitation in mushroom-associated beetles and other insects. Mushroom fruiting bodies provide habitat for a diverse assemblage of insects. While most species visit mushrooms to feed on mycelium and/or spores, predators also may target mushrooms to prey upon fungivores. In turn, these insects may destroy or disperse fungal spores and hyphae, playing a potentially important role in fungal ecology. Because little is known regarding the structure and diversity of mushroom-associated insect communities, I conducted a taxonomically broad survey of mushrooms and their associated insects, primarily adult beetles, at two sites in the Appalachian Mountains. From June-August of 2007, I collected 758 mushrooms representing at least 175 species, and catalogued their associated beetle communities. Eleven orders of arthropods were observed in association with sporocarps, including beetles from 15 families representing ca. 50 morphospecies. Of these, the beetle family Staphyliniidae was represented in the greatest diversity and abundance, with as many as 1,890 individuals of a morphospecies per sporocarp. I used these data to assess the diversity of mushroom-associated insect communities and test for patterns of association across the spectrum of locally common host fungi. Finally, I examined the degree to which sporocarp size, maturity, and phylogenetic relatedness shape the structure and diversity of mushroom-associated beetle communities. Poster

Euady, Douglas M.1*, Khidir, Hana H.1, Porras-Alfaro, Andrea2 and Herrera, Jose.1 1Department of Biology, Truman State University, Kirkville, MO 63501, USA, 2Department of Biology, The University of New Mexico, Albuquerque, NM 87131, USA. douglas.euady@gmail.com. Biogeographic variation in the dark septate endophyte communities of blue grama (Bouteloua gracilis) across central North America. In some plant species, mutualistic relationships with endophytic fungi are thought to ameliorate the effects of the xeric conditions of arid ecosystems. Studying these relationships may aid in developing new understandings of how plants and fungi have evolved and if their current relationships reveal the patterns of co-evolution. Our model plant is blue grama (Bouteloua gracilis), a common forage grass. By comparing the fungal endophyte communities contained within plant samples collected along a latitudinal gradient, we expect to demonstrate the level of consistency among the root associated fungal communities of these distantly growing plants. To answer this question we are continuing to construct a robust dataset containing ITS cDNA sequences from B. gracilis root samples collected over a distance of some 1200 miles, from central Mexico, New Mexico, Kansas, South Dakota and southern Saskatchewan, Canada. So far, our results reveal an interesting pattern of fungal colonization and have provided insight in how geographic variables like water availability affect the community of DSEs and how these fungi have co-evolved with grasses. Poster

Fernandez, Roberto1, Iturriaga, Teresa1* and Castaño, Richard F.2 1Departamento de Biologia de organismos, Universidad Simon Bolivar, Venezuela, Apartado 89000, 2Instituto de Investigaciones Fundamentales en Agricultura Tropical “Alejandro de Humboldt” (INIFAT), Ciudad de La Habana, Cuba, C.P. 17200. fungustym@gmail.com. A new species of Pyriculariopsis (Anamorphic Ascomycetes) from Venezuela. A new hyphomycete species of the genus Pyriculariopsis (Anamorphic Ascomycetes) was found on a decaying leaf of Clusia rosea in “El Avila” National Park, Caracas, Venezuela. This species clearly belongs to the genus due to the conico-truncate shape of denticles in the conidigenous cell, by the presence of rostrate conidia and because some conidial cells (second and third) are darker than the rest. This new species mainly differs from the other ones belonging to the genus by its conidial size and number of septa. Poster

Fischer, M.W.F.1*, Davis, D.J., Stolze-Rybczynski J.J.2 and Money, N.P.2 1Department of Chemistry and Physical Sciences, College of Mount St. Joseph, Cincinnati, OH 45056, USA, 2Department of Botany, Miami University, Oxford, OH 45056, USA. Mark_Fischer@mail.msu.edu. Solving the aerodynamics of fungal flight. Fungi use a variety of mechanisms to launch their spores into air. Mushroom spores are propelled over distances of only a few tenths of a millimeter, sufficient to clear them from the gill surface, and then fall into the air currents circulating beneath the cap. Other fungi, including many ascomycetes, and the zygomycete Pilobolus, use pressurized squirt guns to shoot their spores (or sporangia) over much longer distances. To understand how each mechanism works, it is important to determine the relationship between the launch speed and the range of the spores. Several methods for modeling the dominant viscous drag due to air resistance have been proposed. Two of these models are evaluated in this presentation, by comparing the initial velocity estimates predicted by each approach to novel experimental data obtained using ultra high speed video microscopy. We demonstrate that the simpler Stokes model of drag is far superior to the more complex, but more commonly used, interpolation model of drag. Contributed Presentation

Frank, J.J.1,2, Coffan, R.A.2 and Southworth, D.1 1Department of Biology and 2Department of Environmental Studies, Southern Oregon University, Ashland, OR 97520, USA. southworth@sou.edu. Aquatic gilled mushrooms: Psathyrella fruiting in the Rogue River in southern Oregon. A species of Psathyrella (Basidiomycota) with true gills has been observed fruiting underwater in the clear, cold, flowing waters of the upper Rogue River in Oregon. Fruiting bodies develop and mature in the main channel, constantly submerged, near aquatic vegetation, and were observed fruiting over 11 weeks. DNA sequence data of the ITS region and a portion of the 28S ribosomal DNA gene place this fungus in Psathyrella sensu stricto, in clade v near P. gracilis and P. brooksi. Based on molecular and morphological evidence, we conclude that the underwater mushrooms are a new species. These appear to be truly underwater mushrooms and not mushrooms fruiting on wood recently washed into the river. Substrates include water-logged wood, gravel, and the silty river bed. Water constrains spore dispersal. Spores were observed as wedge-shaped rafts released into a gas pocket under the cap. Underwater gills and ballistospores indicate a recent adaptation to the stream environment. This particular river habitat combines the characteristics of spring-fed flows, clear, cold, aerated water with woody debris in shallow depths on a fine volcanic substrate. The presence of nitrogen-fixing cyanobacteria near fruiting body attachment sites suggests a source of nitrogen in an otherwise clear stream. This observation adds to the biodiversity of stream fungi that degrade woody substrates. This is a new habitat for gilled mushrooms. Poster

Freitag, Camille1, Cabrera, Yohanna1, Williams, Miguel2, Freitag, Michael1 and Morrell, Jeff.1 1Department of Wood Science and Engineering, Oregon State University, Corvallis, OR 97331, USA, 2Department of Biochemistry and Biophysics, Oregon State University, Corvallis, OR 97331, USA. camille.freitag@oregonstate.edu. Fungi colonizing exposed durable wood in Hilo, HI. High production plantation forestry has markedly increased the percentage of non-durable sapwood and decreased heartwood extractive content in naturally durable woods. Improving durability of these species will be critical for helping developing countries realize value from reforestation efforts. Supplemental treatment with protective chemicals may help solve this problem. As part of a project to improve durability of high-value wood species, we treated heartwood and sapwood of teak, redwood and western redcedar (WRC) with three different wood preservatives. Wood samples were exposed under high decay hazard, but non-soil contact conditions near Hilo, HI. Fungi and bacteria colonizing wood samples were isolated after six or twelve months of exposure by traditional methods. We amplified fungal and bacterial 16S rDNA followed by RFLP and/or DNA sequencing to explore the effects of chemical treatment and wood species on community structure. At six months, fungal abundance and diversity were extremely high regardless of wood species or treatment, with the exception of WRC heartwood. Wood-decaying basidiomycota were isolated from both treated and non-treated wood of all species except...
cept WRC heartwood. Further studies are underway to directly isolate fungal DNA from the wood samples; progress has been slowed by the difficulty in overcoming wood extractive interference. Poster

Freitag, Michael, Connolly, Lannelle R. and Smith, Kristina M. Department of Biochemistry and Biophysics, Center for Genome Research and Biocomputing, Oregon State University, Corvallis, OR, USA. freitagm@onid.orst.edu. Centromere and kinetochore proteins of filamentous fungi. Centromeres are complex structures built from DNA, proteins and RNA. They are the foundation for kinetochores, the attachment points for spindle microtubules during nuclear division. Centromeres are now functionally defined by the presence of the centromere-specific histone H3 variant, “CenH3”. We still do not understand how centromeres assemble, how they are maintained and how they are inherited. To address these questions we are using Neurospora crassa and Fusarium graminearum as reference systems. Centromeric regions in Neurospora are of similar complexity as those in most animals, while the F. graminearum genome is virtually repeat-free, which makes these two fungi ideally suited to investigate the relative contributions of DNA composition and epigenetic modifications to centromere identity. To this end we have generated fusions of CenH3 and Cenp-C with fluorescent proteins and affinity tags to study protein localization and function, and to isolate DNA associated with these proteins by chromatin immunoprecipitation (ChIP). CenH3 and Cenp-C-GFP fusions localize to a single “chromocenter” in each nucleus. DNA that contacts CenH3 and Cenp-C maps to previously identified blocks of centromeric or pericentric DNA in Neurospora. Curiously, only trimethylated histone H3 K9, a silencing chromatin mark is found in these regions, while the active dimethylated H3 K4 mark has been found in animals and fission yeast. We are now investigating if trimethylation of H3 K9 (by DIM-5) and heterochromatin maintenance (by HP1) are important for the localization of centromere proteins in Neurospora. Symposium Presentation

Frieders, Elizabeth M. Biology Department, University of Wisconsin-Platteville, Platteville, WI 53818, USA. frieders@uwplatt.edu. Description of a novel doghobble (Eriaceae) endophyte from Great Smoky Mountain National Park. In the last decades foliar endophyte species diversity has increased with most being members of the Ascomycota, and comparatively few from the Basidiomycota. Members of the Eriaceae are best known for harboring root endophytes, not foliar endophytes. In this paper, I describe a new basidiomycetous endophyte isolated from asymptomatic leaves of Leucodendron fontanensis (Eriaceae) from Great Smoky Mountain National Park. Cultures were isolated from sterilized leaves, then inoculated onto autoclaved Eriaceae leaves. Mycelial growth was hyaline and devoid of reproductive propagules. After inoculation onto host leaves, the fungus produced noticeable gelatinous pustules bearing clustered conidiophores. DNA was extracted from cultures and sequences obtained for the rSSU, LSU and ITS regions. Phylogenetic analyses place it within the Atractielloides (Basidiomycota, Pucciniomycotina). A species name and diagnosis will be provided. The Atractielloides contains an ecletic array of highly diverse taxa: hypomycteous and mitosporic (including helicosporous) anamorphs; fruitbodies range from stiltloid to resupinate, bearing holobasidia or heterobasidia with or without prosidia; habitats and nutritional modes include saprobes on wood and plant debris (including bark beetle galleries), mycorparites, lichenicolous. This is the first report of an endophyte in this clade. Poster

Garcia-Sandoval, Ricardo* and Hibbett, David S. Clark University, Worcester, MA 01610, USA. rgarciasandoval@clarku.edu. A six genes phylogeny for the Gloeophylalles. The Gloeophylalles is a group of wood-decaying mushrooms, which includes species from the genera Gloeophyllum, Neolentinus, Veluticeps, Boreostereum and Helioxybe. The monotopic genus Donkioporia also has been included based on the analysis of the nu-ssu region, but a more comprehensive study based on six gene regions places this genus in the Polyporoid clade. Placement of the Gloeophylalles in the context of the Agaricomycetes remains uncertain, as long as different analysis strategies produce different results, and all conditions fail to provide statistical support. Phylogenetic relationships inside the Gloeophylalles place Boreostereum as the most basal group, and account for the monophyly of the remaining genera with the exception of Gloeophyllum, which splits at least in two groups, one including the type species G. sepiarium and the other including G. odora- tum. The evolution of selected morphological characters will be discussed in the context of the phylogeny of the Gloeophylalles, as well as implications for brown-rotting evolution derived from different placements for this group. Contributed Presentation

Gaya, Ester*, Ball, Bernard and Lutzoni, François. Duke University, Department of Biology, Box 90338, Durham, NC 27708, USA. eb62@duke.edu. Resolving deep internodes in the Teloschistales with a multi-gene approach. The Teloschistales, one of the most diverse orders of Lecanoromycetes, currently encompasses two suborders: Physci- ineae (Physciaceae) and Teloschistineae (Letrouitiaceae, Megalosporaceae, and Teloschistaceae). In our most recent studies, we conducted the most exhaustive phylogenetic survey of species within the Teloschis- taceae (the largest family within the Teloschistineae) by restricting the sequencing to ITS. The expected consequence of including so many taxa without adding characters was the loss of significant support for deep internodes. In this context, more loci needed to be sequenced to pursue further phylogenetic studies on the Teloschistaceae and the Teloschistales in general. In order to achieve this aim we sequenced six loci: internal transcribed spacer (ITS), mitochondrial ribosomal small subunit (mitSSU), nuclear ribosomal small and large subunits (nucSSU and nu- cLSU), RNA polymerase II largest and second largest subunits (RPB1 and RPB2), and performed phylogenetic analyses on single and multilo- cus datasets. We will discuss the phylogenetic relationships of these fungi at the ordinal and family level within the context of the current classification of the Lecanoromycetes. Contributed Presentation

Gazis, Romina* and Chaverri, Priscila. Howard University, Department of Biology, 415 College Street NW, Washington D.C. 20059, USA. romingazis@hotmail.com. A preliminary evaluation of the fungal endophytic community in rubber tree (Hevea brasiliensis). Under- standing the role of fungi (i.e. endophytes) in communities and ecosystems has been hampered by little sampling and characterization of fungal diversity. Of the estimated 500,000 plant species in the world, only a few have been studied to determine their endophytic mycobiota. The overall goal of this project is to characterize fungal endophytic species in Hevea brasiliensis and to evaluate their potential role as plant protection agents. This presentation is based on a preliminary survey conducted in a wild rubber population, located in the Amazon basin (Tambopata, Peru). Fifteen trees were sampled for sapwood and leaf endophytes. To identify the isolates, molecular (ITS, 28S, and EF1-alpha for Trichoderma isolates) and morphological data were analyzed. One hundred and eighty fungal endophytes were obtained from 225 samples. Leaves harbored greater fungal endophytic diversity than sapwood. Pestalotiopsis cf. Hughesi was the dominant species, present in leaves and sapwood, but more commonly in leaves. Trichoderma spp. and Xylaria sp. dominated the sapwood isolates. In the future, preliminary in vitro assays will be performed to test the antifungal properties of some of the endophytes against fungal rubber diseases (especially against Microcyclus uleni). Before the present study, the endophytic biota of rubber was unknown; therefore, this project may reveal many new species. Poster

Gibbons, John and Rokas, Antonis. Vanderbilt University, Department of Biological Sciences, Nashville, TN 37235, USA. john.g.gibbons@vanderbilt.edu. Deciphering the functional diversity of intragenic tandem repeats across ten Aspergillus genomes. Intragenic tandem repeats (ITRs) are consecutive repeats of three or more nucleotides found in coding regions. ITRs are the underlying cause of more than forty human genetic diseases, and have been associated with fungal pathogenesis. We have examined the presence of ITRs in ten genomes spanning the genus Aspergillus, a fungal clade of great relevance to med-
Glaser, Jessie A.1,* and Burdsall, Harold H. Jr. 2 1US Forest Service, Northern Research Station, One Gifford Pinchot Dr., Madison, WI 53726, USA, 2Fungal and Decay Diagnostics, 9350 Union Valley Rd., Black Earth, WI 53515, USA. jmclares@fs.fed.us. **Fungi associated with unprocessed wood chips imported from Chile.** International trade in unprocessed wood chips for the pulp and paper industry is a potential source for the introduction of non-native wood-inhabiting pests and pathogens that could pose a severe hazard to U.S. forests. With permission from APHIS, 23 shipments of unprocessed *Pinus radiata* wood chips from Chile were shipped to a processing plant in Bellingham, WA to evaluate the danger of introducing non-native fungal pathogens to the U.S. Fifteen bags of samples were taken from each shipment. Three chips were removed from each bag, surface disinfested by flameing in alcohol, placed on malt extract agar, and incubated at 25C. Over 3400 cultures of fungi were identified to species, genus or higher taxon using light microscopy. Species of *Trichoderma*, *Geotrichum*, *Gliocladium* and *Phialophora* accounted for almost 75% of all isolations. Several potential pathogens were isolated in low numbers, including fungi in the genera *Graphium* (2% of all isolations), *Ophiostoma/Ceratocystis* (0.7%), *Leptographium* (1.8%), *Phoma* (0.1%), *Fusarium* (0.2%) and single isolations of *Moniliformis*, *Phellinus* and *Verticillium*. No pathogenic genera were isolated when the wood chips were not surface disinfested. The introduction of non-native pathogenic fungi by international shipping of wood chips is possible but unlikely due to rapid growth by ubiquitous saprophytic, imperfect fungi. **Poster**

Glenn, Anthony E. 1,* and Bacon, Charles W. USDA, ARS, Russell Research Center, Toxicology & Mycotoxin Research Unit, Athens, GA 30605, USA. anthony.glenn@ars.usda.gov. **Fusarium verticillioides** gene clusters associated with biotransformation of maize allelopathic compounds. Maize produces the benzoazinones DIMBOA and DIBOA, which naturally transform into the more stable benzoazolones MBOA and BOA, respectively. These weed-suppressive allelopathic compounds are also implicated in resistance to microbial diseases and insect feeding. *Fusarium verticillioides* is able to detoxify MBOA and BOA. The biotransformation pathway involves hydrolysis of BOA (encoded by the *FDB1* locus) to produce 2-aminothiazole, which is acetylated (encoded by the *FDB2* locus) to produce N-(2-hydroxyphenyl)malonamic acid. Growth is inhibited on BOA-amended medium if either locus is mutated. Using suppression subtractive hybridization to identify genes up-regulated in response to BOA, two gene clusters were identified that functionally correspond to the *FDB1* and *FDB2* loci. Of nine genes at the *FDB1* locus, three were found to be necessary for biotransformation. The *FDB2* locus consists of 13 genes, including one encoding a putative N-acetyltransferase (NAT). The subcloned NAT gene complemented an *fdhB* mutation, and deletion of the gene eliminated the ability of *F. verticillioides* to metabolize BOA. The other 12 genes at the *FDB2* locus were not essential for biotransformation. This work provides genetic evidence for the biochemistry of benzoazolinone biotransformation, a metabolic process that may enhance the ecological fitness of *F. verticillioides* in the maize field environment. **Contributed Presentation**

Goldmann, Lauren M. 1,* Thompson, Lisa M., and Weir, Alex. Department of Environmental and Forest Biology, SUNY College of Environmental Science and Forestry, 1 Forestry Drive, Syracuse, NY 13210, USA. lmgold01@syr.edu. **Placement of the genus *Ilyomyces* and descriptions of two new species.** Two new species of the rarely collected genus *Ilyomyces* (Laboulbeniales) are described on *Steninaria* from Mexico. The genus *Ilyomyces* is characterized primarily by receptacular, primary appendage, and perithecial characters. Tavares (1985) placed *Ilyomyces* with a number of other genera having a simple 3-celled receptacle (2 of which are below the perithecial stalk cell) in the subtribe *Stigmatomycteae*. Our preliminary molecular data indicate that this is a polyphyletic grouping composed of at least two distinct lineages. One of these lineages (lineage A) includes genera such as *Stigmatomyces*, *Corethromyces*, and *Rhadinomyces*, all of which are characterized by a perithecium with 4 tiers of outer wall cells. The other lineage (B), in which *Ilyomyces* is placed, appears to consist of taxa with 5 tiers of outer wall cells. Precise placement of *Ilyomyces* will, however, have to await additional sequences from other putative 5-tiered relatives e.g. *Phalachryomyces*, *Stenomyces*, and *Synamyomyces*. **Poster**

González, María C.1,*, Anaya-Lang, Ana Luisa1, Glenn, Anthony E. 1, Macías-Rubalcaba, Martha L. 2, Hernández-Bautista, Blanca E. 2 and Hanlin, Richard T. 4 1Departamento de Botánica, AP 70233 Instituto de Biología, UNAM, Ciudad de México DF, 04510, México, 2Departamento de Ecología Funcional, Instituto de Ecología, UNAM, Ciudad de México DF, 04510, México, 4Toxicology & Mycotoxin Research Unit, Russell Research Center, USDA, ARS, Athens, GA 30605, USA, 1Museum of Natural History Annex, University of Georgia, Bogart, GA 30622, USA. mcgv@biologia.unam.mx. **Muscodor yucatanensis, a new endophytic ascomycete from Mexican chakah, *Bursera simaruba*.** During a study on the fungal endophytic associations with some trees of the dry tropical forest of El Eden Ecological Reserve located in the northeast of the Yucatan Peninsula of Mexico, a new fungal species was isolated as an endophyte of a tree named chakah, chachá or huk’up by indigenous mayas. This fungus is characterized by producing a strong musty odor and absence of reproductive structures. Cultures of this fungus on PDA form a white felt colony with an uncolored reverse and a mycelium that grows slowly. Based on morphological and DNA sequence analyses, the Mexican isolate is related to but separated from *Muscodor albus* of the *Xylariaceae* and has not been previously described, therefore, *Muscodor yucatanensis* sp. nov. is described and illustrated. In addition, the new fungus produces a distinctive mixture of new bioactive volatile compounds and their chemical characterization is underway. **Poster**

Greif, Matthew D. 1,*, Stichgel, Alberto M. 2, Miller, Andrew N. 3, and Huhndorf, Sabine M. 1 1Botany Department, The Field Museum of Natural History, Chicago, IL 60605, USA, 2Unitat de Microbiologia, Universitat Rovira i Virgili, 43201 Reus, Spain, 3Section for Biodiversity, Illinois Natural History Survey, Champaign, IL 61820-6970, USA. mgreif@fieldmuseum.org. **Phylogenetic analysis of Chaetomium and its implications on cephalothecoid evolution.** The genus *Chaetomium*, currently residing within *Chaetomiaceae*, accommodates species defined in part by membranous, pigmented cleistothecia bearing long, flexuous setae, and ellipsoidal to limoniform single-celled ascospores with a single apical germ pore. Six described species produce a specific type of cephalothecoid peridium composed of multiple small plates of tightly packed cells that are bound by lines of dehiscence. The abundance of

**Inoculum 59(4), July 2008 31**

Continued on following page
cephalothecoid species in *Chaetomium* provided a model to study the proliferation of this peridial character throughout the genus. Using molecular techniques we assessed the phylogeny of this taxon to examine cephalothecoid peridium evolution and clarify the placement of this genus within the Chaetomiaceae. Phylogenetic analysis using the LSU, beta-tubulin, and RPB2 genes revealed that the genus is currently composed of morphologically similar, yet unrelated, species scattered throughout the Sordariidae. Among cephalothecoid species the peridium was a surprisingly unreliable predictor of monophyly, indicating that this peridial type has arisen independently multiple times, presumably driven by sporidispersal requirements. Additional identified and sequenced isolates will help refine *Chaetomium* and track cephalothecoid evolution among specific lineages. Contributed Presentation

Gremillion, Sara K. 1,*, Hill, Terry W. 1, Loprete, Darlene M. 2, Camara, Kaddy 2, Samuels, Felicia 1 and Mercer, Sarah. 3 1Departments of Biology and Chemistry, Rhodes College, Memphis, TN 38102, USA, 2Department of Biology, Rust College, Holly Springs, MS 38635, USA, 3Department of Biology, Tougaloo College, Jackson, MS 39174, USA. hill@rhodes.edu.

*A mutation in a COG4 homologue affects polarity establishment in* Aspergillus nidulans. We have identified a mutation in *Aspergillus nidulans*, designated swoP (for swollen cell phenotype), causing a temperature-sensitive morphological defect during spore germination and hyphal growth. Conidia typically swell to approximately 1.5 times the normal diameter, and often establish multiple points of polarity, which grow isotropically before arrest. Mutant cells tend to burst when observed under a coverslip. At 42°C, a very small minority of cells eventually produce colonies and asexual spores. Growth at 30°C is essentially normal, though hyphae are slightly wider than wild type and exhibit a minor steering defect. Cells grown at 42°C for up to 18 hours recover normal hyphal morphology upon transfer to 30°C. In hyphae transferred from 30°C to 42°C, both terminal and sub-apical compartments swell irregularly, usually initiated in the basal end of the compartment. The growth defect of swoP is complemented by the wild type allele of AN7462, which shows strong sequence homology to COG4, a component of the Golgi tethering complex associated with retrograde transport of COPF-coated vesicles. Sequencing of the COG4 allele of the swoP mutant reveals a mutation at base pair 2672, introducing a stop codon at amino acid 780. Meiotic mapping produces a ca. 12% recombination frequency between the swoP and AcaK loci, which is consistent with the chromosomal location of AN7462. We are currently working to localize the putative COG4 protein of *A. nidulans* via GFP-tagging and immunolocalization, as well as to demonstrate interactions between *A. nidulans* COG4 and other proteins involved in retrograde vesicle transport in the Golgi apparatus. Poster

Guo, Li*, Jimenez-Gasco, Maria del Mar, Geiser, David M. and Kulka, Gretchen A. Department of Plant Pathology, The Pennsylvania State University, University Park, PA 16802, USA. luck269@psu.edu.

**Spore killing in Fusarium verticillioides.** Spore killing is a fungal example of meiotic drive similar to segregation distortion in animals and plants. Spore killing (SK), found in some ascomycetous fungi, occurs when a killer strain carrying a killer element (SKK) mates with a sensitive strain carrying sensitive element (SKS) giving four normal viable ascospores carrying SKK and four degenerated ones carrying SKS in each ascus. *Fusarium verticillioides* is a worldwide maize endophyte and pathogen producing the mycotoxin fumonisin. Although SK has been reported in *F. verticillioides* and other *Fusarium* spp, SK genotypes are known in only a few *F. verticillioides* strains. The SK locus is genetically mapped to chromosome 5 of *F. verticillioides*. The genome sequence of *F. verticillioides* strain M-3125 has been determined but it carries SKS, making tetrad analysis of the fungus difficult because most *F. verticillioides* strains in nature are SKK and genes of interest may be linked with SK genes. We took 56 *F. verticillioides* strains in the Fusarium Research Center at Penn State and analyzed their SK genotypes by crossing with known killer and sensitive strains. The results will promote our understanding of this interesting phenomenon and benefit functional genomic analysis of *F. verticillioides*. Poster

Haight, John-Erich 1,*, Taylor, Lee* and Laursen, Gary. A. 1 1Biology and Wildlife Department, The University of Alaska, 211 Irving 1, Fairbanks, AK 99775, USA, 2USDA-FS Northern Research Station, One Gifford Pinchot Drive, Madison, WI 53726, USA. jhaight@fs.fed.us.

**Evaluation of Fomitopsis pinicola (Sw.) P. Karst (1881) found in Alaska.** Speciation is a topical area of study in evolutionary biology and population genetics. Researchers of species delimitation have shifted emphasis from sole reliance on morphological characters and mating compatibility to testing proposed species boundaries using molecular evidence. *Fomitopsis pinicola* is an ideal organism to examine for the occurrence of cryptic species because it is an abundant saprotrophic fungus found on decaying logs throughout temperate regions of the world. Phylogenetic research has been conducted on *F. pinicola* isolates collected world-wide but no research has been carried out examining the relationships of *F. pinicola* found in Alaska to those present in the rest of the world. While forms in Interior Alaska exhibit variation in habit and appearance, phylogenetic research is necessary to determine whether these forms can be distinguished genetically. This study evaluates DNA sequences of the ITS region from freshly collected sporophores and herbarium specimens collected in Interior Alaska and compares them to those from Southeast Alaska, other parts of the United States and Europe. Analysis yields three distinct clades: an Interior Alaskan clade, a SE Alaskan clade and a European clade. Evidence implies gene flow between populations is restricted with a possible cryptic species occurring in Interior Alaska. Poster

Hallén-Adams, Heather E. 1,*, and Walton, Jonathan D. 1, 2 1DOE Plant Research Laboratory and 2Department of Biology, Michigan State University, East Lansing, MI 48824-1312, USA. hallenle@msu.edu.

**Amatoxins, phallotoxins and other small peptides are derived from a protein precursor.** The cyclic peptide toxins of poisonous *Amanita* mushrooms, amatoxins and phallotoxins, share a biochemical pathway involving a ribosomally-encoded protein, in which the toxins are flanked by highly-conserved motifs at both the N- and C-termini. We have identified the genes for the primary amatoxins (alpha-, beta- and gamma-amanitin) and phallotoxins (phalloidin and phallacidin) in multiple species of toxin-producing *Amanita*. Additionally, we have identified at least 15 additional members of the amatoxin gene family, encoding putative novel peptides. The genes encoding amatoxin, phallotoxin, and at least two novel peptides are transcribed in the mature *Amanita* fruiting body. *Galenteria marginata* synthesizes amatoxins on ribosomes by a similar mechanism. Contributed Presentation

Harrower, Emma 1,*, Lim, Sean 1, Kroeger, Paul 1 and Berbee, Mary L. 1 1University of British Columbia, Botany, 6270 University Boulevard, Vancouver, British Columbia, V6T 1Z4, Canada, 2Mycological Consultant, 395 East 40th Avenue, Vancouver, British Columbia, V5W 1M1, Canada. salal36@interchange.ubc.ca. Can DNA barcoding *Cortinarius* help identify mycorrhizal roots? Might DNA-barcoding offer a solution to the problem of identification of *Cortinarius* species from roots? DNA-barcoding works on the premise that every organism has a unique sequence of DNA that can be used to identify that particular species. In this study, we are sequencing the ITS regions of over 300 *Cortinarius* herbarium mushroom collections and comparing the sequences to those in GenBank. Our preliminary phylogeny divides sequences from 192 specimens among 72 possible species. This phylogeny allowed us to match 14 ectomycorrhizal sequences from GenBank to actual mushroom specimens. Our study thus links these environmental DNAs that lack voucher material to herbarium specimens that can ultimately be identified. Poster

Harrower, Emma 1,*, Lim, Sean 1, Kroeger, Paul 1 and Berbee, Mary L. 1 1University of British Columbia, Botany, 6270 University Boulevard, Vancouver, British Columbia, V6T 1Z4, Canada, 2Mycological Consultant, 395 East 40th Avenue, Vancouver, British Columbia, V5W 1M1, Canada. salal36@interchange.ubc.ca. A survey of the genus *Cortinarius* in British Columbia. *Cortinarius* Fr. is one of the most

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abundant, diverse and difficult taxonomic genera in the Agaricales with approximately 4000 described species. This genus is commonly misidentified and underrepresented in herbaria. The purposes of this project are: a) to compile an accurate reference collection of Cortinarius sequences from specimens collected in British Columbia; b) to reveal undescribed species of Cortinarius. We sequenced the ribosomal ITS region from as many as possible of 331 specimens collected from the year 2000 onwards. Sequences were compared with GenBank and a preliminary phylogenetic tree using 192 sequences shows 72 possible species. 45 possible species matched sequences in GenBank with >97% identity. 13 possible species only matched mycorrhizal root tips. 14 possible species did not closely match anything in GenBank. 27% (52/192) of the herbarium specimens were either misidentified and re-identified by following up on a GenBank match; or identified for the first time by reference to a GenBank sequence from a well-documented voucher specimen. Using phylogenetic similarity in the ITS region worked effectively to identify described species, to reveal potentially undescribed species and to identify mycorrhizal roots. Contributed Presentation

Hawkins, Lauraine* and Brantley, Elizabeth. Penn State Mont Alto, Mont Alto, PA 17237, USA. lhki1@psu.edu. Macроверag of four mid-Atlantic National Parks. We report on macrofungi inventory work conducted for the National Park Service. At each of four Parks (Antietam Battlefield, Catoctin Mountain, C&O Canal Historical, and Prince William Forest), we sampled two 20 X 20 m plots three times per season in 2005 and 2006. In addition, we conducted forays at each Park annually. Identification work was finished and a project report submitted in fall 2007. Fungi were much more abundant at PRWI (343 fruiting bodies collected) and CATO (329) than at CHO (126) or ANTI (103). This presentation will describe results from this project and address the issues of sampling and assessing biological richness. Contributed Presentation

Hebel, Cassie L.1, Smith, Jane E.24 and Cromack, Kermit Jr.1 Department of Forest Science, Oregon State University, Corvallis, OR 97330, USA. 1USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR 97331, USA. jsmith01fs.fed.us. Invasive plant species and soil microbial response to wildfire burn severity in the Cascade Range of Oregon. Fire suppression in the last several decades has resulted in unprecedented accumulations of organic matter on the landscape, leading to an increase in large, intense wildfires. We investigated the soil microbial community (using PLFA analysis) across 10 blocks of paired burn severity areas within a recently burned forest on the eastern slope of the Cascade Range in Oregon. We examined the effects of the belowground community on the growth of native and non-native plant species in severely burned “red” soil and in less severely burned “black” soil. Long duration, smoldering conditions creating red soils significantly altered both soil nutrients and microbial community structure. Differential growth was observed between native and non-native plant species grown in soil from the two burn severities. Shoot biomass of the aggressive non-native plants grown in red soil was significantly less than non-native plants grown in black soil, when in contrast; growth responses of pioneering native plant species were surprisingly similar, regardless of burn severity or AMF colonization. Although it has previously been reported that fire increases the likelihood of invasion by non-native plant species in burned areas, our results do not support the assumption that red soil conditions are more susceptible than moderately burned soil to non-native, invasive plant species colonization. Contributed Presentation

Hersh, Michelle H.18, Vilgalys, Rytas J. and Clark, James S.3 University Program in Ecology, Duke University, Durham, NC 27708, USA. 1Department of Biology, Duke University, Durham, NC 27708, USA. 2Nicholas School of the Environment and Earth Sciences and Department of Biology, Duke University, Durham, NC 27708, USA. mh34@duke.edu. Effects of fungal and oomycete pathogens on seedling recruitment in a temperate mixed hardwood forest. Fungal and oomycete plant pathogens are believed to be an important mechanism maintaining tree species diversity via control of seedling growth and survival. In this study, we tested a classic ecological hypothesis (the Janzen-Connell hypothesis), which predicts that host-specific pathogens drive spatial patterns of seedling recruitment. We characterized the fungi and oomycetes found in dead or dying seedlings of fourteen southeastern U.S. forest tree species in a North Carolina mixed hardwood forest. Planted seedlings were surveyed weekly for mortality over two growing seasons, and dead or dying seedlings were collected and assayed for pathogens. We used culture-based methods to isolate fungi and oomycetes, and DNA sequencing to identify them to the genus or species level. Germination and survival rates of tree species varied between species, sites, and in time. We have identified at least thirty putative species of potentially pathogenic fungi and five species of pathogenic oomycetes. The majority of the species discovered are relatively rare (<10 isolates). However, two species of fungi, Colletotrichum acutatum and Neonectria radicicola, stand out as potentially influential sources of disease. These fungi are known pathogens of commercially-raised trees, common in both study sites, and have overlapping but distinct host ranges of more than four tree species. The occurrence of C. acutatum is not related to soil moisture or light, but is positively correlated with both conspecific and total adult density. So far, these data do not appear to support the Janzen-Connell hypothesis, since most of the fungi and oomycetes isolated are shared by several hosts. However, since many fungi and oomycetes capable of acting as pathogens are present in the system, pathogens may still have a sizeable impact on plant community structure. Contributed Presentation

