inoculum

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Newsletter of the Mycological Society of America

-- In This Issue --

~ Important Dates ~

June 15: Deadline: *Inoculum* 55(4)

May 25-29, 2003: International Society for Human and Animal Mycology, San Antonio, TX

July 27-31, 2003: MSA-BMS, Alilomar, CA

August 10-15, 2003: 4th International Conf. on Mycorrhizae, Montreal, Quebec

August 17-23, 2003: 4th International Symbiosis Conf., Halifax, Nova Scotia

Editor —

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MSA Homepage:
http://msafungi.org

Fungal Bioterrorism Threat Gaining Public Interest, Yet Not Biggest Concern of Fungal Specialists, Survey Finds

***by* Meredith Stone and John Scally**

Questions or comments should be sent to John Scally, Senior Account Executive, G.S. Schwartz & Co. Inc., 470 Park Ave South, 10th Fl. S., New York, NY 10016, 212.725.4500 x 338 or < jscally@schwartz.com >.

LEADING FUNGAL INFECTION EXPERTS to discuss disease challenges at upcoming mycology medical conference. The threat of fungal agents being misused for bioterrorism will gain the most public attention over the next year, compared with other fungal disease issues, according to one-quarter of fungal (medical mycology) specialists surveyed in an exclusive report. Surprisingly, however, none of those surveyed consider such a bioterrorist threat to be the most significant challenge facing the area of fungal disease.

The survey, conducted by leading medical conference organizer Imedex®, Inc., surveyed 55 clinicians, biochemists, immunologists and other leading professionals in medical mycology — the study of fungi and fungal diseases in humans and animals. Medical mycology experts said the most significant challenge is the continuing increase in morbidity and mortality from fungal infections (43%).

"These survey results tell us that while the public may have fears about biological warfare via fungal pathogens, leading experts believe the greater and more realistic threat comes from a natural progression of fungal disease transmission," said Michael G. Rinaldi, Ph.D. (Dr. Rinaldi is Co-Chairman of the Focus on Fungal Infection Meeting Series at which this survey was conducted, as well as the President of the impending Congress of the International Society for Human and Animal Mycology [ISHAM]).

Imedex, which for 20 years has provided accredited medical education services globally, will release the full study results at the upcoming conference of ISHAM – the leading medical mycology forum which attracts an estimated 1,000 international leaders in the study of fungi and their role in infectious diseases. As noted, the Imedex survey of medical mycology experts was conducted during Imedex's recent conference, Focus on Fungal Infections - 13, in Maui, Hawaii in March.

The potential use of fungal agents in biological warfare and the presence of mycotoxin-producing fungi in foods, plants, crops and animal feed is an intensifying issue of international debate and research. In addition to health concerns, it is estimated that the economic costs resulting from mycotoxins exceed 1.4 billion dollars in the United States alone.

Recent types of fungal disease that generated national awareness include "toxic mold" and "sick buildings," in which certain growth and environmental conditions produce various mycotoxins that are hazardous to human health.

"Fungal disease has recently taken on increasing significance in global health circles and the upcoming ISHAM Congress will serve as a unique forum for leading experts to discuss the latest research and developments," said Dr. Rinaldi. "People generally do not realize the pervasiveness of different forms of fungal infections and this gathering of the foremost researchers will cover medical topics that impact millions of people's lives."

Common forms of fungal disease include ringworm of the scalp or skin, athlete's foot, and fungal infection of the nails. More serious or invasive forms of fungal disease can affect virtually any organ in the body, including the heart, lungs, liver, spleen, eyes and can cause neurological damage.

Additional Survey Highlights

• The method of transmission that currently poses the single greatest public heath threat:
  Air borne **(84%)**
  Human-to-human transmission **(8%)**
  Animal-to-human **(1%)**
  Foodborne **(0%)**

• The area of mycology that has seen the greatest improvement in recent years:
  Improved efficacy of antifungal drugs **(45%)**

• The development expected to have the most promise over the next few years:
  New diagnostic tools for early detection and therapeutic monitoring **(58%)**

About ISHAM Conference (The International Society for Human and Animal Mycology)

ISHAM is a worldwide organization that facilitates the study and practice of all aspects of medical and veterinary mycology. Twenty-three national medical mycology associations are affiliated with ISHAM. The society is a properly recognized non-governmental affiliate of the World Health Organization.

This year's 15th Congress, in San Antonio, Texas May 25 – 29, 2003, will celebrate the 50th anniversary of the foundation of the Society. Over 450 abstracts of new research have been submitted for presentation. The Congress program will follow four separate tracks – Basic Mycology, Applied Mycology, Immunology and Clinical Mycology. Concurrent sessions will allow participants to focus on the area(s) most applicable to their interests.

The scientific program will include detailed discussions on the continued increase in morbidity and mortality from fungal infections, newly emerging pathogens, increasing antifungal drug resistance, new drugs and treatment paradigms, and early detection and monitoring. Additional Congress information is available online at <**www.isham.org**> or by contacting Imedex, the conference secretariat.

About Imedex®, Inc.

Based in Alpharetta, Georgia, USA, Imedex®, Inc. (**www.imedex.com**) is an industry leader in providing accredited medical education services. With 20 years experience in medical education, Imedex concentrates on medical meeting and symposia development worldwide, association management and sponsor acquisition/exhibit management.

Imedex has extensive relationships with leading healthcare professionals and opinion leaders in many fields of medicine. Imedex provides a fully staffed medical resource department as well as in-house business development, project management, marketing and graphic and web-design services. Founded in 1985 in The Netherlands, Imedex established its US-based operations in 1987.

Additional Comments on the REAL Find of the Century

by Peter Austwick

Questions or comments should be sent to Peter K. C. Austwick, 40, Montgomery Ave., Rothesay Bay, Auckland, New Zealand 1310; phone: 64 9 478-7972; peter.joan@clear.net.nz

Brent Heath's contribution to *Inoculum* (53[2]:16, April 2002) quite justly suggests that Colin Orpin's discovery of the presence and role of ruminal chytrids deserves an even greater accolade than that accorded the finding of *Pseudotulostoma* - magnificent though this was itself.

My reason for extolling this claim is that the long delay in the publication of the original paper was seemingly because of the disdain of its reviewers for such an outlandish suggestion that fungi could be involved in such a high temperature anaerobic process as important as rumination ! After all protozoologists knew that THEIR motile specialities were THE organisms responsible along with some bacteria, and no one likes to be told that one''s pet organisms actually belong to another (then) kingdom.

The manuscript was received by the Journal of General Microbiology on 28th October 1974 and eventually found its way to me at the Nuffield Institute for Comparative Medicine at the London Zoo for refereeing, as I was one of the few mycologists involved in animal diseases. Almost incredulously I strongly recommended it for publication but in the event this did not take place until the issue of the Journal Vol.91 pp.249-262 in December 1975.

When going against the grain of contemporary belief the way of a transgressor is hard - after all, having found fungal hyphae in the cotyledon tissue of toxic groundnut (peanut) meal and none whatsoever in the non-toxic, I was told by my superior officer (a protozoologist) that "Turkey - X disease" (i.e. later aflatoxicosis) " was far too important a disease to be caused by a fungus " ! (see Wiley & Morehouse 1978 Mycotoxic Fungi and Mycotoxicoses Vol.2 p 280) !!

From the President's Corner ....

John Taylor, MSA President 2002-2003

The MSA Endowment

"The status quo is the only solution that cannot be vetoed," is one of Clark Kerr's loftier quotes, but my favorite is his response to the question about what tasks took most of his time as president of the University of California. Without hesitation, he replied, "Athletics for the alumni, sex for the students, and parking for the faculty." No one has asked me the same question about being president of the Mycological Society of America, but if they did, the answer would be clear, "The MSA Endowment."

The MSA Endowment, as a whole, is a wonderful institution and accounts for the bulk of the assets of our society. The endowment provides funds for student travel, research, annual lectures, student awards, and the MSA distinctions. The MSA Endowment Committee, chaired by **Tom Harrington** and supported by **Don Hemmes**, **Josephine Taylor**, **Meredith Blackwell**, and **Judi Ellzey**, is responsible for looking after the endowment and encouraging its growth. Just this year, the committee successfully persuaded the MSA Council to recognize the special status of the endowment by formally separating the accounting of the endowment from that of the MSA operating funds. For the first time, the MSA Endowment Committee will know exactly what funds it has for supporting awards.

Why, then, does the endowment take so much time? I think that the root of the problem is that while the endowment is big, the interest that it generates is small, particularly when the economy is down and interest rates are low. As a result, many of our named funds do not producing sufficient income to provide an annual award. When the economy was robust, the council earmarked the interest from uncommitted endowment funds to supplement the awards, but the current council is loath to continue the supplementation in the face of increased costs of publishing and management, especially when combined with reduced income.

What can be done to solve the endowment problem? The solution is simple, each of us should give to our endowment funds of choice. If you are in a lineage of mycologists descended from one of the illustrious mycologists named in a Mentor Student Travel Fund, give to that fund and contact the others in your lineage to encourage them to do the same. The same can be said for the MSA research, lecture and award funds. Unrestricted gifts to the general endowment are also important, so that the officers and council have flexibility to respond to opportunities and emergencies. A list of the Mentor Student Travel Award and Research funds is given below. **Tom Harrington**, <**tcharrin@tcharrin.mail.iastate.edu**> Chair of the MSA Endowment Committee would love to hear from you. MSA Mentor Student Travel Awards are in the names of**: C. J. Alexopoulos, A. Barksdale, H. Bigelow, E. Butler, W. C. Denison, H. M. Fitzpatrick, M. S. Fuller, R. P. Korf, E. S. Luttrell, J. R. Raper, H. D. Thiers, F. A. Uecker, and K. Wells.** Research and Award Endowment funds are in the names of**: Alexander H. and Helen V. Smith Research Fund, Martin-Baker Endowment Fund, Myron P. Backus Award, and the new Clark T. Rogerson Fund.**

Sincerely,
-- John Taylor
MSA President (2002-2003)

From the Editor . . . .

As some of you have heard or read, I will be stepping down as editor of *Inoculum* with the publication of volume 54, number 6 in December, 2003. This move was necessary as I have been elected president of the Indiana Academy of Science and, as such, do not have enough time to be effective at both positions.

I will be replaced by **Richard (Rich) Baird**, Entomology and Plant Pathology Department, Mississippi State University, Box 9655 Dorman Hall, Mississippi State, MS 39762; phone: 662-325-9661; Fax: 662-3258955; email: <**rbaird@plantpath.msstate.edu**>. Rich is an accomplished editor and will continue the high quality of *Inoculum*.

I would like to thank the many of you that have taken the time to make comments about *Inoculum*. As editor, I can tell you that it is these kind comments that make the job very satisfying.

Sincerely,
– Donald Ruch
Editor

Mycological Society of America
Mid-Year Executive Council Meeting

Saturday, March 8, 2003
University of California, Berkeley, CA

1. **President Taylor** called the annual MSA Mid-year Executive Council meeting to order at 9:20 am in the Koshland Hall conference room and extended a formal welcome to Executive Council members (President-Elect Carol **Shearer**, Vice-President David **McLaughlin**, Secretary Lorelei **Norvell**, Treasurer Jim **Worrall**), Managing Editor Jim Ginns and *Mycologia* Editor-in-Chief Joan **Bennett**. Past-President Tim **Baroni** was unable to attend.

2. Secretary Norvell, who distributed the agenda, mid-year reports, proposed MOP revisions, updated roster, and Allen Press "Meeting ASSYSTant" prospectus prior to the meeting, drew attention to motions and actions taken by Executive Council at the 2002 midyear meeting as well as to the midyear reports and/or MOP revisions received from officers and representatives (Vice-President, Secretary, Treasurer, *Mycologia* Managing Editor, *Mycologia* Editor-in-Chief, Webmaster, Historian, and AIBS Council & IMA representatives) and Standing (Electronic Communication & Webpage Management, Endowment, Finance, International Affairs, Nomenclature, Sustaining) and Rotating (MSA Distinctions Awards Committee, Mentor Student Travel Awards, Nominations, Program, Ecology, Environmental Health & Medical Mycology, Phytopathology, and Joint Commission on Common Mushroom Names for North America) committee chairs. Observing that virtually all Society correspondence continues to be handled electronically, Lorelei noted that she had processed 2,430 emails since June 26, 2002.

MOTION (**approved** unanimously): Jim Worrall moved, and Dave McLaughlin seconded, to **approve the minutes** from the February 23, 2002, MSA Executive Council meeting (Cortland, NY) as published in *Inoculum* (53(3): 12-16). Noting that last year the Executive approved extending the Society **credit card limit** to $20,000, Treasurer Worrall announced that he has procured a second card with a $5,000 limit for Society use because the bank does not offer individual cards with such high limits to nonprofit societies.

3. Vice-President McLaughlin reported the names of nominees to be included on the spring ballot. The 2002 slate comprises: *Vice-President* **–** James **Anderson**, Jeffrey **Stone**; *Secretary* – Faye **Murrin**, Josephine **Taylor** *Cell Biology/Physiology Councilor* **–** Harvey **Hoch**, Susan **Kaminskyj**; *Ecology/ Pathology Councilor* **–** Cathy **Cripps**, Jessie **Micales**; *Genetics/Molecular Biology Councilor* **–** Flora **Banuett**, Thomas **Bruns** *Systematics/ Evolution Councilor* – Lisa **Castlebury,** François **Lutzoni**. Bylaws changes to be placed on the ballot include General Council's recommendation to add administration of the MSA Fellows Awards to the duties of the Honorary Members Committee with a necessary name change to the Honorary Awards Committee (**Article IV-E-6d&e**). [Also to be placed on the ballot are **Article II-B** by-laws changes re membership dues increases to cover membership online registration and directory costs (see below).]

4. Treasurer Worrall presented the Treasurer's report and addressed the reallocation of funds proposed by the Endowment and Finance committees. Among the budgetary items discussed at this time were **(i)** the establishment of the Clark T Rogerson Memorial Endowment as a result of the $21,000 generated by Gary Samuels' auction of the Rogerson library; **(ii)** that publishing costs tied to set-up fees to HighWire for placing *Mycologia* online will peak in 2003 and that money might be saved by reducing HighWire's level of customer service from Level 2 ($207/month) to Level 1 ($130/month); **(iii)** that anticipated cash flow problems resulting from advance disbursements for MSA-BMS 2003 might be alleviated by urging the Asilomar convention group to reimburse the Society as soon after the meeting as possible; **(iv)** that the delay in adopting the proposed electronic manuscript submission program, AllenTrack, will enable the Society to save ~$8,000 for fiscal year 2003, which should help offset the lower membership renewals and temporary loss of ~55 institutional subscribers resulting from the Rowecom/divine subscription service bankruptcy; **(v)** the need to renegotiate with Allen Press and HighWire for decreased *Mycologia* publication/ electronic set-up costs; **(vi)** the notification by Managing Editor Ginns that annual institutional subscription rates henceforth should increase ~9% yearly; and **(vii)** the need to inform Society members that post-galley corrections are expensive and that excessive corrections will be charged to authors.

5. Executive Council next considered proposals by **Endowment Chair Thomas Harrington** and **Finance Chair Orson K Miller** to separate operating funds from the endowment funds and to divide endowment monies into two different accounts: **(i)** Endowment Receiving Account and **(ii)** Endowment Account. Chair Harrington "strongly urged the Executive Council to authorize the Finance Committee to create two additional money market accounts for the MSA Endowment."

MOTION (**approved** unanimously): Dave McLaughlin moved and Carol Shearer seconded that MSA separate investments into two primary funds: **Operational** and **Endowment**. The Fundamental Investors mutual fund (ANCFX) will be considered operating funds, and all other current investments (the bond ladders and the Vanguard Index mutual fund (VFINX) will be considered endowment investments.

RECOMMENDATION: The Executive recommends that the Treasurer, in consultation with the Finance Committee, create two new endowment money market accounts: **Endowment Receiving** (to accumulate new endowment donations until such time as they can be invested) and **Endowment** (for existing endowment investments and a new money market account to accumulate interest and dividends until it is spent).

Action to be taken: The Executive also recommends that the Endowment Committee appoint someone to contact Society members willing to "adopt" and

supervise individual funds to help raise each to the recommended minimum sustaining [$10,000] base level.

MOTION (**approved** unanimously): Carol Shearer moved and Lorelei Norvell seconded that Executive Council direct the Endowment Committee that beginning in 2003, General Endowment Funds are not to be used to supplement individually named funds, each of which is, henceforth, to be regarded as self-sustaining.

NOTE: Funds previously earmarked as "Supplement to Mentor Travel Funds" are now transferred to the General Endowment. Beginning in 2003, mentor student travel awards will be covered exclusively by the interest generated in each travel fund. As only travel funds with a minimum $10,000 balance can generate sufficient interest to cover a $500 student travel award, capital from travel funds containing less than $10,000 – at the discretion of the Endowment Committee – may be combined so as to cover "hyphenated" travel awards from the interest dedicated to each award. Travel funds with less than $10,000 will continue to be combined until individual funds reach the required minimum balance. In 2003, for instance, only the Bigelow Travel Fund has sufficient funds to support an individually named Bigelow Student Travel Award; accordingly, other travel funds will have to be combined to cover each $500 mentor travel award (e.g. Denison-Trappe Student Travel Award).]

MOTION (**approved** unanimously): Jim Worrall moved and Dave McLaughlin seconded that the Executive direct the **Endowment Committee to allocate** the awards in coming years so that each individual named fund accrue its interest until its funds are sufficient to make a travel award, e.g. if the fund is below $10,000, there may be several years until an award will be given. It will be the responsibility of the Endowment Committee each year to decide which smaller funds should be combined for granting an award and which are to be withheld to accrue interest to help raise the capital to the $10,000 level.

MOTION (**approved** unanimously): Carol Shearer moved and Dave McLaughlin seconded that henceforth the Alexopoulos Prize and Myron Backus awards be tied to the interest accrued in each individual fund, as is currently done for the MSA Research award grants.

RECOMMENDATION: Executive Council agreed that the MSA Graduate and Undergraduate Fellowship awards are to be funded from the General Endowment.

6. President **Taylor** agreed to contact **AIBS** regarding the double dues situation, where both the Society and the Society Representative to AIBS Council are expected to pay AIBS dues.

MOTION (**approved** unanimously): Dave McLaughlin moved and Lorelei Norvell seconded that the Society underwrite attendance by the MSA representative to AIBS Council at the annual AIBS Executive Council meetings.

7. Managing Editor Ginns presented his report after which the Executive considered the following **(i)** setting fees for paid ads in *Mycologia* based on $1200 for a color full-page ad (see *Biolog's* ad on the front page of the January/February issue); **(ii)** encouraging paid ads in *Inoculum*; **(iii)** investigation of how to cut costs associated with implementation in March of *Mycologia* Online limited access [with1520 addresses potentially available to access HighWire, projected costs include $450 for file maintenance and $300 for file updating; by having AMM implement file updates instead for a minimum $150 / month, the Society might be able to reduce costs); **(iv)** increasing page charges to $60 (from $40) per page and offering a partial pay option to unfunded authors who cannot afford the full rate but who would be willing to pay something; **(v)** the pay-per-view option of *Mycologia* Online in which the Society might receive some money for any amount totaling over $1500 [ME Ginns sounded less than sanguine about the Society ever seeing any money from pay-per-view]; **(vi)** that the memorandum of understanding with NYBG suggests that MSA now holds copyright to *Mycologia* volumes 1-90 while the Garden owns only the physical back issues; and **(vii)** options for dealing with the implications of impact upon the Society arising out of the Rowecom/ divine (subscription service) bankruptcy.

MOTION (**approved** unanimously): Lorelei Norvell moved and Dave McLaughlin seconded that henceforth the ***Inoculum*** **Editor** may accept **paid advertisements** at his/her discretion.

Action to be taken: The Managing Editor should send an invitation offering the 93 institutional subscribers cited in the 1998 New York Botanic Garden agreement the option to subscribe to *Mycologia* Online only (with no hard-copy) at half the institutional rate.

Action to be taken (by Jim Ginns): To contact the institutional subscribers affected by bankruptcy of the Rowecom/ divine subscription service.

8. President Taylor adjourned the meeting at 1:10 pm, reconvening at 2:00 pm after lunch.

9. ***Mycologia*** **Editor-in-Chief Bennett** presented her midyear report, which addressed the following: **(i)** the appointment of Mary Berbee to the Editorial Advisory Committee and the function of that underused Committee; **(ii)** the appointments of Cole, Desjardin, Halling, Longcore, Natvig, Roy, Stephenson, and Woloshuk to bring the total number of Associate Editors to 18; **(iii)** problems resulting from the unanticipated resignation of **Editorial Assistant Mary Langlois** in November; **(iv)** hiring John M. **Donahue**, an applicant with 30 years of journalism experience, to serve as Assistant Editor in her stead for the same salary; **(v)** that problems encountered during test submission of two manuscripts through **AllenTrack**, the proposed new electronic manuscript submission program, resulted primarily from human, rather than technological, failures (Joan foresees few mechanical problems once the system is adopted formally and fully supported by Allen Press); **(vi)** acknowledgement of support by all Associate Editors and reviewers, Managing Editor Ginns, Allen Press staff, Editorial Assistant Langlois, and Assistant Editor Donahue; and **(vii)** EIC Bennett's decision to shorten her tenure as Editor-in-Chief by one year and her recommendation that any future EIC should have served at least one full term as *Mycologia* Associate Editor.

Action to be taken (by the Editorial Advisory Committee): Executive Council recommended that the Editorial Advisory Committee submit in their annual report (due July 10) the names of **six potential Associate Editors** (to replace retiring Associate Editors) and that the

Committee select each new EAC nominee from among Society members who have previously served as *Mycologia* Associate Editors.

EIC Bennett, who noted that there is now a backlog of manuscripts, resulting in part from bringing the new Assistant Editor to speed, expressed a desire to publish all manuscripts as promptly as possible.

MOTION (**approved** unanimously): Lorelei Norvell moved and Carol Shearer seconded that the *Mycologia* Editor-in-Chief be permitted to **increase the number of pages** per issue at her discretion.

Action to be taken (by Editor-in-Chief and the Managing Editor): Executive Council recommends that **AllenTrack be activated by September 1** (with all manuscripts thereafter to be submitted electronically) and that a **tutorial session for the Associate Editors** be offered at the annual meeting at Asilomar.

Recommendation: At Joan Bennett's urging, Executive Council recommended that the Editor-in-Chief search committee be aware of the degree to which the Editorial Office requires hands-on experience, management, and need for institutional support (both monetary and emotional).

10. Executive Council discussed the **Electronic Communications and Web Management Committee** recommendation to consider the **Allen Press Meeting ASSYSTant** for future stand-alone meetings (available on a year-to-year basis). Carol Shearer noted that while such an electronic registration/ abstract submission system is not needed at this time, the Program Committee should track the amount of money and time spent for the 2003 meeting so as to provide a baseline for comparison for what is offered by the Allen Press online abstract submission system and meeting organizer.

MOTION (**approved** unanimously): Dave McLaughlin moved and Carol Shearer seconded to approve the ECWM Committee's request to proceed with renovation of our Abstract submission website and to consider a future modest request for funds (pending receipt of clear cost estimates) to pay for additional programming innovations.