Hesse, Cedar N.*, Sung, Gi-Ho and Spatafora, Joseph W. Oregon State University, Department of Botany and Plant Pathology, 2082 Cordley Hall, Corvallis, Oregon 97331, USA. hessecscience.oregonstate.edu. Illumina-based massively parallel signature sequencing (MPSS) of soil fungi from environmental samples. Current methods for environmental sampling of soil fungi typically involve extensive sample preparation and costly sequencing while yielding a relatively low resolution of fungal communities. Recent innovations in sequencing technologies promise of delivering much greater sequencing depth at a fraction the cost of traditional methods. We are developing a method of massively parallel signature sequencing (MPSS) utilizing the Illumina 1G Genome Analyzer to investigate fungal diversity in forest soils. The Illumina next-generation sequencing platform is capable of reading 25 million short (~35bp) “signatures” per run and circumvents the need for cloning. By targeting the Internal Transcribed Spacer 1 region of rDNA for unique signatures we believe it may be economical to saturate the sampling of a soil system using this method. Previous clone libraries constructed from ectomycorrhizal mats in the H.J. Andrews Experimental Forest will provide a meaningful comparison of this new method. Utilizing an extensive sequence database we hope to assign taxonomic classifications to known fungal signatures in our sample and identify signatures unrepresented in our database. The ease of sample preparation, depth of sequencing coverage, and economical costs could make this an attractive alternative to the traditional clone-and-sequence approach. Symposium presentation

Hibbett, David S.* and Matheny, P. Brandon. Biology Department, Clark University, Worcester, MA 01610, USA. dhibbettclarku.edu. Relative ages of Agaricomycetidae and their ectomycorrhizal hosts. Reconstructing the origins of ectomycorrhizal associations has been a great challenge of evolutionary mycology. The problem has been addressed by ancestral state reconstruction (ASR) analyses, which have yielded conflicting results. ASR is potentially sensitive to taxon sampling, tree topology, and character coding, and even the most sophisticated model-based methods rely on simplistic assumptions about the process of character evolution. An alternative approach uses molecular clock methods to assess the relative ages of ectomycorrhizal hosts and ancestral nodes in the fungal phylogeny. Molecular clock methods also have serious pitfalls, including rate heterogeneity and uncertainty about the placements of fossils used for calibration. To circumvent these problems, we are using Bayesian relaxed clock analyses to simultaneously

Continued on following page

Inoculum 59(4), July 2008 33
estimate the relative (not absolute) ages of clades including ectomycorrhizal Basidiomycota and their potential plant hosts. The main question we address is: Is it plausible that the most recent common ancestor of the Agaricomycetidae (including Agaricales and Boletales) could have been ectomycorrhizal? **Contributed Presentation**

Hiremath, Sanjay S.1,2, Choudhury, A.2, Kowshik, T.2, Randhawa, H.2, Sun, S.1 and Xu, J.1 Center for Environmental Genomics, McMaster University, Hamilton, ON, Canada, 2Department of Medical Mycology, Vallabhbhai Patel Chest Institute, University of Delhi, 110 007 Delhi, India. hiremas@mcmaster.ca. **Population structure of environmental populations of Cryptococcus gattii from India**. The basidiomycete yeast Cryptococcus gattii is a cause of significant morbidity and mortality in humans throughout the tropical and sub-tropical regions. The sporadic nature of the infection and the limited empirical evidence for direct human-to-human transmission have led to the belief that infections in humans are predominantly caused by the inhalation of basidiospores from environmental sources. Therefore, analyzing the structure of environmental populations of C. gattii can significantly increase our understanding of its ecology, evolution, and epidemiology. In this study, we analyzed the population structure of northwestern Indian C. gattii samples obtained from: a) decaying wood in tree holloows of eleven tree species and b) soil underneather the decaying wood. Multilocus sequence typing was conducted using six gene fragments for each of 88 isolates. All isolates belonged to mating type alpha. Population genetic analyses identified significant differentiation among C. gattii populations belonging to both different geographic areas and different host tree species. These data suggest a widespread occurrence of C. gattii in the environment and a locally clonal population structure. **Contributed Presentation**

Hirooka, Yuuri1*, Kobayashi, Takao2 and Ono, Tsuyoshi.3 1Systematic Mycology & Microbiology Laboratory, USDA-ARS Room 330 B011A, 10300 Baltimore Ave., Beltsville, MD 20705, USA, 2Department of International Agricultural Development, Tokyo University of Agriculture, Sakuragaoka 1-1-1, Setagaya-ku, Tokyo 156-8502, Japan, 3Tokyo Metropolitan Agriculture and Forestry Research Center, Fujimi-cho 3-8-1, Tachikawa, Tokyo 190-0013, Japan. Yuuri.Hirooka@ars.usda.gov. **A new nectrioid fungus and its Acremonium-like anamorph on Freycinetia boninensis from Japan.** In 2005, a peculiar nectrioid fungus and its Acremonium-like anamorph were found to cause a leaf blight of Freycinetia boninensis in Hahajima, Bonin Islands, Tokyo, Japan. The Bonin Islands are not connected to the Asian continent and are isolated from all landmasses. The result of this isolation has been the development of many endemic species similar to the better-known Galapagos Islands. The present fungus is characterized by having pale orange perithecia with conspicuous protuberances around the apex, no color change in potassium hydroxide and lactic acid, unitunicate ascii, spinulose ascospores and an Acremonium-like anamorph. This fungus produces pale orange perithecia and an Acremonium-like anamorph, similar to the Ijuhya, Nectriopsis or Lasionectria in the Bionectriaceae, Hypocreales, but it clearly differs from these three genera by its protuberances around the perithecial apex. The conspicuous perithecial warts that characterize this fungus are formed by the uneven, localized development of pseudo-parenchymatous cells of the perithecial apex. Similar development is found in species of Bionectria such as Bionectria lucifer and B. byssicola as well as Viridiospora penicillifera. However, the present fungus is clearly distinguished from these species by its anamorphs (Clonostachys in Bionectria and Penicillium in Viridiospora). Molecular phylogenetic analysis based on beta-tubulin genes also supports the morphological consideration. In these studies, this nectrioid fungus and its Acremonium-like anamorph were proposed as the monotopic species of a new genus in Bionectriaceae. **Poster**

Hodge, Kathie T. Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853, USA. kht1@cornell.edu. **Fungal biodiversity resources on the internet.** Ask a student how she does research for her term papers, or any lay person how he identified the stinky red fungus that appeared in the garden: Google is first on anyone’s list, including mine. We will talk about Google, Wikipedia, and an eclectic handful of websites that surface in Google searches. We will also look at some core sites that are not Google-bouyant, but should be. Information quality; classification system chaos; regionality; identification hazards: all these things will present themselves for examination in light of the range of users interested in fungal biodiversity. Lastly, we will talk about the usability of web resources, and speculate on the historical and future roles of the individualist in mycology. **Symposium Presentation**

Hodkinson, Brendan P.* and Lutzoni, François. Biology Department, Box 90338, Duke University, Durham, NC 27708, USA, bp@duke.edu. **Lichen-associated non-photobiont bacteria: The third symbiont?** Common knowledge dictates that the lichen thallus is formed solely by a fungus that develops a symbiotic relationship with an alga and/or cyanobacterium. However, many lichens are able to grow on extremely nutrient-poor substrates, raising the question of how they are able to maintain themselves without a substantial source of nitrogen and other crucial nutrients. Though non-photobiont bacteria have never been accepted as an essential part of the lichen symbiosis, the metabolic processes that they perform may play a vital role in providing the fungi and algae with necessary nutrients and facilitating interactions between them. Here we present evidence that certain non-photobiont bacteria may be crucial in the maintenance and evolution of the lichen symbiosis. As part of this study, both culture- and PCR-based surveys were conducted on lichen thalli in order to uncover the diversity of bacterial associates. Culture-based studies were conducted in the absence of molecular nitrogen, in order to isolate nitrogen-fixing bacteria for identification and characterization. For PCR-based analyses, we have developed several PCR primer sets that target 16S ribosomal sequences of nearly all Bacteria, but exclude sequences derived from chloroplasts and Cyanobacteria. PCR-based surveys were conducted using a fast new method known as RHPSA-D (Ribosomal Heterogeneous Amplicon Pool Sequence Analysis using Degenerate oligonucleotide-primer bias). Our analyses have revealed a number of interesting and potentially important bacterial lineages associated with lichens. We present several hypotheses concerning the role of non-photosynthetic bacteria in the development, maintenance, and evolution of lichen thalli in nature. **Contributed Presentation**

Hofstetter, V.*, Casieri, L., Viret, O. and Gindro, K. Agroscope Changins-Wadenswil Research Station, Case postale 1012, 1260 Nyon 1, Switzerland. valerie.hofstetter@acw.admin.ch. **The fungal community associated with esca symptomatic plants of Vitis vinifera: Multi-gene phylogeny and development of tef-1 based molecular probes for observation of the fungal community.** Numerous and systematically diverse fungi have been isolated from esca symptomatic wood of Vitis vinifera. The diagnosis of these fungi relies essentially on morphology and ITS specific probes. However the ITS-locus does not offer sufficient variation to unambiguously separate species of the genus Phaeoacremonium, a pioneer invader in the esca disease, nor does it allow the clarification of the systematic position of several mitosporic ascomycetes frequently present in symptomatic wood. Several of these species being also found in healthy vines, their shift from a saprotrophic/endophytic to a pathogenic behaviour suggests a desequilibration in the fungal community. To investigate the fungal community associated with esca symptomatic Vitis vinifera, we choose a sensitive cultivar (Chasselas, rootstock 3309) and isolated and characterized fungi growing from surface-sterilised wood. For frequently isolated ascomycetes we generated partial sequences for five loci (nucLSU, mitSSU, tef-1, RPB1 and RPB2) and combined these data with sequence data produced by the AFTOL project to infer their phylogenetic placement in the Ascomycota. The potential of the tef-1 gene in designing molecular tools for different systematic ranks was explored, not only in view of identification and quantification of particular species during the evolution of esca, but also in view of determining which orders and families compose the fungal community before and after symptoms appear. **Contributed Presentation**

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Hong, S.B.¹, Varga, J.¹, Frisvad, J.C.², Yaguchi, T.³ and Samson, R.A.²
¹Korean Agricultural Culture Collection, NIAB, Suwon, Korea, ²Centralbureau voor Schimmelcultures, Utrecht, The Netherlands, ³Center for Microbial Biotechnology, Biocentrum-DTU, Technical University of Denmark, Lyngby, Denmark, ⁴Medical Mycology Research Center, Chiba University, Chiba, Japan. sbhong@nda.go.kr. **Polypolyphonic taxonomy of Aspergillus section Fumigati and its teleomorph Neosartorya.** Aspergillus section Fumigati (AsF) (teleomorph Neosartorya) is a medically and agriculturally important group. We have studied the section Fumigati using a polypholyphonic taxonomic approach. Phenotypic characters including macro-, micro-morphology, growth temperature regimes and extolitile patterns, and genotypic characters including multiple-locus sequence typing (MLST) of partial β-tubulin, calmodulin and actin genes and RAPD-PCR were examined. MLST of partial β-tubulin, calmodulin and actin genes, growth temperature regimes and extolitile patterns were critical tools for the delimitation of AsF species, although morphological characters were also important to describe the species. The section now consists of 37 taxa: 10 strictly anamorphic Aspergillus species and 27 Neosartorya species. In this presentation, 37 species and their synonyms are listed and their taxonomic positions based on multilocus genes are presented. **Poster**

Horn, Bruce W.* and Dorner, Joe W. National Peanut Research Laboratory, USDA, ARS, Dawson, GA 39842, USA. bruce.horn@ars.usda.gov. **Effect of nontoxigenic Aspergillus flavus and A. parasiticus on aflatoxin contamination of wounded peanut seeds inoculated with agricultural soil containing natural fungal populations.** Peanuts and other seed and grain crops are commonly contaminated with carcinogenic aflatoxins, secondary metabolites produced by Aspergillus flavus and A. parasiticus. Aflatoxin contamination of peanuts in the field can be reduced by 77 to 98% with biological control through the application of nontoxigenic strains of these species, which competitively exclude native aflatoxin-producing strains from developing peanuts. In this study, viable peanut seeds were artificially wounded and inoculated with field soil containing natural fungal populations that were supplemented with conidia of nontoxigenic A. flavus NRRL 21882 and A. parasiticus NRRL 21369. Increasing soil densities of applied nontoxigenic strains resulted in an increase in the incidence of seed colonization by applied nontoxigenic strains, a decrease in seed colonization by wild-type A. flavus and A. parasiticus, and a decrease in aflatoxin concentration in seeds. Reduction of aflatoxins in peanut seeds depended on both the density and the aflatoxin-producing potential of native populations and on the fungal strain used for biological control. **Poster**

Hosaka, Kentaro. Department of Botany, National Museum of Nature and Science, Tsukuba, Ibaraki 305-0005, Japan. khosaka@kahaku.go.jp. **Molecular phylogenetics of the family Mesophilaceae.** The family Mesophilaceae (Hysterangiales, Phallomycetidae, Basidiomycota) is comprised of a number of truffle-like genera exclusively from the Southern Hemisphere (mostly from Australia). Most genera are characterized by having a powdery gleba, and because of this feature, the family has been classified in Lycoperdales, along with Lycoperdales and Geastraceae. A recent molecular study, however, showed that Mesophilaceae is most closely related to Hysterangiales in the order Hysterangiales. This was surprising because most taxa in the order possess a gelatinous to cartilaginous gleba. Furthermore, it is now clear based on the molecular data that Mesophilaceae sensu Zeller is polyphylectic. The type genus Mesophilia belongs to Hysterangiales, but Radiigera belongs to Geastrales, both of which belong to Phallomycetidae. The affinity of the genus Abstoma to other genera, however, remains uncertain. In this talk, we will examine results from multigene analyses of Mesophilaceae including all known genera of the family (Andebbia, Castoreum, Chordrogaster, Gummiglobus, Gumniwena, Malajzukia, Mesophilia, and Nothocastoreanum) and some taxa with uncertain affinity, such as Abstoma. Ecology and biogeography of Mesophilaceae will be discussed as well. **Contributed Presentation**

Hubbard, M.A. and Kaminskyj, Susan, G. W. Department of Biology, University of Saskatchewan, Saskatoon SK S7N 5E2, Canada. susan.kaminskyj@usask.ca **Rapid, tip-directed movement of Golgi equivalents in growing Aspergillus nidulans hyphae suggests a mechanism for delivery of growth-related materials.** Fungal Golgi equivalents (GEs) process and sort materials in the fungal secretory pathway. Despite the importance of localized secretion in fungal tip growth, GE behaviour in living hyphae has not been documented. We used an Aspergillus nidulans strain containing the predicted GE marker CopA:GFP in a hypA1 temperature sensitive polarity defective background (a gift of S. Assinder and A. Breakspear) to study GE distribution in growing wild-type and polarity-defective phenotype hyphae. CopA has been shown to have high homology to Saccharomyces cerevisiae alpha-COP1. Predominant CG localization of CopA:GFP was confirmed by inserting a tagged copy of the established Golgi marker alpha-2,6-sialyltransferase (ST-RFP) and finding a high degree of co-localization. As expected, the patterns of both markers became more diffuse following treatment with brefeldin A. We used CopA:GFP to study GE behaviour in growing A. nidulans hyphae using time-lapse confocal fluorescence microscopy. In wild-type A. nidulans hyphae, GEs were more abundant near hyphal tips than subapically, as had previously been shown with CopA:GFP in fixed cells. Aspergillus nidulans GEs move independently of each other, in all directions, but predominantly and more rapidly toward the hyphal tip. When hypA1 restrictive phenotype cells re-established polarity at 28°C, GEs moved preferentially into the newly formed branches. The average rate of upward GE movement was positively correlated with the ten-fold faster than the hyphal growth rate in the same cells. This relationship held under all experimental conditions tested. At 5 μg/mL, the actin inhibitor latrunculin B significantly decreased tipward GE motility and tip growth rate, whereas at 1 μg/mL, the microtubule (MT) inhibitor benomyl increased tipward GE movement despite decreased growth rate. The MT stabilizing drug, taxol, which we had previously shown to increase cytoplasmic MT number without affecting growth rate, increased tipward GE movement without affecting growth rate. The cytoskeletal basis for GE motility appears to be complex. Our data suggest a model for apical delivery of A. nidulans tip growth materials in which GEs play a role in long-distance transport. **Poster**

Hughes, Karen W.* and Petersen, Ronald H. Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA. khughes@utk.edu. **Can ribosomal ITS sequences be used as indicators of agaric fungal conspecificity?** With improvement of techniques for extracting and amplifying DNAs from soils and other substrates, studies assessing fungal community structure are becoming more common and produce a large number of largely unidentified environmental sequences. Such studies have used various estimates of sequence divergence ranging from 2% to 5% to delineate different species units. For the most part, however, these estimates are not based on experimental data and techniques for calculating sequence divergence are not given. We used two data sets to evaluate sequence divergence within agaric fungal species: 1) Sequence data from the All Taxon Biodiversity Inventory in the Great Smoky Mountains National Park (GSMNP); and 2) Sequence data from a monograph of the genus Megacollybia. Individual collections from the GSMNP were often heterozygous for indels and were cloned to recover haplotypes. Because individual basidiomata represent the product of matings, we assume that the haplotypes represent the same biological species. For this data set, selecting 0-2% ITS sequence divergence as indicating conspecificity accurately recovers 97% of paired sequences from the same organism. For the Megacollybia data set, data were evaluated on the basis of maximum vs. minimum sequence divergence and with and without gap coding. For minimum sequence divergence between species and no gap coding, a 2% estimate of conspecificity would accurately separate 96% of Megacollybia species. **Contributed Presentation**

Huhndorf, Sabine M.* and Lumbsch, H. Thorsten. Botany Department, The Field Museum, 1400 S. Lake Shore Drive, Chicago, IL, 60605, USA. shuhndorf@fieldmuseum.org. **MYCONET, a resource for fungi**

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gual classification. MYCONET is an electronic and printed journal that is devoted to the development of fungal classifications and at the present time is limited to ascomycetes. MYCONET irregularly publishes Notes on ascomycete systematics, and a periodically updated Outline of Ascomycota. The Notes offer information on new concepts at the genus level and above that may necessitate changes in the Outline. MYCONET continues the series of Notes and Outlines that began and ran for many years as hand copy in Systema Ascomycetum (1986-1998) and then moved to the internet and hard copy in 1999. Today, the Notes and Outline are published first electronically and finally available in pdf format which serves as the printed form of the journal. The mission of MYCONET is to continue to provide a place for researchers to go for current classification hypotheses that reflect the latest phylogenies based on molecular and morphological data generated by the mycological community. Symposium Presentation

Hustad, Vincent P.1,2, Methven, Andrew S.1, Meiners, Scott J.1, Pederson, Charles L.1 and Miller, Andrew N.1. Eastern Illinois University, Charleston, IL 61920, USA, 2 Illinois Natural History Survey, Champaign, IL 61820, USA. vphustad@eiu.edu. Analysis of terrestrial macrofungal communities in old-growth prairie groves. This study investigated communities of terrestrial macrofungi in Brownfield (26.1 ha) and Trelease Woods (24.5 ha), Champaign Co., Illinois. These woods are remnants of a larger, pre-settlement prairie grove now encircled by houses, fragmented forests, prairie and agricultural land. Although initially a virgin, deciduous upland forest dominated by oak, ash and maple with a high, closed canopy and fairly open (Brownfield Woods) to moderately dense (Trel ease Woods) understory, sugar maple is rapidly becoming the dominant tree species. Communities of terrestrial macrofungi and macrofungi inhabiting wood fragments <15cm diameter at each forest site were surveyed along twenty separate 100m permanent transects during the Fall fruiting seasons of 2006 and 2007. Over 100 genera of macrofungi were identified from Brownfield and Trelease Woods. Plant litter composition, site precipitation, and relative dominance of tree species were characterized at each site and used to analyze macrofungal diversity. Macrofungal community composition was found to be significantly affected by seasonality and forest division between sites. Correlations between macrofungal communities and environmental variables were examined. Indicator species for distinguishing within- and between-site effects were determined. Contributed Presentation

Hynes, M.M.1,2, Smith, M.E.2, Bledsoe, C.S.1 and Zasoski, R.J.1. Department of Land, Air, and Water Resources, University of California, Davis, CA 95616, USA, 2Falar Herbarium & the Dept. of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA. meg.hynes@gmail.com. Fungal hyphae associated with dominant tree species in the Sierra Nevada Foothills of California. Obtaining information on fungal hyphae in natural systems has been an arduous task for researchers. Recent improvements to harvesting of hyphae from soil have facilitated research in terms of fungal biomass quantification and genetic analysis in forest and woodland systems. Using new techniques, we are investigating the ectomycorrhizal hyphae associated with the four dominant tree species in the lower Sierra Nevada Foothills; these species are Quercus douglasii and wislizeni, and Pinus sabiniana and ponderosa. Hyphae were extracted from root restrictive sand bags. Molecular techniques such as DNA extraction, Polymerase chain reaction (PCR), cloning, and sequencing were employed to determine fungal species. Ectomycorrhizal fungal hyphae species predominantly found were Agaricales, Boletales, Pezizales orders as well as many from the Thelphereaceae family. More ectomycorrhizal fungal hyphae were found as basidiomycetes than ascomycetes. We also compared hyphal taxa found to root tip and fruiting body studies performed at the same field site. Of the 49 taxa found, 24 had been previously found as root tips and 10 as fruiting bodies. By understanding belowground aspects, such as the mycorrhizae associated with the oaks and pines in oak woodlands, managers may be able to enhance regeneration techniques of Quercus douglasii trees in California. Contributed Presentation

Jackson, Jason A.1,2, Vilgalys, Rytas1 and Richter, Daniel D.3. Department of Biology, 2Nicholas School of the Environment and Earth Sciences, Duke University, Durham, NC, USA. jai2@duke.edu. Land use change and the ecological succession of soil fungal communities. Old-field successional theory predicts that species richness, diversity, and function will increase as abandoned agricultural fields advance to mature hardwood stands. These measures often asymptote for plant communities in late successional forests. Fungal communities in soils may respond very differently. Here, ongoing studies of land use change in the South Carolina Piedmont are used to develop a concept of fungal succession. Specifically, soils from agricultural fields, pine forests, and remnant hardwood stands are used to generate molecular data from soil DNA libraries of ITS and SSU genes. Shifts in fungal communities are quantified using phylogenetic and multivariate methods. We infer that fungal communities are species rich in all successional stages, and that species identities shift greatly during the transition from open fields to forests. We discuss the impact that continued land use change may have on fungal communities in piedmont soils. Contributed Presentation

Jaklätsch, Walter1, Poldmaa, Kadri2 and Samuels, Gary, J.3. Faculty Centre for Systematic Botany, University of Vienna, Rennweg 14, A-1030 Vienna, Austria, 2Natural History Museum, University of Tartu, Vane-muse 46, EE-51014, Tartu, Estonia, 3United States Department of Agriculture, Agricultural Research Service, Systematic Mycology and Microbiology Laboratory, Rm. 304, B-011A, BARC-W, Beltsville, MD 20705, USA. wjaklah@uni.wien.ac.at. Reconsideration of Protocrea (Hypocreales, Hypocreaceae). The genus Protocrea is re-defined, based on holotype and recent collections of its type species P. farinosa. Morphology of teleomorphs and anamorphs and phylogenetic analyses of ITS, LSU, tef1 and rpb2 sequences suggest the existence of ca six species. The nontype species earlier described in Protocrea are not accepted in this genus. Species of Protocrea are characterized by perithecia formed in or on a subiculum, bicalculel ascospores that disarticulate at the septum while still in the ascus, by anamorphs belonging to Gliocladium s. str. and polyporiculous habit. For Hypocreafarinosa sensu auct., the new species H. decipiens is introduced. Hypocreapallida is recognized as a species of Protocrea. It is closely related to P. farinosa, morphologically, phylogenetically, and by habitat. The sistergroup of P. farinosa found in the USA is described as a new species. While these two species grow on Skeletocutis nivea, P. pallida has mostly been found on OligoporusTymoconies. The main differences among teleomorphs of Protocrea can be seen in pigmentation and KOH reaction of perithecia and subiculum. While P. farinosa is only known from Europe and the new species only from the USA, P. pallida is probably cosmopolitan. Poster

James, Timothy Y.1,2, Hull, Christina M.2 and Xu, Jianning.1 Department of Biology, McMaster University, Hamilton, ON, Canada, L8S 4K1, 2Department of Biomolecular Chemistry, University of Wisconsin, Madison Medical School, Madison, WI 53706, USA. ja-nest@mcmaster.ca. The molecular mechanism by which the mating-type locus controls uniparental mitochondrial inheritance in Cryptococcus neoformans. Mitochondria are typically inherited uniparentally from only one of the two gametes during sexual reproduction. Isogamous organisms without differentiated gametes (e.g., yeasts) may also display uniparental mtDNA inheritance, and the parent whose mtDNA will be inherited is controlled by the mating-type locus (MAT). The molecular mechanism by which MAT controls mtDNA inheritance is unknown, and may involve polarized cell growth or organelle migration or may involve the specific targeting and degradation of the mitochondria of one parent. We are attempting to distinguish these possible alternatives using the model pathogenic yeast Cryptococcus neoformans. Sexuality in C. neoformans borders on differentiated sexes, MATa and MATα, controlled by a nascent sex chromosome. In crosses of C. neoformans, mtDNA is inherited only from the MATa parent. The master regulatory homeodomain transcription factors Sxi1α and Sxi2a encoded by the MAT locus appear to coordinateately regulate uniparental inheri-
tance as disruption of either gene causes biparental mtDNA inheritance. Candidate genes whose expression is controlled by Sx1/tx/Sx2a have been identified using a whole genome microarray. The effects of genetic disruption of these genes on mtDNA inheritance will be studied using laboratory crosses and in situ hybridization to identify the timing and manner by which mtDNA of the MATa parent is selectively inherited.

**Contributed Presentation**

Janson, Eric M.1, Feeden, Emily R. and Abbot, Patrick. Department of Biological Sciences, Vanderbilt University, Nashville, TN 37235, USA. eric.janson@vanderbilt.edu. Phylogenetic and culture-based examination of the fungal symbiont of a plant galling midge. Tightly integrated symbioses between insects and microbes may frequently involve vertical transmission, strict specificity, and/or co-speciation—especially those that show consistent phenotypic variation within the context of the interaction. Here, we investigated if the phenotypic variation in gall morphology observed in a gall midge-fungal symbiosis could be attributed to genetic divergence of the fungal symbiont and strict specificity of the midge-fungus interaction. Isolates were obtained from the gall tissue of the four gall morphs of the Soldagea gall midge Asteromyia corticifera at two sites near Dayton, OH. DNA was extracted from 64 isolates and sequenced at three nuclear loci (ITS, LSU RNA, and EF-alpha) for identification and phylogenetic reconstruction. In addition, isolates were subjected to a battery of growth rate tests on different media to uncover phenotypic variation that may be uncoupled from any neutral genetic divergence. Haplotypes at all three loci were invariant across all isolates. Moreover, no significant differences were found among isolates for all growth rate tests. These findings suggest that, contrary to the traditional view of integrated symbioses, symbiont specificity in this interaction is low, horizontal transmission of the fungal symbiont may be common, and no co-divergence has occurred between midge and fungus. **Contributed Presentation**

Johnson, James E., Brady, Susan F. and Wagner, R. Steven. Department of Biological Sciences, Central Washington University, 400 East University Way, Ellensburg, WA 98926-7537, USA. jjohnson@cwu.edu. Phyloype diversity and amphibian saprolegniasis. Water molds, primarily in the genus Saprolegnia, have been implicated in large-scale mortality of amphibian eggs under a variety of environmental conditions. Although a number species infect amphibian embryos, the pathogens identified from die-offs or utilized in ecological studies of amphibian saprolegniasis are often identified only as Saprolegnia sp. or are assigned to one of three species (S. ferax, S. diclina, and S. parasitica). This lack of adequate identification makes it difficult to assess factors of host-parasite interaction that contribute to saprolegniasis in amphibians. To investigate diversity of Saprolegnia species associated with amphibian embryos, isolates were obtained from three species of amphibians and traditional morphological characteristics and phylogenetic analysis of the ITS region were utilized to evaluate both types of identification. Analysis of traditionally used morphological characteristics performed poorly and consistently underestimated the number of genetically distinct phylotypes found in the samples. Analysis of the diversity of ITS sequences suggested a number of morphologically cryptic, but genetically very distinct species occur associated with embryos of particular amphibian species. These data also suggest pathogens require precise identification because multiple phylotypes of water molds were isolated from all three amphibian species, but some phylotypes were isolated from only one of the three amphibian species.

**Poster**

Jonesen, Suzanne*, Lutzoni, François and Armaleo, Daniele. Department of Biology, Duke University, Durham, NC 27708, USA. suzanne.jonesen@duke.edu. Upregulated fungal genes in early lichen symbiosis. One fifth of all known fungi are obligatory symbiotic partners with either a green algae, a cyanobacterium, or both. We know nothing of the genetic or molecular mechanisms underlying the nutritional mode of either symbiont. Using the symbiosis between the fungus Cladonia grayi and the green algae Asterocloris sp., we have investigated differentially expressed genes in early lichen development. We used suppression subtractive hybridization to find up-regulated genes in C. grayi and Asterocloris sp. in vitro resynthesis. From this we chose candidate fungal genes from the early stages of lichen development to confirm differential gene expression using quantitative PCR. The results of these experiments will be discussed, and put into the context of putative roles in the lichen symbiosis. **Contributed Presentation**

Jurjetic, Zeljko1 and Peterson, Stephen W.2 1EMSL Analytical, Inc., Westmont, NJ 08108, USA, 2Microbial Genomics and Bioprocessing Unit, NCAUR, ARS, USDA; Peoria, IL 61604, USA. jjurjetic@emsl.com. Penicillium cyjetkovicii, a new species isolated from an air sampler in Northern California. An Anderson air sampler used in a building in Northern California yielded a Penicillium isolate that resembled P. roseopurpureum, but failed to grow or germinate at 5 C, a characteristic assigned to P. roseopurpureum. In order to determine whether the failure to grow was within species variation, we sequenced DNA from four loci, beta tubulin, calmodulin, ITS and lsu-rDNA and RNA polymerase beta. The sequences obtained from the California isolate were quite different from the homologous sequences from the ex type isolate of P. roseopurpureum and consistently showed this isolate to be distinct from P. roseopurpureum. Accordingly we have described and proposed the new species P. cyjetkovicii to accommodate this isolate. **Poster**

Kaminskyj S.G.W.1,2 and Gough, K.M.1 Department of Biology, University of Saskatchewan, Saskatoon SK, 2Department of Chemistry, University of Manitoba, Winnipeg MB. susan.kaminskyj@usask.ca. Using synchrotron FTIR to explore fungal cell biology. Filamentous fungi have been studied for well over a century, are the basis for major biotech industries, and are pre-eminent model systems with a diversity of impacts on humans and the environment. Many fungal genome sequencing projects are underway or completed, and a wealth of experimental tools have been developed. At the same time, the filamentous fungal growth habit, whereby extension is limited to hyphal tips and maturation to more basal regions, has constrained whole-cell composition analyses. We know the function and distribution of many gene products in considerable detail, but have much less information about fungal cell biochemical composition and its relationship to environmental factors. This is likely to be particularly important for cell walls, the interface between a fungus and its surroundings, which are targets for anti-fungal strategies. Synchrotron FTIR (sFTIR) spectroscopy is a new tool for exploring hyphal biochemical composition at high spatial resolution, based on infrared absorbance of characteristic bond types. sFTIR data are diffraction-limited to 3 to 10 μm, depending on the spectral region of interest. sFTIR spectra provide a detailed fingerprint of relative content that clearly distinguishes growing from mature hyphal regions, major taxonomic as well as single gene differences, and growth in optimal vs stressful environments. Most recently, we have been exploring developmental changes in maturing and germinating spores, and nutrient utilization of saprophytes vs endophytes. This has led to new information about metabolite use vs frugality in certain ecological niches and life cycle stages. **Symposium Presentation**

Kang, Hyan-Joo*, Zolan, Miriam E. and Bever, James D. Department of Biology, Indiana University, Bloomington, IN 47405, USA. hyunkang@indiana.edu. Intergenic spacer length measurement using fiber FISH in arbuscular mycorrhizal fungus, Scutellospora fulgida. Arbuscular mycorrhizal (AM) fungi are obligate symbionts of most terrestrial plants. They are very important ecologically, as they improve plant growth, promote plant community diversity, and increase the rate of plant succession. While there is no doubt of the importance these fungi have on plants and the ecosystem, their basic genetics are not well understood. For example, it is still unclear whether these fungi are homor heterokaryotic. Tests of genetic structure and processes depend upon polymorphic markers. The intergenic spacer (IGS) of the rDNA repeat, which has been found to be highly variable and useful as a genetic marker in other fungi, has not been characterized within AM fungi. Fiber flu-

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orescent in situ hybridization (FISH) was used to approximate the length of the IGS in Scutelllospora fulgida. The known rDNA unit repeat length of Coprinus cinereus was used as a control to estimate the unknown IGS length in S. fulgida. The IGS length in S. fulgida was estimated to be approximately 17 kb, while each rDNA unit repeat was around 22 kb. This is the first study to use fiber FISH on AM fungi. **Poster**

Kang, Seogchani*, Park, Bongsoo1, Park, Sook-Young1, Mansfield, Michele A.; Blair, Jaime E.; Geiser, David M.; Coffey, Michele M.; Ivors, Kelly1 and Martin, Frank.4 Dept. of Plant Pathology, Penn State University, University Park, PA 16802, USA, 2Dept. of Plant Pathology, University of California, Riverside, CA 92521, USA, 3Dept. of Plant Pathology, NC State University, Fletcher, NC 28732, USA, 4USDA-ARS, Salinas, CA 93905, USA, 5School of Agricultural Biotechnology, Seoul National University, Seoul, Korea. sxk55@psu.edu. **Phytophthora Database: A model cyberinfrastructure for pathogens.** Non-indigenous pathogens and variants of indigenous ones continuously threaten human and agricultural and ecological system. The rapid expansion of global commerce and human travel has greatly increased this threat. Given the pathogen movements across political boundaries and the interconnections among national economies, our response should also be coordinated with international partners. However, to date efforts to study and manage this threat have been fragmented, mostly regional, and limited to coping with immediate crises. Due to their virulence and ability to spread rapidly, *Phytophthora* is one of the most destructive groups of plant pathogens. Given the global nature of *Phytophthora* problems, efforts to map and document the diversity and distribution of *Phytophthora* worldwide and to share this information are essential to significantly improve our ability to track and manage *Phytophthora*. The goal of the *Phytophthora* Database project (http://www.phytophthoradb.org) is to archive genotypic and phenotypic diversity of *Phytophthora* in a highly integrative cyberinfrastructure that can easily be searched and updated. The database provides a number of data search, analysis and visualization tools to support identification and risk assessment of newly isolated *Phytophthora*. Geographic Information Systems tools will be incorporated to support the visualization of the distribution and change of *Phytophthora* species and their diseases across environmental, geospatial and temporal contexts. The database and associated tools can easily be adapted to create similar cyberinfrastructures for different plant or animal pathogen groups. **Contributed Presentation**

Kaonongbua, Wittaya and Bever, James D. Indiana University, Department of Biology, Bloomington, IN 47405-3700, USA. wkaonong@indiana.edu. **Interesting and undescribed species of arbuscular mycorrhizal fungi from the US grasslands.** During our work attempting to understand the range and distribution of taxonomic diversity of arbuscular mycorrhizal (AM) fungi by exploring the biodiversity of these fungal symbionts in grasslands of the US, we came across several previously undescribed species of AM fungi. Here we use both morphological (light microscopy and SEM) and molecular data to determine the taxonomic positions of two of these fungi. The first one is a putative *Acaulospora* (*Acaulospora* “knobby”) producing spores resembling those of members of Acaulosporaceae. Spore color is hyaline, sub-hyaline or occasionally pale yellow in water. Spores are potentially composed of 3 bi-layer walls: single spore wall and two germination walls. None of the walls react in Melzer’s reagent. The distinctive character of this species is the minute, round-tip knobs ornamenting the spore wall. The ml5U sequence of this species also indicates close affinity with other members of Acaulosporaceae. The second species (*Acaulospora* “red eyeball”) also produce spores resembling those of members of Acaulosporaceae. Spore color is reddish brown in water. Spores are potentially composed of 3 bi-layer walls: single spore wall and two germination walls. None of the walls react in Melzer’s reagent. The distinctive character of this species is the hyaline outer germination wall. The previous attempts at establishing a single-species culture of these fungi failed and thus all work described here was based on field collected specimens. **Poster**

Keirle, Matthew R.1,*, Hemmes, Don E.2 and Mueller, Gregory M.3 The Committee on Evolutionary Biology, University of Chicago, Chicago, IL 60637, USA, 2University of Hawaii, Hilo, HI 96720, USA, 3The Field Museum, Chicago, IL 60605, USA. mkeirle@uchicago.edu. **Investigating the allelic evolution of a compound microsatellite locus in the Hawaiian mushroom *Rhodocollybia laulaha*.** A population-level study of the Hawaiian mushroom *Rhodocollybia laulaha* is underway to investigate microevolutionary processes particular to the macrofungi. The development of genetic markers for this project has yielded a microsatellite locus (G28) which in combination with other markers tracks genets within the *R. laulaha* population and discerns intra-population level patterns. Seven G28 alleles have been recovered from 153 individuals. The G28 locus contains a tri-nucleotide, imperfect motif which permits examination of the relationships among alleles and allows for detection of potential size homoplasy within the repetitive element. Alignment of G28 allele sequence data across multiple unrelated individuals suggests that alleles of like size are homologous. A variety of gap coding methods are explored in the inference of allelic evolution. Some methods provide a clear pattern of allelic evolution while others yield equivocal results. Length differences between alleles appear to be the result of polymerase slippage at multiple positions in the repetitive element suggesting an intricate process of allelic evolution which might be sequential but not necessarily stepwise. Complex migration scenarios must be invoked to explain the current geographic distribution of G28 alleles if their evolution was in fact sequential. **Contributed Presentation**

Keller, Harold W.4, Kilgore, Courtney M., Everhart, Sydney E., scarborough, Angela R., Ely, Joseph S. and Pottorff, Charly. Department of Biology and Earth Science, University of Central Missouri, Warrensburg, MO 64093, USA. haroldkeller@hotmail.com. **Adventures in tree canopy exploration: The search for corticolous myxomycetes using the double rope climbing technique highlighted in the “Wild Chronicles” television series.** The double rope climbing technique is commonly used in research because all climbing gear can be carried in backpacks, both hands can be used to collect samples, and the climber can advance the rope higher in the tree canopy. A Big Shot slingshot was used to shoot a weighted throw bag attached to a slick line over crotches and branches usually at heights of 18 to 24 meters. Dress, gear and vertical climbing techniques are described here along with a hand-held foot loop used by female climbers. All students participated in a tree climbing school taught by professional arborist Charly Pottorff and passed the knot-tying test consisting of the Figure Eight stopper knot, Anchor Hitch, Blake’s Hitch (friction knot), and a series of Half Hitches. The buddy system was used where each climber was paired with a ground crew member instructed in safety procedures. Episode 318 of “Wild Chronicles” aired on some Public Broadcasting Stations as “Smoky Mountains Treetop Exploration” produced by National Geographic Television. Boyd Matson served as the host and narrator. Courtney Kilgore and Sydney Everhart demonstrated how to access, climb, and gather samples from the tree canopy. Financially supported by the National Science Foundation Award DEB-0079058 and 0343447, Discover Life in America 2001-26 and 2002-17, and National Geographic Committee for Research and Exploration 7272-02. **Contributed Presentation**

Kernaghan, Gavin4 and Patriniq, Glenn. Biology Dept., Mount Vincent University, 166 Bedford Hyw., Halifax, Nova Scotia, Canada B3M 1J6. gavin.kernaghan@msvu.ca. **Fungal communities associated with Cenococcum geophilum ectomycorrhizae in the eastern boreal forest.** The boreal forest is dominated by ectomycorrhizal (ECM) tree species. However, individual ECM root tips are also co-colonized by a wide variety of fungi other than the dominant symbiont. These include competing ECM species, endophytes and external saprophytes. Fungal species assemblages also vary among tree species, due to host-symbiont specificity. To reveal patterns in the diversity and specificity of ECM associated fungal communities, we analyzed root tips colonized by the ubiquitous Cenococcum geophilum on balsam fir, white spruce and
white birch in eastern Canada. ECM were collected from each host in mixed stands and the fungal ITS amplified. Following size exclusion from C. geophilum DNA, PCR products were cloned, sequenced and compared to GenBank references by maximum parsimony. The ECM of all 3 hosts supported diverse fungal communities and several taxa occurred on only one host. The majority of fungi detected were ascomycetes, with members of the Helotiales accounting for a large proportion of the diversity. Within the Helotiales, several commonly encountered sequence types remain unidentified, although they are similar to other un-named, root associated GenBank sequences. Species accumulation curves are non-asymptotic, indicating that more intensive sampling would reveal even greater fungal diversity.

Kerrigan, Julia*, Evans, Joshua, Hughes-Murphee, Sherri and Krodel, Anna. Dept. Entomology, Soils, and Plant Sciences, Clemson University, Clemson, SC 29634-0315, USA. jkerrig@clemson.edu. Fungal diversity in the Clemson Experimental Forest. A survey to document fungal species in the Clemson Experimental Forest is being conducted as a Creative Inquiry project. Creative Inquiry projects are undergraduate research studies that are intended to be intensive, discovery-oriented approaches to learning and promote reasoning, critical thinking, and communication skills. This research project is designed to introduce undergraduate students to the field of mycology, with emphasis on the importance of fungi in forest ecosystems and the identification of fungi with different tools. Since January 2007 fungi have been collected from a variety of forest types and locations in the Clemson Experimental Forest. Samples are being identified based on morphological characteristics and, when necessary, DNA sequences. Voucher specimens and records are being maintained and will be deposited in the herbarium at the Campbell Museum of Natural History at Clemson University. Thus far, most of the species identified have been macrofungi such as mushrooms and shelf fungi. This study is a starting point for documenting the fungal diversity in the Clemson Experimental Forest and an important addition to the preexisting species lists of flora and fauna.

Khidir, Hana1a, Eudy, Douglas M.1, Porras-Afario, Andrea1 and Herrera, Jose.1 1Department of Biology, 100 E. Normal, Truman State University, Kirksville, MO 63501, USA, 2Department of Biology, MSC03 2020, The University of New Mexico, Albuquerque, NM 87131-0001, USA. hkh467@truman.edu. Characterization of root-associated fungal communities inhabiting Bouteloua gracilis, Bouteloua eriopoda, Sporobolus cryptandrus, and Yucca glauca. Unlike the extent of research on plant-fungal interactions focused on vesicular arbuscular mycorrhizae (VAMs), knowledge about the ecological significance of non-VAM root-associated fungi (RAF) is limited. Recent research has shown that some RAF are necessary for the success of plants in harsh environments. Few studies have specifically examined how RAF communities vary between different species of plants coexisting in arid environments. We examined RAF communities inhabiting four common and co-occurring plants. Bouteloua gracilis, Sporobolus cryptandrus, and Yucca glauca were collected at six points along a 9km transect within the semiarid grasslands of the Sevilleta National Wildlife Refuge (SNWR; New Mexico). Bouteloua eriopoda plants were also collected within the same field site, but at a different time. The most common Operational Taxonomic Units (OTUs) from the grasses were sequences related to Phoma sp. and Ctinjelliis sp. Conversely, OTUs from Y. glauca greatly differed from the grasses with the major RAF identified as Fusarium sp., Alternaria sp., and Sporothrix sp. Regression analyses using Morisita-Horn and Sorensen qualitative similarity values of all pair-wise comparisons of OTUs within each plant species showed no significance and thus no effect of inter-plant distance on RAF community similarity.

Kilgore, Courtney M.*, Keller, Harold W., Ely, Joseph S. and Wilson, Stephen W. Department of Biology and Earth Science, University of Central Missouri, Warrensburg, MO 64093, USA. opsonize@hotmail.com. Variation in myxomycete species assemblages and richness related to pH of living trees and herbaceous prairie plants. One of the most important environmental parameters that influence myxomycete species distribution is the pH of the substratum. Although myxomycetes may have a wide range of pH tolerance, many have an optimal pH range. This study compared the myxomycete species assemblages of acidic trees with basic and circumneutral pH trees and herbaceous plants. The working hypothesis stated there was a significant difference in myxomycete species assemblages between acidic and basic plant species and that plant species with a circumneutral pH had the highest species richness. Seven acidic trees were studied: Picea rubens (pH 3.7 ± 0.05), Pinus strobos (pH 3.9 ± 0.36), Pinus echinata (pH 3.9 ± 0.88), Abies fraseri (pH 4.07 ± 0.06), Tsuga canadensis (pH 4.1 ± 0.08), Taxodium distichum (pH 4.6 ± 0.58), and Liriodendron tulipifera (pH 5.2 ± 0.49). Nine basic and circumneutral pH herbaceous plants and trees were studied: Cercis canadensis (pH 6.3 ± 0.51), Quercus alba (pH 6.7 ± 1.03), Fraxinus americana (pH 6.9 ± 0.35), Ulmus americana (pH 7.0 ± 0.28), Juniperus virginiana (pH 7.4 ± 0.27), Yucca spp. (pH 7.1 ± 0.51), Echinacea spp. (pH 7.4 ± 0.57), and Asclepias syriaca (pH 7.9 ± 0.88). Plants with circumneutral pH had higher species richness than basic or acidic plants. Unique species assemblages occurred on different plants. Supported by NSF DEB Award 0343447 and NGS Award 7272-02.

Kim, Min-Ji*, Kim, Jae-Jin, Choi, Yong-Seok, Lim, Young Woon and Kim, Gyu-Hyeok.1 Division of Environmental Science & Ecological Engineering, Korea University, Seoul, 136-701 Korea, 2National Institute of Biological Resources (NIBR), Environmental Research Complex, Incheon, Korea, kimmj@korea.ac.kr. Basidiomycetous decay fungi on logs of pine trees exposed in the forest land. The successional diversity of basidiomycetous fungi was established on Korean pine (Pinus koraiensis) and pitch pine (Pinus rigida) logs exposed on the forest floor. The fungal surveys were carried out three times after 18, 42, and 54 months of exposure. A total of 128 basidiomycetous isolates were obtained and grouped by their cultural morphology. For accurate fungal identification, traditional methods were complemented with molecular methods, including BLAST search on large subunit 28S rDNA sequences in GenBank and phylogenetic analysis. From the first survey, the isolation frequency and fungal diversity were more than two times higher from pitch pine than Korean pine. The dominant species from pitch and Korean pine logs were Phlebiopsis gigantea and Hypocnemium karstenii, respectively. From the second and third surveys, primary basidiomycetous species were significantly replaced by successive

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species, such as Hypoclinium eichleri, Phanerochaete velutina, Phlebia radiata, Rhizochaete sp., and Trametes versicolor. These results suggested that decay fungi have host preference according to the tree species or raw wood materials. Poster

Kirk, Paul M. CABI, Bakeham Lane, Egham, Surrey TW20 9TY, UK. p.kirk@cabi.org. Index Fungorum and the Catalogue of Life. The Index Fungorum is the global fungal nomenclator for which the Index Fungorum Partnership are the custodians. It contains the scientific (Latin) name applied to the organisms studied by mycologists (true fungi, protozoan fungi and stramenopiles), the authority for the name, where these names were published and, for recent names, information of the type collection and it geographical origin. Authors names are standardized against the recommended forms in Brummitt & Powell (Authors of Plant Names) and on-line additions, homotypic names are linked together, Code compliance is indicated and references to related names included in previous compilations are given. The Species Fungorum derives names from the Index Fungorum and applies a subjective taxonomic opinion, from a range of sources, to those names. The aim is to produce a consensus checklist of the world’s fungi – it is currently 43% complete – and contribute to the Species2000-ITIS Catalogue of Life. The Catalogue of Life aims to produce a consensus checklist of life on earth comprising AVC (Accepted/Valid/Correct) names and synonyms, with references, vernacular names and nominal distributional data. It is compiled from a federation of 52 databases and the 2008 Annual Checklist comprises 1,105,589 names and 461,182 common names.

Poster

Klich, Mareni, Tang, Sean1 and Denning, David. 2 USDA, ARS, Southern Regional Research Center, New Orleans, LA 70124, USA, 2Education Research Centre, Wythenshawe Hospital, Manchester M23 9LT, UK. Maren.Klich@ars.usda.gov. Potential involvement of aflatoxin and ochratoxin in ascgillus. Aspergillus is an increasingly important human pathogen. It is not known whether aflatoxin or ochratoxin could act as virulence factors for pathogenic species producing these toxins. We examined a number of isolates for toxin production in ‘near human’ conditions. Eight of the 21 aflatoxin-producing isolates screened produced aflatoxin at 37 °C on the general medium Yeast Extract Sucrose agar (YES). However, none of them produced toxin on Brain Heart Infusion agar (BHA), a medium that mimics human tissue. Five of the eight ochratoxin-producing isolates produced toxin at 37 °C on YES. Three of these isolates, including two A. alternata strains, produced toxin at 37 °C on BHA, indicating that this toxin is a potential virulence factor. Poster

Kretzer, Annette M., Bai, Shasha, King, Zachary R., Dunham, Susie M. and Burke, David J. 3 State University of New York, College of Environmental Science and Forestry, 1 Forestry Drive, Syracuse, NY 13210, USA, 3Oregon State University, Department of Forest Science, Corvallis, OR 97331, USA, 3The Holden Arboretum, 9500 Sperry Road, Kirtland, OH 44094, USA. kretzer@esf.edu. Molecular analysis of bacterial communities associated with Douglas-fir (Pseudotsuga menziesii) ectomycorrhizae from Oregon. We have designed a new 16S rDNA primer pair for the analysis of bacterial communities from ectomycorrhizae (ECM). Primers were tested on tuberculate ECM of Rhizopogon vinicolor and vesiculosa. Amplification success was low, but three 16S rDNA libraries were obtained that were dominated by sequences from the Alphaproteobacteria, Gammaproteobacteria, and Actinobacteria with some Bacteroidetes, Planctomycetes, Actinobacteria, and Verrucomicrobia present as well. Primers were also used to compare bacterial communities from non-tuberculate Douglas-fir ECM colonized primarily by Russula spp., Lactarius spp., and Tomentella spp. Cluster analysis of terminal restriction fragment length polymorphism (TRFLP) profiles indicated that there were different bacterial communities; however, the communities did not seem to be affected by the taxonomic identity of the ectomycorrhizal fungi. Multi response permutation procedures confirmed that bacterial communities were not significantly different between different fungal genera (P = 0.15), and observed community differences must therefore be driven primarily by other factors such as soil micro-heterogeneity and/or ECM developmental stage. TRFLP profiling and sequencing of cloned 16S rDNA genes indicated that Alphaproteobacteria were again particularly common followed by Gammaproteobacteria and Bacteroidetes. Contributed Presentation

Kroken, Scott, Milani, Nicolas, Wasmann, Catherine and VanEttten, Hans. Dept. of Plant Sciences, Div. of Plant Pathology & Microbiology, University of Arizona, Tucson, AZ 85721-0036, USA. kroksen@ag.arizona.edu. Origin and inheritance of a gene product necessary for pathogenicity of divergent Fusarium spp, on host plants in the Fabaceae that produce the phytoalexin pisatin. Polyphyletic fungal pathogens of pea all have the ability to detoxify the plant phytoalexin pisatin that otherwise wards off fungal infections. The enzyme pisatin demethylase (PDA) has been characterized in (Haemato)nectria haematococca MPVI (in the Fusarium solani species complex), and other ologos of encoding gene have been found in other Fusarium spp. that demonstrate the same biochemical activity, including closely related Neocosmospora (Haemato)nectria bonitoides and more distant Fusarium oxyssporum f. sp. pisii. The acquisition of this gene among these species has been attributed to recent horizontal gene transfer (HGT) events, due to their discontinuous distribution, the distinct coding and nucleotide bias compared to other genes in the genome of H. haematococca, and the presence of the PDA gene on a conditionally dispensable (CD) chromosome in H. haematococca. However, a comparison of the range of sequence divergences of orthologous genes in the genomes of H. haematococca and F. oxyssporum indicates that the divergence rates of PDA are consistent with vertical descent. Additionally, a gene genealogical analysis of these genes is consistent with descent from a common ancestor of Fusarium sensu lato. The genealogy also suggests that the gene originated by duplication and divergence from a paragolous P450 cytochrome oxidase that is part of an uncharacterized gene cluster, which is currently present in the genome of H. haematococca (and perhaps other Fusarium spp.). Therefore, a gene that is putatively used in the production of a secondary metabolite has been co-opted for a novel function of modifying an exogenous secondary metabolite of plant origin. This novel function allowed for the evolution of a new lineage of pathogens that may colonize a range of other species in the Fabaceae (bean family), as (-) pisatin is found in phylogenetically diverse and discontinuous lineages. The origin of this successful family of 20,000 plant species has been dated to 60 million years ago, which is within the range of the estimated origin of PDA. Thus, Fusarium spp. and Fabaceae have been in a co-evolutionary arms race that far predates the presence of these fungal pathogens of pea in agricultural settings. Alternative explanations will be discussed for observations that were previously invoked as evidence for HGT, including frequent gene loss among lineages of Fusarium, the endogenous variation in nucleotide and codon composition within genomes, and the origin of CD chromosomes and their inheritance at the population and species levels. In conclusion, these currently polyphyletic fungal pathogens of pea appear to have a monophyletic ancestor that evolved the ability to utilize one the largest plant families in terms of species and biomass as a food source. Contributed Presentation

Kropp, B. R.1 and Matheny, P. Brandon. 2 Biology Department, Utah State University, 5305 Old Main Hill, Logan, UT 84322, USA, 2Department of Ecology and Evolutionary Biology, 569 Dabney Hall, University of Tennessee, Knoxville, TN 37996-1610, USA. bkropp@biology.usu.edu. A preliminary phylogeny of the Inocybe geophylla complex from Europe and North America. Inocybe geophylla is one of the most widespread, toxic, and easily identified species of the ectomycorrhizal (ECM) genus Inocybe. Between two and nine varieties have been proposed based largely on color variation of fruit bodies. The species appears to lack host specificity, forming ECM associations with up to twelve genera of angiosperms and gymnosperms from North America and Europe. The most widely accepted European concept for this taxon comprises two varieties, var. geophylla and var. lilacina that are separable by fruit body color. The rather complex

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nomenclature of these varieties along with field observations, which indicate substantial phenotypic and ecological variation can be found within the two varieties, prompted a phylogenetic study of the *I. geophylla* complex. Results are presented from a preliminary phylogenetic analysis using material representing the two varieties of *I. geophylla* along with additional related species from North America and Europe. **Poster**

Krüger, Dirk*1, Hommel, Kerstin1, Arnold, Norbert2 and Tarkka, Mika.1 1UFZ, Helmholtz-Centre for Environmental Research, Department of Soil Ecology, Theodor-Lieser-Strasse 4, D-06120 Halle/Saale, Germany, 2Department of Bioorganic Chemistry, Leibniz Institute of Plant Biochemistry, Weinberg 3, D-06120 Halle/Saale, Germany. dirk.krueger@ufz.de. **Bacterial associates of bolete fruiting bodies.** The microbial communities inhabiting fruiting bodies of ectomycorrhizal fungi have gained little attention thus far, especially regarding functional characters of these assemblages. We expect bacteria to be a rich source of secondary metabolites, which is already established for Boletales (pigments) themselves. We have investigated the bacterial community on fruiting bodies of *Xerocomus badius* and *Xerocomus chrysenteron* (Boletales). These boletes are the substrate for parasitic mitosporic fungi of the genus *Sepedonium*. Hence, they present an opportunity to study the interactions and co-evolutionary trajectories of ectomycorrhizal mushroom, parasites, and bacteria in a multiparticle symbiotic association. Here we report first evidence on *Xerocomus chrysenteron* cultivable and non-culturable bacterial diversity, and present examples of antagonistic and synergistic actinobacterial-fungal interactions. **Poster**

Lauer, Carrie K.* and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. laure.carr@students.uwlax.edu. **Seasonal moisture effects on ectomycorrhizal communities of *Pinus ponderosa*.** Ectomycorrhizae are a mutualistic symbiotic association between the roots of plants such as forest trees and fungi. Trees, such as pines, are thought to grow poorly in the absence of their mycorrhizal symbionts, but few ectomycorrhizal communities are well characterized and how they change along moisture gradients is currently unknown. Monotypic stands of ponderosa pine (*Pinus ponderosa* Lawson) from sites in the transition zone between forests and shrub steppe in central Washington were selected for this study. These stands experience periods of extreme high and low soil moisture due to water available from spring melt and extremely low summer precipitation due to the rain shadow of the Cascade Range. Percent soil moisture was monitored and the ectomycorrhizal communities in these fairly ecologically uniform pine forests assessed. This research utilized both molecular methods and the identification of fruiting structures to characterize the biodiversity, species composition, and relative abundance of ectomycorrhizal fungi associated with pine. DNA sequences of the ITS region allowed the identification of a total of 54 different phylotypes associated with mycorrhizal pine root tips, including 13 genera of basidiomycetes and 11 genera of ascomycetes. However, sampling of fruiting bodies yielded representatives of only three ectomycorrhizal taxa during two years of sampling. During periods of extremely low soil moisture (<1%), the abundance of mycorrhizal root tips observed in samples declined and a large proportion of senescent root tips was observed. Although species richness was not significantly different over the growing period, major shifts in ectomycorrhizal community composition were observed in relatively short time periods. These data suggest that the ectomycorrhizal community structure for these sites is largely driven by seasonal moisture. **Poster**

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Lee, Hyang B.*1, Mun, Hye Y.1, Kim, Kyong M.2 and Kim, Hyo J.2 1Division of Applied Bioscience & Biotechnology, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 500-757, Korea, 2Department of Life Sciences, Seoul National University, Seoul 151-747, Korea. hblee@jnu.ac.kr. **Seasonal diversity of airborne fungi in oriental pear farms located in Naju, Korea.** This study was performed to investigate the seasonal diversity of airborne fungi in oriental pear (* Pyrus pyrifolia*) farms located in Naju, Jeonnam Province, Korea. From February 2007 to February 2008, the outdoor samples of airborne fungi were taken in two locations of the pear farms by opening the medium (PDA) plate lid for 10 to 30 min. The air plates were incubated at 23C for 7-14 days after sampling. Each isolate was identified based on the cultural, morphological characteristics and 18S and 28S ribosomal RNA gene analyses. *Alternaria, Cladosporium, Sporidesmium* and *Pleosporales* were the most prevalent airborne fungi, followed by *Aspergillus* and *Penicillium*. Some coelomycete fungi including *Phoma* and *Phomopsis*, and several genera such as *Leptosphaeria*, *Phaeosphaeria* and *Phaeosphaeriopsis* belonging to the order *Pleosporales* were also frequently detected in the air samples. In addition, our poster will consider the other minor fungal genera and show their morphological and phylogenetic diversities. **Poster**

Lee, Maria* and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. lee.mari@students.uwlax.edu. **Differentially expressed proteins in *Penicillium marneffei*, a thermal dimorphic pathogen of immunocompromised individuals in Southeast Asia.** *Penicillium marneffei* is a unique thermal dimorphic fungus initially causing pulmonary infection, which then disseminates to other organs among immunocompromised patients in Southeast Asia. It can be fatal if diagnosis is not done early with prompt treatment. The main objective of this research was to characterize some of the proteins produced by *P. marneffei* that effect dimorphism. *Penicillium marneffei* was cultured at 25°C (mold) and 37°C (yeast), processed in 2-D gel electrophoresis and sequenced via mass spectrometry. In addition, we also developed a mathematical program within Matlab to consistently select protein spots on 2-D gels based on their intensity measurements. Twenty-two protein spots were designated as a landmark or upregulated/downregulated when the fold increase of the intensity was near 1 or greater than 1, respectively. Proteins common to both the mold and yeast phase of *P. marneffei* were involved with general metabolism and signal transduction. Many of the proteins upregulated in the yeast phase were involved with stress response vital for survival within the host macrophages. One of the most interesting proteins, highly upregulated in the mold phase, is a 55kDa immunogenic protein, with potential use as diagnostic marker or antifungal target. These data represent a contribution to a molecular-based understanding of dimorphism in *P. marneffei*. **Contributed Presentation**

Lefevre, Emilie*, Letcher, Peter M. and Powell, Martha J. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487, USA. letch006@bama.ua.edu. **Ecological roles of chytrids in aquatic communities.**

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systems: use of a new molecular technique, the qPCR. Despite their ubiquity in aquatic systems, chytrids, which possess few distinctive morphological features for identification using conventional microscopic techniques, have been ignored in studies that proposed models of the microbial food web. In light of recent microbial ecological studies, molecular approaches seem to be a promising way to assess in situ diversity and abundances of such conspicuous microorganisms. In this context, the present work will focus on the development of a sensitive molecular technique, the quantitative PCR, for the identification and quantification of chytrid zoospores in lakes. To this end, three lakes (Lakes Tuscaloosa, Nicol and Lurleen) situated in the Black Warrior River Basin of Alabama and differing in their trophic status were seasonally sampled by (1) chytrid isolation, (2) in situ genomic DNA extraction, and (3) measurements of physico-chemical and biological parameters. Ribosomal RNA genes from chytrids cultured will provide a reference database for primer design, qPCR optimization and characterization of chytrid diversity. Comparison of the results obtained by qPCR with other physico-chemical and biological parameters of the lake will provide a better understanding of the ecological role of chytrids in lakes and their interaction with other components of the microbial food web.

**Contributed Presentation**

Letcher, Peter M.*, Powell, Martha J. and Churchill, Perry F. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487, USA. leetch006@bama.ua.edu. *Rhizophlyctis rosea finds a new home in Chytridiomycota. *Rhizophlyctis rosea* (Chytridiomycota) is an apparently ubiquitous soil-inhabiting, cellulose-degrading chytrid that is the type for *Rhizophyctis*. Previous studies have revealed multiple zoospore subtypes among morphologically indistinguishable isolates in the *R. rosea* complex sensu Barr. In this study we analyzed zoospore ultrastructure and combined nuclear rRNA gene sequences (partial LSU and complete ITS1-5.8S-ITS2) of 49 isolates from globally distributed soil samples. On the bases of molecular monophyly and zoospore ultrastructure, this group of *Rhizophlyctis rosea*-like isolates is designated as a new order, the Rhizophyctidales. Within the Rhizophyctidales are four new families (*Rhizophlyctidaceae*, *Sonoraphlyctidaceae*, *Arizonaphlyctidaceae*, and *Borealophlyctidaceae*) and three new genera (*Sonoraphlyctis*, *Arizonaphlyctis*, and *Borealophlyctis*). **Contributed Presentation**

Li, Mochan. Life Science Building, 1280 Main Street, West Hamilton, Ontario, Canada L8S 4K1. lim7@mcmaster.ca. Genetic diversity of *Russula* sp. nov. from China. *Russula* is one of the larger known genera of ectomycorrhiza-forming basidiomycetes. It has been previously identified in the US and Europe. Not many species have been documented from Asia. Our study is interested in resolving phylogenetic relationships of *Russula* species collected from Southwest China. Multiple molecular markers, such as specific rRNA ITS, LSU, RPB2, etc., are applied to identify the phylogeny of the isolates from this study and how they are related to known species. If novel species could be identified, then both morphological and molecular methods are applied in order to fully characterize new species. Within population study can also be done within the AL group. A genomic library of *Russula* is constructed using short-gun cloning method, and then sequence-specific primers, which are designed towards individual fragments, are used to amplify the rest of strains within the AL population. Finally single nucleotide polymorphisms (SNP) can be identified by either comparing sequences among different AL strains or by examining restriction length polymorphisms. SNP are valuable genetic markers for strain-specific genotyping. **Poster**

Lindner, Daniel L.*, Banik, Mark T. and Ortiz-Santana, Beatriz. US Forest Service, Northern Research Station, Center for Forest Mycology Research, One Gifford Pinchot Drive, Madison, Wisconsin 53726, USA. dlindner@wisc.edu. Molecular phylogeny of the genus *Wolfiporia*. The genus *Wolfiporia* is comprised of resupinate polypore species that produce brown-rots in a variety of conifer and hardwood species throughout many areas of the world. The most well-known species in the genus, *W. cocos*, produces large, edible sclerotia (“tuckahoes”) that are highly valued in traditional Asian medicine. To investigate relationships within *Wolfiporia*, the nuclear large subunit (LSU) and intergenic spacer region (ITS) of ribosomal DNA were sequenced from three species of *Wolfiporia: W. cartilaginea*, *W. cocos* and *W. dilatohypha*. Based on analyses of LSU sequences, the genus is polyphyletic. Although all three species fall in the “Antrodia clade” of polypores, *W. cartilaginea* and *W. dilatohypha* are closely related to *Laetiporus*, while *W. cocos* is not closely related to any species for which data are available. LSU sequences from *W. cocos* fell into three distinct clades: one containing collections from Japan, China, the Dominican Republic and Malawi; one containing collections from the western US; and one containing collections from the eastern US. Further work is needed to delineate species within the *W. cocos* complex, although this may be hampered by multiple insertion events in the ITS region. **Poster**

Liu, M.*, Hambleton, S. and Tropiano, R. Biodiversity (Mycology and Botany), Agriculture & Agri-Food Canada, 960 Carling Ave. Ottawa, ON K1A06C, Canada. liumi@agr.gc.ca. Molecular detection and identification of yellow rust (*Puccinia striiformis*) by Taqman real-time PCR. In recent years, the incidence of yellow rust of wheat has increased drastically in USA and Canada causing major losses. Early detection and identification of the pathogen in certain regions is important for control of the disease. However, morphological identification of this fungus can be challenging. DNA sequence data suggested that a high percentage of specimens from multiple herbaria labeled as *P. striiformis* were not correctly identified, therefore the use of DNA sequence-based techniques for detection and identification of *Puccinia striiformis* became particularly important. In the present study, we designed Taqman real-time PCR probes and primers based on protein coding genes and developed assay protocols. The assay sensitivities were tested on 10-fold serial dilutions of a DNA extract from pure urediniospores. Assay specificities were evaluated on more than 20 *P. striiformis* specimens and a broad sampling, both geographically and taxonomically, of rust fungi occurring on cereal crops and other grasses. The technique proved to be sensitive for the detection of stripe rust infections and could be used for identification of the pathogen in environmental samples. **Poster**

Lodge, D. Jean¹, Laessoe, Thomas², Aime, M. Catherine³ and Henkel, Terry.¹ US Department of Agriculture, Forest Service, Northern Research Station, Center for Forest Mycology Research, PO Box 1377, Laquillo, PR 00773-1377, USA. ²Dept. of Biology, University of Copenhagen, Universitetsparken 15, DK-2100 Copenhagen, Denmark, ³Dept. of Plant Pathology and Crop Physiology, Louisiana State University Agricultural Center, 302 Life Sciences Bldg., Baton Rouge, LA 70803, USA, 4Dept. of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA. maime@agcenter.lsu.edu. Meta-analysis of rare neotropical Xylariaceous fungi to detect cloud forest specialists endangered by climate change. We compared records of 121 neotropical *Xylaria* taxa from Belize, Ecuador, the Guianas, Mexico, Puerto Rico and Venezuela in order to determine if there were tropical montane or cloud forest specialists that might be endangered by climate change. All of the global climate change models indicate increased drought in the Caribbean. Lifting of the cloud base has also been indicated in Central America and the Andes. Determining habitat specialization is difficult for rare species as detection is an issue, so we focused on widespread species recorded in two or more countries. Three widespread but rare neotropical montane specialists were strongly indicated. An additional seven widely distributed *Xylaria* taxa occurred primarily in montane forests and might also be affected by climate change. Another 28 species reported from only one country probably includes additional montane specialists, indicating that these species may be adversely impacted by climate change, but their risk is difficult to evaluate. Foliicolous and fruit inhabiting species were overrepresented among montane species as compared to their representation among all taxa. *Xylaria* taxa on fruit and leaves are frequently host-specific while those on wood are not. Host-specialization may be an additional risk factor among *Xylaria* species restricted to cloud forests. **Poster**

Continued on following page
The Tree of Life Web Project (http://tolweb.org) (Tol.) is a collaborative effort by biologist providing a collection of information, available over the Internet, about the evolutionary history and diversity of life on Earth. The current data is available in about 9000 web pages, each illustrating and discussing an individual species or a group of many species, linked together in the form of the evolutionary tree of life. Its goal is to contain information on every clade and species of organism, living and extinct, as well as proposals on their origin and relationships. There are currently over 600 biologists in more than 20 countries contributing to the project. An overview of the Tree of Life Web Project will be presented, beginning with its current design and content, with a focus on Fungi, and a discussion of successes and failures. Plans for the future of the project, including integration with the Encyclopedia of Life, will be emphasized. Symposium Presentation

Maldonado-Ramírez, Sandra L.1,*, Kauffman, Frank 1, Oliver, Jeffrey 2,3, Miadlikowska, Jolanta 1, Lenards, Andrew 2 and Maddison, David. 2 Department of Biology, Duke University, Durham, North Carolina, USA, 3Department of Entomology, University of Arizona, Tucson, Arizona, USA, 4Department of Ecology and Evolutionary Biology, Yale University, New Haven, Connecticut, USA. flutzoni@duke.edu. Past, present, and future of AFTOL phylinformatics. This presentation will focus on phyloinformatic tools that have been developed for all fungal groups covered by AFTOL and used downstream of phylogenomic data mining and data processing – i.e., tools developed within and around WASABI. An update on the alignments of all sequences generated by AFTOL-1 together will all fungal sequences of loci selected for AFTOL-1 that are available in GenBank will be presented, along with a description of the concept developed for the management of these alignments, their phylogenetic analysis, and tools developed within Mesquite to visualize the resulting trees. A description of the WASABI-Mesquite environment developed for the AFTOL-2 project will be presented along with long-term goals of the WASABI-Mesquite interconnectivity for large-scale phylogenetics. Symposium Presentation

Maddison, David R. Department of Entomology, University of Arizona, Tucson, Arizona, USA, 3Department of Biology, PO Box 9012, University of Puerto Rico, Mayaguez Campus, Mayaguez, PR 00681-9012, USA, 2Department of Chemistry and Biochemistry, Brigham Young University, Provo, UT 84602, USA. smaldonado@uprm.edu. Molecular and metabolic dissection of the novel Arabidopsis-endophyte. A recent survey of root colonizing endophytes at Konza Prairie, a native tallgrass prairie, has shown that plant endophytes are equally or more abundant than arbuscular mycorrhizal fungi. Endophytic isolates of A. fumigatus, P. janthinellum, and Trichoderma reesei inhibited the growth of various unknown endophytic bacteria but formed biofilms with the same bacteria on sterile filters. We also analyzed fungal extracts using HPLC techniques, mass spectral analysis, and antibacterial testing. Due to the low concentration of the compounds we were unsuccessful in characterizing the compounds. Poster

Mandyam, Keerthi* and Jumpponen, Ari. Division of Biology, Kansas State University, Manhattan, KS 66506, USA. kgm9595@ksu.edu. Molecular and metabolic dissection of the novel Arabidopsis-endophyte. A recent survey of root colonizing endophytes at Konza Prairie, a native tallgrass prairie, has shown that plant endophytes are equally or more abundant than arbuscular mycorrhizal fungi. Endophytic isolates of A. fumigatus, P. janthinellum, and Trichoderma reesei inhibited the growth of various unknown endophytic bacteria but formed biofilms with the same bacteria on sterile filters. We also analyzed fungal extracts using HPLC techniques, mass spectral analysis, and antibacterial testing. Due to the low concentration of the compounds we were unsuccessful in characterizing the compounds. Poster

Manoch, Lek, Jeamjitt, Ounma, Dethoup, Tida, Kokaew, Jitra and Eamvijarn, Amnat. Department of Plant Pathology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand. agrilkm@ku.ac.th. Hyphomycetes from soil, fallen leaves and dung in Thailand. The purpose of this research was to study diversity of Hyphomycetes from soil, fallen leaves and dung from various locations. Different isolation methods such as the moist chamber, direct isolation, Wurzig’s direct plating, dilution plate and heat and alcohol treatment were used. Glucose ammonium nitrate agar, half strength potato dextrose agar (1/2 PDA), 2% malt extract agar and water agar were employed. Identification of the fungal isolates was based on morphological characteristics of colony growth on agar media and examination of the spores and fruiting bodies using stereo, light and scanning electron microscopes. Eighty-three isolates comprising 36 genera and 41 species of Hyphomycetes were recorded. Soil fungi were Alternaria plumipes, Arthrinium phaeospermum, Cladosporium cladosporioides, Curvalaria lunata, C. tuberculata, Gilmaniella humicola, Humicola grisea, Mammaria echi-
nobotyroides, Memnoniella echinata, Myrothecium cinctum, M. roridum, M. verrucaria, Nigrospora oryzae, Phialophora cyclaminis, Pithomyces maydics, Scopulariopsis brevicaulis, Scytalidium lignicola and Stemphylium sarcoforme. Fungi isolated from various fallen leaves were Arthrinium phaeospermum, Bipolaris maydis, Beltranihuma rhombica, Cladosporium cladosporioides, Curvularia eragrostidis, Ellipsopis gallesiae, Gilmaniella humicola, Helicomyces, Humicola grisea, Memnoniella echinata, Myrothecium verrucaria, Nigrospora sphaerica, Periconia digitata, Stachybotrys nephropora, S. kampanensis, Tetraploa aristata, Torula herbarum and Wiesenertomyces javanicus. Coprophilous Hyphomycetes from cow, deer, eld’s deer, goat and toad dung were Arthrobotrys oligospora, Cephalophthora irregularis, Nodulosporium gregarium, Oidiodendron griseum and Pithomyces karoo. **Poster**

Mansfield, M. A.; Balci, Y. B.; Kim, S.; Park, S.Y.; Jones, H.J.; Hong, S.; Blair, J.; Coffey, M.; Geiser, D. and Kang, S. The Pennsylvania State University, Dept. Plant Pathology, University Park, PA 16801, USA. West Virginia University, Division of Plant and Soil Sciences, Morgantown, WV 26506, USA, Pennsylvania Department of Agriculture, Bureau of Plant Industry, Harrisburg, PA 17120, USA, National Institute of Agricultural Science and Technology and National Institute of Agricultural Biotechnology, Rural Development Administration, Suwon 441-707, Korea. Amherst College, Dept. of Biology, Amherst, MA 01002, USA. Department of Plant Pathology and Microbiology, University of California, Riverside, CA 92521, USA, man203@psu.edu.