The ECWM Committee also recommended strongly that it is now time to bundle a number of services under one roof, which could be done by adopting the Enhanced Options package at Allen Marketing and Management at Allen Press. Estimated annual costs of $8,000 would cover on-line secure renewals; on-line ballot/polls; real time updated secure membership directory maintained by AMM; member address changes and updates; email announcements; officer access to several reports; suggestion area for members; and miscellaneous additional items, such as a shopping cart (back issues, books). The extra costs could be partially offset by raising the dues and dedicating the full amount of the raise during this and successive years to pay for the enhanced services. Although reluctant to ask membership to vote for a dues increase two years in a row, all present agreed that the Society has encountered problems by keeping dues artificially depressed for so long. Managing Editor Ginns and President Taylor pointed out that even with an annual increase of ~9% for institutional subscriptions, *Mycologia* institutional rates are still well below those of comparable journals.

MOTION (**approved** unanimously): Carol Shearer moved and Lorelei Norvell seconded that Council consider **increasing annual membership dues** as follows: Individual, Family, & Affiliated Society memberships from $92 to $98, and Student, Associate, & Emeritus-subscriber memberships from $46 to $50. If approved, the dues increase would be dedicated to defraying costs associated with the adoption of the AMM Enhanced Option package. [Vice-President **McLaughlin** placed these proposed changes to Bylaws Article II-B on the ballot after Email approval by Full Council on March 13.]

Executive Council also discussed the incompatibility of the current web server with the MSA Bulletin Board so that it is currently unavailable on the MSA homepage. Taylor and Secretary Norvell both noted that Webmaster Halling has stepped into the breach by erecting a webpage devoted to job announcements. Roy Halling has indicated that he will continue to post such announcements, provided they are appropriately formatted and do not require further editing by him.

Action to be taken (by Secretary Norvell): The Executive recommended that Roy Halling be complimented on his management of the Society website and be asked formally to continue to post job announcements on the webpage he has already set aside for that purpose.

11. President Taylor noted that Dr Richard Baird has expressed a desire to serve as next *Inoculum* Editor and that current Editor Ruch supports Baird's candidacy. Full Council will consider Baird and other potential candidates at its annual meeting at Asilomar in July 2003.

Action to be taken (by President Taylor, Secretary Norvell): Executive Council expressed heartfelt thanks to *Inoculum* Editor Donald Ruch, who will end his term with the final issue of Volume 54, for a job very well done.

12. Executive Council next considered the report from **International Affairs Chair Cantrell** (see *Inoculum* 54(2): 10-11), in particular her discussion of the terms "Sister" or "Allied" to be used for fellow mycological societies for listing on the annual Mycological Society of America Roster and linking on the MSA website. [The Secretary has already informally added the African Mycological Association, Australasian Mycological Society, British Mycological Society, Latin American Mycological Society (with whom a formal memorandum of understanding was signed in 1999), Mycological Society of China, Mycological Society of Japan, and the North American Mycological Association to the current Roster.)

MOTION (**approved** unanimously): Dave McLaughlin moved and Lorelei Norvell seconded that the Society list and link such fellow mycological societies on the roster and website under the name "Allied Mycological Societies." No financial obligation is implied or should be inferred; the name "**Affiliated Mycological Societies**" remains reserved for those societies (currently the Boston Mycological Club, Illinois Mycological Association, and the Oregon Mycological Society) who pay regular membership and receive *Mycologia*, *Inoculum* and one vote in return.

13. The Executive next discussed **Memorials Committee member & Historian Pfister's** request for additional guidelines and/or help for **Memorials Committee** (currently composed of the Editor-in-Chief, the President, and the Historian).

Recommendation: Executive Council suggests that henceforth the Historian formally chair the Memorials Committee.

14. John Zak, who has served MSA well (first in *Mycologia* and then in *Inoculum)* as the Society's **Book Review Editor,** recently tendered his resignation. Executive Council greeted **Amy Rossman's** offer to serve as new Book Review Editor with loud huzzahs and general enthusiasm.

15. MSA 2006, MSA 2007: MSA-NAMA 2004 will be held in Asheville, North Carolina jointly with the North America Mycological Association. MSA-MSJ 2005 will be held jointly with the Mycological Society of Japan in Hilo, Hawaii. Executive Council next considered locations (e.g., Edmonton, Alberta; Minneapolis/St Paul, Minnesota; University of Texas at Austin; Madison, Wisconsin; Mexico; and Florida) and potential co-hosting organizations (e.g., ALM (Latin-American Mycological Society), SSE (Society for the Study of Evolution), BSA (Botanical Society of America), and MMSA (Medical Mycological Society of the Americas) for not-yet-scheduled future meetings.

Recommendation: Executive Council recommended that the following potential meetings be explored: **MSA 2006** in **Minnesota** (provisionally with the **Society for the Study of Evolution (SSE)**; Dave McLaughlin agreed to investigate) and **MSA 2007** in **Miami**, Florida (provisionally with the **Latin-American Mycological Society (ALM)**; with Jack Fell, Jim Kimbrough, and Diane Te Strake to be contacted as potential ad hoc Committee members).

16. Executive Council also considered and made recommendations on the following items:

(i) MOTION (**approved** unanimously): Jim Worrall moved and Lorelei Norvell seconded that the Society send Linda Hardwick a bouquet of flowers and letter of appreciation in return for her hard work for the Society.

(ii) Action to be taken (by President Taylor, Editor-in-Chief Bennett): The following duties should be added to the President's and Editor-in-Chief's guidelines in the Manual of Procedure: **(i)** The President is to write and send letters of appreciation to department heads of retiring Associate Editors that laud their contribution both to the Society and to science in general and explain how such volunteer efforts keep *Mycologia* standards high and costs low. **(ii)** The *Mycologia* Editor-in-Chief is to send a Certificate of Appreciation to retiring **Associate Editors** in recognition of their hard work on behalf of the Society.

Lorelei L. Norvell, MSA Secretary

(iii) President Taylor noted that he has sent the **American Type Culture Collection** names of three prospective Society representatives as requested, one of whom will be selected by ATCC to serve as MSA representative to that group.

17. President Taylor adjourned the meeting at 5:30 pm for social adjustment in his lab with graduate students. Executive Council and Editors extended thanks to President and Delia Taylor for their gracious hospitality, warm companionship, and delicious brisket on Friday evening.

Respectfully submitted,
***-- Lorelei L Norvell,* Secretary**

Change of Address

Send all corrections of directory information, including e-mail addresses, directly to Allen Press

Mycological Society of America
Attn: Linda Hardwick, Association Manager
PO Box 1897 [810 E 10thSt]
Lawrence, KS 66044-8897

Vox 800.627.0629 (US and Canada)
or 785.843.1221
Fax 785.843.1274
Email **lhardwick@allenpress.com**

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

The Clark T. Rogerson Student Award: A new Award

The Mycological Society of America is happy to announce the establishment of a new student research award from proceeds from the auction of Clark Rogerson's mycological library. Clark T. Rogerson (1918-2001) was Curator of Cryptogamic Botany at the New York Botanical Garden between 1958 and his retirement in 1990; he continued as Emeritus Curator until 1997, when illness kept him at his family home in Utah. The two areas of Clark's life that brought him most pleasure were collecting and identifying. He emphasized ascomycetes in his collecting, but he was equally adept at identifying fungi in all groups, and was a close advisor to the COMA mycological group in New York. He was among the most generous contributors to MSA graduate student awards. It is therefore appropriate that the Clark T. Rogerson award should be used to encourage undergraduate and graduate students to participate in field work and/or herbarium studies. To this end, beginning in 2004 one award for approximately $1000 will be given annually. Details of the application procedure will be announced in a future issue of *Inoculum*.

Each year the MSA gives many awards in support of student travel and research. These awards are funded thanks to generous contributions from MSA members. Maintaining the high number, and monetary level, of these awards requires continuing donations from the membership. All MSA members are encouraged to contribute annually to the Society awards funds. To donate, or to obtain information about the many funds, please contact the MSA Endowment.

***-- Gary Samuels,* PhD**
gary@nt.ars-grin.gov

Managing Editor's Mid-Year Report

Distribution - Publication of *Mycologia* is on schedule! 2122 copies of the November/December issue of volume 94 were mailed December 11, 2002. The January/February issue of volume 95 was mailed in mid-February and the online version is available.

Advertising - One of the first ads in Mycologia appeared in the Jan/Feb issue. It is a full page by Biolog Inc.

On-line version - Launched in March of 2002 *Mycologia* on-line has been available free to the public.

A) Limited Access: On February 18, 2003 limited access was implemented. A considerable amount of editing was needed to prepare the site. Jim Worrall is owed a large vote of thanks for handling this. The Managing Editor dealt with the logistics between Mycologia, Allen Press and HighWire. Members and institutional subscribers were notified in January about the move to limited access. Activating access to the site by members and institutional subscribers will result in some queries, but Linda Hardwick does not seemed phased by that and is providing HighWire with updates on 2003 memberships and institutional subscriptions.

B) Pay-Per-View: In the near future PPV will be available to nonsubscribers. The demand for PPV is not expected to be great and to encourage PPV use the fees to users will be reasonable.

C) Loading Back Issues: The plan to make available online volumes 91 through 93, that is, all the volumes under the control of MSA, was given lower priority due to budgetary constraints.

Page Charges - All authors are asked to pay page charges, but payment is optional. Charges are set at $40 per page and this rate has been in effect for several years. Approximately 50% of authors in volume 94 agreed to pay page charges and that should yield about $22,000.

Indexing - Glassman Indexing Services of Ankney, IA, indexer of volumes 92, 93, and 94, is under contract to prepare the Author & Subject, Fungus Taxa and Host indexes for volume 95.

Institutional subscriptions - As of July 2002 there were 922 institutional subscribers. 603 subscriptions went to addresses in the USA. The others were distributed over 41 countries. In 2003 the fees are $175 for US, $190 for other countries and $160 for online access only.

Most disturbing was the bankruptcy of a journal subscription agency, Rowecom Inc. Allen Press said that 55 subscriptions to *Mycologia* were submitted by Rowecom in 2002. If that number applies to 2003 then *Mycologia's* income will be down by about $9,700, because Rowecom collected funds from libraries but did not forward funds to the journals.

We do not want to loose these 55 subscribers. Thus we will be trying to contact these subscribers to discuss accommodating those libraries.

Publishers have been discussing the option of "gracing" those subscribers who paid Rowecom for 2003.

Membership directory - The 2002-2004 version was mailed mid July with Mycologia 94(4). Eight membership categories are recognized. They are, with the number of individuals in parentheses, Member (916), Student (165), Life (60), Emeritus (122), Associate (46), Family (8), Sustaining (23) and Honorary (22). Thanks to Linda Hardwick for preparing the initial draft and inputting revisions. And thanks to a past president from Maryland, who prefers to remain anonymous, for proofreading two drafts.

Managing editor's expenses - In 2002 $440.00 has been spent mainly on postage and phone calls. This does not include attendance at the Executive meeting in Cortland. In addition, most photocopying is available at no cost to MSA.

Queries - In 2002 about 300 e-mails, letters and phone calls were sent/made on *Mycologia* related business, such as questions of copyright, page charges, galleys, sale of MSA mailing list, advertising in *Mycologia*, and members comments and complaints.

-- J. Ginns
ginnsj@telus.net

ITEMS NEEDED FOR THE ANNUAL AUCTION

It's time to begin thinking about items to bring to the annual auction to be held during the social gathering on the last night of the MSA Annual Meetings in Pacific Grove, Callifornia, July 27-31. Old books and manuscripts and historical artifacts are especially appreciated. Nor do we shy away from silly, outlandish objects of mycologicl interest. Bring your items to the meeting and contact **Don Hemmes** before the social and he will organize the materials for the auction. If you might not make the meetings and want to send items, let Don know at hemmes@hawaii.edu.