**Cyber-sleuthing in the 21st century to protect US agriculture and ecosystems:** Using an online platform to identify and monitor the plant pathogenic genus *Phytophthora*. The identification, management and tracking of existing and emerging plant diseases has become increasingly difficult with the rapid exchange of agricultural commodities and human movement. To competently manage existing and emerging diseases across global boundaries and within the US, it is important to coordinate efforts via an efficient information exchange platform. The plant pathogenic genus *Phytophthora* includes several notorious species that have historically shaped the development of policies that control horticultural and agricultural commerce within the US and globally. To support the rapid diagnosis of *Phytophthora* species and to make that information available to a world-wide community, an initiative was taken to develop an online, publicly available forensic database of *Phytophthora* species. This presentation will use examples to illustrate how the *Phytophthora* database (PD) has assisted in the identification of novel *Phytophthora* species from natural and agricultural environments and describe how data from the PD has been used to determine evolutionary relationships among these potentially destructive plant pathogens. This study was supported by the USDA-NRI Plant Biosecurity Program (award number 2005-35605-15393). **Contributed Presentation**

Mardones, Melissa and Ibarra, Teresa. Departamento Biología de Organismos, Universidad Simon Bolivar, Venezuela, Apartado 89000. fungustyn@gmail.com. **Two new species of Strossmayeria (Helotiales) from Venezuela.** Two new species, belonging to the genera *Strossmayeria* (Helotiales, Helotiales) are reported from a cloud forest in El Avila National Park, Venezuela. They were found growing on bamboo and on an unknown monocotyledonous host. *Strossmayeria* species are almost always found in association with its *Pseudosporopipes* anamorph. They have tiny, turbinate, sub-stipitate to sessile apothecia. The genus is characterized by a + reaction under Melzer’s reagent of ascospores and ectal excipular tissues, a most unusual and particular characteristic. The new species are very distinct from previously described ones by their ascospore lengths, up to 110 µm, and number of septa. Between these two species there are differences such as excipular characters and ascospore amyloid reaction. As well there are differences in relation to the anamorphic states. **Poster**

Martin, W. Wallace; James, Timothy; Vilgalyas, Rytas and Longcore, Joyce. Randolph-Macon College, Ashland, VA 23005, USA, Department of Biology, Duke University, Durham, NC 27708-0338, USA. **Phytophthora describe how data from the PD has been used todetermine evolutionary relationship amongst these potentially destructive plant pathogens:** This study was supported by the USDA-NRI Plant Biosecurity Program (award number 2005-35605-15393).

Mata, Juan L. Murphy, Peter, Mayer, Ben and Pyakurel, Subha. Department of Biology, University of South Alabama, Mobile, AL 36688, USA. jmata@usouthal.edu. **Linear growth of worldwide Lentinula strains.** The shiitake mushroom, *Lentinula edodes*, is second to the button mushroom in terms of commercial importance. Five other extant morphological species in the shiitake complex are recognized: L. lateritia, L. niveoazelandiae, L. boryana, L. raphanica, and L. acuicullospora. Numerous physiological assays on *L. edodes* have been performed. Such trials include determination of growth curves with the intention of maximizing efficiency for mycelium production as a source of inoculum. Optimum growth rates have been determined for *L. edodes* and L. boryan – the American Shiitake – in certain synthetic media, but there are no publications for any such work that includes comparison of mycelium growth for species within *Lentinula*. Here, we present our results of linear mycelium extension for 14 strains representing five species of *Lentinula*. Strains were grown in five different synthetic media, in triplicate sets, at set temperatures of 15, 20, 25, 30, and 35 C. **Poster**

Matheny, P. Brandon and Hibbett, David S. Biology Department, Clark University, 950 Main Street, Worcester, MA 01610, USA. pmatheny@clarku.edu. **Historical patterns of diversification in the Inocybaceae, a cosmopolitan family of ectomycorrhizal fungi.** The Inocybaceae is only one of few ectomycorrhizal (ECM) clades of Agaricales with a worldwide distribution in major ectotrophic areas of the north temperate zone, North World tropics, Old World tropics of Africa and southeast Asia, and the south temperate zone. A relaxed molecular clock analysis combined with a secondary calibration procedure supports the hypothesis that almost all major lineages of the family were in place by the late Cretaceous, but that diversification did not rapidly proceed until the early Tertiary. This pattern of evolution is consistent with a “long fuse” diversification model shaped by the mass extinction event that occurred at the end of the Cretaceous. Between 25-28% of nodes receive significant support during the Paleocene and Eocene in contrast to 50-71% of nodes from the Oligocene onwards, a result consistent with an early Tertiary radiation. Diversification of the family, however, sharply decreased during the Oligocene, a period of dramatic global cooling and massive vegetational changes. This was followed by a recovery in diversification during the Miocene. **Contributed Presentation**

Mayor, Jordan R.; Schuur, Edward A.G. and Henkel, Terry W. University of Florida, Department of Botany, Gainesville, FL 32611, USA. jmayor@ufl.edu. **Fungal ecophysiology revealed: A global meta-analysis of sporocarp 13C and 15N isotope values**
tifies trophic roles regardless of ecosystem origin. Fungi perform keystone roles in terrestrial nutrient cycles through uptake of mineral nutrients by mycorrhizal and return of elements by saprotrophic (SAP) decomposition. Linking ecological roles to fungi is necessary to refine understanding of fungal ecophysiology and biogeochemical cycling. We analyzed published and original fungal nitrogen (delta15N) and carbon (delta13C) isotope values across multiple ecosystems to test if global differences among trophic groups could be used to identify fungi with unknown ecological roles. Inclusion of our novel dataset from a rain forest in Guyana bolstered comparisons of fungal isotope variability using multivariate and mixed model regression techniques. Collector based categorization of ectomycorrhizal (ECM) and SAP fungi were confirmed in 92.5% of 840 species (discriminant analysis). Additionally, predicted probabilistic classifications for fungi of unknown trophic status were achieved in fungi from boreal, temperate, and tropical ecosystems. The difference between ECM and SAP delta15N and delta13C values were of comparable magnitudes (6‰ and -2.2‰) across the 32 sites suggesting that fungal physiology is globally uniform. Combined, these findings support the use of stable isotope values to define ecological roles of fungi and provide a foundation for more advanced isotope-based applications in fungal ecology. Contributed Presentation

McDonald, Tami R.*, Armaleo, D. and Lutzoni, F. Department of Biology, Duke University, Durham, NC 27708, USA. trms@duke.edu. DNA methylation in lichen-forming fungus Cladonia grayi. CS DNA methylation is an epigenetic modification of cytosine that is associated with gene silencing in eukaryotic genomes and genome protection. Although DNA methylation is widespread in plants and animals, it is relatively rare among the fungi. When DNA methylation is present in fungal genomes, usually only repetitive elements or regions of foreign DNA are subject to methylation. However, DNA from lichen-forming fungi appears to be heavily methylated genome-wide (Armaleo and Miao, 1999). Interestingly, the DNA is methylated only when the fungus is in association with the alga, and is unmethylated when the fungus is grown alone, suggesting a link between lichenization and DNA methylation. We attempt to determine which genes or regions of DNA are subject to DNA methylation in a symbiosis-specific manner. We use Methylated DNA Immunoprecipitation (MeDIP), which allows methylated portions of the genome to be isolated. A library of putatively methylated genomic fragments from the fungal portion of the lichen Cladonia grayi was screened for fragments that were methylated in the symbiotic state and unmethylated in the aposymbiotic state. Candidate regions were further screened by southern blotting and bisulfite sequencing. Poster

McKay, Doni* and Smith, Jane E. USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR 97331, USA. dmckay@fs.fed.us. Investigating soil fungal recovery during the first two years after wildfire. Post-fire forest recovery is dependent on functioning soil fungal communities. We investigated the effects of burn severity on soil recovery by measuring fungal diversity (TRFLP), fungal communities (cloning and sequencing) and soil nutrients from a recent fire in the Cascade Range of Oregon. Soil samples were collected immediately after the fire and then in May, July, and October of 2004 and 2005. At each of 5 stands, 3-to-6 paired plots were established that included soils from the severely burned ”red soils” and from the less severely burned “black soils”. Long duration, smoldering conditions creating red soils altered both fungal species richness and soil nutrients. A single species in the Pezizales was detected immediately after fire and continued to be detected in most samples, regardless of fire severity, throughout the study. Approximately 100 TRF species have been detected. Of these, 12 species were detected in 15% or more of the samples in both red and black soils. Not surprising, sequence data show many TRF species are fire-loving Ascomycetes; our cloning efforts produced 36 different genera primarily in the Ascomycetes. At each sampling period, cumulative fungal species richness was slightly less in the red soils than in the black soils. Knowledge of post-fire soil recovery is essential to long-term forest management. Contributed Presentation

Mejia, Luis C.*, Castlebury, Lisa A.*, Rossman, Amy Y.*, Sogonov, Mikhail V.1 and White, James F.1 1Department of Plant Biology and Pathology, Rutgers University, 59 Dudley Road, Foran Hall, New Brunswick, NJ 08901, USA, 1Systemic Mycology and Microbiology Laboratory,USDA-ARS, Rm. 304, B011A, 10300 Baltimore Ave., Beltsville, MD 20705, USA. mejial@eden.rutgers.edu. Taxonomic and systematic studies on wood inhabiting fungi from the Gnomoniaceae (Diaporthales). The fungal family Gnomoniaceae (Diaporthales) has been traditionally considered to include genera with species that grow exclusively on leaves of herbaceous plants and hardwood trees principally from temperate zones of the Northern Hemisphere. However recent molecular data has shown that there are a number of species that infect woody tissues, currently excluded from the Gnomoniaceae on the basis of morphology, that are highly supported to belong to this family on the basis of multiple gene sequence analysis. This work presents a reviewed taxonomy and phylogenetic placement for available species from the genera Amphiploiothe, Ditopella, Cryptodiaporthe, and Cryptosporella, all of them known to occur mostly on woody tissues. We confirm the placement of the type species of these genera within the Gnomoniaceae and present phylogenetic analyses at the genus level based on multiple gene data analysis. Furthermore we will present information on the relationship between host identity and the speciation patterns and geographic distribution of these fungi. Poster

Mena Ali, Jorge I.1,2, Gibson, Amanda1, Oxelman, Bengt2, Antonovics, Janis3 and Hood, Michael E.1 1Dept of Biology, Amherst College, Amherst, MA 01002, USA, 2Dept of Plant & Environmental Sciences, University of Gothenburg, Sweden, 3Dept of Biology, University of Virginia, Charlottesville, VA 22904, USA. jmenaali@amherst.edu. The worldwide occurrence of the anther-smut fungus Microbotryum on species of the Caryophyllaceae as assessed from herbarium surveys. Invasion/infection of pathogens onto a new host can be affected by various traits of the host that limit the pathogen’s survival, reproduction and spread to more individuals in the population. The effect of these traits will in part depend on the life history of the pathogen, as well as its specificity and virulence. Microbotryum violaceum causes anther-smut disease in members of the Caryophyllaceae. Obligate pathogens with very restricting life cycles such as M. violaceum are expected to preferentially infect perennial host species. Here we greatly expand this hypothesis by surveying over 28 thousand herbarium specimens of Silene and allied genera of the Caryophyllaceae to determine the worldwide distribution of M. violaceum. These data was then examined for associations between the probability of infection and life history of the host, floral morphology, and breeding system. Our analyses expand the assumed range of the pathogen from an exclusively temperate Northern distribution to a worldwide presence, to include subtropical locations. These results are discussed in light of host distribution over a broad geographic range and the role of potential host shifts in dispersal at an inter-continental scale. Poster

Methven, Andrew S.*, Pederson, Charles L. and Hustad, Vinc P. Department of Biological Sciences, Eastern Illinois University, Charleston, IL 61920, USA. asmethven@eiu.edu. Site variation in corticolous lichen assemblages on sweet bay in coastal floodplain forests. Weeks Bay National Estuarine Research Reserve, a microtidal estuary located on the eastern shore of Mobile Bay in Alabama, embraces a variety of terrestrial habitats including coastal floodplain forests. Forests adjacent to Weeks Bay are dominated not only by deciduous species such as tupelo, water oak, live oak and sweet bay but gymnosperms including bald cypress, slash pine and longleaf pine. While some of the forests are relatively undisturbed, others have been negatively impacted by agriculture, timber cutting, and turpentine production. Although the effects of these disturbances on biotic communities within the reserve are largely unknown, a previous study of corticolous lichens in the reserve revealed that: 1) rather than considering all known lichen species in a community analysis, a subset of lichen species could be effectively utilized; and 2) it is more efficacious to examine a single sentinel tree species, sweet bay, along three permanent transects rather than all of the trees. Lichen as-
semblages were analyzed using multidimensional scaling (MDS) based on the Bray-Curtis Index of Similarity. Differences in lichen assemblages on sweet bay were determined with an Analysis of Similarity test (ANOSIM). Overall, corticolous lichen assemblages on sweet bay in the C-1 transect differed (p < 0.01) from those on the C-2 and R-1 transects but the C-2 and R-1 lichen assemblages did not differ significantly. Spatial homogeneity of lichen assemblages was observed on sweet bay in the R-1 and C-2 transects (both of which differed from C-1 sweet bay). 

**Contributed Presentation**

Miller, Bradley W.1 and Fox, Thomas R. 228 Cheatham Hall, Virginia Tech, Blacksburg, VA 24061, USA. bwmillergk@hotmail.com. **Phosphorus desorption in the ectomycorrhizal rhizosphere of lobolly pines.** Some ectomycorrhizal fungi secrete low-molecular-mass organic acids such as oxalate that have the potential to solublize P from mineral surfaces. Soils analyzed 28 years after fertilization suggest that the majority of P applied is now sorbed to Fe- and Al oxides with a small but significant increase in organic P. Recently, it has been suggested that the classification of ectomycorrhiza based upon morphology into “exploitation types” may be related to physiological adaptations of the symbionts to heterogeneous soil environments. We will present our results of the ectomycorrhizal rhizosphere (ER) on total P concentrations in a lobolly pine stand 28 years after fertilization. The ER of mature lobolly pines were collected and classified based on ectomycorrhizal exploitation types. Amorphous Fe- and Al oxides were analyzed using acid ammonium oxalate and citrate-bicarbonate-dithionite extractions. The total P concentration of the soil and the ER were compared using a K oxalate extraction procedure. Results showed that total P concentrations in the ER have been depleted in comparison to the non-ER soil. Exploitation types did not differ in the total P concentrations of the ER at 10 mM K oxalate. Results from these tests will advance our understanding of the ER on soil P pools in forest soils and the possible role of ectomycorrhiza in fertilized pine forests. 

**Contributed Presentation**

Minnis, Andrew M.1*, Sundberg, Walter J.2 and Methven, Andrew S.3 1Systematic Mycology & Microbiology Laboratory, USDA-ARS, Rm. 304, B011A, 10300 Baltimore Ave., Beltsville, MD 20705, USA, 2Department of Plant Biology, Southern Illinois University Carbondale, Carbondale, IL 62901-6500, USA, 3Department of Biological Sciences, Eastern Illinois University, Life Science Bldg. 2070, 600 Lincoln Ave., Charleston, IL 61920, USA. Drew.Minnis@ars.usda.gov. **Pluteus phaeocyanoalus sp. nov. from California, USA.** During our ongoing monographic studies of *Pluteus*, a eugonic genus found commonly on xyloidal substrates, *Pluteus phaeocyanoalus* sp. nov. was discovered. This distinctive fungus has a dark brown pileus and whitish stipe that becomes grayish green toward the base after bruising in a manner similar to *Pluteus salicinus*. Microscopically, the relatively narrow, lageniform pleurocystidia, brown pigmented lamellar cystidia, and cellular pileipellis lacking elongate cystidial elements characterize this taxon. *Pluteus phaeocyanoalus* occurs on dead *Quercus* logs and is currently known only from the San Francisco Watershed in San Mateo Co., California, USA. **Poster**

Money, Nicholas P. Department of Botany, Miami University, Oxford, OH 45056, USA. moneynp@muohio.edu. **Capturing the mechanism (and beauty) of fast movements in fungi: New work with ultra high speed video.** Fungi are the evolutionary champions of fast movement and use a variety of mechanisms to propel themselves into the air. Examples include the pressurized squirting of microscopic spores from cells called asci, the ejection of larger sporangia by the explosive eversio of a flexible membrane in the artillery fungus, and the intriguing surface-tension catapult that launches the spores of mushroom-forming fungi and their relatives. Because many of these processes occur at very high speeds, the most influential studies on fungal movements in the last century relied upon clever inferences rather than direct observation. In the last few years, technological advances in the area of high speed video microscopy have provided the first unambiguous information on the operation of these processes. This presentation will showcase experiments using this technology. **Symposium Presentation**

Moore, Geromy G.1,2, Horn, Bruce W.3, Elliott, Jacalyn L.1, Hell, Kerstin3, Chulze, Sofia N.4, Wright, Graeme5, Naik, Manjunath K.5 and Carbone, Ignazio5 1Department of Plant Pathology, North Carolina State University, Raleigh, NC 27606, USA, 2National Peanut Research Laboratory, Agricultural Research Service, U.S. Department of Agriculture, Dawson, GA 39842, USA, 3International Institute of Tropical Agriculture, Cotonou, Republic of Benin, 4Departamento de Microbiologia e Inmunologia, Universidad Nacional de Rio Cuarto, Cordoba, Argentina, 5Department of Primary Industries, Queensland, Kingaroy, Australia. **Meeting type**

**Contributed Presentation**

Morell Rodríguez, Gloriner4*, Román, Roberto, Ortíz, Miguel, Morales, Coral, Benítez, Alexander, Uzcategui, Julia and Maldonado Ramírez, Sandra L. Department of Biology, PO Box 9012, University of Puerto Rico, Mayagüez Campus, Mayagüez, PR 00681-9012, USA, smaldonado-do@uprm.edu. **Halotolerant endophytic fungal diversity in sea grass beds of Thalassia testudinum.** Prairies of *Thalassia testudinum* provide an essential habitat for economically important invertebrates, fishes, and endangered species. Although the productivity of sea grass beds is critical for the marine ecosystem, no previous studies have focused on the endophyte-host interaction. Our main objective was to identify fungal endophytes with the potential to provide *T. testudinum* an additional salt tolerance mechanism in the marine environment. Plants were collected
from sampling sites near the solar saltmerns and Buyé Beach (Cabo Rojo), La Pargueru (Laajas), and Vieques Island. Nine fragments (1cm²) from two surface-sterilized leaves from each plant were plated in Petri dishes containing Marine Agar amended with chloramphenicol, and incubated at 25°C for 7 days. We screened endophytic isolates from Cabo Rojo and Vieques able to grow only on Marine Agar supplemented with up to 12.5% sodium chloride. Isolates of Blastomyces dermatitidis and Gliocephalis hyalina required concentrations of at least 2.5% NaCl to grow whereas Cladosporium cladosporioides and C. oxycesrum grew at different concentrations of NaCl ranging from 1% up to 12.5%. This is the first report of B. dermatitidis as a fungal endophyte of T. testudinum and the first report of G. hyalina as a fungal endophyte and as a component of the marine environment. **Poster**

Mourino-Perez, Rosa R.¹, Roberson, Robert W.², Freitag, Michael¹ and Bartnicki-Garcia, Salomon.¹ ¹Departamento de Microbiología, Centro de Investigación Científica y Educación Superior de Ensenada, Ensenada B. C., Mexico, 'School of Life Sciences, Arizona State University, Tempe, AZ, USA, ²Department of Biochemistry and Biophysics, Center for Genome Research and Biocomputing, Oregon State University, Corvallis, OR, USA. rmourino@ciece.mx. **Nuclear dynamics in Neurospora crassa.** Nuclear movement and localization in fungi have been intensely studied over the last two decades. Here we report the results of a study to evaluate nuclear dynamics in the apical and subapical regions of Neurospora crassa hyphae. By confocal microscopy, the nuclear displacement of five strains that express histone H1-tagged with sGFP was compared. We included in this study mutants deficient in Mutator related motor proteins, rpy1, rpy3, nkin and ropy1/nkin double mutant and a wild type strain as control. Additionally, we treated the H1-GFP strain with benomyl to inhibit microtubule (Mt) formation and with cytochalasin A to inhibit actin filaments. In all strains, most nuclei advanced in antrangrade and retrograde movements of nuclei were observed in all strains, except the double mutant. The displacement rate of nuclei was highly correlated to hyphal elongation rate. The exception was the nkin mutant and cells treated with cytochalasin A. The shape of nuclei in growing hyphae was different: In the control, almost all nuclei were elongated, while in all other strains varying numbers of spherical nuclei were observed. The distance between the hyphal apex and the first nucleus varied between all strains and treatments. The rpy1 mutant showed the largest exclusion region and the cytochalasin A-treated cells completely lacked this nucleus exclusion zone. In conclusion, the movement and distribution of nuclei in mature hyphae appear determined by a combination of forces, with cytoplasmic bulk flow being a major determinant. Nevertheless, motor proteins bind nuclei to Mts and actin microfilaments appear to act as a scaffolding to move all components in unison with the cytoplasm. **Symposium Presentation**

Mugambi, George K.¹,² and Huhndorf, Sabine M.¹ Botany Department, The Field Museum, 1400 S. Lake Shore Drive, Chicago, IL 60605, USA, ¹University of Illinois at Chicago, Department of Biological Sciences, Chicago, IL 60607, USA, gmugam1@uic.edu. **Additional molecular systematics of the Coronophorales.** Taxonomic relationships within the Coronophorales have received varied treatments over the years. The order has been predominantly recognized as consisting of one family, the Nitschkiaceae, or comprising two families, Nitschkiaceae and Bertiaeaceae. Most recently at least three families were recognized within the order using sequence data from partial sequences of the ribosomal, large subunit, nuclear DNA (LSU). To confirm the monophyly of the families and to further assess generic circumscription within the group, a detailed taxon sampling representing a wide variety of genera was targeted for phylogenetic analyses using LSU and ribosomal polymerase II subunit 2. Four families, Bertiaeaceae, Cheterosphaerellaceae, Scortechinellaceae and Coronophoraceae are accepted in this study. The analyses show that the genus Scortechinia is polyphyletic. **Poster**

Mullaney, Edward J.*, Sethumadhavan, Kandan, Boone, Stephanie and Ullah, Abul H. J. Southern Regional Research Center, ARS, USDA, New Orleans, LA 70124, USA. ed.mullaney@ars.usda.gov. **Comparison of the catalytic properties of Aspergillus niger and Escherichia coli phytase.** Phytic acid (myo-inositol hexakisphosphate, InsP6) is a ubiquitous phosphate storage compound in plants. During germination and growth, plants employ an array of special phosphatases, phytases, to release the sequestered inorganic orthophosphates. With the increasing amounts of soybean and other plant meals in swine and poultry feed, a market for a phytase suitable for use as a feed additive has developed. This is because simple-stomached animals lack an effective phytase in their digestive system to hydrolyze phytic acid. Feed trials on a select group of phytases have demonstrated their efficacy in making phytin phosphate available to monogastric animals. This also benefits the environment by reducing phosphorus levels in the animals’ manure. The need for an effective phytase has been the subject of numerous scientific studies over the past four decades. Of all the enzymes characterized, only a few have the stability, high specific activity, and other required catalytic features to merit commercialization. A comparison of two native phytases adopted by the animal feed industry, A. niger PhyA and E. coli AppA2, highlights what properties are necessary for a marketable product. It is also instructive to know how knowledge-based modifications of these enzymes now have the potential to produce an enhanced biocatalyst animal feed additive. **Poster**
Murrin, Faye. Department of Biology, Memorial University of Newfoundland, St. Johns, NL, Canada, A1B3X9. fmurrin@mun.ca. Moose and mycorrhizal mushrooms. Moose (Alces alces andersonii) are native to much of Canada, but were introduced on to the island of Newfoundland in 1878 and again in 1904. The present populations of moose are densely distributed, particularly within the National Parks where hunting is prohibited. Within the boreal forest of Terra Nova National Park, moose browsing suppresses the regeneration of stands of Balsam Fir (Abies balsamea) previously disturbed by insect infestations. This has a significant impact on the landscape, reducing biodiversity within the Park.

In the present study, we investigated the impact of these disturbances on the ectomycorrhizal mushroom communities in Balsam Fir stands. As described earlier, fruiting bodies were collected in control and moose enclosure plots within five previously established study sites with different levels of past insect disturbance; species identifications and fruiting body numbers were recorded to determine species richness, frequency and similarity among plots and sites. This report will summarize our findings from a three-year study on the impact of moose on the mycorrhizal fungi and discuss some of the challenges involved in such a study. Poster

Nalim, F.A.*, Bettmann, G.T. and Sterling, T.M. Department of Entomology, Plant Pathology and Weed Science, New Mexico State University, Las Cruces, NM 88003, USA. FANALIM@NMSU.EDU. Swainsonine production in an endophyte-plant interaction using pipocic acid as a precursor. The antitumor agent swainsonine is an alkaloid found in several plant species including the locoweeds, Astragalus and Oxytropis, and in fungi such as Metarhizium and Rhizoctonia, and is responsible for neurological damage to cattle that feed on plants that contain the toxin. L-Popicic acid is an important precursor to many microbial secondary metabolites including swainsonine. Recent work has shown that the locoweed endophyte, Undulifilum, also produces swainsonine. The goal of this project was to determine if both the plant and the fungus synthesize swainsonine or if it is produced only by the endophyte. We investigated the production of swainsonine in locoweed with and without the endophyte using radiolabeled pipocic acid and non-radio-labeled pipocic acid in two parallel studies. Preliminary results of HPLC and UPLC-MS analysis of the samples indicate that the pipocic acid is being converted to swainsonine by the fungus when the fungus is in the plant. Further experiments to understand this pathway and the results will be discussed. Poster

Norvell, Lorelei L.* and Exeter, Ronald L.2 Pacific Northwest Mycology Service, Portland, OR 97229-1309, USA, USDI Bureau of Land Management, Salem, OR 97306-1720, USA. lnorvell@pnw-ms.com. Return to the elusive Phaeolocybilla 2. Oregon – the phaeolocybilla Eden? Although Phaeolocybilla species are rarely collected worldwide, the center of biodiversity for the mycorrhizal agaric genus seemingly resides in the temperate rainforests of Oregon. While preparing a full-color monograph of western North American phaeolocybillas to be published by the USDI-BLM in 2008, the authors collected or identified during a three month period over 400 collections representing 24 of 25 species known to the Pacific Northwest. The prolific 2007 autumn field season provided important insights for P. californica, P. gregaria, P. lilacifolia, P. phaeogaleroides, P. radicata, P. lateosquamulosa and its small-spored look alike, the newly described P. ochraceocana. One new locality brings to twelve the known sites in Oregon (9), Washington (1), and British Columbia (2) for P. oregonensis, infrequently collected and not yet verified from California or Idaho. Other Oregon phaeolocybillas collected in 2007 include P. ammiratii, P. attenuata, P. bentzkogafmannii, P. hirtellus, P. fallax, P. kauffmannii, P. olivaceus, P. piceae, P. pseudo-festiva, P. redbeadii, P. ruffipes, P. scatesiae, P. sipei, P. spadicea, P. tibikogafmannii, and the vernal P. pleuropolydota. The sole species not reported for the state is P. rufotubulina, now in need of further molecular analysis to determine its separation from the closely related and earlier described P. californica. Poster

Oliver, Jason P.* and Jellison, Jody. School of Biology and Ecology, University of Maine, Orono, ME 04469, USA. jason.oliver@umit.maine.edu. Inky cap wood decay physiology. Many of the inky cap species have been reorganized in the new genera Coprinopsis and Coprinellus in the family Psathyrellaceae based on phylogenetic research. Most species in this family are considered forest litter and debris decaying fungi. This restructuring warrants investigation into the wood decay physiology of the inky caps, which traditionally have been considered soil and dung fungi. The inky cap species are known to efficiently metabolize many hemicellulose polymers and results support this claim. Preliminary investigations suggest a preference for hardwood with the greatest percent of decay by the Coprinellus isolates. Differences between hardwood and softwood hemicellulose structure are likely responsible for the inability to decay sound softwoods. Physiological research focused on these fungi will support changes in taxonomy and will improve our understanding of the ecology of these fungi and the processes of forest litter and debris degradation. Contributed Presentation

Onyemachi, Felix C. Department of Science and Technology, University of The Gambia, P.O. Box 3530, Banjul, The Gambia. chiadikobi@yahoo.com. Mushroom-based nutriceuticals versus herbal preparations. A system of traditional medicine which is based on the belief and practices of the African people includes treatment using medicinal plants and mushrooms. Traditional preparation of medicinal plants involves the reduction of plant parts into powders, infusions and smoke or fumes. In addition to patient safety issues, there is the risk that a growing herbal market and its great commercial benefits might pose a threat to biodiversity through the over harvesting of the raw material for herbal medicines and other natural health care products. These practices, if not controlled, may lead to the extinction of endangered species and the destruction of natural habitats and resources. Mushrooms are highly treasured in African’s rural village communities. There is a rapidly growing interest in mushroom products as a source of high value dietary supplements, which have great potential for therapeutic applications. Several mushroom nutriceuticals have been shown to enhance host resistance in the treatment of various cancers, immunodeficiency diseases or immunosuppressant after drug treatment, as adjuvant for vaccines and for combination with antibiotics. The overwhelming majority of mushroom products used for production of nutriceuticals are cultivated commercially (not gathered from the wild). This guarantees proper identification, and pure and unadulterated products - in some cases it also means genetic uniformity. Mushrooms are easily propagated vegetatively, which safeguards clonality. Mushroom mycelia can be stored for a long time and genetic and biochemical consistency can be tested after a considerable time. Contributed Presentation

Onyemachi, Felix C. Department of Science and Technology, University of The Gambia, P.O. Box 3530, Banjul, The Gambia. chiadikobi@yahoo.com. The role of traditional knowledge in African traditional medicine. Large parts of the population in developing countries depend on traditional medicine and treatment for survival. Traditional medicine is practiced in different ways in different parts of Africa, but one characteristic feature of traditional medicine—wherever in Africa it is practiced— is the belief that serious illness can be caused by a supernatural agency, for example, ancestor spirit anger. It is a common belief in Africa that the spirits of the ancestors protect their living descendants. Divination and incantation play a role in Traditional African Medicine (TAM). Divination (the consultation of an oracle) is the diagnostic mechanism used in TAM to discover a hidden sin (ancestor spirit anger). The rituals that are undertaken to appease the angered ancestors are not initiated until confessions of the misdemeanors have been extracted from the ill patient. The rituals accompanying the use of herbal medicines are referred to as “incantation”. It is a collection of carefully chosen words used to bring out the healing effect of the medicine. The other common feature of traditional medicine in Africa is the widespread use of plant and animal parts for the preparation of medicines. The age of the plant being harvested is also an important factor. It is also important to know whether the medicinal parts of the plant should be prepared fresh from the plant, dried or squeezed. The time of the day
during which it is harvested is also taken into consideration. Some invoke the name of the gods when preparing their concoctions and use certain verses of the Quran when preparing certain herbs. **Contributed Presentation**

O’Reilly, Bernadette D.¹ and Vilgalys, Rytas. Duke University, Box 90338, Durham, NC 27708, USA. bdo2@duke.edu. **Interspecies dating**

**Armillaria and Entoloma involvement in carpophoroid formation.** *Armillaria* is a common fungal root rot pathogen that produces abundant fruiting bodies (honey mushrooms) and rhizomorphs. This fungus, in turn, has a fungal pathogen — *Entoloma abortivum*. *Entoloma* causes *Armillaria* to form aborted fruiting bodies called carpophoroids that are composed of tissue from both fungi. Since it is common to find normal fruiting bodies of both *Armillaria* and *Entoloma* juxtaposed with carpophoroids, it has been widely assumed that the species of *Armillaria* involved in the carpophoroids reflects the species generally found in that locality. This study designed genus specific primers to amplify the rDNA of both the *Armillaria* and *Entoloma* species within carpophoroids and then sequenced a portion of the LSU and ITS region. Phylogenetic analyses, including parsimony, maximum likelihood and Bayesian, were used to determine the species of *Armillaria* and *Entoloma* involved in carpophoroid formation across the geographical range of samples collected. **Contributed Presentation**

Ortiz-Santana, Beatriz ¹ and Lodge, D. Jean. ² Center for Forest Mycology Research, Northern Research Station. US-Forest Service, One Gifford Pinchot Drive, Madison, WI 53726-2398, USA. ³ Center for Forest Mycology Research, Northern Research Station, US-Forest Service, Laupillo, PR 00773-1377, USA. boritzsantana@fs.fed.us. **New species and records of Agaricus from the Greater Antilles and Virgin Islands.** *Agaricus* specimens from the Dominican Republic (10 collections), Puerto Rico (25 collections), and the islands of Guana (6 collections) and St. John (7 collections) in the Virgin Islands were studied using morphological and molecular data (rDNA ITS region). Collections fell into Sections Arvenses, Dupleanulati, Sanguinolentii and Xanthoderma, the latter with the highest representation. The identification of two collections of *A. roralis* from Puerto Rico was supported by morphological and molecular data. Sequence data placed some Dominican Republic collections close to *A. californicus*, *A. pocillator*, *A. subfloccosus* and *A. subrufescens*, although certain morphological characters differed from species descriptions. As many as 12 undescribed species may be represented among these collections from the eastern Greater Antilles (four from the Dominican Republic and five from Puerto Rico) and the Virgin Islands (two from Guana and one from St. John). **Poster**

Osmundson, Todd W.¹,² and Halling, Roy E.¹,² Institute of Systematic Biology and the Lewis B. and Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458, USA. ³Department of Ecology, Evolution and Environmental Biology, Columbia University, New York, NY 10027, USA. tosmundson@nybg.org. **Systematics of Tylopius (Boletaeae): Biogeographic and evolutionary insights.** As one of the largest genera in the Boletaceae, *Tylopius* is central to the classification of this family. Like other speciose bolete genera (e.g., *Boletus*, *Leccinum*), *Tylopius* as currently circumscribed is morphologically heterogeneous and appears to be polyphyletic in preliminary molecular analyses. Our study uses molecular (rDNA-LSU, atp6, EF1-a, RPB1) and morphological data to study systematic relationships in *Tylopius*, with the goals of (i) assessing its monophyly; (ii) evaluating the infrageneric classifications of previous authors; and (iii) examining relationships within several difficult species complexes. Due to the putative polyphyly of the genus, a broad sampling of *Boletus* and other Boletaceae was employed, including genera that have either been segregated from, synonymized with, or hypothesized to be closely related to *Tylopius* by some authors: *Porphyrellus*, *Austroboletus*, *Fistulinella*, *Rubinobolus*, and *Xanthoconium*. In addition, phylogeographic analyses of *T. balouii* were conducted to examine evidence of a widespread geographic distribution for this species. Results thus far do not support the monophyly of *Tylopius* as currently circumscribed, but instead support as monophyletic a core group of species centered around the type species *T. felleus* yet containing a broad array of morphologies. Likewise, previously-erected infrageneric groups do not represent monophyletic lineages. Based on the results of molecular and morphological examinations, an evaluation of the evolution and systematic utility of various morphological characters in the Boletaceae will be presented. **Contributed Presentation**

Osorio, Jhon A., Inácio, Carlos A. and Di Nancy, José C. Departamento de Fitopatología, Universidade de Brasília, 70910900 Brasília, DF, Brasil. jcarmine@unb.br. **Sphaero dothis species on leaves of Maprounea brasiliensis (Euphorbiaceae) from the Parque Nacional em Brasilia.** Small tar spots (ca. 0.3-0.7 mm diam), circular-elliptic, sometimes with reddish margins, isolated or coalescent, were observed on leaves of *Maprounea brasiliensis* (Euphorbiaceae UB 10.083). Sections using a freezing microtome revealed a *Sphaerodothis* species characterized by: *stromata* amphi genous, single or sometimes multiloculate, mostly epiphyllous; *ascosporas* 250-400 × 245-362 µm in cross section, mostly ovoid to spherical, periphrasate, paraphrasate; *paraphyses* 3-4 µm diam, hyaline, septate, branched; asci 59-102 × 9-19 µm, cylindrical to cylindric-clavate, 8-spored; *ascospores* 13-18 × 5-8 µm, uniseriate or sometimes biseriate, globose to ovoid, characteristic at first hyaline with gelatinous sheath but becoming brown, guttulate when hyaline. Apparently, *Phyllachora maprouneae* described by Hennings in 1904 is the same fungus, thus probably deserving a recombination into *Sphaerodothis*, a genus established five years later in 1909 by Shear. The only difference between the two materials is the fact that Hennings described only hyaline ascospores, however the dimensions and morphology of all structures are identical, thus indicating the need for a study of the type material before a final conclusion is reached. **Poster**

Padamsee, Mahajaben ¹, McLaughlin, David J. and the AFTOL2 working group. Dept. of Plant Biology, Univ. of Minnesota, St. Paul, MN 55108, USA. pada0003@umn.edu. **Morphology: Sampling strategy, integration with molecular data, and the development of ontologies.** One of the main objectives of AFTOL2 is to resolve the deep nodes of the fungal tree of life using subcellular and molecular characters. Subcellular structures such as the Spitzenkörper and meiosporangium are being studied to add to the considerable data collected from published and continuing studies of septa, spindle pole body, and nuclear division during AFTOL1. Taxa from basal fungal lineages and other key phyla are being targeted to trace transitional morphology and evolutionary events. Organisms examined for AFTOL2 will be presented as models for obtaining complete datasets. Integration with molecular data is being achieved by a coordinated sampling strategy to allow combined phylogenetic analyses. The AFTOL Structural and Biochemical database (SBD) serves as a resource and repository of subcellular characters but was initially developed as a static, albeit web-accessible database. In AFTOL2 the SBD will be reconfigured to work on an ontological basis. Structured, controlled vocabularies or ontologies are being developed in consultation with other fungal morphologists to make the data available and searchable from other databases. A full set of illustrated character states will be developed for the SBD. Various morphological image databases are being explored to ascertain ways to illustrate and store images of characters and states and to link these to the SBD. **Symposium Presentation**

Parrent, Jeri L.¹,² and Taylor, A.F.S.¹ Institute of Systematic Biology, University of Guelph, Guelph, Ontario, N1G 2W1, Canada. ³Department of Forest Mycology and Pathology, Swedish University of Agricultural Sciences, Uppsala 75007, Sweden. jparrent@uoguelph.ca. **Friend or foe? Evolutionary history of genes encoding sucrose utilization in fungi and its implication for fungal symbiosis.** Symbiotic fungi belong to a number of distinct ecological guilds that either share or differ in the benefit they confer to plant hosts. It is unknown whether functional trait conservatism among guilds of similar interaction type (e.g. mutualists) may explain similarity in symbiotic outcomes. One trait

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in which plant-associated fungi may vary is their ability to procure different forms of plant carbon. Culture-based studies have suggested that mycorrhizae cannot utilize sucrose but pathogen pathogens can. Is the capacity to use sucrose a functionally conserved mutualistic trait? Many symbiotic fungi are unculturable; thus, to address this question I used the presence of glycosyl hydrolase family 32 (GH32) genes that encode sucrolytic enzymes as a proxy for sucrose utilization. Fungal genomes were examined and a phylogenetically and ecologically diverse array of fungi was assayed for GH32 presence. 6 clades of GH32 ranging from 0-6 genes per species were recovered. GH32 distribution showed little phylogenetic signal but a strong link to ecology; 91% of mycorrhizal taxa lacked GH32 genes, and 84, 54 and 43% of endophytes, pathogens and lichens possessed them. These data show functional diversity does exist within ecological guilds. They also reveal a striking contrast between mycorrhizal and other symbiotic fungi in their potential to utilize sucrose, suggesting this is a convergent- not conserved-trait among fungal mutualists, and that carbon dynamics in mycorrhizal interactions are distinct from that of other plant-fungal mutualisms. Contributed Presentation

Pey, Kabir G.1,2, Garbelotto, Matteo1 and Bruns, Thomas D.2 1Dept. of Environmental Science, Policy & Management, UC Berkeley, Berkeley, CA, USA, 2 Dept. of Plant & Microbial Biology, UC Berkeley, Berkeley, CA, USA. kpey@nature.berkeley.edu. Is landscape scale dispersal an important determinant of fungal species richness and community composition? Dispersal is one of the most important and yet least understood aspects of fungal ecology. At large spatial scales molecular data show a clear imprint of dispersal limitation in population genetic and phylogeographic structure. However, few fungal studies have examined how landscape scale dispersal patterns affect important ecological processes such as competition, succession and community assembly. In this study we used virtual islands - patches of pine trees located in a non- ectomycorrhizal scrub matrix - to examine the effects of dispersal on ectomycorrhizal community dynamics. We analyzed these communities in the context of an island biogeography model where increasing island isolation (i.e. reduced dispersal) is predicted to lower fungal species richness. This study follows on previous work in 10-year old pine islands where we found a strong effect of island size on ectomycorrhizal richness. However, the strong effects of island size and limited sampling prevented us from drawing strong conclusions about the direct effects of dispersal. For the current study we sampled a new batch of islands, this time holding island size constant and looking across a larger range of isolation. In addition, we included only mature trees (>20 years) to see how succession affected community dynamics. As predicted, increased isolation was correlated with decreased ectomycorrhizal species richness. Dominant species from 10-year old trees were rare or absent on mature trees. Despite this, succession appears to have caused an overall increase in species richness compared across similar sized islands. We also conducted analyses of fungal community structure in conjunction with measurements of important soil chemical properties, such as nitrogen, phosphorous, and pH, for individual pine islands. In conclusion, it appears that landscape scale dispersal patterns are important and deserve greater consideration in fungal ecology studies. Symposium Presentation

Pekarek, Elizabeth* and Vilgalys, Rytas. Department of Biology, Duke University, Durham, NC 27708, USA. elizabeth.pekarek@duke.edu. Characterization of postzygotic isolation of interspecific hybrids in the genus Pleurotus. The idea that good species do not cross to produce fertile offspring is a cornerstone of the biological species concept. Yet, a collection of Pleurotus pulmonarius from New Zealand (NZP) shows mating compatibility with three putatively separate biological species of Pleurotus (P. ostreatus, P. eryngii and P. pulmonarius). Interspecific hybrids of NZP and P. eryngii and P. ostreatus were examined for aspects of postzygotic reproductive isolation, such as hybrid inviability, hybrid sterility and hybrid breakdown. No fitness loss was observed in the vegetative growth of hybrid dikaryons and 75% of these dikaryons were able to form fruiting bodies. However, a substantial reduction in spore viability was observed in hybrid mushrooms. In addition, vegetative growth rates of germinated hybrid spores were highly variable and typically slower than those of nonhybrid individuals. AFLP mapping was employed to examine the meiotic behavior of species-specific molecular markers in progeny derived from these hybrid mushrooms. Poster

Pfister, Donald H.* and Warming, Judith. Harvard University Herbaria, 22 Divinity Ave., Cambridge, MA 02138, USA. dpfister@oeb.harvard.edu. Digital literature resources. The literature that describes and discusses organisms is at the heart of organismic studies and forms the biodiversity canon. The books and journals are scattered, often rare, and linguistically and bibliographically challenging. A number of projects are exploiting digital technologies and developing new tools to deliver these essential resources to the global research community. Several of these projects will be discussed with an emphasis on the Biodiversity Heritage Library (BHL), a consortium of ten public and private institutions. In less than three years BHL partners have combined and analyzed their holdings, developed strategies for prioritizing subject areas, created new public and private partnerships, developed new discovery tools, secured funding, and delivered more than 3.500.000 pages to the web. The underlying principles of open access, international participation, and broad, but focused, subject support make this project unique. The BHL and similar projects like the Royal Botanic Garden of Madrid’s digital library, France’s Gallica, Google Books, the Internet Archive, and Project Gutenberg, deliver thousands of books to researchers’ desktops. OCR indexing, while still imperfect, enhances the discovery of these works when searching the web. Improved optical character recognition (OCR) for languages and fonts are being closely monitored and tested. Copyright restrictions will continue to limit access to some 20th century literature, but publishers are motivated to deliver retrospective titles digitally, and legislation to free “orphaned works” is being followed closely. For the first time in human history there is the prospect that much of the specialized descriptive literature covering fungi will be available to the scientific community – and eventually from a hand-held device. Symposium Presentation

Picard, Kathryn T.*, Letcher, Peter M. and Powell, Martha J. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487, USA. leetch006@bama.ua.edu. A new genus and zoospore type within the Chytridiales. Unrealized diversity among zoosporic fungi (Chytridiomycota) is being revealed as taxonomic surveys are being refined with molecular and ultrastructural analyses. Recently, we have discovered a new chytrid nested in a clade of unknown taxa within the Chytridiales. This new chytrid was isolated from soil on pollen, though it is also capable of metabolizing chitin. Thallus morphology is heavily influenced by substrate. On pollen, the thallus is comprised of a large, spherical sporangium with ornamented walls. The uniaxial rhizoidal system develops into an extensive network of divericate branches. Morphology on chitin substrates is characterized by a renate or angular sporangium and reduced rhizoidal complexity. The sporangium in both

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phenotypes is oculpulate with a discharge plug, and zoospores are released in a vesiculate mass. Transmission electron microscopy revealed that the zoospore was fundamentally Chytridialian, reaffirming molecular placement of the isolate within the order. However, the zoospore also exhibits subcellular characteristics unique to this taxon, most notably two large vesicles located in an anterior vesicle-rich region of the cell. Characterization of these vesicles is ongoing. Based on molecular phylogeny, thallus development and morphology, and zoospore ultrastructure, a new genus and zoospore type will be described for this chytrid. Contributed Presentation

Plishka, Marcie J.R.*, Tsuneda, Akihiko and Currah, Randolph S. Department of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9 Canada. plishka@ualberta.ca. A structural analysis of convergent cleistothal fungi representing the Leotiomyctes and Sordariomyctes. Pleuroascus nicholsoni and Nigrosabulum globosum are coprophilous cleistothal ascomyctes that were once placed among the Pseudeurotiaceae on the basis of having a dark, membranous peridium, a plectomycetous centrum, and hyaline non-porate asciiopes. Recent molecular phylogenies indicate that this suite of characters represents a convergence that has arisen in both apothecial and perithecial lineages. In P. nicholsoni, there is little overt evidence of a putative affiliation with the Leotiomyctes although whole ascomata show limited signs of polarity with the characteristic tightly coiled appendages generally arising along or below the equatorial region and a marked thinning of the subicular hyphae over the crown of the ascoma. However, electron microscopy indicates that the globose ascis contain uniseriate arrangements of ascospores within a delimiting membrane system, and sterile elements dispersed throughout the centrum represent vestigial, apically branched paraphyses. Morphological characteristics indicating a relationship between N. globosum and its perithecial relatives among the Bionectriaceae (Hypocreales) are also cryptic but detectable using light and electron microscopy. Centrum development in this species involves the proliferation of ascogenous filaments that grow up between the cells of pseudoparenchyma. First formed ascis are clavate, but those formed later in development are subglobe and distorted in shape. We surmise that the convergent form represented by these two species arose in response to the demands of a coprophilic lifestyle. Contributed Presentation

Porras-Alfaro, Andrea1,2, Herrera, Jose2, Sinsabaugh, Robert L.1 and Natvig, Donald O.1. Department of Biology, MSC32020, The University of New Mexico, Albuquerque, NM 87131, USA. 2Department of Biology, 100 E. Normal, Truman State University, Kirkville, MO 63501, USA. annpas@ummn.edu. Distribution patterns of soil and plant-associated fungal communities in a semiarid grassland. We analyzed diversity and structure of fungal communities found in biological soil crust, rhizosphere soils and in association with different dominant grass species in a semiarid grassland located at the Sevilleta National Wildlife Refuge, a Long Term Ecological Research site in New Mexico. Internal Transcribed Spacer (ITS) rDNA sequences were amplified using fungal specific primers. More than 3000 sequences were obtained. Species richness was high, with more than 23 orders represented, and rarefaction curves and diversity estimators did not show saturation. Soil and plant-associated fungal communities were dominated by dark septate fungi belonging to the Pleosporales with a substantial overlap among rhizosphere and biological soil crust. Roots of dominant grasses were colonized by a consortium of fungal endophytes that included dark septate fungi, coprophilous, mycorrhizal, saprophytic and plant pathogenic fungi. Differences among the fungal communities colonizing different plant structures such as crown, leaves, seeds and roots of one of the dominant plants, Bouteloua gracilis, will be discussed. Contributed Presentation

Porter, Terri M.1,2, Vilgalys, Rytas1 and the AFTOL2 Working Group. 1Duke University, Biology Department, Campus Box 90338, Durham, NC 27708, USA. terri.porter@duke.edu. Assessing support for the basal fungal lineages: Mitochondrial versus nuclear-encoded markers. Understanding evolution of the earliest fungal lineages remains one of the major challenges facing the Fungal Tree of Life initiative (AFTOL). In addition to the canonical AFTOL genes (nuclear-encoded SSU, ITS, LSU, RPBI, RB2, EF1A; mitochondrial-encoded SSU, ATP6), new sources of comparative gene data are still needed to resolve phylogenetic relationships among basal lineages. Preliminary comparisons among nuclear and mitochondrial small subunit ribosomal genes and mitochondrial protein-coding genes COX1 and COX3 (cytochrome c oxidase subunits 1 and 2, respectively) have demonstrated that mitochondrial protein coding genes can also be useful for inferring organizational evolution of fungi (Paquin et al., 1995). Here, we report on studies utilizing combined nuclear and mitochondrial genome data, including data from AFTOL, and from sequenced mitochondrial genomes of basal fungi (Fungal Mitochondrial Genome Project, Lang research group). We constructed a phylogeny for basal fungi using sequenced mitochondrial gene data for several genes including COX1 and have supplemented the dataset with gene sequences from strains in the current study (AFTOL2). In this preliminary report, we compare the support for basal fungal nodes in mitochondrial versus nuclear-encoded markers. Poster

Powell, Martha J.1*, Letcher, Peter M.1 and Longcore, Joyce M.2 1Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487, USA, 2School of Biology and Ecology, The University of Maine, Orono, ME 04469, USA. mpowell@biology.as.ua.edu. A new oculpulate genus in the order Rhizophydiales. Molecular phylogenetic analyses of Chytridiomycota have revealed that the modes of zoospore discharge through inoperculate and oculpulate openings have arisen repeated times in separate lineages among chytrids. However, an oculpulate genus among members of the monophyletic order Rhizophydiales has only recently been described. We have discovered another oculpulate chytrid in a second molecular lineage within the Rhizophydiales. This new chytrid was isolated from soil on keratin, but it could utilize additional substrates, including pollen and chitin. No species described for other oculpulate genera exhibited the thallus features of this chytrid. Encysted zoospores germinated with a single, primary rhizoidal axis, which evidently branched out additional axes, often times in threes. Secondary rhizodial branches typically occurred some distance from the sporangiun. Walls of sporangia were covered with minute warts that were detectable with light microscopy, but the finely encrusted nature of the wall ornamentation was best visualized with scanning electron microscopy. At the time of zoospore discharge, a large hinged operculum folded back, zoospores were released as a motionless mass, and zoospores soon swam away. Thick-walled resting spores were also produced. Transmission electron microscopy revealed that the zoospore architecture was characteristic of the Rhizophydiales, and most similar to zoospores of organisms in the Rhizophysdiaceae. However, the kinetosome-associated structure (KAS) was more prominent than in the type genus, Rhizopodium. Consequently, based on molecular phylogeny, thallus morphology, and zoospore ultrastructure, a new genus will be described for this oculpulate chytrid. Poster

Price, Relf L.1, Keller, Harold W.2* and Stumpfner, Ted.11Valles Caldera National Preserve, P.O. Box 359, Jemez Springs, NM 87025, USA, 2Department of Biology and Earth Science, University of Central Missouri, Warrensburg, MO 64093, USA. 20 Colle San Martin, Santa Fe, NM 87506, USA. haroldkeller@hotmail.com. Myxomycetes of New Mexico. The southwestern, semiarid state of New Mexico is partly dissected by the Continental Divide. The north-central part lies within the Southern Rocky Mountains; the northwest forms part of the Colorado Plateau; the eastern two-fifths falls on the western fringes of the Great Plains; and the south is part of the Chihuahuan desert. Seven Life Zones are present from desert (lowest point 867m) to alpine (highest 4,014m). Characteristic vegetation in each zone includes desert shrubs and grasses; pithon/jumper woodland, sagebrush, and chaparral; ponderosa pine and oak woodlands; mixed conifer and aspen forests; spruce/fir forests; and tundra wild flowers and riparian shrubs. This diversity produces a large

Continued on following page
geographic area high in myxomycete biodiversity. Macbride published a list of 25 myxomycetes in “The Slime Moulds of New Mexico”; others have added 13 more species. Price in his 1971 Master’s Thesis entitled “The Myxomycetes of Montane Northern New Mexico” recorded 31 additional state records. The Valles Caldera National Preserve in the Jemez Mountains yielded many new records, including a new species, Comatricha calderaeensis, the second collection of Lamproderma cristatum in the USA, and the rare Kellomomyxa finicola. Since 1971 our forays have included all of the Life Zones and habitats throughout the entire state. Supported in part by NSF Award DEB-0343447 to HWK. Contributed Presentation

Pringle, Anne. Organismic and Evolutionary Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA. pringle@oeb.harvard.edu. What tools do ecologists and others need from fungal bioinformatics resources? Many of the ecologists now working with fungi have never had training in mycology. When faced with a fuzzy green isolate taken from soil, a common coping strategy is to extract DNA and sequence. Sequences provide some information but often do not provide a definitive identification. Sequences taken from otherwise unidentified cultures, or directly from soil or other substrates, languish on ecologists’ computers because without a positive identification they cannot be submitted to NCBI. Ecologists and other scientists (including physicists) need training in mycology, and the web provides unprecedented access to both basic information about fungi, and the protocols needed to handle fungi. However, fungal bioinformatics resources should also provide the infrastructure to warehouse unidentified sequences, the capacity to link sequences collected from one site to similar sequences collected from other sites, and the tools to connect sequences to organisms. Efforts to create these resources are underway and both the FESIN research coordination network and UNITE database provide a focus for future endeavors. Symposium Presentation

Pringle, Anne*, Cross, Hugh B., Wolfe, Benjamin E. and Richard, Franck. Organismic and Evolutionary Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA. pringle@oeb.harvard.edu. Biogeographic patterns in the body size and phenology of an introduced ectomycorrhizal fungus. The biogeographic patterns associated with the autecologies of fungi are poorly understood. By using both historical records and molecular data, we have established the fungus Amanita phalloides as an introduction currently expanding its range on the West Coast of North America. The fungus is native to Europe. Although it has also been introduced to the East Coast of North America, on the East Coast A. phalloides grows as isolated populations and is not spreading. By collecting mapped populations of fungi from California, Europe, and the Northeast U.S., and using genetic fingerprints created with AFLP protocols to map genetic individuals, we show that most mushrooms in a habitat are unique genetic individuals. Data suggest that genets of A. phalloides are typically less than 1 m in diameter. The pattern holds across California, Europe, and the Northeast, and is the same for sites where populations are assumed to be young and sites where A. phalloides has been collected for over 30 years. There appears to be no correlation between body size and geographic origin or age of a population. In contrast, although the mushrooms of A. phalloides appear at specific times of year in Europe and on the East Coast, in California mushrooms can form at any time of year. Moreover, mushrooms are twice as large in California, as compared to mushrooms on the East Coast or in Europe. Contributed Presentation

Raja, Huzefa A.*, Ferrer, Astrid and Shearer, Carol A. University of Illinois, Department of Plant Biology, 265 Morrill Hall, 505 South Goodwin Avenue, Urbana, IL 61801, USA. raja@uiuc.edu. Three new freshwater ascomycetes from Florida. A new genus, Ocala scalariformis gen. et sp. nov., and two new species, Ayria nubispora sp. nov., and Rivulicola cygnea sp. nov. are described and illustrated from submerged woody debris. The new taxa were collected during a distributional study of freshwater ascomycetes along the Florida peninsula. Ocala scalariformis (Pleosporales, Dothideomycetes) has a combination of morphological characters that excludes its placement within any existing family and genus in the Pleosporales. These characters include: membranous ascomata, broad cellular pseudoparaphyses, bitunicate ascii, and hyaline phragmospore, thick-walled ascospores with ephemeral, amorphous, bipolar gelatinous appendages. Ayria nubispora and Rivulicola cygnea belong to the Sordariomycetes and are discussed in relation to other species in their respective genera. Ascospores of each of the three taxa are equipped with a gelatinous sheath and/or appendages, structures thought to serve as flotation and/or substrate attachment devices in aquatic habitats. Poster

Reynolds, Hannah* and Vilgalys, Rytas. Duke University, Biological Sciences, Box 90338, Durham, NC 27708, USA, htr@duke.edu. Where in the Eurotiales are the macroscopic asccorcaps? The Elaphomycetaceae consist of two ectomycorrhizal genera: the false-truffle Elaphomyces and the epigean fungus Pseudotulostoma. Recent molecular work has shown the Elaphomycetaceae to be closely related to the saprobe Trichocoma in the Eurotiales. These fungi represent an independent evolution of the complex, macroscopic asccorcap, as they are rooted in an order famed for its dominant anamorphic stages and microscopic teleomorphs. They also represent an independent origin of mycorrhizal fungi. The placement of this family within the Eurotiales is largely based on ribosomal sequences and, due to the limited genetic information, is only weakly supported by the molecular data. Other than the link to Trichocoma, the relation of these complex, macroscopic asccorcaps with the other Eurotiales is unresolved. We expanded taxon sampling and used a multi-locus sequence approach to further resolve the placement of the Elaphomycetaceae in the Eurotiales. Poster

Riquelme, Meritxell. Department of Microbiology, Center for Scientific Research and Higher Education of Ensenada (CICESE), Km 107 Ctra., Tijuana-Ensenada, 22860 Ensenada, Baja California, México. riquelme@cicese.mx. Characterization of the Spitzenkörper and the exocyst in Neurospora crassa. Vegetative hyphae display an apical body or Spitzenkörper (Spk), whose behavior and robustness determine the growth and morphology of the fungal cells. Early transmission electron microscopy studies showed that the phase-dark Spk observed by phase-contrast light-microscopy corresponded mainly to an outer layer of macrovesicles surrounding a macrovesicular core. To investigate the nature of the Spk vesicles and analyze their role in cell-wall formation in the model fungus Neurospora crassa, we have tagged with fluorescent proteins several enzymes involved in cell-wall synthesis. We found that chitin synthases (CHS-1, CHS-3, and CHS-6) localized at the core of the Spk, whereas an enzyme required for glucan synthase activity (GS-1) localized at the external layer of the Spk. At the plasma membrane of the apical dome, just in front of the Spk, we found an accumulation of Exo- cyst components (SEC-5, SEC-15). These results suggest: 1) a spatial and possibly functional specialization of the cell wall synthesis machinery within the Spk, and 2) exocytosis of Spk vesicles at a much delimited area of the hyphal apex. Symposium Presentation

Rittenour, William R.* and Harris, Steven D.1,2 Department of Plant Pathology and Center for Plant Science Innovation, University of Nebraska-Lincoln, Lincoln, NE 68588, USA. written1@bigred.unl.edu. Inventorying and characterizing glycosylphosphatidylinositol (GPI)-anchored proteins in the wheat pathogen Fusarium graminearum. Fusarium graminearum is the causal organism of head blight on wheat and barley. Little is known about the role of surface proteins during growth of plant pathogenic fungi. One class of cell surface proteins is anchored to the cell surface by a GPI moiety. We used the publicly available Big Pifungal predictor software to inventory the GPI-anchored proteins in the proteome of F. graminearum. Our analysis yielded 205 predicted GPI-anchored proteins, 147 of which also were predicted to contain a signal peptide. Of these 147 proteins, 57 showed similarity to proteins of known function, whereas 90 had unknown functions. Of the proteins with predicted function, most were carbohydrate-modifying enzymes likely involved in altering the cell wall during growth. However, Continued on following page
some proteins were identified that may have a role in pathogenicity, including a Cu-Zn superoxide dismutase, a cutinase, and several aspartyl proteases. Of the unidentified proteins, two (FGSG_08844, FGSG_01588) were selected for gene deletion studies based on the presence of variable internal repeats within the coding sequences, which is indicative of adhesion proteins in other fungi. Although no phenotypes have yet been established for these two genes, there are major gaps in their sequences among F. graminearum isolates collected in Nebraska, suggesting a possible utility in population studies of this pathogen. Our research will provide much needed insight into how the cell surface contributes to fungal growth and pathogenicity. Poster

Rivera, Karol12 and Siebert, Keith A.12 1Department of Biology, University of Ottawa, Ottawa, ON, Canada, K1N 6N5, 2Biodiversity, Agriculture and Agri-food Canada, Ottawa, ON, Canada, K1A OC6, krive081@uottawa.ca. A putative new species of Penicillium related to P. herquei revealed by phylogenetic analysis. Penicillium herquei, a species of biverticillate penicillia belonging to Penicillium subgenus Furcatum, is widely distributed, but has been reported infrequently. Agar colonies are distinguished by brilliant yellow, green or orange colours. Colony characters are quite variable. A beta-tubulin gene tree of twelve strains identified as this species revealed the existence of a group of four strains isolated from Southern Ontario that forms a sister clade to the type with high bootstrap support. The same group appears in the ITS tree but with lower bootstrap support. Additional gene trees for calmodulin, translation elongation factor 1-alpha and cytochrome oxidase 1 will be generated to determine whether this clade meets the criteria of the phylogenetic species concept. Micromorphological characters of the putative new species will be compared with those of strains conforming with the ex-type strain to determine whether the clade represents a cryptic or morphologically distinct species. Poster

Robbertse, Barbara1, Reeves, John, Yoder, Ryan, Schoch, Conrad L. and Spatafora, Joseph W. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA. robberb@science.oregonstate.edu. Phylogenomics of fungi. The collaborative research project AFTOL2: resolving the evolutionary history of the Fungi will depend heavily on phylogenomics for resolving deep node relationships. The strategy of the first tree of life project was to sample many (~2000) species and available loci (8) whereas the strategy of AFTOL2 is to sample approximately ten times less species but ten times more loci. The orthogonal loci are chosen according to a set of criteria such as copy number, amplicon size, informativeness and use in other tree of life or phylogenomic studies. At the time of writing this abstract, released and annotated genomes (>47) represented four phyla (8 subphyla) of the fungal kingdom. Mining genomes for orthologs in a time-phylogenetic context. A pipeline was developed to assemble the orthologs present in all fungal genomes and align them into a super matrix. Phylogenetic analyses were performed using a variety of methods, including Maximum Likelihood and Bayesian approaches. The results of these analyses are consistent with previous findings, indicating that the fungal kingdom is highly diverse and contains multiple evolutionary lineages. Poster

Roberson, Robert W. School of Life Sciences, Arizona State University, Tempe, AZ 85287, USA. robb2@asu.edu. In search of the lost Spitzenkörper. Hyphal growth and morphogenesis are complex processes that have allowed the fungi to successfully utilize a wide range of ecological habitats and develop multiple lifestyles. Cytological studies, and more recently molecular studies, of hyphal tip biology have placed great emphasis on the Spitzenkörper. The Spitzenkörper appears to have evolved only in the filamentous fungi where it is present in all members of the Basidiomycota and Ascomycota studied thus far. Among the ‘lower fungi’, Spitzenkörpers have been verified only in Alternaria macrognosy (Chytridiomycota). Though progress is being made to better understand the cellular and molecular biology of the Spitzenkörper, its specific function(s) in hyphal growth and its distribution among the fungi remain important questions. In this presentation, bioimaging methods will be used to review Spitzenkörper behavior, structure, and existence among fungal taxa. Symposium Presentation

Rodrigues, Tatiana T. M. S.1a, Lourenço Jr., Valdir1, Silva, Mychele B.1, Berbee, Mary L.2 and Mizubuti, Eduardo, S. G.1 1Department of Plant Pathology, Universidade Federal de Viçosa, Viçosa, MG, 36570-000 Brazil, 2Department of Botany, University of British Columbia, Vancouver, BC, V6T 1Z4 Canada. tatianatozzi@yahoo.com.br. Mycelial compatibility, AFLP marker and mating type genes suggest that Brazilian population of Alternaria solani is clonal. Brazilian populations of A. solani are highly variable, despite their lack of a known sexual cycle. A marker-based approach was used to investigate factors that could affect recombination in population pathways. Mycelial compatibility (MC) was tested for 85 isolates that were sampled from potato and tomato and then paired in all possible combinations. From 7,225 pairings, 6,141 were compatible. No sexual structure was observed from any pairing. Most of the incompatible pairings involved isolates from different hosts. Of the incompatible reactions, 453 resulted from pairing isolates from potato with isolates from tomato. 213 incompatible reactions resulted from pairings between isolates from potato and tomato were from pairings between isolates from tomato. The AFLP marker revealed high genetic diversity. Of 31 loci, 29 were polymorphic (93.6%) and Nei’s gene diversity was 0.42. Significant linkage disequilibrium (LD) and allele association (IA), LD= 808 (P<0.05), IA=1.51, (P<0.001); LD=5760 (P<0.05), IA=4.97 (P<0.001), for AFLP and MC data, respectively, suggested clonality. Primers were used to amplify the HMG box of the MAT1-2 and Alpha box of the MAT1-1 idiomorphs of 30 isolates. Only MAT1-2 idiomorph was detected. The absence of the second mating type and the high levels of LD and IA strongly support a clonal population structure of A. solani in Brazil. Acknowledgement: CAPES. Contributed Presentation

Rojas, Enith L.1,2, Herre, Edward A.2, Rehner, Stephen1, Van Bae1, Sun-shine2, Chen, Rui2, Pang, Junfeng3, Wang, Ruixiu2, Sha, Tao2, Zhang, Yaping3 and Samuels, Gary J.1 United States Department of Agriculture, Agriculture Research Service, Systematic Mycology & Microbiology Laboratory, B-011A, Rm. 304, 3030 Baltimore Ave., Beltsville, MD 20705, USA, 2Smithsonian Tropical Research Institute, Apartado Postal 0843-03092, Balboa, Ancon, Republic of Panama, 3State Key Laboratories, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650223, Yunnan, China, 4Laboratory for Conservation and Utilization of Bio-resource, Yunnan University, Kunming 650091, China. enith.rojas@ars.usda.gov. Phylogenetic relationships among endemic and pathogenic isolates of Colletotrichum gloeosporioides s.l. associated with Theobroma cacao in Panama and China. In a survey of Theobroma cacao and tree species native to Panama, the morphological species Colletotrichum gloeosporioides was frequently isolated both as asymptomatic endophytes and also as presumptive foliar and fruit pathogens. Colletotrichum gloeosporioides was also the dominant endophyte in asymptomatic leaf samples collected from T. cacao plants that had been introduced via seeds in Xingshuabanna Botanical Garden in Southern China. Sequence typing with the widely used ITS and LSU provided insufficient resolution and support to test for phylogenetic correlations among isolates and their host association, ecological mode, or geographic origin. However, data from additional nuclear loci (e.g., tef1, B-tub, rpb1, 2) resolved the isolates into cohesive groups, in some cases as host-specific pathogens, and in other cases as generalist endophytes and weak pathogens. The Asian isolates of C. gloeosporioides from T. cacao yielded clades of isolates related to, yet distinct

Continued on following page
from, Neotropical clades. These results suggest that these additional nuclear loci will be useful in developing refined phylogenetic hypotheses for characterizing the systematics, ecology and biogeography of phylogenetic species within Colletotrichum. **Contributed Presentation**

Rosique-Gil, Edmundos*, González, María C.1 and Cifuentes, Joaquín.2 1Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, DF 04510, México, 2Herbario FCME, Facultad de Ciencias, Universidad Nacional Autónoma de México AP 70-399, Coyoacán México DF 04510, México. mgc@biologia.unam.mx. **New records of three freshwater ascomycetes from an urban lagoon of Tabasco, Mexico.** During the past two years a biodiversity project to study lignoncolous freshwater ascomycetes of the State of Tabasco was undertaken because it is located in one of the highest precipitation regions of México which results in an elevated diversity of natural and urban lentic habitats. A survey of ligneicolous freshwater ascomycetes was carried out in Las Ilusiones Lagoon located in the metropolitan area of Villahermosa City, the State of Tabasco, Mexico. Anipodera inflataciscera, Ascosacculus heteroguttatus and A. aquaticus are recorded for first time in Mexico. This study is an important contribution to the knowledge of the worldwide distribution of these three species from tropical freshwater ecosystems. **Poster**