***Don Hemmes*, Aution Coordinator**
hemmes@hawaii.edu

MSA Council Email Express

Since March 3, Executive Council and Council have taken the following actions by Email:

Email Council Poll 2003-01 – On March 3, Executive Council approved a proposal from the Endowment Committee to create the Clark T Rogerson Fund, the income from which will be used to support research-related travel of a graduate or undergraduate student for field study and/or herbaria.

Email Council Poll 2003-02 – On March 13, General Council approved polling the membership on the 2003 ballot regarding raising dues $6 (from $92 to $98) for Individual, Family, & Affiliated Society memberships and $4 (from $46 to $50) for Student, Associate, & Emeritus subscriber members, with the monies accrued from this increase [i.e. $6 of the $98 and $4 of 50] to be dedicated to helping to defray costs associated with adoption and maintenance of the Allen Marketing & Management's (AMM) Enhanced On-line Services Package.

Email Council Poll 2003-03 – On April 17, General Council approved Dr Richard Baird to succeed Don Ruch as *Inoculum* Editor (2003-2006).

Email Council Poll 2003-04 – On April 21, General Council approved transfer of the "Supplement to Mentor Travel Award Funds" to the General Endowment, with income from those funds no longer to be used to supplement individually named funds. Each individually named Mentor Travel Award fund is henceforth to be regarded as self-sustaining.

Email Council Poll 2003-05 – On April 21, General Council also approved that interest accrued from the "Supplement to Mentor Travel Award Funds" fund during 2002 could be used for purposes other than supplementing Mentor Travel Awards in 2003.

Other news from the Secretary:

- **Welcome, New Members!** Although candidates for MSA membership cannot vote until formally approved at the annual general business meeting, they do receive *Mycologia* and *Inoculum* immediately after Allen Press processes their applications. During February, the following 7 people applied for MSA first-time (or returning) membership: CANADA – Shaun R **Kay**; PUERTO RICO – Angel M **Nieves-Rivera,** Beatriz Ortiz **Santana**; UNITED STATES – Daniel J **Friedman**, Ainslie **Little**, Miao **Liu**, Bernadette D **O'Reilly**. March and April applications will be noted in the next issue.
- EMERITUS – James H **Ginns**, John **Haines**, and Edson C **Setliffe** have applied for **MSA Emeritus** status, which will be formally conferred after approval is voted by the general membership at the Society's annual business meeting at MSA-BMS 2003 in Asilomar.

-- Lorelei Norvell
MSA Secretary

ABLER, REBECCA and MILLER, ORSON K. Dept. Biology, Virginia Polytechnic Institute and State Univ., Blacksburg VA 24061 USA. rebellin@vt.edu **Intraspecific variation in metal tolerance within the ectomycorrhizal species *Suillus granulatus*.**

Ectomycorrhizal (ECM) fungi are known to enhance plant growth under trace metal stress. In order to colonize the host plant, the mycobiont must employ strategies to tolerate high concentrations of potential toxic metals. Although adaptive metal tolerance has been determined for several groups of organisms, including plants and bacteria, there is little evidence to support adaptive changes in response to metals within ECM species. To better understand the nature of ECM tolerance for trace metals, several species were grown on agar plates amended with Cu^{2+} and/or Zn^{2+}. *Suillus granulatus* exhibited a sectoring response on several of the high-zinc plates, resulting in different patterns of pigmentation and colony growth for the same isolate. Sectors were sub-cultured and grown on agar plates amended with up to 1000 ppm Cu^{2+} or Zn^{2+}. Differences in growth rate, colony diameter, and morphology were seen among the sector isolates on both copper- and zinc-amended media. Inter-simple sequence repeat (ISSR) analysis was performed on the sectors and the parent strain of *Suillus granulatus* to determine whether the sectors differed genetically from the parent strain, or whether the culture exhibited adaptive phenotypic plasticity. The results presented contribute toward an understanding of intraspecific heterogeneity in ECM metal tolerance. *Poster*

*ADAMS, GERARD. Dept. Mycology & Botany, American Type Culture Collection, Manassas, VA 20110 USA. gadams@atcc.org **A review and revision of the subgenera and sections of *Cytospora*.**

The coelomycete genus *Cytospora* has been subdivided into sections by some authors and into subgenera by others, based on morphological characteristics. The teleomorph *Valsa*, a stromatic pyrenomycete, has similarly been subdivided. A specific section/ subgenus of the teleomorph corresponded to a specific section/ subgenus of the anamorph. The collection and description of several new species of *Cytospora* and *Valsa* has initiated a revision of the genera and of subgenera and sections. A new species of *Valsa* has only solitary perithecia without an apparent stroma. Two new species of *Leucostoma* have *Cytospora* anamorphs with the features of both sections Torsellia and Leucocytospora. Two new species of *Cytospora* have the combined characteristics of three sections/ subgenera. A third species has a unique stroma. Character traits that have been distinct for subgenera and sections appear in multiple lineages on an ITS-rDNA gene tree. Nevertheless, inoculation of a "universally susceptible" host with many distinct *Cytospora* species has provided evidence that subgenus and section morphologies are apparently stable in different tree bark habitats. *Contributed Presentation*

ALFARO, MICHAEL[1], ZOLLER, STEFAN[2] and LUTZONI, FRANCOIS[2]. [1]Dept. Evolution and Ecology, Univ. California, Davis, CA 95616 USA; [2]Dept. Biology, Duke Univ., Durham, NC27708-0338 USA. mealfaro@ucdavis.edu **Bayes or bootstrap? A simulation study comparing the performance of Bayesian Markov chain Monte Carlo sampling and bootstrapping in assessing phylogenetic confidence.**

Despite the growing use of Bayesian Markov chain Monte Carlo sampling as a method for both estimating the maximum likelihood topology and for assessing nodal confidence, the relationship between the Bayesian measure of confidence and the most commonly used confidence measure in phylogenetics, the non-parametric bootstrap proportion, is poorly understood. We used computer simulation to investigate the behavior of three phylogenetic confidence methods: Bayesian posterior probabilities (BMCMC-PP), maximum likelihood bootstrap proportion (ML-BP), and maximum parsimony bootstrap proportion (MP-BP). We simulated the evolution of DNA sequence on seventeen-taxon topologies under 18 evolutionary scenarios and examined the performance of these methods in assigning confidence to correct and incorrect monophyletic groups, as well as the effects of increasing character number on support value. Contrary to MP-BP, ML-BP was often strongly correlated with BMCMC-PP, but the latter two methods could provide substantially different estimates of support on short internodes. For a given threshold value, more correct monophyletic groups were supported by BMCMC-PP than by either ML-BP or MP-BP. BMCMC provided high support values for correct topological bipartitions with fewer characters than was needed for non-parametric bootstrap. *Symposium Presentation*

ALLEN, M.F. Center for Conservation Biology, Univ. California, Riverside, CA 92521 USA. michael.allen@ucr.edu **Responses of mycorrhizae to environmental change: perspectives from semiarid ecosystems.**

Mycorrhizae are a sink for C, taking sugars from the host plant in exchange for limiting soil nutrients. However, there is no single limiting factor. Mycorrhizae exist along a gradient from high to low C, and high to low nutrients. In most wildland ecosystems, nutrients or water is limiting. In these cases, the plant becomes nutrient limited stimulating mycorrhizal formation. As nutrients increase, especially near urban or agricultural areas with N deposition, the plant can reduce dependency on mycorrhizae and infection declines. This process also occurred in the past under conditions of lower atmospheric CO_2. C was limiting and experimental studies show a decline in mycorrhizae in the same manner as increasing N. Alternatively, as CO_2 in the atmosphere increases, N becomes more limiting, and mycorrhizae increase. However, as CO_2 continues to increase, or N becomes extremely limiting, mycorrhizae and plant health both decline. Data from many experiments in my lab have demonstrated that the complex interactions between nutrients, plants, and atmospheric CO_2 alter species composition and structure soils. These complex interactions will result in changing limitations and structure- function relationships in wildland ecosystems in the future. *Symposium Presentation*

*ALLEN, M.F., QUEREJETA, J.I. and EGERTON-WARBURTON, L. Center for Conservation Biology, Univ. California, Riverside, CA 92521 USA. michael.allen@ucr.edu **Complex vertical and horizontal transport of water in a 3-dimensional oak woodland by roots and mycorrhizal fungi: implications to nutrient cycling.**

Mycorrhizae move soil resources. However, resource movement occurs in many different directions depending on the gradients between soil, fungus, plant, and atmosphere. During drought, some mycorrhizal fungi remained active. These occur in ecosystems with deep root plants. Many plants perform hydraulic lift, whereby during the night, water moves from deep layers to the surface, then moves laterally in response to water potential gradients. Hydraulically-lifted water moves through the fungal hyphae of both ecto- and arbuscular mycorrhizae. The hyphae near the roots are hydrophobic, reducing loss into the soil. Water moves rapidly to the tips because the flow has a direct pathway as opposed to the surrounding soil, where flow is unsaturated. The hyphal tips are hydrophilic, and water moves into the soil. N mineralization and hyphal transport even when soil water potentials are as low as -5 MPa, a value too low for normal mineral-

ization. If the hyphae are connected to an adjacent shallow-rooted plant, isotopic and dye data demonstrated that some hydraulically-lifted water moves into the shallow-rooted plants and can form a significant amount of the transpiration stream. These data demonstrate that mycorrhizae not only move water directly from shallow soils to roots, but also from deeper- rooted plants into surface hyphae and even connected plants. *Symposium Presentation*

ANDREW, CARRIE, LANDIS, FRANK and *GARGAS, ANDREA. Dept. Botany, Univ. Wisconsin, Madison, WI 53706 USA. agargas@wisc.edu **Identification of plant-associated fungal spores and spore-like organisms.**

Fungal-plant root symbiotic associations play critical roles in determining plant community structure, yet identification of specific fungi from soil samples remains vexing. Since species in phylum Glomeromycota do not form complex fruiting bodies, morphological species identification requires informed assessments of variable spore wall characteristics. Identifications are complicated by decomposition processes, the growth of other fungi on or within spores, or morphological similarity to organisms such as animals, protists, plant megaspores, or non-glomalean fungal spores. We are identifying unknown yet extremely common spores and spore-like structures within Wisconsin oak savanna soil samples using morphological and PCR-amplified ITS rDNA sequence characters. We present these results to detail rhizosphere diversity, and also to satisfy the curiosity of those who, like us, have wondered what these things were. *Poster*

*ARCHER, DAVID, ALCOCER, MARCOS, AL-SHEIKH, HASHEM, BARNES, SALLY and WATSON, ADRIAN. School of Life and Environmental Sciences, Univ. Nottingham, University Park, Nottingham NG7 2RD, UK. david.archer@nottingham.ac.uk **The secretion of heterologous proteins by fungi.**

Filamentous fungi are exploited as hosts for the secreted production of heterologous proteins. Some heterologous proteins are produced in bulk on a commercial scale and find uses in food processing and detergents. Other proteins are used as research tools or, potentially, in clinical applications. Irrespective of the end-use, the two main concerns are the quality of product (its authenticity) and its yield. Although many fungal species are effective natural secretors of some native proteins, they have proven to be less adept at secreting heterologous proteins. The secreted yields depend on the particular target protein and the expression host/vector combination. Some success stories will be contrasted with some problem proteins. Those proteins that are difficult to express from fungi provide an opportunity to investigate the stress responses, especially the unfolded protein response (UPR), that are established within the fungus. Our increasing knowledge of the molecular detail of protein expression in fungi, including stress responses, is providing new opportunities for manipulating the expression host in order to control, and improve, protein production. Current strategies for improving secreted yields of heterologous proteins from fungi will be discussed. *Symposium Presentation*

*ARNOLD, ELIZABETH and LUTZONI, FRANCOIS. Dept. Biology, Duke Univ., Durham, NC 27708 USA. aearnold@duke.edu **Foliar endophytes of *Magnolia grandiflora*: morphological plasticity, molecular diversity, and species composition inferred using two isolation media.**

The degree to which isolation media influence inferences regarding abundance, diversity, and species composition of foliar endophytes has not been studied in detail, but is important for understanding the utility of culture-based surveys. Using two common isolation media (potato dextrose agar [PDA] and malt extract agar [MEA]), we surveyed endophytic fungi associated with leaves of *Magnolia grandiflora* (Magnoliaceae) in Durham, NC, USA. From three focal trees in a mature hardwood stand, we isolated endophytes from 60 leaf segments/leaf (N=3 leaves/tree/medium). Endophytes occurred in all leaves and in 209 of 1080 leaf segments (19.4%), with similar rates of infection inferred from PDA and MEA. Axenic cultures were grouped to morphospecies using vegetative characters and were used to estimate species richness on each medium. A subset of morphotypes was subcultured on both media to estimate morphological consistency under different nutrient regimes. Finally, nrDNA sequence data were used to identify all isolates, and to quantify species richness. We will discuss the abundance, diversity, and species composition of foliar endophytes of *M. grandiflora* as inferred from these isolation media; the utility of morphospecies in approximating species boundaries; and phylogenetic placement of fungal endophytes associated with leaves of this species, part of a basal lineage of angiosperms. *Contributed Presentation*

*ASHKANNEJHAD, SARA and HORTON, THOMAS. Dept. Environmental Forest Biology, SUNY-ESF, 350 Illick Hall, Syracuse, NY 13210, USA. sashkenn@syr.edu **The role of large mammal mycophagy on dune ecosystem succession.**

Pinus contorta seedlings are establishing in isolated locations on the Oregon Dunes, south of Florence, Oregon, U.S.A., hundreds of meters from neighboring forest mycorrhizal networks. We examined mycophagy as an alternative inoculum source for the isolated dune seedlings. Small mammals are well-known vectors of mycorrhizal fungi. However, the vast unvegetated spaces on the dunes ecosystem may inhibit much small mammal movement from the forests where the fungi fruit to seedlings in remote areas. We looked instead to large mammals due to their greater mobility in traveling across the dunes. Most deer feces collected contained incredible quantities of spores. In a bioassay, sterile seedlings inoculated with these deer fecal pellets developed mycorrhizae dominated by the fungal genera *Suillus* and *Rhizopogon*. We compared the fungal species composition of the deer pellet bioassay with the fungal species composition of isolated seedlings collected on the dunes. The ectomycorrhizal fungal species on the isolated dune seedlings almost mirrored those found in the bioassay seedlings. Our results show that deer vector large, concentrated spore packages that readily inoculate seedlings in a laboratory setting. We suggest their mobility across the dunes and consequent spore packages may aid in the establishment of mycorrhizal seedlings under primary succession. *Contributed Presentation*

BAKER, CHRISTINE and *HARRINGTON, THOMAS. Dept. Plant Pathology, Iowa State Univ., Ames, IA 50011 USA. cjbaker@iastate.edu **Population genetics of *Ceratocystis fimbriata* f. *platani* in the southeastern USA and Europe.**

Introduced fungal plant pathogens such as *Ceratocystis fimbriata* can cause devastating losses. *C. fimbriata* f. *platani* is a serious pathogen of *Platanus* species (London plane, oriental plane, and American sycamore) used as street trees or in plantations. Phylogenetic analyses suggest this pathogen is native to North America. We used fingerprints of nuclear DNA [(CAT)5] and mitochondrial DNA (*Hae* III restrictions) and PCR-based microsatellite markers to compare the genetic variability of populations of this fungus from the southeastern USA and southern Europe. Nuclear and mitochondrial

fingerprints together delineated 19 haplotypes among 33 isolates collected from seven sites in the southeastern USA. The 26 European isolates from 18 sites had identical fingerprints. Isolates from the southeastern USA had many alleles (based on length of the PCR products) at the microsatellite loci. Microsatellite markers were monomorphic within the European population, except that three Italian isolates shared a unique allele at one locus, which differed from the rest of the population by 3 bp, perhaps due to a recent mutation. The genetic variability of *C. fimbriata* f. *platani* in the southeastern USA suggests this population is native. The lack of variability in the European population supports the hypothesis that it resulted from an introduction of the pathogen through Italy. *Poster*

BARTNICKI-GARCIA, SALOMON. Centro de Investigacion Cientifica y de Educacion Superior de Ensenada (CICESE), 22860 Baja California, Mexico. bart@citrus.ucr.edu **Quantitative approaches to the cell biology of hyphal morphogenesis.**

In the last 15 years, new concepts and techniques have brought us closer to a quantitative description of cell behavior of fungal hyphae, and thus closer to understanding their morphogenesis. The arrival of video microscopy and image analysis made possible high-resolution studies of single growing hyphae. Ephemeral events lasting seconds or less (growth pulses, cytoplasmic contractions) were discovered. A close correlation was established between Spitzenkörper trajectory and morphogenesis. The availability of a mathematical equation (hyphoid), based on the concept of a vesicle supply center (VSC), provided the framework for comparative morphology and for predicting the gradient(s) of wall formation needed to attain specific shape(s). Manipulations with laser tweezers proved that the Spitzenkörper governs growth direction and shape of a hypha, as predicted by the VSC model. Currently, the goal is to visualize and quantitate the polarized traffic of secretory vesicles in a hypha. The challenge is to dissect and measure the interactions between secretory vesicles and cytoskeleton components to understand what initiates and regulates the pattern of polarized exocytosis that generates a hyphal tube. Confocal microscopy combined with rapid advances in molecular genetic tagging of specific cell components makes it an attainable goal. *Symposium Presentation*

*BATES, SCOTT[1], ROBERSON, ROBERT[1], and DESJARDIN, DENNIS.[2] [1]Dept. Plant Biology, Arizona State Univ., Tempe, AZ 85287 USA. [2] Dept. Biology, San Francisco State Univ., San Francisco, CA 94132 USA. Scott.Bates@asu.edu **Arizona puffballs and earthstars (Lycoperdaceae and Geastraceae, Basidiomycota, Fungi).**

The importance of studying biodiversity across the globe is widely recognized. However, fungi are often overlooked in such studies even though they are essential components of the Earth's ecosystems. In Arizona, vascular plants found throughout the state have been documented in many publications; however, only a few mycologists have systematically collected, described, and reported on groups of fungi found there. This poster presents preliminary results from a continuing investigation of the Lycoperdaceae and Geastraceae (i.e. puffballs and earthstars) as they are found within the diverse biotic communities of Arizona. Classical taxonomic methods are employed in studying specimens of these fungi collected in the field as well as herbarium material. Examples of taxonomic treatments are presented here that include standard macroscopic and microscopic morphological descriptions. As part of the larger investigation, a study of spore morphology is undertaken using scanning electron microscopy (SEM). This aspect of the study will contribute to taxonomic knowledge of these families as spore morphology is a conserved character and, therefore, phylogenetically informative. Examples of SEM micrographs exhibiting various spore morphologies are also included here. Overall, data collected in this ongoing study will help in establishing baselines of fungal biodiversity in Arizona. *Poster*

*BENNETT, REBECCA[1], MILGROOM, MICHAEL[1], CUNFER, BARRY[2], and BERGSTROM, GARY [1] [1]Dept. Plant Pathology, Cornell Univ., Ithaca, NY 14853 USA. [2]Dept. Plant Pathology, Univ. Georgia, Griffin, GA 30223 USA. rsb21@cornell.edu **Population structure of seedborne *Stagonospora nodorum* on wheat.**

Infected seed has been shown to be a potentially important source of inoculum in the *Stagonospora nodorum* pathosystem. Despite the fact that high incidence of infected seed is common in commercial seedlots of wheat, the seedborne aspect of *S. nodorum*'s biology has yet to be examined within a population genetic framework. Using flurorescent-labeled AFLPs, we are analyzing the genetic structure of seedborne populations of *S. nodorum* sampled from commercial seedlots and/or production fields of winter wheat in New York and Georgia. *Poster*

*BERGEMANN, SARAH[1], VANSANT, WILLIAM[1], KORDESCH, NICHOLAS[1], METZ, TIMOTHY[2], and GARBELOTTO, MATTEO[1] [1]ESPM-ES, 151 Hilgard Hall, Berkeley, CA 94720 USA. [2]Restoration Forestry, 1593 Old Briceland Rd, Garberville CA 95542 USA. sebergemann@nature.berkeley.edu **The effects of *Phytophthora ramorum* on the biomass of ectomycorrhizal fungi associated with tanoak (*Lithocarpus densiflorus*).**

Phytophthora ramorum was identified as the lethal agent of stem cankers in oaks (*Quercus* spp.) and tanoak (*Lithocarpus densiflorus*) in coastal regions of California. Girdling of trees results in a reduction of carbon allocation with subsequent loss of fungal biomass; however, the differential impact on species remains unknown. Through experimental manipulations and repetitive sampling, the goals of this research are to determine whether shifts in dominance or relative abundance of ectomycorrhizal biomass occur as a result of altered carbon supply. A randomized block design was implemented with six blocks (20 x 60 m) divided into 3 (20 x 20 m) plots per block. Root tips and soil were sorted from cores sampled along 2 transects per plot. Dominance of taxa was assessed from ITS PCR products cloned from root pools and individual root tips. After baseline sampling, treatments (physical girdling of all trees, 1/2 girdling of all trees, and control) were randomly assigned to plots. Probes utilizing Taqman chemistry were developed that can target selected species in mixed root pools and quantify abundance from DNA template concentrations. The results of the relative abundance of ectomycorrhizal biomass from roots and mycelia from selected taxa at baseline sampling and successive periods will be discussed in terms of the effects of a reduction in carbon. *Contributed Presentation*

*BINDER, MANFRED[1], HIBBETT, DAVID,[1] and FARNHAM, WILLIAM.[2] [1]Biology Dept., Clark Univ., Sackler Science Center, 950 Main Street, Worcester, MA 01610, USA. [2]Marine Laboratory, Univ. Portsmouth, Ferry Road, Hayling Island, Hants, PO11 0DG, UK. mbinder@clarku.edu **Phylogenetic relationships of the marine phyco-parasite *Mycaureola dilseae* (Agaricales).**

Marine homobasidiomycetes are among the smallest fungal groups with only nine described species. Our previous studies suggest that marine forms primarily evolved from cyphelloid agarics (minute cup-shaped terrestrial saprotrophs) *via* transitions through mangroves to

fully marine habitats. Additional results, based on four rDNA regions (nuc-ssu, nuc-lsu, mt-ssu, mt-lsu), indicate the existence of a second lineage of marine fungi in the Agaricales. *Mycaureola dilseae* is a parasite on *Dilsea carnosa* (Porter and Farnham 1986), a red alga distributed in subtidal areas along the northern temperate shores of Europe. The *M. dilseae* infection causes necrotic lesions on algal blades locally breaking down photosynthetic pigments. Clusters of tiny gasteroid fruiting bodies are later produced around the edges of the degrading lesion's center. A parsimony ratchet analysis shows that another group of reduced agarics includes the closest relatives to *M. dilseae*. It is nested in *Gloiocephala* spp., a group of minute stipitate-capitate saprotrophs that does not contain cyphelloid forms. *G. aquatica*, a fresh water fungus discovered in eutrophic ponds in Argentina (Desjardin et al. 1995), is closely related to *M. dilseae*. *Contributed Presentation*