Rossman, Amy Y. Systematic Mycology & Microbiology Laboratory, USDA-ARS, Rm. 304, B011A, 10300 Baltimore Ave., Beltsville, MD, 20705, USA. Amy.Rossman@ars.usda.gov. **What do plant pathologists want from the Fungal Barcoding Initiative?** Plant pathologists want from the Fungal Barcoding Initiative what everyone wants, specifically a fast, accurate identification of their causal plant pathogen resulting in a scientific name that synthesizes current knowledge of that organism. It sounds so easy! Yet, accurate DNA barcodes can only be developed once the fungal pathogen and related species have been adequately defined, characterized and placed in their phylogenetic context. For some groups of plant pathogens and many serious disease-causing fungi the systematic foundation for developing DNA barcodes for species does not exist, while for other groups, such as the genus Phytophthora, that have recently received considerable attention, developing DNA barcodes is possible. The quest to develop DNA barcodes for plant pathogens will result in highlighting those groups that are in serious need of systematic attention. Similar to DNA barcoding of fungi in specific ecological habitats such as indoor air, it may be possible to target just the most threatening plant pathogens. With DNA barcodes for fungi used by plant quarantine diagnosticians, it may be possible for incoming plant products and germplasm to be declared safe prior to shipment saving time and money while protecting U.S. agriculture and natural resources. **Symposium Presentation**

Rumburg, Jess R., Moskalenko, Maria, Muska, Dave and Horton, Thomas R.* Department of Environmental and Forest Biology, State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13210, USA. thorton@esf.edu. **The invasive orchid Epipactis helleborine (L.) Crantz forms mycorrhizae with truffles (Tuber spp.) and other Ascomycetes in New York state. Epipactis helleborine is a member of the Orchidaceae family that is native to Europe. The plant is viewed as an invasive species in North America and is now found in thirty U.S. states from Maine to California, as well as three Canadian provinces. Limited data suggest the plant is associated with Tuber (Ascomycota – true truffles) in North America. Here we sampled the orchid from a wide variety of locations in New York state and identified its fungal associates using molecular methods. All samples of E. helleborine were colonized by members of Ascomycota with the majority being members of the genus Tuber. We were unable to identify the species of the Tuber in our study, largely because this fungus is undersampled in the northeast and as a consequence, there are few sequences deposited in Genbank for comparison. Surprisingly, Tuber spp. appear to be common in New York given the orchid is widespread and frequently encountered in the state. These results suggest mycorrhizal fungi play a role in the invasion biology of the orchid.** **Poster**

Saunders, Megan* and Kohn, Linda M. Department of Ecology and Evolutionary Biology, University of Toronto, 3359 Mississauga Rd., Mississauga, ON L5L 1C6 Canada. megan.saunders@utoronto.ca. **Elucidating biotic factors that influence assembly of fungal endophyte communities.** Maize was used to assess the influence of two factors on fungal endophyte communities: production of host defense compounds, and presence of a primary colonizer. Maize has been selectively bred to produce high quantities of benzoazinoids (BXs). To determine the influence of BX production on communities, fields were planted with genotypes differing in their ability to produce BXs. Endophyte communities were characterized and tested for tolerance to a toxic BX byproduct, 2-benzoazolinone (BOA). In seedling roots and mature leaves, the community proportion with low BOA tolerance was significantly greater in BX non-producers than in producers. Mean abundance of *Fusarium* species, including agents of animal toxicosis and corn diseases, was up to 35 times higher in mature leaves of BX producers than in non-producers. Next, we investigated the effect of a seed endophyte on community assembly. Fields were planted with BX producing and non-producing genotypes that were either sterilized or inoculated with *Fusarium verticillioides*. Results from the field and related in vitro experiments indicate that *F. verticillioides* facilitates colonization by closely related species. Results suggest that selective breeding for BX production may have unintentionally increased colonization by *Fusarium*. Host defense compounds and presence of a primary colonizer significantly altered endophyte community structure. **Contributed Presentation**

Schmidt, John Paul*, Avis, Peter2, Leacock, Patrick3 and Mueller, Greg,3 Smithsonian Environmental Research Center, Edgewater, MD, USA, 2Biology Dept, Indiana University Northwest, Gary, IN, USA, 3Dept of Botany, The Field Museum, Chicago, IL, USA. john.pauls@operamail.com. **Use of occupancy estimation in fungal ecology.** Fungal ecologists often wish to determine if experimental treatments or environmental factors can influence the distribution of a fungal species. These studies are challenging as it can be difficult to detect a species even when it is present in a site. Species may appear to be absent, but in reality are present and missed during sampling. These “false absences” make it difficult to assess differences between areas or the effects of an experimental treatment. This problem is also found in studies of cryptic animal species. In recent years animal ecologists have developed...
op a new type of analysis, “occupancy estimation”, to address this prob-
lem. Occupancy estimation uses repeated sampling to determine the
probability of finding a species when it is present in a site, referred to as
the “detectability” of the species. The detectability can then be used to
estimate the % of sampled sites where a species occurs but was missed
during sampling. The analysis can also estimate the effects of covariates,
such as an experimental treatment or environmental factor, on both oc-
cupancy of the species and its detectability. We demonstrate an occu-
pancy analysis on data collected for a study of the effects of N addition
on mycorrhizal fungi in an eastern deciduous forest. In particular we ex-
amine the influence of N addition on the occupancy and detectability of
a variety of species. Symposium Presentation

Schreiner, R. Paul. USDA-ARS-HCRL, 3420 NW Orchard Ave., Cor-
vallis, OR 97330, USA, paul.schreiner@ars.usda.gov. Arborcular my-
corrhizal fungi (AMF) amplified from grape roots are dominated by
Glomus species while spores retrieved from vineyard soil are not.

The diversity of AMF in vineyards was assessed using both classical and
molecular approaches. Grape roots or AMF spores were isolated from
soil collected in the planting row of 10 ‘Pinot noir’ vineyards in Oregon.
Spores were mounted in PVLG and identified to species, while AMF in-
side grapevine roots were indentified after sequencing PCR products
amplified from root DNA extracts. A total of 17 morphotypes (species)
were found as spores in soil, including 7 species in the Acaulosporaceae.
PCR products gave a total of 18 AMF phylotypes, which were dominat-
ed by Glomus >99% but completely devoid of clones from the
Acaulosporaceae. Four Glomus phylotypes (including Glomus in-
traradices) were found in every vineyard and comprised 81% of all
clones examined. G. intraradices has been repeatedly isolated in trap-
cultures; however, the remaining 3 common phylotypes have not been
obtained in pot-culture after extensive efforts to do so. Three Acaulospo-
ra species were shown to colonize ‘Pinot noir’ roots under controlled
conditions and PCR products obtained from these root extracts matched
Acaulospora sequences. These results indicate that AMF within the
Acaulosporaceae are excluded from the symbiosis with grapevines
under field conditions, even though spores are commonly found in vine-
yard soils. Contributed Presentation

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ment of Botany, University of British Columbia, Vancouver BC, V6T
1Z4, Canada, 2Division of Biology, Newcastle University, Newcastle
upon Tyne, NE1 7RU UK, 3Department of Biology, Konan University,
Kobe 658-8501, Japan. sekimoto@interchange.ubc.ca. Evolution and
phylogeny of the marine oomycete endoparasites. Oomycetes are
morphologically and ecologically diverged organisms, such as thallus
morphology ranging from single-celled to highly developed hyphae and
ecological behavior as saprophytes or parasites. In spite of their large
morphological and ecological diversity, the origin and evolutionary
development of oomycetes were still uncertain. In this study we investi-
gated the molecular phylogeny and ultrastructural comparative mor-
phology of some little-studied marine oomycetes, which include
unicellular obligate endoparasites of marine algae. In our trees based on
both the SSU rRNA and cox2 genes, saprolegnian and peronosporalean
oomycetes each formed a monophyletic clade whilst our marine en-
doparasite species branched before both clades. Many of the morpho-
logical features of marine endoparasite species were shared with the
saprolegnian oomycetes rather than the peronosporalean species, sug-
gestting that the peronosporalean oomycetes are the most derived and
specialized group in the oomycetes. Our data indicated that oomycetes
may have originated from the marine environment as unicellular en-
doparasites. Saprolegnian oomycetes then diverged in the freshwater en-
vironment largely as saprophytes and weak parasites of plant roots, crust-
tacea and fish, and peronosporalean oomycetes advanced into the
terrestrial environment predominantly as necrotrophic and biotrophic
pathogens of land plants. Contributed Presentation

Shadwick, John D.1, Powers, Donna Moore2, Spiegel, Frederick W.1,*
and Stephenson, Steven L.1 1Department of Biological Sciences, Uni-
versity of Arkansas, Fayetteville, AR 72701, USA, *Biology/Chemistry
Division, Cornell Community College, Corning, NY 14830, USA.
spiegel@uark.edu. Distribution and occurrence of protostelids in
Australia. The continent of Australia, with a total area of more than
7,600,000 km², covers about 5% of the earth’s land area. Most of the
continent is low, flat and dry; deserts, dry grasslands and woodlands are
the predominant vegetation types. Although many elements of the biota
are relatively well documented, this is not the case for the protostelids, a
group of unicellular amoeboid slime molds commonly found on dead
plant substrates. During the period of 1997 to 2007, samples for isolation
of protostelids were collected at a number of localities throughout main-
land Australia, in Tasmania and on subantarctic Macquarie Island. These
samples yielded 23 described species of protostelids and one species of
myxomycete (Echinostelium hisprium) often recorded from the same
substrates examined for protostelids. Protostelium mycophaga and
Schizoplasmodiopsis pseudoendospora were the most common proto-
stelids, occurring in 23 and 12% of all samples, respectively. Sixteen
species were recorded from the aerial litter microhabitat, whereas 18
species were recovered from the ground litter microhabitat. Poster

Shaw, Brian D.*, Upadhyay, Srijana and Lee, Soo Chan. Department of
Plant Pathology and Microbiology, Program for the Biology of Fila-
mentous Fungi, Texas A&M University, College Station, TX 77843,
USA, bdshaw@tamu.edu. Connecting endocytosis and hyphal tip
growth. Filamentous fungi are ideal model systems to study the process
of polarized growth, since their life cycle is dominated by hyphal growth.
The importance of endocytosis through the Spitzenkörper is well estab-
lished, however, mounting evidence also suggests an important role for
endocytosis in maintaining the polarization site. Here we propose a novel
apical recycling model to explain a role for endocytosis in hyphal tip
growth. In actively growing hyphae, cortical ActA::GFP and FimA::GFP patches were highly mobile throughout the hypha and were
concentrated near hyphal apices. A patch depleted zone occupied the api-
cal 0.5 μm of growing hypha. Actin patches are well established to be
sites of endocytosis. Disruption of fimA resulted in delayed polarity es-
establishment during conidium germination, abnormal hyphal growth and
endocytosis defects in apolar cells. To further probe the role of endocy-
tosis in hyphal growth we examined the function of ArfB. A. nidulans
ArfB is an ortholog of S. cerevisiae arf3 and human arf6, two proteins
known to be involved in vesicle formation, endocytosis and actin local-
ization. Disruption of arfB resulted in a loss of hyphal polarity phenotype
delay in endocytosis. Our data support a novel apical recycling model which indicates a critical role for actin patch mediated endocy-
tosis to maintain polarized growth at the apex. Symposium Presentation

Short, Dylan*, O’Donnell, Kerry2, Zhang, Ning3 and Geiser, David.1
Department of Plant Pathology, Penn State University, University Park,
PA, USA, *Microbial Genomics and Bioprocessing Research Unit, Agri-
cultural Research Service, USDA, Peoria, IL, USA, 1Department of
Plant Pathology, Cornell University, Geneva, NY, USA, dps191@psu.edu.
Phylogenetics and population biology of a mono-
phyletic group within the F. solani species complex that is widely asso-
ciated with human infections. The F. solani species complex (FSSC)
is a group of ascomycete plant and human pathogens that are common
in many environments. The FSSC comprises several dozen phyloge-net-
ic species, seven of which correspond to known biological species, but
are otherwise morphologically cryptic. We are investigating the phylo-
genetics, taxonomy and population biology of “Group 2” of the FSSC, a
monophyletic group commonly found in the human environment and
also frequently in human infections, particularly in the 2006 outbreak
of contact lens-associated fungal keratitis. DNA sequence analysis of pro-
tein-coding genes suggested that Group 2 may actually comprise more
than one phylogenetic species. Using the complete genome sequence of
Nectria haematococca Mating Population VI (NhMPVI) as a guide, we
identified polymorphic microsatellites in intergenic regions and in other
portions of the genome useful as genetic markers for studying Group 2
and other members of the FSSC. Ten out of fifteen markers tested were

Continued on following page
successful in amplifying an expected band in Group 2, “Group 1” (NihMPV, which also commonly infects humans), as well as in the source species NhMPV1. Based on DNA sequence analysis of these regions, microsatellite polymorphism was observed in addition to non-microsatellite insertion/deletion polymorphism and nucleotide substitutions. Inferences about phylogenetic species boundaries, recombination and taxonomy will be presented. **Contributed presentation**

Simmons, D. Raben1,2, Chambers, James G.2, Churchill, Perry F.2 and Wakefield, W. Scott.2 1School of Biology and Ecology, University of Maine, Orono, ME 04469, USA, 2Department of Biological Sciences, University of Alabama, Tuscaloosa, AL 35487, USA. david.t.simmons@umit.maine.edu. **Diversity within the genus Poellomyces (Spizellomycetes, Chytridiomycota).** Since it was described in 1995 Poellomyces (Spizellomycetes), a genus of chytrids with exogenous (endobiotic) development, has contained only two species (P. hirtus and P. variabilis), which differ in location of rhizoidal axes and pigmentation when grown on nutrient agar. We commonly encounter this genus inside of pollen packets placed in water cultures of soil or dung samples. The diversity of the genus is unknown, and as a part of a project to update the taxonomy of spizellomycetanalean chytrids, we amassed over 40 strains from four continents. We extracted DNA from these cultures with standard methods or Whatman FTA cards. We cloned and sequenced amplified fragments of the nclSU rDNA and ITS1-5.8S-ITS2 regions. Our preliminary molecular phylogeny suggests that the number of species in this genus is underestimated. Our next steps will be to produce a multi-gene phylogeny and report ultrastructural and physiological differences of isolates to further document the morphological and ecological diversity within Poellomyces. **Poster**

Simonin, Anna1, Pett-Ridge, Jennifer2, Fricker, Mark3, Watkinson, Sarah1 and Glass, N. Louise.1 1University of California Berkeley, Dept Plant & Microbial Biol, Berkeley, CA 94720, USA, 2Lawrence Livermore Natl Lab, Livermore, CA 94551, USA, 3University of Oxford, Dept Plant Sci, Oxford OX1 3RB, England. annasimonin@berkeley.edu. **Fusion events influence resource distribution within and between Neurospora crassa colonies.** Vegetative hyphal fusion events occur often within colonies of higher order fungi, and more rarely between two established fungal colonies. Presumably, fusion events influence cytoplasmic and organelar movement within a hyphal network due to changes in architecture and connectivity. We tested the ability of two N. crassa fusion mutants, so and prm-1, to translocate 2-aminoisobutyric acid (AIB) throughout a colony as compared to a wild type colony. AIB is a non-metabolizable amino acid analogue that has been used as a tracer in other fungal systems. so mutants have a growth rate similar to WT but are deficient in hyphal fusion, while prm-1 mutants also have a similar growth rate to WT but have been shown to exhibit about a fifty percent fusion rate defect in germcells. The effects of these mutations on nutrient movement in a colony are discussed. We also assessed the ability of an established WT colony to share AIB with another colony via inter-colony fusion. Preliminary evidence suggests that there is no translocation from one established colony to another despite complete resource sharing observed between fused germcells. These and further studies will allow us to quantify and elucidate differences between intra-colony, inter-colony, and germling resource sharing and translocation. **Poster**

Sjokvist, Elisabet*, Larsson, Ellen and Larsson, Karl-Henrik. Department of Plant and Environmental Sciences, Göteborg University, Box 461, SE-405 30 Göteborg, Sweden. elisabet.sjokvist@dpes.gu.se. **Podoscyphaceae - polyphores after all?** Stipitate steroid basidiomycetes have previously been classified on the basis of morphological characteristics. They share the following common features: stipe, pileus, a smooth hymenophore, and hyaline smooth spores. Four genera of stipitate steroid fungi were included in molecular phylogenetic analyses in an attempt at assigning them to the orders recently described. All analyses were made on nuclear rDNA, using parsimony and Bayesian inference. The results clearly show that these fruiting body types have evolved many times independently. Genus Cotyliida belongs in the Hydrochaetales. Cymatoderma and Podoscypha cluster within Polyporales, and along with the poroid fungus Abortiporus biennis they form a monophyletic group. The type species of Stereopsis, Stereopsis radicans, clusters with the corticioid species Clavulicium globosum, but could not be placed in any of the present orders. It is likely that a new order will have to be described within Agaricomycetes to encompass Stereopsis. **Poster**

Skosireva, Irina*, Sun, Sheng and Xu, Jianping. Department of Biology, McMaster University, 1280 Main Street West, Hamilton, Ontario, L8S 4K1, Canada. jpix@mcmaster.ca. **Mitochondrial inheritance in diploid-haploid matings in Cryptococcus neoformans.** It is known that in Cryptococcus neoformans in the haploid-haplloid (HH) crosses between haploid mating type allele a (MATa) and alpha (MATα) strains, most progeny inherit mtDNA from the MATα parent. Besides mating between haploid strains, haploid-diploid (HD) mating can also occur in C. neoformans. However, the pattern of mitochondrial inheritance in these HD crosses is unknown. To determine the pattern of mitochondrial inheritance in the HD crosses, I used YZX1 (MATα) and YZX2 (MATa), which are two isogenic serotype D strains that differ only at MAT locus and both possess serotype A mitochondria. Each of these two haploid strains was crossed with 7 diploid serotype AD strains, which have serotype D mitochondria and various MAT genotypes. Four types of crosses were set up: 1) MATa x MATα/Ea/Es; 2) MATα x MATa/αa; 3) MATa x MATα/Es, and 4) MATα x MATa/Es. The mtDNA genotype of 425 progeny was determined using five molecular markers located in genes COX1, ND2 and ND5 in the mitochondrial genome. MtDNA leakage was observed in all crosses of MATα x MATα/Ea/Es and MATα x MATα/a types. These results demonstrate that for HD matings in C. neoformans mtDNA inheritance is not completely uniparental. The higher leakage (from 47.7 % to 86.4 %) was observed in HD crosses involving diploid parents which are supposedly heterozygous for three putative mitochondrial-related genes (aim17, aim28, and aim38). **Poster**

Smith, Matthew E.* and Pifeter, Donald H. Farlow Herbarium and Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA. msmith@oeb.harvard.edu. **Fungi in the Boletaceae form tuberculate ectomycorrhizae with Quercus.** The ectomycorrhizal symbiosis (EM) is a widespread interaction between diverse plants and fungi from several major lineages. Despite the polyphyletic nature of this symbiosis, the overall morphology of EM roots is similar with most plant-fungus combinations. Tuberculate ectomycorrhizae (TEM) are an unusual EM type where aggregates of roots are scattered on the soil. Conifer TEM, formed by species of *Poolemys* (Fagaceae) and Engelhardia (Juglandaceae) from Taiwan, Eucalyptus from Australia, *Photinia* (Rosaceae) from the USA, and Quercus from Japan. Little is known about these angiosperm TEM and their fungal symbionts remain unidentified. We collected TEM under Quercus in a tropical cloud forest (Xalapa, Mexico) and in a mixed deciduous forest (Massachusetts, USA). We present data from two discrete DNA regions (rDNA, ATP6) to show that these TEM fungal symbionts from geographicly distant forests are closely related species of Boletaceae. Although the exact identity of the EM symbionts is not yet known, they are phylogenetically distant from known TEM-forming fungi. The ecological and phylogenetic implications of these findings will be discussed. **Contributed Presentation**

Spiegel, Frederick W.* and Shadwick, John D. Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville, AR 72701, USA. fspiegel@uark.edu. **The global distribution of protosteloid
amoebae, *Protostelium mycophaga*. Protosteloid amoebae, more commonly known as protostelids, are an assemblage of terrestrial amoebzoans that produce simple sporocarps which consist of a microscopic stalk and a single spore or small sporangium. Until recently, it has been difficult to make any generalizations about their biogeography. However, as a result of worldwide sampling over the last decade, it has become possible to discern some patterns. The most commonly encountered morphological species is *Protostelium mycophaga* Olive & Stolzen. On a global scale, it is encountered in nearly 40% of substrate samples. However, it is not evenly distributed. It is found with high frequency in temperate North America, Hawaii i, the Caribbean, Western Eurasia, Eastern Africa, and New Zealand. However, it is uncommon in Argentine Patagonia and Tierra del Fuego, Oman, and Central Asia. It is unlikely that one explanation accounts for its rarity in all of these areas. Southern South America appears to have numerous substrates that would support protosteloid amoebae, yet all are rare, with *P. mycophaga* being least rare, suggesting that conditions select against the presence of protosteloid amoebae in general. However, in Oman and Central Asia, while protosteloid amoebae are relatively common, *P. mycophaga* makes up only a small portion of the biota, suggesting that conditions select against this species in particular. While patterns of distribution can now be discerned, it appears to be premature to speculate on cause and effect. 

Stalpers, Joost. Centraalbureau voor Schimmelcultures, PO Box 85167, Utrecht NL-3508, Netherlands. justalpers@hotmail.com. MycoBank: MycoBank was initiated by the Centraalbureau voor Schimmelcultures of the Royal Academy of Science of The Netherlands in 2004. It is a database in which all newly described fungi and new names of fungi can be deposited and stored along with key nomenclatural and descriptive material. MycoBank can serve as a central storage for the around 1,400 new scientific names for fungi introduced each year, which are now dispersed through a multitude of scientific journals. Each name that is registered is checked against a nomenclatural database (Index Fungorum) and is given a unique reference number. The deposition numbers are cited when names are published in the journals in a parallel manner to the way GenBank numbers are used. As with GenBank, MycoBank will never apply any form of censorship. The International Mycological Association (IMA), which constitutes the IUBS Section for General Mycology, has now assumed responsibility for MycoBank, and a board to govern MycoBank has been established. Several leading mycological journals (e.g. Fungal Diversity, Mycological Research, Mycotaxon, Studies in Mycology) have made the prior deposition of new names in MycoBank a requirement for publication. Proposals to make registration of new names in MycoBank mandatory after the next International Mycological and International Botanical Congresses in 2010–2011 are in process. Symposium Presentation

**Poster**

Stolze-Rybczynski, J.L.,1* Fischer, M.W.F.2 and Money, N.P.1 1Department of Botany, Miami University, Oxford, OH 45065, USA, 2Department of Chemistry and Physical Sciences, College of Mount St. Joseph, Cincinnati, OH 45065, USA. stolzel@muhiohio.edu. **Biomechanics of spore discharge in *Armillaria tabescens***, Ballistospore discharge is a feature of the majority of the 30,000 species of basidiomycete fungi. A few seconds prior to the launch of the spore, a drop of fluid (called Buller’s drop) develops at its base which enlarges until it contacts fluid on the spore surface, and then spore and fluid are catapulted into the air. We hypothesize that the mechanism has been adapted in mushrooms to avoid spore loss via impaction on the crowded surfaces of gills and spines, or within tubes. Until recently, the launch process eluded analysis, but spore motion has now been studied using ultra high speed video microscopy. Videos obtained from gilled basidiomes of *Armillaria tabescens* at a camera speed of 50,000 frames per second reveal the initial mean velocity of ballistospore discharge to be 0.64 ± 0.08 m/s (n = 9). Based on this measured velocity, the application of a mathematical model for drag provides an estimated discharge distance of 0.1 mm. The model is validated by remarkable video sequences showing the entire motion of the spore, including the stalling process between adjacent gills. These videos and estimates of energy usage during spore discharge reveal how the discharge distance is controlled to prevent spore loss within the basidiome. Research on the biomechanics of spore discharge is a vital part of efforts to understand and manage the spread of fungal pathogens. **Poster**

Suh, Sung-Oui* and Zhou, Jim. Mycology Program, ATCC (American Type Culture Collection), Manassas, VA 20110, USA. ssuh@atcc.org. **Two novel and three common ambrosia yeasts associated with the beetle Xyloterinus politus (Curculionidae).** Because lignified cellulse, the major component of wood, is not easily digested by most insects, fungi that colonize wood serve as ambrosia for certain beetle groups. Although several phylogenetically distinct yeasts and sordariomycete fungi have been reported as ambrosia fungi, their ecology and roles in this symbiotic relationship with beetles are largely unknown. In this study, we report two additional ambrosia yeasts and several common species associ-

Continued on following page
ated with *Xylotereus politus*, the ambrosia beetle that attacks black oak. Seven yeast strains isolated from this beetle were deposited in the 1980s as ATCC 62895T through ATCC 62901T but have not been formally described. Our recent studies, based on rDNA sequence comparisons and other taxonomic criteria, indicate that five of the strains belong to *Saccharomycopsis microsora*, *Pichia hamphiresinis*, and *Candida mycetangi*, which are also found in the galleries of several other ambrosia beetles. The rest were identified as novel species within the genera *Candida* and *Pichia*. ATCC 62898T, an ascospore-producing strain, is a sister taxon of *Pichia dorogenensis*. ATCC 62899T is phylogenetically close to *Candida sophiae-reginae* and *C. palmocephila* and lacks ascospores. Details of those ambrosia yeasts will be discussed indicating their molecular phylogeny and other taxonomic information. *Poster*

Sun, Qihong*, Choi, Gil H. and Nuss, Donald L. Center for Biosystems Research, University of Maryland Biotechnology Institute, 9600 Gudelsky Dr., Rockville, MD 20850, USA. choi@umbi.umd.edu. Hypovirus-responsive transcription factor gene pro1 of *Cryptophenctria parasitica* is required for female fertility, asexual spore development and stable maintenance of hypovirus infection. We report characterization of the gene pro1 encoding a putative transcription factor, identified in transcriptional profiling studies as being down-regulated in the chestnut blight fungus *Cryptophenctria parasitica* in response to infection by a virulence-attenuating hypovirus. Sequence analysis confirmed that pro1 encodes a zinc finger protein with significant sequence similarity to the pro1 gene that controls fruiting body development in *Sordaria macrospora*. Targeted disruption of the *C. parasitica* pro1 gene resulted in two phenotypic changes that also accompany hypovirus infection: a significant reduction in asexual sporulation that could be reversed by exposure to high light intensity and loss of female fertility. The pro1 null mutant, however, retained full virulence. Although hypovirus CHV1-EP713 infection could be established in the pro1 null mutant, infected colonies continually produced virus-free sectors, suggesting that pro1 is required for stable maintenance of hypovirus infection. These results complement the recent characterization of the hypovirus-responsive homologue of the *Saccharomyces cerevisiae* Ste12 transcription factor, cpsi2, that was shown to be required for *C. parasitica* female fertility and virulence. *Poster*

Sun, Sheng* and Xu, Jianping. Department of Biology, McMaster University, 1280 Main Street West, Hamilton, Ontario, Canada, L8S 4K1. suns6@mcmaster.ca. *Inter-variety chromosomal rearrangements in Cryptococcus neoformans*. Cryptococcus neoformans is a major human pathogenic fungus that causes meningitis in immunocompromised hosts. *C. neoformans* has two different varieties, var. neoformans and var. grubii. Inter-variety hybridization results in both a low level of recombinant and progeny with low viability, suggesting chromosomal rearrangements may exist between the varieties. In this study, we compared chromosomal differences between the two varieties. Using the available genome sequences for H99 and JE2C1, we determined that although the two genomes displayed overall synten, there were 31 chromosomal rearrangement regions involving transpositions, translocations and inversions. Significantly lower levels of inter-variety recombinant were observed in these rearranged chromosomal regions compared to syntenic chromosomal regions. Using a direct PCR strategy, we further studied the polymorphism of eight simple inversions in a collection of 64 natural *C. neoformans* strains including both varieties as well as inter-variety hybrids. We found that at all of the eight inversion regions, strains belonging to the same variety had the same variety-specific chromosomal arrangement. Naturally occurring inter-variety hybrids showed different levels of heterozygosity at the eight regions. Results from our study will help us to better understand the ecology, population structure and evolutionary history of *C. neoformans*. *Contributed Presentation*

Taylor, D. Lee†*, McFarland, Jack W.†, Booth, Michael G.†, Herriott, Ian C., Lennon, Niall J.‡ and Nusbaum, Chad.‡ University of Alaska, Institute of Arctic Biology, 311 Irving Building, Fairbanks, AK 99775, USA. *Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA. flt@uaf.edu. Sequencing the boreal forest: What do 70,000 new sequences tell us about fungal ecology? Fungi are key players in nutrient cycling in the boreal forest, yet their diversity and specific roles are completely undescribed. Boreal forest soils contain roughly one quarter of Earth’s labile organic carbon, but climate warming and climate-driven changes in disturbance regimes are likely to substantially alter carbon dynamics. We are characterizing fungal community structure across habitats, successional stages, and soil horizons, primarily within the Bonanza Creek LTER site of interior Alaska. Here we present an overview of results from high throughput sequencing of 14 PCR clone libraries constructed from 2100 soil cores collected across 21 sites sampled twice in consecutive years. Nine of the sites represent early (willow-aspen), mid (birch-aspen) and late (white spruce) successional stages in Bonanza Creek upland ecosystems, while 12 of the sites represent four distinct black spruce community types. To date, the project has generated roughly 70,000 bidirectional clone sequences which reveal that boreal forest soil fungal communities are remarkably diverse in species numbers and in deep phylogenetic breadth. Approximately 2000 operational taxonomic units (OTUs) were recovered from the black spruce sites and diversity was even higher in the upland sites. Fifty-eight percent of the black spruce OTUs occurred once in the dataset (i.e. “singltons”), suggesting that even with our massive sequencing efforts, we have not fully captured the diversity present. Fungal community composition varied relatively little between years, while shifts in species composition through successional stages were apparent. We also observed differences among communities in acidic and non-acidic black spruce sites, with higher diversity indices (due to greater evenness of dominants) in the non-acidic sites. However, community composition was much more strongly correlated with soil horizon (litter vs. humic vs. mineral) than any other factor in every study site. Because we sequenced a rapidly evolving marker, the nuclear ribosomal ITS plus LSU, we were able to identify many of the OTUs to species or genus and infer the trophic guilds to which they belong. Plant-associated taxa (especially ericoid or ectomycorrhizal) were far more abundant (typically >60% of clones) than classical decomposers, i.e. “saprophytes” (typically <15% of clones) in each study site. Because clone numbers are roughly proportional to biomass, our results strongly suggest that plant-associated fungi account for a much greater fraction of the living mycelium in soil than do decomposer fungi. This observation has implications for plant nutrition and the dynamics of carbon sequestration and release from the massive pools present in boreal forest soils. *Symposium Presentation*

Thaler, Andrew†*, Schultz, Tom†, Vilgalys, Rytas‡ and Van Dover, Cindy.† Duke University Marine Lab, Beaufort, NC 28516, USA, ‡Duke University, Durham, NC 27708, USA. adt5@duke.edu. Dominant fungi from Gulf of Mexico methane seeps represent an undescribed ascomycete clade. The extent of fungal diversity in marine ecosystems is poorly characterized. Marine fungi may represent a reservoir of previously unexplored diversity. Fungi have been reported at deep-sea hydrothermal vents and methane seeps. Methane seeps are formed when methane is released from gas hydrate reservoirs, are hydrocarbon rich, and may contain populations of ecologically significant fungi that differ from those of the surrounding sediment. Sediment cores were collected from the Alaminos Canyon methane seep in the Gulf of Mexico and environmental DNA was extracted using a commercial extraction kit. Partial sequences of the large ribosomal subunit were amplified and sequences were compared against the NCBI Genbank and AFTOL databases. Results were aligned with their closest matches and a phylogeny was assembled. Eurkaryotic diversity was greatest in the upper 0-2 cm of the sediment. There was an increase in the number and percentage of fungal phyotypes recovered from the redox boundary at 2-4 cm. Within this zone, the most common sequences recovered were from an unidentified phylotype that aligns within the ascomycetes. This phylotype could represent an undescribed group of fungi endemic to the deep sea. The presence of a novel ascomycete clade at the redox boundary suggests the presence of a specialized fungal group that can exploit this microhabitat. *Poster*
after 6 days of incubation on MEA and PDA they formed in concentric rings and became orange in color after 2 wk. All isolates had hyaline, growth occurring at 30°C. The isolates produced sclerotial-like structures but did not produce asexual or sexual spores. On MEA and PDA amended with 0.5% tannic acid, all isolates produced a green, orange, and red similar to a sequence deposited in GenBank (accession no. AY969953) from an uncultured basidiomycete. Research is currently in progress to better characterize and identify this basidiomycete fungus.