*BISCHOFF, JOSEPH, STRUWE, L., and WHITE, JAMES, JR. Dept. Plant Biology and Pathology, Cook College, Rutgers Univ., New Brunswick NJ 08901 USA. jbischof@eden.rutgers.edu **Evaluation of anamorphic states in Clavicipitaceae (Hypocreales) and their use in determining monophyly within the family.**

Historically, fungi identified by their asexual (anamorphic) states have been taxonomically placed in the phylogentically uninformative group, Deuteromycotina (Fungi Imperfecti). Deuteromycotina is a phenetically assembled group whose nomenclature, theoretically, provides no information regarding evolutionary history or relationships. Recent analyses of the 28S rDNA, anamorphic morphology, and teleomorphic morphology of clavicipitalean species suggest the contrary. Preliminary results support the monophyly of anamorphic groups within Clavicipitaceae (Hypocreales), while finding paraphyly in teleomorphic genera. This may suggest that a reassessment of how we determine generic groups in Clavicipitaceae is necessary. *Contributed Presentation*

*BLACKWELL, MEREDITH[1], SUH, SUNG-OUI[1], MARSHALL, CHRISTOPHER[2], and McHUGH, JOSEPH. [3] [1]Dept. Biological Sciences, Louisiana State Univ., Baton Rouge, LA 70803 USA. [2]Dept. Entomology, Smithsonian Institution, National Museum of Natural Science, Washington, D.C. USA. [3]Dept. Entomology, Univ. Georgia, Athens, Georgia 30602 USA. mblackwell@lsu.edu **Did yeasts accompany beetles as they radiated into wood?**

In a survey of insect gut yeasts, we isolated close relatives of *Pichia stipitis* (Saccharomycetes) from the gut and surface of wood-ingesting beetles (Coleoptera: Passalidae). The yeasts were collected from a broad geographical range in the southeastern USA and Panama. Phylogenetic analyses of SSU and LSU rRNA sequences of 300 taxa distinguished a well-supported clade consisting of the passalid yeasts and *Pichia stipitis*, *P. segobiensis*, *Candida shehatae*, and *Candida ergatensis*, all of which ferment and assimilate xylose or hydrolyze xylan, major components of hemicellulose. The passalid yeasts also synthesize a wide range of B-complex vitamins *in vitro*, which many insects require. Minor genetic and phenotypic variation among some of the passalid yeasts was detected by ITS sequences and *in vitro* metabolic tests. We do not know if the yeasts benefit from the association. The consistent association of the xylose-fermenting yeasts with wood-ingesting passalid beetles across a wide geographical range, however, suggests that microbial metabolites may have aided the beetles in a radiation and expansion into woody habitats. *Contributed Presentation*

BOK, J. W. and *KELLER, N. P. Dept. Plant Pathology, Univ. Wisconsin-Madison, 1630 Linden Dr., Madison, WI 53706 USA. npk@plantpath.wisc.edu **Global regulation of secondary metabolism.**

Secondary metabolites are low molecular weight natural products that are not essential to the producing cells but likely have a survival function in nature. They are of intense interest to humankind due to their pharmaceutical and/or toxic properties. We have identified a novel *Aspergillus nidulans* protein, LaeA, which regulates gene expression of several secondary metabolites. This protein is conserved in *A. fumigatus* and likely other ascomycetes. LaeA is a nuclear located protein that positively regulates sterigmatocystin biosynthesis, mycelial pigment formation, penicillin biosynthesis, lovastatin biosynthesis and asexual spore pigment biosynthesis in *A. nidulans*, and mycelial pigment formation, asexual spore pigment biosynthesis and gliotoxin biosynthesis in *A. fumigatus*. mRNA studies of both *laeA* and over expression *laeA* strains suggest this regulation is transcriptional. Two signal transduction molecules (protein kinase A and RasA) which negatively regulate sterigmatocystin biosynthesis and asexual sporulation in *A. nidulans* also negatively regulate *laeA* expression. However *laeA* strains show little difference in asexual spore production from wild type thus suggesting the primary role of LaeA is to regulate secondary metabolism. Current studies are aimed at deciphering the mechanism of this regulation. *Symposium Presentation*

*BREAKSPEAR, ANDREW and ASSINDER, SUE. School of Biological Sciences, Univ. Wales, Bangor, Bangor, Gwynedd LL57 2UW, UK. bsp81b@bangor.ac.uk **Using GFP constructs to study the endomembrane system of *Aspergillus nidulans*.**

The eukaryotic secretory system functions to regulate the modification and delivery of newly synthesised proteins, lipids and carbohydrates. To allow this, mispackaged proteins in the Golgi are returned to the Endoplasmic Reticulum by retrograde transport via COPI-coated vesicles. *Aspergillus nidulans* is an ideal model organism in which to study this process, displaying a highly polarised form of growth that is concentrated to a defined region of the hyphal tip. We have tagged the *A. nidulans* alpha-COP protein, a constituent of COPI, with the reporter Green Fluorescent Protein (GFP). In wild-type strains, the alpha-COP:GFP appears to localise to Golgi equivalents at the hyphal tip. Further work is underway using immunocytochemistry and transmission electron microscopy to confirm this. To investigate positioning and locomotion of Golgi equivalents, an alpha-COP:GFP expressing strain has been treated with cytoskeletal drugs. In addition a variety of temperature-sensitive mutant strains, deficient in normal polarised growth, have been transformed with the alpha-COP:GFP. Results will be reported of analysis of these strains by confocal microscopy. *Symposium Presentation*

*BRIERE, S. C. [1], KRISTJANSSON, G. T.[1], FAVRIN, R. [1], and CALLAN, B. [2] [1]Canadian Food Inspection Agency, Ottawa Laboratory Fallowfield, Ottawa, Ontario Canada K2H 8P9. [2]Pacific Forestry Centre,Victoria, BC V8Z 1M5. email brieresc@inspection.gc.ca **Surveys for *Phytophthora ramorum*, the causal agent of Sudden Oak Death, in Canada.**

Plant diseases caused by the fungus *Phytophthora ramorum* have become increasingly important since it's interception in 1993 in both Germany and the Netherlands. The pathogen has since been detected in Belgium, Denmark, France, Poland, Spain, Sweden, the United Kingdom and the United States. The pathogen has caused devastating losses in the oak and tanoak forests of coastal Northern California. Starting in November 2001, Canada has acted to limit imports of

known hosts of *P. ramorum* and soil from affected areas. In concert with this regulatory action, Canada initiated a survey to determine if *P. ramorum* had been introduced into Canada. The first survey was started in the summer of 2002 and a total of 2857 samples were collected and analyzed from the provinces of British Columbia, Ontario, Québec, Nova Scotia and New Brunswick. The survey concentrated on known host species cultivated in Canada including *Rhododendron, Azalea, Lonicera, Acer, Arctostaphylos* and *Quercus*. We did not detect *P. ramorum* in any of the samples from the 2002 survey. Approximately 40 *Phytophthora* isolates were recovered. Most were identified as *P. cactorum, P. citricola,* or *P. cinnamomi*. Two of the isolates recovered during the 2002 survey appear to be previously undescribed *Phytophthora* spp. The 2003 survey results are pending. *Poster*

*BURGESS, JOSHUA, SCHWAN, WILLIAM, and VOLK, THOMAS. Dept. Microbiology and Biology, Univ. Wisconsin-La Crosse, La Crosse WI 54601 USA. burgess_joshua@hotmail.com
Development of a rapid PCR-based assay to detect the human pathogen *Blastomyces dermatitidis* in soil samples.

Blastomyces dermatitidis is the dimorphic fungal agent of blastomycosis, a disease that primarily affects humans and dogs. The clinical appearance of this mycosis is well characterized but there is still little known about its environmental niche, having been isolated from nature only about 20 times. We have developed a PCR-based assay to detect *B. dermatitidis* from soil samples using primers specific to a portion of the virulence gene *BAD*1. An internal standard control was designed to ensure that negative results from soil samples are not the result of PCR failure due to soil inhibitors; a plasmid, pTJV2-1, was developed by excising 50 bp from the center of *BAD*1 and cloning it into pGEM-3z. The sensitivity of the plasmid, using *Blastomyces* specific primers (BSP), is 10 femtograms. To test specificity of the assay in the environment, soil was seeded with *B. dermatitidis*. The extracted DNA was amplified using BSP. The specificity was determined by co-seeding with actinomycetes and fungi, especially those closely related or found in the same geographic areas, such as *Histoplasma capsulatum* and geophilic dermatophytes. This method will later be tested quantitatively on soil samples collected from sites that are likely positive for *Blastomyces* based on recent epidemiology, ultimately leading to a more accurate picture of the distribution of this fungus in nature. *Poster*

CAFARO, MATIAS. Dept. Ecology and Evolutionary Biology, Univ. Kansas, Lawrence KS 66045 USA. matcaf@ku.edu **Eccrinales (Trichomycetes) are not fungi, but a novel clade of the class Mesomycetozoea, in the early divergence of animals and fungi.**

Eccrinales and Amoebidiales have been considered members of the class Trichomycetes (Zygomycota) for the last 150 years. These organisms inhabit the gut of a wide range of arthropods (Crustacea, Insecta Diplopoda) in varied habitats. The order Eccrinales is characterized by unbranched, nonseptate, multinucleate thalli and sporangiospores that are formed basipetally from the thallus apex. The order Amoebidiales has coenocytic, multinucleate thalli that produce amoebae, which typically encyst and produce cystospores. Most of their taxonomy is based on a few micromorphological characters. Sexual reproduction is not known in either group. Only one species, *Amoebidium parasiticum*, has been axenically cultured so far, which has permitted several biochemical and phylogenetic analyses. As a consequence, Amoebidiales were removed from the Trichomycetes and placed in the Mesomycetozoea. The affinity of Eccrinales and Amoebidiales was suggested early on when the class Trichomycetes was erected in 1948. Molecular markers were developed to study the relationship of these orders to other groups. Ribosomal gene (18S and 28S) sequence analyses do not support a close association of these orders to the Trichomycetes, their putative sister taxon, or to other fungi. Eccrinales have common ancestry with the Amoebidiales and belong to the Mesomycetozoea, placed at the animal-fungi boundary. *Contributed Presentation*

CAMPBELL, JINX and *SHEARER, CAROL. Dept. Plant Biology, Univ. Illinois, Urbana, IL, 61801 USA. jcampbe2@life.uiuc.edu
Untangling the confusion in the Aliquandostipitaceae.

The family Aliquandostipitaceae was erected for the genus, *Aliquandostipite*, which contained two species of tropical ascomycetes. In a later study, molecular phylogeny indicated that one of these species, *A. sunyatsenii*, was more closely related to *Jahnula* and was thus transferred. At the same time a new species of *Jahnula*, *J. siamensiae* was described, although molecular analyses indicated this species had closer affinities to *Aliquandostipite*. A new genus, *Patescospora* was erected for a species that also had phylogenetic affinities with *Aliquandostipite*. To better understand the relationships of species within Aliquandostipitaceae, molecular phylogenetic analyses were performed using 18S rDNA sequences on six species of *Jahnula*, two undescribed species of *Jahnula*, one species of *Aliquandostipite*, two undescribed species of *Aliquandostipite* and one species of *Patescospora*. *Jahnula sunyatsenii*, is placed on a monophyletic clade with four species of *Jahnula* and the two undescribed species of *Jahnula*, indicating that it was correctly moved into *Jahnula*. The type species of *Aliquandostipite*, *A. khaoyaiensis*, is placed on a monophyletic clade with *Patescospora separans*, *Jahnula siamensiae* and two undescribed species of *Aliquandostipite*. Based upon these molecular results, and confirmed with morphological comparisons, generic transfers are proposed and new species are described. *Poster*

CANTRELL, SHARON. Science & Technology, Univ. del Turabo, P. O. Box 3030, Gurabo, P. R. 00778 USA. scantrel@suagm.edu
Sampling methods to study Discomycetes diversity in a subtropical rain forest.

Most of the studies that have used a systematic collecting scheme have not included the Discomycetes. For this reason, I have undertaken a study to test two sampling methods at two sites in the Caribbean National Forest, Puerto Rico. For a plot-sampling method, two 10x10m plots divided into one hundred 1x1m subplots were established; for each sample twelve subplots were selected at random with replacement. Two 60m transects were established and in each, twelve 1x1m subplots were randomly placed at the beginning of the study. The study was conducted from Oct. 2001-Sept. 2002. A total of 46 and 51 morpho-species were identified between transects and plots, respectively. There was a 32% overlap and 68% complementarity between sites. The Sorensen Similarity Index between sites was 0.74 for both methods, and 0.75-0.80 between methods within sites. The species accumulation curve indicates that the minimum number of subplots needed is 10 per transect and 60-70 per plot to obtain between 70-80% of the species. In terms of sampling effort, I concluded that at least 12 samples distributed throughout a year at more frequent intervals during the rainy season are needed. There was no difference between using transects or plots based on the number of species and similarity indexes. Based on a Chi-Square analysis using the frequencies of species, however, transects were better than plots. *Contributed Presentation*

*CARPENTER-BOGGS, LYNNE[1], CARRIS, LORI[1], and CASTLEBURY, LISA[2] [1]Dept. Plant Pathology, Washington State Univ., Pullman WA 99164 USA. [2]USDA ARS Systematic Botany and Mycology Lab, 10300 Baltimore Avenue, Beltsville MD 20705 USA. carris@wsu.edu **Multi-locus phylogenetic analysis of *Tilletia* species infecting hosts in grass subfamily Pooideae.**

Phylogenetic analysis of Tilletiales (Ustilaginomycetes, Basidiomycota) based on large subunit nuclear rDNA shows that *Tilletia* species infecting hosts in grass subfamily Pooideae form a well-supported monophyletic group (bootstrap >95%). In addition to infecting Pooids, these species are characterized by reticulate or cerebriform teliospore ornamentation. The objective of this study is to resolve relationships within the Pooid-infecting clade, which includes the wheat bunt pathogens *Tilletia controversa*, *T. laevis* and *T. tritici*. Nine loci, including those proposed for the Assembling the Fungal Tree of Life and Deep Hypha Projects, were screened for variability by sequencing *T. controversa*, and two closely related species from wild grasses, *T. bromi* and *T. fusca*. Beta-tubulin, COX3, and ATP6 were less than 2% variable among these species, RPB1 and IGS1 showed 2-5% variability, and TEF-1 alpha, actin, RPB2 and IGS2 were 5-10% variable. The 5-10% level of variability is necessary to differentiate closely related, but host-specific taxa. Preliminary analyses indicate that a number of the accepted species are polyphyletic, although in general host plant remains a good indicator of species identity. *Poster*

*CASTLEBURY, LISA, ROSSMAN, AMY, and FARR, DAVID. USDA ARS Systematic Botany and Mycology Lab, 10300 Baltimore Avenue, Beltsville MD 20705 USA. lisa@nt.ars-grin.gov **Phylogenetic placement of the anamorph genus *Sirococcus*.**

The anamorph genus *Sirococcus* contains the causal agents of Sirococcus shoot blight of conifers (*S. conigenus*) and butternut canker (*S. clavigignenti-juglandacearum*). The butternut canker fungus was recently introduced into North America and threatens the extinction of the butternut tree (*Juglans cinerea*). *Sirococcus* is characterized by the production of fusiform, hyaline, mostly 1-sepate conidia from globose or flattened, simple to multilocular pycnidia. Teleomorphs for these fungi, if they exist, have not been reported. Internal transcribed spacer region sequences indicate that the type species *S. conigenus* is most closely related to diaporthalean fungi. Approximately 1200 bp of LSU nrDNA were sequenced to determine a more exact placement in the Diaporthales. Parsimony and Bayesian analyses firmly placed both species in the Gnomoniaceae. *Sirococcus conigenus* is most closely related to isolates of *Discula destructiva*, while *S. clavigignenti-juglandacearum* is closest to an isolate *Gnomonia padicola*. These data suggest that the butternut canker fungus does not belong in the genus *Sirococcus*. Correct placement of *S. clavigignenti-juglandacearum* may help to determine the origin of this devastating disease. *Poster*

*CHAN, WAI YEE, LAW, KIT MEI, and VRIJMOED, L. L. P. Dept. Biology and Chemistry, City Univ. Hong Kong, Tat Chee Avenue, Kowloon, HKSAR. 50182548@student.cityu.edu.hk **A comparative study of qualitative sampling methods for the analysis of the indoor air molds.**

Accurate and informative sampling methods are very important in the evaluation of fungal exposure in indoor air quality (IAQ) investigations. We have investigated the relationship between indoor viable airborne and dustborne fungi and compared the performance of viable and non-viable air samplers - Reuter Centrifugal Air Sampler (RCS) and Zefon Air-O-Cell ™ (AOC). Two 12hr investigations were conducted in two typical Hong Kong office premises in autumn and winter in 2001. Viable samples were incubated on Dichloran Glycerol 18 and 2% Malt Extract Agar at 25ºC. The results indicate a more diverse and abundant fungal species was present in dust samples than in air in both seasons. Simpson's Diversity Index values in dust samples were 16 - 18% higher than air samples with much higher counts (>500 times) recorded. Our investigations also show that more abundant fungal species but with similar species diversity was collected by AOC, compared with RCS. The AOC recorded 25 - 110 times higher counts than the RCS but showing the Orchiai Similarity Index 0.81 - 0.86 in both seasons. The dominant fungi collected in dust and air were *Penicillium*, *Aspergillus* and *Cladosporium*, with increased dominance of *Cladosporium* in winter. This study suggests that more informative IAQ investigations can be conducted by collecting viable samples in dust and non-viable samples in air. *Symposium Presentation*

*CHAVERRI, PRISCILA[1], and SAMUELS, GARY.[2] [1]Pennsylvania State Univ., Dept. Plant Pathology, University Park, PA 16802 USA. [2]USDA-ARS, Systematic Botany and Mycology Laboratory, Beltsville, MD 20705 USA. priscila@nt.ars-grin.gov **Teleomorph and anamorph evolution in *Hypocrea/Trichoderma*: towards a species concept.**

The taxonomy of *Hypocrea/Trichoderma* has been historically difficult. Species definitions based on morphological characters such as conidiophore type, synanamorphy, color of the ascospores and conidia, and stroma morphology have not been supported by DNA sequence analyses. Classification of the holomorph based on combined attributes of teleomorph and anamorph has been somewhat more successful but still conflicts with the sequence data. The objective of this study was to study species of *Hypocrea* with green ascospores and their anamorphs; ascospore pigmentation has been used as a generic character in the Hypocreales. Comparative analyses of phenotype and DNA sequence data show that the character of green ascospores is a recently derived and not useful as a generic character. In addition, simple, acremonium- and verticillium-like conidiophores are probably primitive characters, lost in recent species; the majority of the recently derived species have complex conidiophore types. As a result of the combination of multiple phenotypic and genotypic characters, many more new species are described in *Hypocrea/Trichoderma*. A species concept is discussed. *Contributed Presentation*

CHEN, MO-MEI. University Herbarium, 1001 Valley Life Sciences Building #2465, Univ. California, Berkeley, CA 94720-2465 USA. mmchen@nature.berkeley.edu. ***Cronartium ribicola* and *Cronartium quercuum* in California.**

Because rusts are obligate parasites, rusts will appear when the rust host does. This leads us to ask: "When does the rust host occur on California earth?" This is the California phytogenous scenario. Sugar pine rust (*Cronartium ribicola* Fisher) is an obligate parasite and an indigenous species in California. *Ribes roezli* is prevalent in the five needled sugar pine (*Pinus lambertiana* Dougl) areas. Sugar pine white pine blister rust is characterized by the Pacific Mediterranean flora. Systematic biological specializations and taxonomic treatments frequently utilize formae speciales, such as *C. ribicola*. f. sp. *roezli*. Recent results from cladistic analyses of morphological and molecular characters have suggested that these fungi have had a longer co-evolutionary relationship with five needle pines than *Ribes* hosts. The occurrence of

white pine blister rust floras in virgin forests indicates the blister rust has evolved as part of the indigenous ecosystem in each region. It is proposed here that the pine-oak gall rust (*Cronartium quercuum* (Berk.) Miyabe) exists in California as an evolved ecotype for the Pacific West Coast rust flora. The pycniospores and aeciospores evolved simultaneously with Monterey pine (*Pinus radiata* D. Don) and Bishop pine (*Pinus muricata* D. Don) and the teliospores and urediospores with coast live oak (*Quercus agrifolia* Nee). *Symposium Presentation*

CHEN, MO-MEI. University Herbarium, 1001 Valley Life Sciences Building, Berkeley CA 94720 USA. mmchen@nature.Berkeley.edu **The edible mushroom species characteristic: America and China.**

A rich and large variety of mushroom species can be found in the forests of the California Pacific coast and Sierra Nevada Mountains. Four main edible species are prevalent throughout the Pacific coast: *Morchella esculenta, Boletus edulis, Cantharellus cibarius*, and *Tricholoma magnivelare*. San Francisco itself has a unique mushroom natural heritage in mycology with up to over 1,000 wild species around the Bay. The cultivation mushroom industry in America traditionally started with *Agaricus bisporus* and has begun to diversify their products with the *Lentinus edodes, Hericium* species fungi. The Chinese have a 2,000-year history in cuisine and medicinal fungi that exceeds 25 species for cultivation and 256 species used for specific pharmaceutical needs. Over the years the Chinese have developed unique agroforest techniques in cultivating the mushrooms, presently producing 40 million tons of mushrooms annually, which is 60% of the world's production. According to recently mushroom biogeography and systematic studies, edible mushroom can be classified into 6 mushroom regions in China and possess 938 species, 166 genera, 54 families and 14 orders. As the abundance of diverse mushroom species become better known throughout the world, humans will come to enjoy the natural healthy food and medicinal properties of these fungal treasures. *Symposium Presentation*

*CHIU, SIU-WAI and LUK, WING-YAN. Dept. Biology, Chinese Univ. Hong Kong, Shatin, N. T., Hong Kong SAR, China. siuwaichiu@cuhk.edu.hk **Breeding of medicinal lingzhi by protoplast fusion.**

Lingzhi is a traditional medicinal fungus gaining worldwide popularity. It refers to *Ganoderma lucidum, G. tsugae* and other species belonging to genus *Ganoderma* subgenus *Lucidum*. Protoplast fusion by polyethylene glycol was carried out to introduce the wild germplasm of a native *G. lucidum* isolate into an exotic commercial *G. tsugae* cultivar. Both species bear red laccate pilei and are commonly cultivated for medicinal use. The selected hybrids as confirmed by DNA fingerprinting showed expansion of growth temperatures and increasing growth rates in comparison to those of the parental cultivar favoring commercial production using natural climatic conditions in Hong Kong. Sequences of the nuclear and mitochondrial genes reflect the selective advantages of one parent in the artificial hybridization. However, the other parent dominated in a mycelial confrontation test. Thus the sensory system in the wall-membrane layer and the production of secretory lytic enzymes are the first line of defence against non-self. *Poster*

*CHIU, SIU-WAI, CHEUNG, KA-WAN, CHUANG, PHILIP and CHU, MABEL. Dept. Biology, Chinese Univ. Hong Kong, Shatin, N. T., Hong Kong SAR, China. siuwaichiu@cuhk.edu.hk **Pathogenesis of a medicinal fungus *Ganoderma lucidum*.**