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Thomas, Elizabeth* and Kropp, Bradley R. Department of Biology, Utah State University, 5305 Old Main Hill, Logan, UT 84322, USA. bkropp@biology.usu.edu. **Expression analysis of iTCP79B2 during the rust infection of Dyer’s Wood by Puccinia thlaspeos.** Glucosinolates and their hydrolysis products are part of a plant defense response to pathogens. Dyer’s wood (Isatis tinctoria) has been shown to produce unusually high levels of indole glucosinolates. In this study, a sequence encoding CYP79B2 was isolated from dyer’s wood. iTCP79B2 from dyer’s wood has 97% percent sequence identity to CYP79B2 from Arabidopsis thaliana and 89 percent sequence identity to CYP79B3 from A. thaliana. Because of high sequence identity, it could be inferred that the dyer’s wood sequence, like that of A. thaliana, is likely involved in synthesis of indole glucosinolates. The kinetics of iTCP79B2 expression during the first 72 hours of infection by P. thlaspeos was also studied using real time PCR. There was a significant down-regulation of iTCP79B2 during the first 8 hours after infection, an up-regulation after 16 hours, followed by continued down-regulation through the rest of the 72 hour period. **Poster**
**RNA editing of cryptic mitochondrial genes in Didymium iridis.** The mitochondrial genome of the myxomycete Didymium iridis lacks Open Reading Frames (ORFs) for most gene products. Research in a related organism, Physarum polycephalum, has revealed extensive co-transcriptional editing of mRNA transcripts to produce functional gene products. Editing events were primarily single-nucleotide insertions, but also included dinucleotide insertions and C to U conversion events. We sequenced the cDNAs of six mitochondrial genes in D. iridis: atp1, atp6, cox1, cox2, cyb, and nad7. We compared the edited sequence to the genomic sequence and characterized the editing events. In addition, we compared the RNA editing patterns of D. iridis and P. polycephalum. We identified 286 additional bases not found in the genome, representing 278 separate editing events. Of these, 197 events were unambiguous in their location. Many of the patterns previously reported in P. polycephalum were found in the D. iridis sequence, including the preponderance of single C nucleotide insertions (257 of 286), the correlation between purine-pyrimidine dinucleotides immediately upstream of editing sites (56.4% of unambiguous editing events), and the high frequency of 3rd codon position editing events (55% of the unambiguous events). There was some conservation of specific editing sites between the two organisms, though this varied on a gene by gene basis. **Poster**

Trphin, D.1*, Stolze-Rybczynski, J.L.1, Fischer, M.W.F.2 and Money, N.P.1 1Department of Botany, Miami University, Oxford, OH 45056, USA, 2Department of Chemistry and Physical Sciences, College of Mount St. Joseph, Cincinnati, OH 45056, USA. tmind2@muohio.edu. **Spore launch by drying:** The cavitation-based mechanism of conidial discharge in the banana pathogen Deightoniella torulosa. The anamorphic ascomycete Deightoniella torulosa (Syd.) M.B. Ellis is a pathogen of banana, causing “black spot” and other diseases of this globally-threatened fruit crop. Its large conidia are discharged from the surface of banana fruits and vegetative tissue in response to dry airflow. The spore is launched by the explosive formation of a gas bubble (cavitation) in the bulbous tip of the subtending conidiophore. This extraordinary mechanism was first hypothesized in the 1960s, but could not be verified because gas bubble formation and the separation of the spore from the conidiophore occurred too swiftly to be visualized using conventional microscopy. In this poster, we present new information obtained using an ultra high speed digital video camera. Analysis of video data obtained at camera speeds of up to 75,000 frames per second show how this mechanism is capable of launching conidia at a mean initial velocity of 0.22 ± 0.18 m/s (n = 23). Based on this measured velocity, the application of a mathematical model for drag provides an estimated discharge distance of up to 0.93 mm from the host, which is sufficient to drive the conidia into the prevailing wind. Our research has contributed to the understanding of the biology of an important fungal pathogen and has important implications for the study of biometrics. **Poster**

Tsui, Clement K.M.1,2,4*, Kaocharoen, Sirad2, Wang, Bin3, Trilles, Luciana3, Fanrong, Kong4 and Meyer, Wieland.1,4 1Molecular Mycology Research Laboratory, Centre for Infectious Diseases and Microbiology, Westmead Millennium Institute, Westmead Hospital, Westmead, Australia, 2Inter-Department of Medical Microbiology, Graduate School, Chulalongkorn University, Bangkok, Thailand, 3Retroviral Genetics Laboratory, Centre for Virus Research, Westmead Millennium Institute, Westmead Hospital, The University of Sydney, Australia, 4Laboratório de Micologia, Instituto de Pesquisa Clínica Evandro Chagas, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil, 5Centre for Infectious Diseases and Microbiology-Public Health, Institute of Clinical and Medical Research, Westmead Hospital, Westmead, Australia, 6Faculty of Medicine, The University of Sydney, Western Clinical School at Westmead Hospital, Sydney, Australia, 7Department of Forest Science, University of British Columbia, Vancouver, BC, V6T 1Z4, Canada. clementtsi@gmail.com. **Hyperbranched rolling circle amplification as a rapid and sensitive method for species identification within the Cryptococcus species complex.** The Cryptococcus species complex contains two closely related basidiomycetous yeasts: Cryptococcus neoformans and C. gattii, which cause cryptococcosis in humans and other animals. The species and varieties are characterized by different clinical, epidemiological, biochemical and molecular features. The currently used identification methods are either time consuming or no longer commercially available. However, a rapid, sensitive and robust assay for the detection of these pathogens is vital for early diagnosis and appropriate treatment decisions. To overcome those limitations, four padlock probes targeting species-specific single nucleotide polymorphisms at the internal transcribed spacer (ITS) of the RNA gene locus were developed and applied during isothermal hyperbranched rolling circle amplification (HRCA). The probes were tested against 99 samples, including 94 clinical cryptococcal cultures, three closely related Cryptococcus species, and two clinical specimens. The use of the padlock probes and the combination of probe signal amplification by HRCA provided a quick and sensitive assay for the accurate identification of C. neoformans var. grubii, C. neoformans var. neoformans and C. gattii. HRCA was also useful to detect hybrids, when they were heterozygous at the ITS locus. The HRCA results were in agreement with previous genotyping data based on PCR fingerprinting, AFLP and ITS sequencing. **Contributed Presentation**

Upadhyay, Srijana*, Chang, Dauwon, Ebbole, Daniel J., Wilkinson, Heather H. and Shaw, Brian D. Department of Plant Pathology and Microbiology, Program for the Biology of Filamentous Fungi, Texas A&M University, College Station, TX 77843, USA. srijanapadhyay@tamu.edu. **Comparative analysis of fluG function in Aspergillus nidulans and Neurospora crassa.** Asexual reproduction, conidiation, is an important phase in the life cycle of fungi, which in Aspergillus nidulans initiates with the emergence of an aerial conidiophore stalk, followed by the development of an elaborate multicellular conidiophore that produces unineucelar haploid spores called conidia. Genetic regulation of conidiation is well characterized in A. nidulans, but comparative analysis of the function of these genes in other fungi is limited. In A. nidulans flug is involved in generation of an extracellular signal required for activation of asexual development. In Neurospora crassa, deletion of the flug ortholog (NCU04264) produced a mutant that displayed no detectable phenotype. Surprisingly we found that complementation with the NCU04264 gene restored the conidiation defect of the A. nidulans flug mutant. Overexpression of NCU04264 in A. nidulans via the alcA promoter also conferred the ability to initiate conidiation in submerged culture. Our results demonstrate conservation of biochemical function of the flug product between the two species, even though the flug ortholog apparently does not function in conidiation in N. crassa. **Poster**

URen, Jana M.1*, Lutzoni, François2, Miadlikowska, Jolanta2 and Arnold, A. Elizabeth.1 1Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA, 2Department of Biology, Duke University, Durham, NC 27708, USA. juren@email.arizona.edu. **Evolutionary relationships of endophytic, endolicenichic and saprotrophic fungi in the Chiricahua Mountains.** We examined the evolutionary relationships and diversity of endophytic, endolicenichic, and saprotrophic Ascomycota from phylogenetically diverse plants and lichens in the Chiricahua Mountains of Arizona. We cultured 732 endlichenic and endophytic fungi from 10 lichen species and 10 plant species (mosses, ferns, conifers and angiosperms), as well as 355 saprotrophs occurring in dead leaves in the canopy and host-associated leaf-litter. To estimate diversity, host specificity and taxonomy, the internal transcribed spacer rDNA region was sequenced for all isolates. Fungi from all trophic modes are highly diverse; we recovered > 200 genotypes and 5 classes of Pezizomycotina. Fungal
communities isolated from living tissue were significantly more diverse than fungi recovered from dead tissue. At the class- and genotype levels, endophytes and endolichecnic fungi are more similar to each other than to saprotrophs, especially when compared against fungi from leaf litter. Preliminary assessments indicate that phylogenetically distinct lichens share multiple genotypes of endolichecnic fungi, regardless of growth form or substrate. Phylogenetic analyses for focal genera will consider the evolutionary relationships and evolution of trophic modes of these novel fungi. **Contributed Presentation**

Vellinga, Else C.1,6 Hemmes, Don E.2, Mueller, Ulrich G.3, Sysoyphanthong, Phongeun3, Kasm, Søytong2 and Bruns, Thomas D.1 1University of California, Berkeley, CA 94720, USA, 2University of Hawaii, Hilo, HI 96720, USA, 3University of Texas, Austin, Austin, TX 78712, USA. 4Mushroom Research Centre, Chiang Mai 50150, Thailand, 5King Mongkut’s Institute of Technology Ladkrabang, Bangkok 10520, Thailand. vellinga@nature.berkeley.edu. **Leucoagaricus and Leucocephorinus (Agaricaceae): A systematic and phylogenetic approach.** The two saprotrophic genera Leucoagaricus and Leucocephorinus form a monophyletic clade within the Agaricaceae, but are not monophyletic themselves. Their geographic distribution is in the tropics, subtropics and temperate zones, and they are absent from high altitude and latitude regions. Collections from four different biodiversity hotspots are analyzed to gain insight in the phylogeny of the group and the placement of this clade in the family, and to learn the species composition for each region. All four areas, California, Hawai’i, Panama and northern Thailand, have a unique set of species. Only a few species are widespread, and these occur in man-made habitats. California is rich in species of Leucoagaricus section Piloselli (species that have a strong auto-oxydativ reaction) and section Rubroineci (species with a cutis as pileus covering), Hawai’i has a relatively high number of traditional ‘Leucocephorinus’ species; species from Panama and Thailand are diverse and group in unnamed clades. In all regions, some habitats host a large number of species. This is the first comprehensive study of the group for all four regions; finding names for the species is a challenge. Questions such as is it possible to divide the clade into morphologically defined subclades and where did this group originate will be addressed. **Poster**

Virag, A.1, Semighini, C. P.1, Upadyay, S.2, Shaw, B. D.2 and Harris, S. D.1,6 1Department of Plant Pathology and Center for Plant Science Innovation, University of Nebraska, Lincoln, NE 68588-0660, USA, 2Department of Plant Pathology and Microbiology, Texas A&M University, College Station, TX, 77843, USA. **Function -
al characterization of pxillin homologues in Aspergillus nidulans.** Paxillin is a well-characterized protein that links the extracellular matrix to the actin cytoskeleton in animal cells and is intimately involved in multiple aspects of cellular morphogenesis. Characteristic features of pxillin include the presence of multiple C-terminal LIM domains. Here, we report that the filamentous fungus Aspergillus nidulans possesses two distinct pxillins, PxA and PxB. PxA possesses two LIM domains and localizes to a surface crescent at hyphal tips that likely corresponds to the polarisome. Analysis of deletion mutants shows that PxA is not required for polarization but does play a role in the maintenance of a stable polarity axis and is needed for normal rates of hyphal extension on minimal media. These observations implicate PxA in polarization some function. By contrast, PxB possesses three LIM domains and localizes to the septum where it forms a constricting ring. Analysis of deletion mutants suggests that PxB is required for formation of a stable cytokinetic actin ring that constricts in a timely manner. Addition -

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Volk, Thomas J., Curland, Rebecca4 and Jarvis, Elisabeth4 Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. volk.thom@uwlax.edu. **Plant pathology vs. medical mycology: Battle of the fungi.** Although humans and plants are clearly different disease hosts, the study of fungal diseases in plants and humans share many matching ITS phylotypes to voucher collections and photographs of field specimens, species-level identification was possible for many common saprobcic and mycorrhizal Agaricomycetes groups, including Russula, Suillus, Mycena, Gymnopus and others. Using ITS sequences as the primary sampling unit, we have been able to identify a broad variety of fungi collected through both specimen-based and culture-independent surveys. Based on these data, it is reasonable to assume that within a restricted geographic area such as Duke Forest, sequence overlap between closely related species of macrofungi is rare, and intra-specific ITS variation is less common. **Poster**

Vigilas, Rytas1,2, Parente, Jeri L.2, Williams, Gwendolyn1, Jackson, Jason1, O’Brien, Heath1, Johnson, James L.1 and Moncalvo, Jean-Marc. 1Department of Biology, Duke University, Durham, NC 33333, USA, 2Department of Integrative Biology, University of Guelph, Ontario, N1G 2W1, Canada. **Molecular-based survey of fungal diversity across changing Piedmont Forest communities: Still hammering away with the ITS region.** The Duke Forest, located in the central North Carolina piedmont plateau, is an important research site for many studies on forest community dynamics, environmental change, and the effects of land use history on natural communities. Using a combination of specimen- and clone-based approaches, we contrasted fungal community diversity within the Duke Forest from two Permanent Sample Plots (PSPs) representing different major piedmont forest soil communities. Soil clone libraries were prepared from separate litter, organic, A-horizon, and B-horizon samples. Taxonomic identification was enhanced by additional sequencing of sporocarp and mycorrhiza samples from several PSPs. As reported earlier (O’Brien et al., 2006), fungal diversity in these forest types is very high, with estimates of upwards of 1000 species per PSP, and a total estimated forest diversity (ACE) of 2845 species. The Duke Forest soil fungal community is dominated by several groups, including many saprobcic and mycorrhizal taxa of Agaricomycetes. **Poster**

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more characteristics than are generally acknowledged. Plants and humans share some commonality in the taxa of fungal pathogens (Koch’s postulates!), modes of infection, and how the pathogen travels through the organism. Plants and humans share broad categories of infections such as superficial diseases of the epidermis, traumatic implantation, and systemic pathogens. Conditions such as stress / weakened defense system or high heat and humidity can favor fungal growth in both groups. However, given the dissimilarity between the two hosts, the signs, symptoms, host defenses, and treatment methods differ greatly. Where is the disease triangle in medical mycology? Most fungal plant pathogens are specific to one host species, but can easily spread between individuals. In contrast, almost all fungal human diseases affect other mammals, but are typically not contagious. Human mycoses are typically more difficult to treat because of similarities between fungal and animal cells and their close phylogenetic relationship. The main purpose of this poster is to show that Plant Pathology and Medical Mycology are not so different after all, and, despite different terminology for the same processes and structures, both groups have much to learn from the other. Poster

Walberg, Eric D.* and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. walberg.eric@students.uwlax.edu. Much ado about radiotrophs: Preliminary study of effects of ionizing radiation on carotenoid-containing fungi. UV-protective pigments are ubiquitous in nature, and highly selected for in habitats with high UV exposure. Examples of these are carotenoids, melanins, and a diverse group of small aromatic molecules (SAMs), such as many ‘lichen compounds.’ All these compounds contain series of conjugated double bonds that confer a wide absorbance spectrum, melanin being the extreme case. Previously, these have all been thought to serve merely photoprotective and antioxidant roles in fungi. Recent studies (Dadachova et al. 2007) have suggested, however, that melanin-containing fungi may be able to capture energy from ionizing radiation for metabolic use. However, melanins are large extracellular polymers, while carotenoids and SAMs are small, usually intracellular compounds. It is possible, however, that carotenoids and SAMs may also be useful in energy capture, depending on the mechanism of energy transfer. We have selected several species of fungi that contain either carotenoids or SAMs for experimentation. Our initial experiments deal with the phenomenology of exposure of these fungi to various kinds of radiation (e.g. gamma, neutron, UV, and visible light). Fungi containing SAMs and/or carotenoids, as well as derived colorless mutants, will be tested to see if growth parameters are affected. Practical implications in terms of raditrophy and radiotolerace will be discussed. Poster

Walker, Allison* and Campbell, Jinx. University of Southern Mississippi Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39564, USA. allison.kennedy@usm.edu. Marine fungi as indicators of human disturbance on Mississippi Gulf Coast beaches. Marine fungi are principally found in intertidal habitats such as beaches where they play an important role in nutrient cycling. Human impact can drastically change a coastal environment and because fungi are sensitive to anthropogenic influence, they may have utility as indicators of human disturbance levels. The purpose of this project was to investigate differences in marine fungal communities found on barrier island beaches compared to those found on Mississippi Gulf Coast beaches variously impacted by human disturbance. Substrates including driftwood, algae, sand and flotsam were collected from pristine and disturbed beaches in fall and spring and examined for the presence of marine fungi using morphological and molecular (ITS T-RFLP) techniques. Marine fungal species richness, density and community composition were compared among beaches and effects of salinity, pH, water temperature, season and beach disturbance levels were assessed. Poster

Walker, Donald M.*, Rossman, Amy Y.*, Castlebury, Lisa A.*, Mejia, Luis*, Sogonov, Mikhail V.* and White, James F.1 Department of Plant Biology and Pathology, Rutgers University, 59 Dudley Road, Foran Hall, New Brunswick, NJ 08901, USA. Systematic Mycology & Microbiology Laboratory, USDA-ARS, Rm. 304, B011A, 10300 Balti-
orobutyric anhydride and gas chromatography with electron capture detection was used to identify the compounds of interest. The detection limits for DON and ergosterol were 10 and 500 pg/µL, respectively. Results regarding disease incidence, fungal growth and DON translocation will be discussed. **Contributed Presentation**

Wilson, Andrew W.*, Binder, Manfred and Hibbett, David S. Department of Biology, Clark University, Worcester, MA 01610, USA. awilson@clarku.edu. Is gastromycetization in the Agaricomycetes represent an evolutionary dead-end or a key innovation? A study with emphasis on the Sclerodermataceae. Gasteroid Agaricomycetes have enclosed hymenophores and have lost ballistospory (forcible discharge). The loss of ballistospory is thought to be irreversible, and therefore lineages that have evolved a gasteroid morphology are unable to revert to hymenomycetous forms. In other words, gastromycetization constrains morphological evolution. We are interested in determining if gastromycetization also constrains taxic diversification (i.e., species proliferation), as well as morphological diversification. We focused on the Sclerodermataceae (Boletales) and several other lineages, such as the Lycoperdaeae and Phallomycetidae, which include morphologically diverse gasteroid and hymenomycetous genera. Recent molecular studies in the Sclerodermataceae suggest that the group experienced a period of early rapid diversification, possibly indicating that gastromycetization was a key innovation within the lineage. We used stochastic mapping methods to analyze a five-gene dataset for the Sclerodermataceae, and other available datasets of gasteroid Agaricomycetes to address the question: is gastromycetization in the Agaricomycetes an evolutionary dead-end, or a key innovation? **Contributed Presentation**

Wilson, Nathan. 1037 N. Rose St.Burbank, CA 91505, USA. nathan@mushroomobserver.org. Harnessing user generated content: Blurring the distinction between amateur and professional mycologists. Amateur and professional mycologists have had a long and fruitful relationship. However, there remains a great deal of potential that can now be realized using the emerging tools of taxonomic bioinformatics. The key is to enable user generated content through the internet. Amateurs are eager to get access to professional experience, literature and tools. In return they can now provide an unprecedented level of worldwide coverage including photographs, macroscopic and microscopic descriptions as well as habitat and distribution data. The amateur community can help correct errors that have been made in interpreting existing literature, help spread new knowledge, and be effective collaborators in the creation of new knowledge. The best way to achieve these goals is to create effective internet-based tools for disseminating original source literature, providing access to professional tools such as DNA sequencing hardware and most importantly facilitating active conversations between the people in the professional and amateur communities. **Symposium Presentation**

Winton, Loretta M.*, Zhang, Mingchu 2, and Sparrow, Steven D.1 USDA ARS, Subarctic Agricultural Research Unit, Fairbanks, AK 99775, USA, 2School of Natural Resources & Agricultural Sciences, University of Alaska Fairbanks, Fairbanks, AK 99775, USA. lori.winton@uaf.edu. Fungal diversity and chemical properties in agricultural and forest soils in Alaska. Fungal species diversity and community structure in soil is currently an active area of research but the majority of cultivation-independent studies have focused on soils in natural systems. We took replicate mineral phase soil samples from actively managed barley fields, partially managed fields in the Conservation Reserve Program (CRP), and unmanaged forest lands near Delta Junction, Alaska. Soil pH was similar among the three land uses. Soil total carbon was highest in samples from barley fields and lowest in forest samples. Ten-week incubations indicated that forest soil samples had the lowest active carbon pool and mineralizable N. We sequenced ITS clone libraries to compare soil fungal diversity among the three land uses. In barley, 77% of the clones were assigned to 11 orders of Ascomycota, 14% to five orders in Basidiomycota, 8% to Zygomycota, and 1% to Glomeromycota. In CRP, 60% of the clones were in four orders of Ascomycota, 36% to six orders in Basidiomycota, 4% were in Zygomycota, and <1% in Glomeromycota. In forest soils, 52% were in eight orders of Ascomycota, 47% in 11 orders of Basidiomycota, and 1% in Zygomycota. The successive increase of Basidiomycota (and corresponding decrease of other taxa) from barley to CRP to forest correlates well with plant type, soil type, and management regime. **Poster**

Wolfe, Benjamin E.1,2, Tulloss, Rodham E.2, Jahren, A. Hope3 and Pringle, Anne.1 Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA, 2Herbarium Rooseveltensis Amanitarum, Roosevelt, NJ 08555, USA, 3Earth and Planetary Sciences, Johns Hopkins University, Baltimore, MD 21218 USA. bwolfe@fas.harvard.edu. Evidence for a single origin of the ectomycorrhizal symbiosis within the genus Amanita. The ectomycorrhizal (EM) symbiosis has evolved repeatedly across the kingdom Fungi, but the evolutionary stability of this trait at finer taxonomic scales has not been assessed. Amanita is an iconic fungal genus with most species forming EM associations. However, some Amanita species are found in grassland ecosystems without woody plant hosts and are assumed to be saprotrophic. These putatively non-mycorrhizal species are rarely collected, but may provide clues to the origin of the EM symbiosis within this diverse clade. Using a multilocus phylogenetic reconstruction and stable isotope data from a global collection of Amanita species, we estimated the number of times the EM symbiosis has evolved in Amanita. We find evidence for a single origin of the EM symbiosis with strong support for a monophyletic clade of mycorrhizal Amanita species and all non-mycorrhizal Amanita species forming basal clades in the phylogeny. Stable isotope signatures of putatively non-mycorrhizal species are similar to other saprotrophic homobasidiomycetes and significantly different from mycorrhizal Amanita species, confirming that these basal Amanita species are saprotrophic. Our results suggest that the evolution of the EM symbiosis may have served as a key innovation in the diversification of Amanita. **Contributed Presentation**

Yafetto, L.1*, Davis, D. J.2 and Money, N. P.3 Department of Botany, Miami University, Oxford, OH 45056, USA, 2Department of Chemistry and Physical Sciences, College of Mount St. Joseph, Cincinnati, OH 45233, USA. yafettll@muohio.edu. How rhizomorphs work. Fungal rhizomorphs are complex, multicellular, root-like organs formed through the aggregation, interlacing, and adhesion of millions of tip-growing hyphae. There has been very little research on the invasive mechanism utilized by rhizomorphs to penetrate compacted soils and woody substrates. The pathogen Armillaria mellea forms rhizomorphs in culture and serves as an excellent model for developmental studies. This presentation addresses (i) features of rhizomorph anatomy in this fungus that support its invasive behavior; (ii) the adaptive growth response of rhizomorphs subjected to mechanical stress; (iii) the biochemical basis of turgor generation and nutrient translocation within rhizomorphs, and (iv) novel measurements of the forces exerted by growing rhizomorphs. Our experiments provide the first clear picture of the mechanical processes that allow rhizomorphs to function as migratory organs in low-moisture and nutrient-poor environments that present substantial obstacles to fungal colonization. **Contributed Presentation**

Yun, Hye Young. Systematic Mycology and Microbiology Lab., Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, USA. hye.yun@ars.usda.gov. An investigation of Korean Gymnosporangium species causing cedar rust. A study of the biodiversity, distribution, host specificity and phylogeny of Korean Gymnosporangium species using morphology, artificial inoculation and molecular phylogenetic analysis was performed. Nine species were recognized and distributions were constructed for South Korea. Gymnosporangium uncirne sp. prov. and five additional species were reported from South Korea for the first time. New morphological characters, hosts and regional habitats were observed. Phylogenetic relationships of nine representative Gymnosporangium taxa were studied with nuclear 28S rDNA sequence data. Sequences varied at the species rank

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and were useful for species delineation. Collections initially identified as *G. asiaticum* formed sister clades with strong bootstrap support. Further analysis with AFLP data and a reexamination for unique morphological characters showed that *G. uncinum* was distinct from its sister taxon, *G. asiaticum*. Phenotypic variation of primarily morphological, telial and aecial characters was evaluated by mapping on the molecular phylogenetic tree. Among seven telial characters, telial host, position of telia, telial shape, telial length and teliospore length appeared well conserved and could be used to differentiate species. Nine aecial characters were similarly evaluated for some taxa and, seven were relatively well conserved. A revised identification key for Korean *Gymnosporangium* species was offered. 

**Contributed Presentation**

Yun, Hye Young¹,², Kim, Young Ho³, Hong, Soon Gyu¹, Huang, Yun⁴ and Lee, Kyung Joon.⁵ ¹Systematic Mycology and Microbiology Lab, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, USA, ²Department of Agricultural Biotechnology, Seoul National University, Seoul 151-921, Republic of Korea, ³Polar BioCenter, Korea Polar Research Institute, KORDI, 7-50 Songdo-dong, Yeonsu-gu, Incheon, Republic of Korea, ⁴Department of Plant Protection, Sichuan Agricultural University, Ya’an, Sichuan, China, ⁵Department of Forest Science, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Republic of Korea. HyeYoung.Yun@ARS.USDA.GOV. **Distribution, morphology and molecular phylogeny of Gymnosporangium species in Northeastern China.** This study was an investigation of the distribution and biodiversity of the causal agents of cedar rust, *Gymnosporangium* species, in Northeastern China. Morphological and phylogenetic characters were used to compare Chinese taxon with those found in Korea. During the survey of the fungi in the three northeastern provinces of China, Jilin, Liaoning and Heilongjiang Provinces, from 2003 through 2006, *G. asiaticum*, *G. japonicum* and *G. yamadae* were identified and, detailed morphological descriptions and listings of several unrecorded telial and aecial host species from Jilin and Liaoning Provinces were produced. Nuclear 28S rRNA gene sequences of the three *Gymnosporangium* species showed variability at the species rank. However, populations of the same species from China and Korea were not differentiated phylogenetically or morphologically. The northeastern provinces and the Korean Peninsula have similar vegetation consisting of the same telial and aecial host species and may be geographically close enough to allow spore dispersal between them, except for the inhospitable, cold Heilongjiang Province where no or few telial and aecial host plants grow. These results suggest that populations of the same species have opportunities for genetic recombination during their heteroecious life cycle. Thus, speciation has not occurred due to interbreeding of Chinese and Korean populations. **Poster**

Zitomer, Nicholas C.*, Glenn, Anthony E., Bacon, Charles W. and Riley, Ronald T. USDA-ARS, Toxicology and Mycotoxic Research Unit, Athens, GA, USA. nik.zitomer@ars.usda.gov. **A single extraction method for the analysis by liquid chromatography/tandem mass spectrometry of fumonins and biomarkers of disrupted sphingolipid metabolism in tissues of maize seedlings.** The fungus *Fusarium verticillioides* is a pathogen of many plants and is known to produce fumonisins. These toxins have been shown to contribute to the development of maize seedling disease. Fumonisin disruption of sphingolipid biosynthesis has been demonstrated to occur during such pathogenesis. A liquid chromatographic/mass spectrometric method was developed for the analysis of fumonisin content in maize leaf tissue, as well as the elevation of biomarkers of sphingoid base disruption in those tissues. This method involved a quick extraction and subsequent analysis on a mass spectrometer. To test the efficacy of the method, seed of susceptible and resistant maize lines were inoculated with a pathogenic, fumonisin-producing strain of *F. verticillioides*. The maize seedlings were then harvested and analyzed for fumonisins, as well as sphingoid bases and their 1-phosphates. Fumonisin accumulation was evident in the leaves of inoculated plants and was significantly greater in the leaves of the susceptible maize variety than the resistant variety, as well as elevation of sphingoid bases and sphingoid base 1-phosphates. Unexpectedly, FB1 was preferentially accumulated in the leaf tissues over FB2 and FB3. The method developed was effective, fast, and sensitive for use in determining these indicators of disease induced by infection and toxin production. **Poster**

**MYCOLOGICAL NEWS**

**Fungi Cause Many Disease Outbreaks but Mostly Ignored**

**American Academy of Microbiology News Release:**

**Report Calls for New Resources for Studying Fungi That Impact Human Health and Agriculture**

Washington, DC – June 24, 2008 – Fungi can cause a number of life-threatening diseases but they also are becoming increasingly useful to science and manufacturing every year. However, many people, scientists among them, are largely unaware of the roles fungi play in the world around us. Research on fungi and fungal diseases are seriously neglected as a result – a situation with grave negative repercussions for human health, agriculture, and the environment – according to the *Fungal Kingdom: Diverse and Essential Roles in Earth’s Ecosystem*, a new report from the American Academy of Microbiology.

The report is the product of a colloquium convened by the Academy in November, 2007, where experts in mycology, medicine, plant pathogens, and ecology discussed the current state of research in mycology and compiled a list of specific recommendations for future work.

“The average person is at risk for several fungal diseases, from toenail infections to athlete’s foot to life threatening systemic infections,” says Arturo Casadevall of the Albert Einstein College of Medicine and one of the co-chairs of the colloquium. “Fungi may also predispose people to asthma and allergic diseases,” says Casadevall. Despite the frequency of fungal infections, according to the report they are relatively understudied, making fungal infections difficult to diagnose and treat. When faced with an undiagnosed fungal infection, doctors are forced to treat their patient without a firm grasp of which drugs will work and which drugs will only cost the patient valuable time.

But fungi are more than just a medical problem; as the cause of more than half of all plant diseases, fungi are also an expensive drain on agriculture. The economic repercussions of managing fungal pathogens on crops – the money and effort spent, the numerous pesticide applications, the consequences of these applications for surface water and soil quality, and the impacts on crop yields – are extraordinary.

In the environment, fungi are not seen as a liability but...
as an integral part of their ecosystems. They break down dead plants and animals (organic matter) into the building blocks plants need for growth and they engage in beneficial symbiotic relationships with plants, all functions necessary for maintaining healthy ecosystems. When an ecosystem is disturbed, fungi can behave in unexpected and often destructive ways, as in the case of the black mold that is overrunning the areas surrounding the Chernobyl nuclear power plant in Ukraine and outbreaks of coral bleaching that are destroying coral reefs. Scientists still do not understand fungi well enough to predict how these organisms will behave when their environment is disturbed.

Industry and food manufacturing benefit in many ways from the work fungi do. “Fungi are workhorses for research and biotechnology,” according to Joseph Heitman of the Duke University Medical Center, the other co-chair of the colloquium. “Both the hepatitis B vaccine and Gardasil (the vaccine for papilloma virus) are produced in yeast,” he notes.

The importance of fungi to human health, agriculture, the environment, and industry demands that we gain a better understanding of these organisms. Some of the report’s key recommendations include:

**Evaluate the Impacts of Mold in Homes and Businesses.** There is a serious lack of scientific data to support any stance with respect to indoor mold toxicity or remediation. More effort should be devoted to testing and long-term monitoring of mold contamination and human health in New Orleans and other areas flooded by Hurricane Katrina. Natural disasters like Hurricane Katrina provide natural laboratories for understanding how fungi respond to disturbance and the subsequent impacts they have on human health.

**Create a Fungal Genomes Database.** Researchers involved with fungi must focus efforts on developing a comprehensive fungal genomics database in order to make the vast quantities of sequence data more available and to enable the field to fully capitalize on the promise of genomics.

**Report and Track Fungal Infections.** Public health agencies should implement formal programs to report cases, track disease progress, and design interventions in outbreaks of fungal disease. The lack of reporting and tracking systems has made it difficult to control the spread of fungal pathogens, because good epidemiological data on the scope of infection is usually not available.

A full copy of the report and further recommendations can be found on the Academy website at www.asm.org/colloquia/ext.

The American Academy of Microbiology is the honorary leadership group of the American Society of Microbiology. The mission of the Academy is to recognize scientific excellence, as well as foster knowledge and understanding in the microbiological sciences. For more information about the American Society for Microbiology, contact Barbara Hyde at 202-942-9206 or visit.
Humboldt Institute

ANNOUNCING ...The complete redesign of the Humboldt Institute website, now with a color flyer for each seminar, easier site navigation, and more complete information about the Institute, its programs, and eastern coastal Maine: http://www.eaglehill.us

EAGLE HILL NATURAL HISTORY SEMINARS

In support of field biologists, modern field naturalists, and students of the natural history sciences, Eagle Hill offers specialty seminars and workshops at different ecological scales for those who are interested in understanding, addressing, and solving complex ecological questions. Seminars topics range from watershed level subjects, and subjects in classical ecology, to highly specialized seminars in advanced biology, taxonomy, and ecological restoration. Eagle Hill has long been recognized as offering hard-to-find seminars and workshops which provide important opportunities for training and meeting others who are likewise dedicated to the natural history sciences. Eagle Hill field seminars are of special interest because they focus on the natural history of one of North America’s most spectacular and pristine natural areas, the coast of eastern Maine from Acadia National Park to Petit Manan National Wildlife Refuge and beyond. Most seminars combine field studies with follow-up lab studies and a review of the literature. Additional information is provided in lectures, slide presentations, and discussions. Seminars are primarily taught for people who already have a reasonable background in a seminar program or in related subjects, or who are keenly interested in learning about a new subject. Prior discussions of personal study objectives are welcome.

June 29 - July 5
Lichens and Fungi: Identification, Ecology, and Role in Assessing Forest Continuity
Steven Selva

July 6 - 12
Lichenicolous Fungi: North America’s Second Sick Lichen Masterclass
David L. Hawksworth

Aug 3 - 9
Polypores, Tooth Fungi, and Crust Fungi
Thomas Volk and Sean Westmoreland

Aug 31 - Sept 6
Mycology for Naturalists: Diversity, Biology, and Ecology of Fungi and Fungal-like Organisms
David Porter

Sept 28 - Oct 4
Advanced Mycology: Freshwater and Marine Ascomycetes
Carol Ann Shearer

Seminar information may be found at

For more information, please contact the Humboldt Institute, PO Box 9, Steuben, ME 04680-0009. 207-546-2821. Fax 207-546-3042. E-mail: office@eaglehill.us

Publisher of three science journals: Northeastern Naturalist (www.eaglehill.us/rena); Southeastern Naturalist (www.eaglehill.us/sena); and Journal of the North Atlantic (www.eaglehill.us/jonat).

—Anne Favolise-Stanton
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Student Awards

Christopher D. Crabtree, a MSA student member, was recognized as the outstanding graduate student at the annual University of Central Missouri Department of Biology and Earth Science Annual Banquet. This is the second year in a row Chris has received this honor. The UCM Sigma Xi Chapter honored Chris at their Spring Banquet for the best graduate research paper entitled “Macrofungi, myxomycetes, and soil attributes associated with five communities at Ha Ha Tonka State Park, Missouri.” Angela R. Scarborough also received the UCM Sigma Xi best undergraduate research paper award based on her paper “Species Assemblages of Tree Canopy Myxomycetes Related to Bark pH.” Angela also was recognized as the Outstanding Tri-Rho Member and currently serves as President of our UCM Chapter. Courtney M. Kilgore, a MSA student member, was inducted as a full member in the UCM Chapter of Sigma Xi. (Harold W. Keller, harold-keller@hotmail.com)

55th Annual Charles Peck Foray

55th Annual Charles Peck Foray, 19 - 21 September 2008, Brauer Field Station of SUNY Cortland, near Albany NY. Visit the Website: http://www.eaglehill.us/CUPpages/Peck.html or contact Roy Halling (email: rhalling@nybg.org).

MSA 2009 Symposia Solicitation

The program committee of MSA is currently soliciting proposals for symposia and workshops for the upcoming joint meeting with the Botanical Society of America (BSA) in Snowbird Utah in 2009. To propose a symposium or workshop, please provide the following information: 1) a title; 2) a very short summary of why this topic is particularly timely or appropriate; and 3) a tentative list of speakers. For the list of speakers, we assume that there will be a maximum of six, but the entire list need not be completed at this point. In fact, we encourage you to save at least two slots to be filled after reviewing abstracts submitted for the contributed oral and poster presentations. Also, please indicate whether the proposed symposium or workshop will involve only MSA members or both BSA and MSA members. We are very interested in soliciting ideas for joint symposia and workshops involving both MSA and BSA members. Proposals can be sent via electronic mail to any of the following members of the program committee: Marc Cubeta (marc_cubeta@ncsu.edu), Tom Horton (trhorton@esf.edu) or Fred Spiegel (fspiegel@uark.edu). The deadline for receipt of the proposal is September 1, 2008.

Mycology Education Mart

A Mycology Education Mart has just been established in parallel to the existing Lichenology Mart (http://www2.bio.ku.dk/lichens/courses/), where all relevant courses that you want highlighted in order to attract students can be posted. It is housed at Copenhagen University (Ulrik Søchting, UlrikS@bio.ku.dk) and can be found at: http://www2.bio.ku.dk/mycology/courses/. (Thomas Læssøe, thomasl@bio.ku.dk)
Fungi Educates and Entertains Readers With All Things Mycological

A brand new mycological journal was launched to much fanfare this spring. Fungi magazine promises to educate and entertain all those having an interest in mycology from amateur mycophile to professional mycologist. “I am delighted to see the birth of Fungi. It looks beautiful and has much interesting information…It feels just right! If the promise of the first issue holds up, it will fill a dire need for amateur mycologists,” proclaimed Moselio Schaechter, Distinguished Professor, emeritus, Tufts University and author of In the Company of Mushrooms.

Each issue of Fungi will explore the world of mycology from many different angles: regular features ranging from toxicology to medicinal mushrooms; with how-to articles on photography, cooking and mushroom cultivation. “Great first issue! I actually read it cover to cover and can’t wait to read the next one!” beamed Gary Lincoff, author of The Audubon Society’s Field Guide to North American Mushrooms. And along with the regular features, each issue also will publish peer-reviewed technical papers ranging from original research findings to reviews of taxonomic groups to new records of North American species.

Many of the Contributing Editors of Fungi have won awards nationally for their photography, writing, or pedagogical efforts. Most are leaders in regional North American mycological societies and share a feeling that North American mycologists should have a magazine of their own that is the equal of what the Europeans are publishing. Several recent events, including the termination last year of the British journal The Mycologist led them to the conclusion that something new had to happen. “Of course launching a new periodical is a bit nerve-racking and I found myself asking, ‘If we build it, will they come?’” confides Britt Bunyard, Fungi Publisher and Editor in Chief, who is cautiously optimistic. So far, the response from the mycological community has been overwhelming. George Hudler, author of Magical Mushrooms, Mischiefous Molds, recently wrote a letter of encouragement to Bunyard saying, “Thanks a bunch and congratulations for having the courage, foresight, and dedication to launch this new journal!” Mycology professor Cathy Cripps has called Bunyard “The Savior of Amateur – Professional Mycopublishing.”

Fungi is to be published five times per year (four seasonal issues plus a special issue) by FUNGI, P. O. Box 8, 1925 Hwy. 175, Richfield, Wisconsin 53076-0008 USA. Subscriptions are $35 for five issues, for USA residents; $38 for residents of Canada and Mexico; $40 for all others. Author instructions, credit card orders, archives, and all other information can be found at the website: www.fungimag.com.

If you would like more information about FUNGI or to schedule an interview with Britt Bunyard or any of the Contributing Editors, please call Britt at 262.677.0876 or email at bbunyard@wi.rr.com.
Trees, Truffles, and Beasts


The introduction to this book accurately describes the scope of the information contained within, “…from the Microlevel to Infinity”. By using trophic interactions in ectomycorrhizal forests as a common thread, these authors weave together a broad array of personal observations and pertinent scientific research into a sweeping account of forest ecology and conservation. The combined geographical experiences, technical expertise, and grand vision of the authors provide a rare and complementary perspective on the Pacific Northwest U.S. and southeastern Australian forested ecosystems with a general focus on the truffle. This well-written book will be useful for introductory mycology students interested in learning the components of ectomycorrhizal forests, and for more advanced students or professionals seeking technical information on mycophagy, nutrient cycles, and forest management. In addition, amateur mycologists will enjoy reading the interesting case studies regarding the interconnected role of truffles in forest ecosystems – tales certain to impress your dinner guests.

The first two chapters are largely background ecological information on the structure and function of forests within the two major geographical regions explored in great detail within the book – the Pacific Northwest forests of the U.S., and southeastern Australia. A detailed introduction to soil development in chapter 2 helps to better characterize the subterranean home of the truffle. The more advanced (or busy) reader may simply skip over these introductory chapters and hurry on to the core thesis of the book (Chapters 4 & 5), but doing so would mean missing out on some interesting information and well written prose. Chapter 3 brings the reader up to speed on the evolutionary history of mycorrhizal fungi and provides a good primer on the major ecological services provided by fungi in forest ecosystems. This chapter also foreshadows the book’s thesis: that much can be learned through examining the co-evolutionary interactions among mycorrhizal truffles, host trees, and animal spore dispersers. Through examination of the complexity of evolutionary pressures exerted on the truffle, we learn about how the environmental stresses of fire and desiccation possibly drove Australia’s fungi below ground, an adaptation requiring ‘faith’ in zoochorous dispersal.

Chapters 4 and 5 remind us how un-alone we mycophagists really are in the world. From potoroos to red-backed voles, we are introduced to the real movers-and-shakers of truffle spore dispersal. And for those seeking alternative sources of selenium or other micronutrients in their diet, the reader is referred to the detailed nutritional evaluation of mycophagy provided in Chapter 5, replete with anecdotal stories about animal dependency on hypogeous fungi for nourishment during part, most, or all of their lives. Chapters 6 and 7 examine the role of fire disturbances on maintaining landscape structure and function, a necessary addition to fully understand the books study sites, but a bit of an uncomfortable transition for the reader. Close attention is paid to how mismanagement in the western U.S. and Australia has quickly created a very different landscape – one that undoubtedly has altered forest functioning and the role of mycorrhizae. Here we are presented too with Chris Masers’ alluring vision for sustainable forest management.

Chapter 8 returns to the theme of forest complexity with further examination of detailed case studies from both the U.S. and Australia. It is here we learn of the intricacies of tripartite interactions. The breadth of animal and fungal taxonomic information is a great source of reference material to trophic, food web, mammalian, or mycological ecologists conducting research in the western U.S. or Australian *Eucalyptus* forests. Chapter 9 concludes with a summary of the book and leaves the reader with a new appreciation of a complex and delicate interdependency that is largely hidden from the casual observer. This book is well written and a timely treatise on truffle ecology—one eagerly anticipated by all those who have ever seen Dr. Trappe speak on the subject. This book is an interesting and well-priced addition to the mycologist’s bookshelf.

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Taming the Truffle—

Over the last several decades, dozens of books on truffle cultivation have been published in Italian, French and Spanish. Much new has been learned about the topic during those decades. Now a definitive book in English has at last appeared, one that brings the science and art of cultivating truffles up to date for the English-speaking audience. As a government scientist in New Zealand, Ian Hall pioneered the establishment of truffle orchards, or truffières; since his retirement he has devoted full time to this activity. He established the program on a carefully designed, scientific footing and continues that approach today. Alessandra Zambonelli of the University of Bologna is among the foremost European researchers on truffle cultivation. Hall and Zambonelli combine their expertise and, with the participation of professional writer and editor Gordon Brown, reveal the state of the art and science of producing the “ultimate mushroom” in a splendidly interesting and informative way.

Not only is the prose a delight, but also the illustrations, all in color, are both informative and pleasing. The reader encounters a visual treat of many kinds of truffles and their spores and tissues, of truffières, of truffle hunters and their dogs, of truffle festivals, cooks and truffle dishes, and of truffly landscapes. Obviously much time and care went into that, and each photograph fulfills its destiny of being worth a thousand words. The authors begin with a narrative on the history and lore of truffles from the second century B.C. through the dark ages and medieval times into the “Golden Age of Truffles” initiated in the 14th century in Italy and France. They then note the discovery of mycorrhizae by A. B. Frank, occasioned after he was commissioned by the King of Prussia to find out how to grow truffles. They take us through the decline of truffle production and its causes in early 20th century Europe to the emergence of truffle science and how it is applied to present day truffle production.

Next comes an extensive chapter on truffle identification, including not only the more popular edibles but also unpalatable and potentially, if mildly, toxic ones. Habitats of selected commercial species are discussed in detail; anyone who has a few acres and aspires to make a fortune growing truffles on them needs to study this and the following chapter on establishing a truffière. It is a tricky and uncertain business, at least when done outside the normal range and habitats of the species of interest, and each species differs from the others in those respects.

Establishing a truffière is not the end of the challenge. Sustaining productivity requires continuing vigilance in maintaining soil health, controlling host tree density and unwanted vegetation, and discouraging invasion by competing mycorrhizal fungi and insect truffle browsers. One curiously slighted topic, just mentioned offhandedly in a single sentence, is the harvest of truffles by mycophagous mammals. In North America, squirrels and assorted other rodents are skilled and voracious truffle enthusiasts. Perhaps no proven control methods have been developed, but some truffle growers use poison baits during the truffle fruiting season, a practice that may be illegal in some areas. I have visited truffières in Australia that have electrified mesh fences to keep out small mycophagist marsupials and rodents, outside of which are three electric wires strategically placed to discourage wombats from crashing through or digging under the mesh. Mice can also gnaw at the bark of young host trees in spring when the sap is rising; stems may need to be wrapped in a gnaw-resistant material where that is a problem.

If all goes according to plan, the owner of a successful truffière may have a first harvest sometime between five and ten years after planting. Outside of areas where the Périgord and other cultivated truffles occur naturally, the longer times seem more usual. The final chapter in Taming the Truffle deals with many topics: finding and harvesting the truffles, regulations governing harvest and sale in different countries, yields and prices, packaging and marketing, exporting, and more.

After the text come 13 appendices, including diverse but useful topics such as names of host and non-host tree and shrub species for various truffle species, common names of truffles and host plants in four languages, production of Périgord truffles in France and Spain in recent years, climatic data for known truffle-producing areas around the world, and chemical characteristics of various fertilizers. For reasons not obvious to me, the list of references is not keyed to their use in the text. Chapter endnotes could have accomplished this without interrupting the flow of the text. Instead, we are given a website to consult for that purpose, but we are told that web information is constantly changing. If we don’t find what we need from the cited website, “go to the home page and try the search option if there is one,” and if that fails, do a Google search. I have never seen such advice in an otherwise excellent book, and I hope never to see it again.

That said, I return to my evaluation that this book is outstanding, a must for anyone interested in, planning to establish, or already managing a truffière.

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Fungi in the Environment

The prime objective was to produce a volume that would highlight the roles and importance of fungi in the environment together with the modern approaches and tools that are now revealing the importance of fungi in a wider biological context. This sweeping goal would fill libraries if taken literally, were it not for the term “highlight,” which reduces it to a realm of possibility. And that limited realm is mostly realized well for the included chapters. The book is divided into six topic areas: 1) Imaging and modelling of fungi in the environment, 2) Functional ecology of saprotrophs, 3) Mutualistic interactions in the environment, 4) Pathogenic interactions in the environment, 5) Environmental population genetics of fungi, and 6) Molecular ecology of fungi in the environment. Adding “environment” to most of the topic titles was evidently felt necessary to remind readers that the environment can be at the molecular level. All 18 chapters embodied in these topical sections are competently written, but they range from extremely complex and specialized to highly informative for students and generalists.

In Topic 4, pathogenic interactions, the functional genomics of the rice blast fungus are described along lines similar to the preceding chapter on arbuscular mycorrhizal fungi. The implications to ultimate disease control are substantial. After reading these two genomic papers, the preceding one on mutualists and this one on pathogens, I was left with curiosity on how the two types of fungi are similar and how they differ genetically in their interactions with their host. I could not really pull it out of the two papers myself, so I hope genomics researchers will do so before long. That could tell us much about why some fungi increase plant health and others subvert it. The chapter on use of DNA microarrays to
study interactions between nematode-trapping fungi and nematodes details the morphologic and DNA activities of the fascinating trapping phenomenon; these studies are just beginning but show considerable promise. The role of glucans is illuminated in the life of human fungal pathogens, but much remains to be learned about how fungal glucans affect the biochemistry of the pathogenesis and the host immune defenses. The final chapter in topic 4, “Plagues upon houses and cars: the unnatural history of Meruliporia incrassata, Serpula lacrymans and Sphaerobolus stellatus,” wins the prize as the most readable and entertaining yet immensely informative contribution to the symposium. Whether you live in a house, a yurt, or out of an automobile, you will enjoy learning about its potential plagues through author Nicholas Money’s superb pedagogic craftsmanship.

Topic 5 on environmental population genetics deals with recognition, maintenance and selection of species, matters of special interest about fungal phylogenetics in respect to speciation, adaptation, geography and taxonomy. The companion chapter on application of multilocus sequence typing and multilocus microsatellite typing in fungal population genetics and epidemiology updates these specialized techniques, at least for the specialist. And finally, topic 6 on molecular ecology of fungi in the environment includes an exposé of the astonishing diversity of fungi in the guts of beetles and a summary of the importance of ascomycete laccase genes for decomposition of salt marsh plants.

The symposium that engendered this book was held in 2004, thus it is fair to ask how up-to-date these review chapters are, especially because many of the topics are rapidly advancing. The cited literature shows a scattering of 2005 papers, so authors were given some opportunity for updating. Still, most references are dated 2003 and before. Readers interested in the topics presented will nonetheless find lots of meaty food for thought. Perhaps a third of the chapters require an advanced knowledge of the subject matter to find them meaningful. Look at the book in a library to see if it meets your needs before committing the rather spendy purchase price. The cover, binding and paper are all of the high quality typical of Cambridge University books.

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The Study of Plant Disease Epidemics


This book fills a need for a comprehensive plant epidemiology textbook. Apparently built upon the previous work of Campbell and Madden in the 1990 “Introduction to Plant Disease Epidemiology,” this book provides the theoretical background and skill development to complement an advanced undergraduate course or a graduate course in plant disease epidemiology. It would be extremely useful for a student beginning to develop an epidemiology project, and with its clear sections and handy index it can also serve as a practical epidemiological statistics reference for any plant pathologist.

The text is organized into 12 sections, most of which are heavily analytical. The first section provides a brief introduction to some concepts and some history. The next two sections describe the basics of measuring plant disease and model construction and interpretation and, in the remainder of the book, the authors draw upon these concepts to build a very practical approach to understanding plant disease epidemiology. The sections are packed with model development and cover a dizzying array of approaches and specific problems. The sheer depth of the analytical topics covered includes much exploration of the underlying questions. Organisms are left behind but so too is any indication of what the major problems of plant disease epidemiology might be, and there is little in the way of development of new questions here. However, at the end of each section, there is some useful discussion and guidance about interpretation and model design. Each section is referenced and also includes suggestions for further reading, which presumably provide more discussion and/or connection to real world examples. Certainly not all of the text is likely to be relevant to any particular study, but the completeness of the work means that virtually every epidemiological study will draw heavily on the concepts and analyses outlined here. It includes a good number of practical examples worked in SAS, but not R, the now standard open source software for statistical analysis.

Although the book is clearly aimed at a mathematically literate audience, it has enough introductory information and simple examples to remain accessible to those who are interested and focused but not expert epidemiologists. It is not an interesting or easy read, but its completeness and accessibility make it very well suited as a reference book. It is a great companion to understanding the dense and abundant epidemiology literature. Probably every plant pathologist should have this text, and any mycologist who wants to keep a foot in the world of plant epidemiology would find this book quite useful.

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Aspergillus Systematics in the Genomic Era


Yet another outstanding compilation of papers on the topic of Aspergillus genomics as one comes to expect in the journal Studies in Mycology. The 14 chapters in this issue discuss various aspects of Aspergillus taxonomy and biology, ranging from the current status of species recognition, strain recognition using genomics, secondary metabolites in species recognition, and important mycotoxins. Most of the chapters, however, deal with taxonomy and genomics of various groups of Aspergillus.

When my students isolate Aspergillus species I tend to discourage them from working further on these taxa as identification using conventional approaches is nearly impossible. As I read through this book I had the following question in mind. Will this issue improve the chances of my students identifying Aspergillus species? Read on for the answer.

Aspergillus is one of the most economically important genera of microfungi, so any book dealing with it taxonomy must be highly prized. Aspergillus species produce many important metabolites and toxins, which various entities might like to patent; therefore the taxonomy of the genus is extremely contentious. Any book that can deal with and make recommendations that could stabilize the taxonomy and put forward ways to identify species is very useful. This book achieves these desirable aims and therefore is a very important text.

The first paper deals with the current status of species recognition and identification in Aspergillus. It reviews the history and importance of Aspergillus taxonomy and provides a list of new taxa described since 2000. There is a discussion on the roles of molecular, morphological and physiological characters in species recognition. The genomics approach, especially so called “DNA barcoding” is discussed in more detail. Paper 2 asks the question what can comparative genomics tell us about Aspergillus species concepts. Four cases studies are detailed to provide answers. They conclude that it is unlikely that genomics will solve all taxonomic problems in the group but hope that genomics can provide an arsenal of data that can aid more accurate delineation of species.

Sexual and vegetative compatibility genes are discussed in Chapter 3 and I found this chapter rather hard going. Paper 4 advocates using secondary metabolite profiles, growth profiles and other tools on top of morphological and molecular approaches for species recognition. If all approaches are used, a polyphasic classification can be developed for Aspergillus species. Paper 5 deals with the clinically important Aspergillus species and is significant in that it makes recommendations for clinical species recognition. This is followed by a brief paper (6) on strain typing, while Paper 7 deals with Aspergillus diversity in agricultural products. Two rather nice color micrographs of Aspergilli in culture are presented and the polyphasic approach to species identification is subscribed. Paper 8 deals with nomenclatural considerations and is significant in that it makes proposals for describing new taxa in Aspergillus and their teleomorphs.

Paper 9 provides the most significant data in the issue. Important recommendations are made here concerning Aspergilli species concepts and these are applicable to many speciose genera. Topics dealt with are: 1) which and how many genes are required to delimit species; 2) how to deal with dual nomenclature; 3) standards for describing and storing type cultures; and 4) required databases. These section discussions are followed by 14 important recommendations, many of which should be followed by all mycologists when describing new species in any, but particularly speciose genera.

The polyphasic approach to species recognition is emphasized throughout this issue and the remaining Chapters deal with polyphasic taxonomy in various Aspergillus sections; Paper 10, section Candidi; Paper 11, section Clavati; Paper 12, section Usti; Paper 13, black aspergilli; Paper 14, section Fumigati and its teleomorph Neosartorya.

This book is fantastically illustrated with numerous pages of color plates – the micrographs are wonderful. I recommend that every mycologist and every library associated with a mycologist or plant pathologist should have this book on their shelves.

Returning to the question concerning my student’s chances of identifying Aspergillus species – well, I guess identification is beyond the average mycologist unless they have plenty of time and funds to carry the experiments needed for the polyphasic approach.

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Note: All Studies in Mycology are available on-line at Centraalbureau voor Schimmelcultures (http://www.cbs.knaw.nl/).
needs further investigation. Secretion systems in several species of bacteria, effectors and receptors involved in plant cell recognition and virulence factors for several pathosystems are also presented.

Regarding the non-pathogenic plant-microbe interactions, the symbiotic systems between nitrogen fixing bacteria and legumes are fully addressed. Two alternative models responsible for the switching between the Nod and Myc signaling pathway (cross talk pathway involved in mycorrhization and nodulation) are presented. The discovery of a novel pre-penetration apparatus formed in the plant cell that prepares and directs penetration of the arbuscular mycorrhizal fungi in root epidermis is included as well. Several papers are dedicated to the role of calmodium-like proteins and Ca²⁺ in signaling pathways of symbiotic interactions.

Since this book covers pathogenic and non-pathogenic plant-microbe interactions, its content gives the reader the chance to contrast the cellular and physiological responses as result of different interactions. For example, the cellular mechanism involving cytoplasmatic aggregation and reorganization of cytoskeleton in invasions of pathogenic fungi and the function of the cytoskeletal microtubule in initiation of legume-rhizobia symbiosis are presented. The fact that certain cellular plant mechanisms are shared as response of initial encounters of rhizobia and root-knot nematodes is also noteworthy.

This book is useful for a broad range of students and researchers who might be interested in the latest advances or short reviews related to plant-microbe interactions. Furthermore, it gives insights in future directions that should be undertaken by scientists in the field. Therefore, microbiologists, virologists, plant pathologists and physiologists, and mycologists, among others, can refer to this book as a useful and valuable resource. Since two sections focus on fungi-plant interactions (mycorrhizas and pathogenic fungi), the book can certainly be of usefulness and enjoyment for the mycological audience.

In the majority of the papers the methodologies are not fully detailed; however, the content of the manuscripts might help the reader become familiar with cutting-edge techniques (i.e. functional genomics, transcriptome and metabolome analyses, transformation, GFP technology) that can be applied or adapted in this or related fields. The organization of the individual papers could be improved for they do not follow a specific format. As aforementioned, this book compiles presentations given in a conference, and therefore, it is understandable that reviews, lectures and research papers follow different structures. In this regards, a note specifying the nature of the paper could improve the overall organization and easiness of reading.

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The Fusarium Laboratory Manual


John Leslie and Brett Summerell have taken years of expertise and compiled that information into a comprehensive and practical approach to Fusarium identification and taxonomy. Fusarium species are prolific worldwide. Their role as causal agents of plant diseases, endophytes and inhabitants of seed and other plant parts, soil-borne decomposers, producers of toxins and secondary metabolites, as well as causes of infections in animals and humans make them a group of fungi dealt with and identified by many. Workshops on Fusarium identification have been popular, since they first were held at Penn State and Minnesota in the 1970’s and 1980’s. Leslie and Summerell have taken information from Fusarium workshops, research, and publications; and put it into print to reach a wider audience and serve as a reference.

Published on stock paper with a large spiral binding, the book can be placed next to a workbench or microscope station with ease. The first few chapters serve as a methods, media, and techniques primer, stressing consistency to reduce variation. The detail given for techniques is extensive, almost anticipating any trouble one might encounter. Vendors and catalog numbers complete the detail. Thorough discussions of vegetative compatibility groups and fertility concepts in Chapters 4 and 5 provide historical information and strategies along with methods and interpretations.

Advances in nucleic acid and molecular marker techniques are reviewed, and DNA extraction methods given that are viable alternatives to more expensive kits. PCR and AFLP analysis, and resultant genetic maps, population studies, and GenBank database information (as of 2006) is well covered. DNA primer pair development is noted as lacking in large scale applicability for those developed using ribosomal ITS regions, but sequence data from nuclear and mitochondrial rRNA coding regions, β tubulin, and others show promise for greater applicability.

The section on Taxonomy and Identification gives a historical perspective of the early work by plant pathologists and the variability and confusion that has been difficult to avoid, especially in Sections such as Liseola. Morphological species concepts are discussed, followed by biological species defined as more than merely mating populations. Shared characteristics within a species are emphasized as being more important than differences, and populations are stressed rather than individuals – a very important point. Phylogenetic species characteristics based on DNA sequences identifying clades...
and molecular markers for characters, either morphological or physiological, can support identification. Numbers of strains, geographic locations, and host variation lead to rationale that 60 to 300 isolates should be examined to determine a new species. Guidance is given on where to draw lines and how to view gray areas.

Species naming and name conservation remains a topic for discussion, with *F. verticillioides* offered as an example. The use of “variety” rather than “forma specialis” is argued. Teleomorphs are discussed in Chapter 10, including *Albonectria, Gibberella, and Haematonecetria* listed with their known anamorphs. Chapter 11 stresses points made in previous chapters to delineate a process or general identification strategy, following the species concepts discussed earlier. Beginning with disease and isolation, the reader is lead through an identification approach, including a flow chart, which should be applicable to many isolates encountered in plant diagnostics. Special consideration is given to *Fusarium oxysporum* and the confusion in that group with *forma specialis*, vegetative compatibility groups (VCGs), and names based on hosts.

The focus then comes back to morphological characters as the first differentiation between species. Images and drawings illustrate differences in spore morphology and phialide structure and development. The emphasis again is on observation of similarities rather than differences within isolates. A chart for recording observations is included and may be photocopied to use at the lab bench. Rather than including or referencing a key, readers are encouraged to make comparisons to known species descriptions in the book, or to purchase “standard” sets of cultures from the organizers of *Fusarium* workshops. That next step beyond notation of morphological characters could be a frustrating one for an identifier who may not know where to take that next step. Standard culture sets might be difficult for users to maintain. Beyond morphology, it is emphasized that fertility and molecular work may be the next step to make a complete identification or for an uncertain identification, due to the concept of “running out of morphological characters before you run out of species to be separated”.

The second half of the book consists of species descriptions for 70 of the most common and clearly accepted species. Each description includes the accepted name, teleomorph and any synonyms. Reported Geographic and Host Distribution is followed by Media to Examine and Key Characters, which give details about color on CLA and PDA, growth, phialides, conidial morphology, and presence of features such as chlamydomes. Sections follow on Taxonomy, Pathology, and Ecology including information on hosts, populations, mating types, DNA primer work, secondary metabolites and toxin production, and other cited information. Each species description ends with a Current Species Description reference.

Overall, the book is a very comprehensive yet usable volume. The Table of Contents has each chapter split into sub-chapters with page numbers listed. The detail in each chapter is impressive, yet understandable. The photographs by Suzanne Bullock are superb. There are 2,425 references cited throughout the book. The species name is included in parentheses behind each reference, a very helpful feature. The book is well-indexed, including an index to species names under “F”, including cross references for synonyms. Techniques and methods described may be applicable to research with other fungal genera.

The *Fusarium Laboratory Manual* will be used extensively by all researchers and teachers working with *Fusarium*, no matter what their level of expertise. Nothing can replace the “hands-on” experience of attending a *Fusarium* workshop, but this book takes that experience and puts it in a “take-home” package to be used over and over.

—Nancy Fisher Gregory
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**Fungal Families of the World**


*Fungal Families of the World* is a long awaited book by those who need a major reference book providing comprehensive information and illustrations about all families of fungi in a single volume. This book has arrived at a great moment in fungal systematics, and the names of the families used represent the state-of-the-art in fungal taxonomy at the family or higher ranks. All the 536 accepted families of fungi are featured in this book and the classification system used is based on the consensus of recent results obtained by the exciting projects Deep Hypha and Assembling the Fungal Tree of Life. Names of taxa for higher taxonomic ranks are those accepted in Hibbett et al (2007). This book is suitable for a wide audience including fungal enthusiasts, students, and specialists. The authors’ goal for this book is to extend the information presented in the Dictionary of the Fungi by providing full descriptions of each family along with images or illustrations of key genera for most groups.

Following the introduction the authors present a brief history of the classification of fungi followed by a list of important, recent references on fungal phylogenetics. Groups such as the Oomycota and Myxomycota, traditionally studied by mycologists, but no longer belonging to the true Fungi are not included. The book is ordered alphabetically by families making it easy to find information about them. The authors present a concise de-
scription for each family followed by a list of significant genera, and subsections on their distribution, ecology and economic significance. This information highlights the relevance of fungi in the environment, the roles that they play, and how humans have benefited or been affected by them. Additionally there are notes about relationships with other groups, classification issues, or interesting observations. Each of the family sections ends with an updated list of references to major phylogenetic and taxonomic works for each family.

A major feature of this book is the high quality color pictures and illustrations for more than 400 of the 536 families. Minor disadvantages for non-specialists readers of this book are the lack of an index to taxa, as well as the lack of a phylogenetic arrangement of the families. This would help in finding key genera and species and for locating families belonging to the same order and phyla. Without doubt, this book offers a view of the great morphological diversity of the kingdom Fungi. The book also includes a glossary of technical terms relevant to mycology useful for beginners and specialists. At the end the authors present a list of the 536 families of fungi accepted in this work including their authorities, references and synonymy. This must-have book for everyone interested in fungi is of extraordinary quality with the potential to be a classic reference!


---Luis C. Mejia
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Systematic Mycology & Microbiology Laboratory
USDA-ARS Beltsville, MD 20707
mejial@eden.rutgers.edu

Recently Received Books


Previously Listed Books


• Fungi in the Ancient World: How Mushrooms, Mildews, Molds, and Yeast


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**Mushroom Modoku #1**

This puzzle uses the same rules as Sudoku, but with letters instead of numbers. Put one of the nine letters – P S I L O C Y B E – in each empty cell. Each row, column and 3x3 block will contain all of the 9 different letters. There cannot be more than one of the same letter in each row, column or 3x3 block.

—Juliet Pendray

aloet.netover.com

Vancouver Mycological Society

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**TAKE A BREAK**
An MS graduate assistantship is available at The Department of Coastal Sciences (http://www.usm.edu/gcrl/coastal_sciences/) at the University of Southern Mississippi (http://www.usm.edu) for a highly qualified student wishing to conduct research on the role of root associated fungi in saltmarsh restoration success.

Saltmarsh communities are important vegetated habitats that are classified as essential fish habitat, reduce wave energy, enhance sedimentation, stabilize the sediment, clean coastal waters and provide coastal defense from erosion. Saltmarshes, however, are declining with the most dramatic coastal wetland losses in the United States are in the northern Gulf of Mexico. This area comprises 41% of all national wetlands and from 1955–1978 this region lost 12,700 ha of wetlands, the same land area as Rhode Island. In efforts to overcome the loss of these valuable habitats, saltmarsh restoration projects are on the increase. In the northern Gulf of Mexico restoration efforts have focused on planting of saltmarsh species, primarily *Juncus* and *Spartina*, often on reclaimed or created dredge spoil islands. Nursery-raised plants are the major source of plants used in restoration projects.

This research assistantship will investigate the role of symbiotic root-associated fungi (VAM) in raising saltmarsh nursery plants. The interaction between VAM and saltmarsh plants is an understudied area that has many implications for future restoration efforts. The objectives of this study are to determine if VAM increase the growth and health of nursery-grown saltmarsh plants, and whether this results in higher restoration success with fewer plants dying from, among other things, transplant shock.

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

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**Graduate Assistantship at UMN**

I am welcoming applications from prospective graduate students interested in ecological and evolutionary interactions between fungi occupying plants, both endophytes and pathogens. Assistantship funds are available and students could enter through the graduate program in Plant Biological Sciences (PBS) or the program in Ecology, Evolution, and Behavior (EEB). Please contact me for more information.

—Georgiana May

gmay@umn.edu

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**Mold Testing and Identification Services**

Identification and contamination control for buildings, food technology, animal and plant diseases. Specializing in identification of parasitic watermolds on Amphibians and Fish. ASTM & Mil-Spec testing for fungal resistance of materials. 10% discount for regular and sustaining MSA members. Email microbe@pioneer.net Voice mail 541.929.5984; Surface mail Abbey Lane Laboratory, LLC, PO Box 1665, Philomath, OR 97370 USA. For more information see www.abbeylab.com.

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**Wanted: Specimens and Cultures of Fungi**

Wanted: specimens and cultures of fungi in the genus *Pestalotiopsis* and the related genera: *Bartalinia*, *Monochaetia*, *Pestalotia*, *Seiridium* and *Truncatella* to assist taxonomic research at Mississippi State University. Contact Paul Scott PScott@plantpath.msstate.edu, (865) 548-5688, 206 Dorman Hall 32 Creelman St. Mississippi State University 39762-9655.

—Paul Scott

PScott@plantpath.msstate.edu
McCrone Research Institute

McCrone Research Institute (McRI) is an internationally recognized institute specializing primarily in teaching applied microscopy (www.mcri.org). We are a small not-for-profit educational institute in Chicago.

**Indoor Air Quality: Fungal Spore Identification (#1630)**


The goal of the week is for the participants to be able to place virtually all visible particles into meaningful categories and also to relate those particles to problems in buildings and to human health. Emphasis is on slit samples like those from the Air-O-Cell and Burkard and also on tape pull samples, and viable sampling will be discussed.

Tuition: $1500.00 per student


**Indoor Air Quality: Advanced Fungal Spore Identification (#1631)**


In this course, working analysts with moderate experience will perfect and expand spore identification skills for slit-type samplers like those from the Air-O-Cell and Burkard and also from tape pull samples from building materials. Class structure will be flexible enough to work on specific needs of the enrollees.

Tuition: $975.00 per student


**About the Instructor**

John Haines, PhD, Scientist Emeritus. New York State Museum, Albany, NY. John has degrees in biology and mycology from the University of Washington and Oregon State University. He retired in 2005 from the New York State Museum’s Biological Survey after 34 years as the state’s mycologist and has been teaching mycology at the McCrone Institute and building a new home for the last few years. Dr. Haines has taught many courses and workshops on mycology and airborne fungus spores starting in the 1970s and has helped many mold analysts get started or to hone their skills. He has collaborated with the New York State Health Department, the Pan American Aerobiology Association, the International Aerobiology Association, The Mycological Society of America, Union College, and has been involved in research on asthma and composting hazards. He also formed a laboratory for identifying building mold for New York State and county health departments. John’s approach to fungi in buildings is from a natural history as well as a health viewpoint.

Full articles on our history, the work of Dr. Walter McCrone (our founder), our courses, and publications are available on our website, www.mcri.org.

—Lauren Logan
Registrar
McCrone Research Institute
2820 South Michigan Avenue
Chicago, IL 60616
(p) 312-842-7100
(f) 312-842-1078
llogan@mcri.org

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**Mycological Society of America — Gift Membership Form**

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

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or FAX to (785) 843-1274, Attn: Processing Department

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

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

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

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

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

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

Cordyceps Website
www.mushtech.org

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

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

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

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

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

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

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

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

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

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

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

German Mycological Society DGfM
www.dgfm-ev.de

HighWire Press (58-3)
mycologia.org

Humbo ldt Institute — Located on the eastern coast of Maine, the institute is known for the extensive series of advanced and professional-level natural history science seminars it has offered in Maine since 1987, along with ecological restoration seminars and expeditions to the neotropics. It publishes the Northeastern Naturalist and Southeastern Naturalist, two scholarly, peer-reviewed, natural history science journals which provide an integrated publishing and research resource for eastern North America, including eastern Canada. 59(4)
www.eaglehill.us
www.eaglehill.us/programs/nhs/natural-history-seminars.shtml
www.eaglehill.us/nena
www.eaglehill.us/sena
www.eaglehill.us/jona

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

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

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

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

JSTOR (58-3)
jstor.org

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

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

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

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

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

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

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

www.pnwfungi.org/

Pleurotus spp.
www.oystermushrooms.net

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

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

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

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

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

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

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

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

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

U.S. National Fungus Collections (BPI)
Complete Mushroom Specimen Database (57-1)
www.ars.usda.gov/ba/psi/sbm1

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

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

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

CALENDAR OF EVENTS

June–October, 2008
Seminars at the Humboldt Institute
Humboldt Institute, Maine
www.eaglehill.us/mssemdes.html

July 11-21 and July 11-28, 2008
Mycotour Ecuador
Ecuador

July 14–26, 2008
Fleshy Fungi of the Highlands Plateau
Highlands Biological Station
Highlands, NC
www.wcu.edu/hbs

July 26–30, 2008
APS Centennial Celebration
Minneapolis, Minnesota
www.apsnet.org

July 27–August 2, 2008
Myxomycete Seminar
Humboldt Field Research Institute, Maine
www.eaglehill.us

July 28–August 5, 2008
China-Japan Asia Pacific Mycology Forum 2008
Changchun, China
www.junwusu.com

August 2–3, 2008
FESIN workshop
Milwaukee, WI
www.bio.utk.edu/fesin

August 3–8, 2008
Ecological Society of America (ESA) Meeting
Milwaukee, WI
www.esa.org/meetings/

August 5–10, 2008
IUMS (International Union of Microbiological Societies)
Congress 2008
XII Bacteriology and Applied Microbiology
XII International Congress of Mycology
XIV Congress of Virology
Istanbul, Turkey
Abstract deadline: 31 January 2008
www.IUMS2008.org/

August 10–13, 2008
Mycological Society of America Meeting
Penn State University, State College, PA
www.outreach.psu.edu/programs/mycology/index.html

September 4–7, 2008
North American Mycological Association (NAMA) Annual Foray
In memory of Dr. Orson K. Miller
Hosted by:
Southwest Idaho Mycological Association (SIMA)
McCall, Idaho

September 19–21, 2008
55th Annual Charles Peck Foray
Brauer Field Station of SUNY Cortland, near Albany, NY
www.plantpath.cornell.edu/CUPpages/Peck.html

October 4–10, 2008
Sixth International Congress on the Systematics and Ecology of Myxomycetes
Nikita Botanic Garden, Yalta, Ukraine
www.icsem6.org

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

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