Ganoderma lucidum complex is a well-known group of white rot fungi with medicinal properties. They are also commonly found in both dead and live woody trees as pathogens in urban and reserve areas of Hong Kong. The identities of the field pathogens were determined using electron and microscopic techniques, DNA sequencing and sexual compatibility with mating testers obtained by protoplast isolation. Field observation shows that the live tree hosts for *G. lucidum* include exotic *Acacia confusa, Lophostemon conferta, Alizia lebbeck, Leucaena lecucocephala, Cerbera manghas* and native *Litsea cubeba*. *In vitro* pathogenesis study indicates that *L. cubeba* was the most susceptible host. Both basidiospore suspension and mycelium-colonized wheat grain as inocula artificially infected all seedlings of *L. cubeba* but few seedlings of *A. confusa* and *L. conferta*. Molecular detection using species-specific primer for polymerase chain reaction was the most sensitive method to reveal the invasion of the pathogen in host tissues than microscopic detection and chitin assays for early diagnosis. The pathogen ramified not just the vascular tissues but invaded the pith and spread bidirectionally from the site of infection. Consequently, basidiocarps of *G. lucidum* were observed on stem and roots of the infected trees. *Contributed Presentation*

*CHIU, SIU-WAI[1], LEE, PUI-NIN[1], TANG, PATRICK[1], CHUNG, ANTHONY, H.Y. [1], WONG, YUM-SHING[1], and NG, TZI-BUN. [2] [1]Dept. Biology, [2]Dept. Biochemistry, Chinese Univ. Hong Kong, Shatin, N. T., Hong Kong SAR, China. siuwaichiu@cuhk.edu.hk **A comparison on pigment yield and volatile profiles by submerged and solid-state fermentation of *Monascus purpurens*.**

High yield of red water-soluble *Monascus purpurens* pigments was obtained by a formulated medium-containing glutamate. The roles of glutamate were: serving as both carbon and nitrogen-sources and enhancement of production of water-soluble extracellular pigments. Submerged fermentation yielded faster pigment production rate than did conventional solid-state-fermentation. Strong cheese flavour was obtained with the former, while alcohol production was prominent in the latter as revealed by gas chromatography-mass spectrometry. In both fermentation protocols, citrinin, a hepato- and nephrotoxin, was not detected by high performance liquid chromatography. The red flavoured fermentation products free of citrinin showed antioxidant bioactivities and contained inhibitors of HMG-CoA reductase, cholesterol-lowering agents. *Contributed Presentation*

*COLE, GARRY T. and HUNG, CHIUNG-YU. Dept. Microbiology and Immunology, Medical College of Ohio, Toledo OH 43614 USA. gtcole@mco.edu **Dysregulation of host immune response to *Coccidioides* infection.**

We have reported the isolation of a *Coccidioides* gene (*SOWgp*) that encodes an immunodominant, spherule outer wall glycoprotein. This antigen is a component of a parasitic phase-specific, membranous layer (SOW) produced at the cell surface. The crude SOW fraction is easily obtained from liquid shake cultures, and is rich in ìlipid complexes.î SOWgp is the only detectable polypeptide in the SOW fraction and has been isolated from the membranous material by TX-114 detergent extraction. The translated *SOWgp* gene of isolate C735 predicted a protein composed of a signal peptide and propeptide, six randomly repeated proline- and aspartic acid-rich motifs, and a GPI anchor signal consensus sequence. Deletion of the *SOWgp* gene by homologous recombination resulted in a significant reduction in virulence and loss of patient antibody recognition of the SOW layer. C57BL/6 mice challenged intranasally with the mutant strain mounted a protective Th1 response to infection, while mice inoculated with the parental strain developed disseminated disease characterized by persistent inflammation and activation of a

dominant, non-protective Th2 pathway of immunity. SOWgp appears to play a pivotal role in the virulence of *Coccidioides* by dysregulation of host immune response to infection that exacerbates the onset of disease. *Symposium Presentation*

*COLLINS, KELLY[1], DUNHAM, SUSIE[2], CRONN, RICH[3], and MOLINA, RANDY.[3] [1]Dept. Forest Science, Oregon State Univ., Corvallis OR 97331 USA. [2]Dept. Biology, Albertson College of Idaho, 2112 Cleveland Blvd. Caldwell, ID 83605 USA. [3]USDA-Forest Service, Forestry Sciences Laboratory, Corvallis, OR 97331 USA. Kelly.Collins@orst.edu **Microsatellite markers reveal rampant gene flow among subpopulations of *Cantharellus formosus* in the central Cascade Mountains of Oregon.**

Conservation genetic approaches for conserving allelic diversity are well developed for animals and plants, but are in their infancy in the conservation of rare and commercially important mushrooms. Population genetic surveys of mushrooms are complicated by a high frequency of cryptic species in many groups; in addition, total below-ground abundance and diversity may show a poor correspondence to ephemeral fruiting bodies, which can be the focus of intense commercial harvest. In order to establish a conservation strategy for the commercially important chanterelle of the Pacific Northwest (*Cantharellus formosus*), we are determining population genetic structure for eight populations of this species located on the 15,000 acre H.J. Andrews Long-Term Ecological Research site. Sporocarp samples from two time points (240 individuals from 1997; 215 from 2000) have been evaluated for multi-locus genetic variation at six microsatellite loci. Data from the 1997 sample reveal minimal interpopulation genetic differentiation, with an Fst of 0.02 across sites, and a high interpopulation migration rate (Nm = 1.3 per generation). Results obtained from the H.J. Andrews LTER from 1997 show that loss of individual subpopulations of *C. formosus* are unlikely to result in a substantial reduction in overall genetic diversity. *Contributed Presentation*

CRIPPS, CATHY. Plant Sciences and Plant Pathology Dept., Montana State Univ., Bozeman, MT 59717 USA. CCripps@montana.edu **Interesting distributions of ectomycorrhizal alpine fungi along the Rocky Mountain cordillera.**

The Rocky Mountain cordillera connects the arctic along the continental divide to the Colorado alpine. The alpine flora of the Beartooth Plateau (Northern Rockies) has a strong arctic component (50%), as does that of the Southern Rockies (41%). In documenting the alpine mycota of the RM for a NSF-sponsored project, comparison of the regions revealed interesting distributions of ectomycorrhizal fungi. Fungi associate with *Salix arctica, S. reticulata, S. planifolia, S. glauca, Dryas octopetala,* and *Betula glandulosa* (rare). Two Amanitas are prevalent in the RM alpine: *A. absarokensis* sp.nov., restricted to the Beartooth Plateau (BT), and *A. nivalis* only from CO. Arctic-alpine species *Lactarius nanus* and *L. salicis-reticulata* associate with dwarf willow, *L.glyciosmus* with *Betula*, and *L. repraesentaneous* with *S. glauca* above timberline in both areas. *Russula nana, R. norvegica*, and *R. pascua* occur both N and S, while *R. delica* is with *Dryas* in CO. *Leccinum rotundifolia* is with birch in both areas. Only a subset of alpine *Laccaria* species from CO occur on the BT. *Inocybe* is a diverse genus in the CO alpine with over 20 species; less than half occur on the BT. Saprophytic arctic-alpine indicator species *Marasmius epidryas* and *Arrhenia auriscalpium* are reported only from the southern Rockies. Possible explanations for distributional data will be discussed. *Contributed Presentation*

CROMACK, KERMIT. Oregon State Univ., Corvallis OR 97331 USA. Kermit.Cromack@orst.edu **Roles of mycorrhizal fungi in biogeochemical processes.**

Ectomycorrhizal fungal mats from *Hysterangium setchellii* colonized an average of 15% of the mineral soil surface area and 9.6% of the top 10 cm of mineral soil volume in a western Oregon Douglas-fir forest ecosystem. Dense mineral soil colonization by these fungal mats results in significantly higher soil respiration rates and in substantially greater accumulations of calcium oxalate than occurs in adjacent non-mat soil areas. Microbial biomass estimates made using the chloroform fumigation method were about three times greater in fungal mats than in adjacent non-mat areas. Fungal biomass estimates that were indexed using calcium oxalate fungal tissue concentrations and soil oxalate extractions were found to be substantially greater in fungal mats of *H. setchellii*. This ectomycorrhizal fungal species was estimated to contribute approximately 2.7% of total belowground biomass in a Douglas-fir forest ecosystem. Fungal mat tissue and foliar nutrient concentrations of N, P, and K were similar in this Douglas-fir forest, but Ca concentrations were substantially greater in fungal mat tissue than in foliage. *Symposium Presentation*

*CZEDERPILTZ, DANIEL [1,2], and STENLID, JAN[1]. [1]Swedish Univ. Agricultural Sciences, Inst. for Forest Mycology and Pathology, Uppsala, Sweden. [2]Univ. Wisconsin-Madison, Dept. Plant Pathology, Madison, WI, USA. dlindner@wisc.edu **Development of a model system to study adaptation of the forest pathogen *Heterobasidion annosum* to the biocontrol agent *Phlebiopsis gigantea*.**

The use of biocontrol agents is an emerging field with promising applications for forestry and agriculture. However, the regular use of biocontrol agents may cause pathogen populations to change over time, thus reducing the efficiency of control. In order to study possible outcomes of interactions between a plant pathogenic fungus and its respective biocontrol agent, we are developing a system in which the root-rot pathogen *Heterobasidion annosum* is challenged by the biocontrol agent *Phlebiopsis gigantea*. In this system, *H. annosum* and *P. gigantea* are co-inoculated on spruce discs and the exact concentration of *P. gigantea* spores needed to suppress *H. annosum* is determined. *H. annosum* is then reisolated from the discs containing the highest *P. gigantea* concentrations, and these isolates are again challenged with *P. gigantea*. This cycle is repeated many times to determine if increasing concentrations of *P. gigantea* are needed to suppress *H. annosum*. *H. annosum* isolates are archived at each step so that genetic changes can be tracked, and certain isolates will be tagged with *gfp* (encoding green fluorescent protein), thus making it possible to visualize mycelial interactions *in situ*. These techniques will be useful for understanding the mechanisms that underlie biocontrol of *H. annosum*. *Poster*

*DADER, LAURA and ELLZEY, JOANNE. Biological Sciences, Univ. Texas at El Paso, El Paso, TX 79968-0519 USA. ldader@utep.edu; jellzey@utep.edu **A study on asthma and allergic rhinitis incidences and environmental associations.**

Emergency room visits (ER) and hospital admissions attributable to respiratory diseases have been on the rise worldwide since the early 1970's. Air pollution, namely ozone and particulate matter less than PM10, including pollen and fungal spores, have been implicated as causative agents in ER visits. Due to the limited publications concerning allergic rhinitis, asthma and air pollution in the El Paso/Ciudad Juarez area, a retrospective study was conducted using linear

regression to compare the numbers per day of allergic rhinitis and asthma ER visits in a William Beaumont Army Medical Center (WBAMC) pediatric population to the levels of maximum temperature, precipitation, average wind speed, dew point, ozone, pollen and fungal spores from July 27, 2000-September 30, 2001. Forty-eight thousand cases of ER visits due to respiratory illnesses during this period were filtered to 1450 cases of allergic rhinitis and asthma. When the case numbers for allergic rhinitis and asthma were combined, temperature, pollen, fungal spores and ozone appeared to have synergistic influences over the case numbers. PM10 and PM2.5 data are being collected and all of the data is being analyzed by SAS Proc Reg for further statistical analyses. *Poster*

DESJARDIN, DENNIS. Dept. Biology, San Francisco State Univ., San Francisco, CA 94132 USA. ded@sfsu.edu **Unusual macromycetes from Thailand: an update on a NSF-PEET project.**

A NSF-PEET project designed to monograph marasmioid and mycenoid fungi of southeast Asia has yielded collatoral benefits. Thailand harbors a number of unusual and seemingly ancestral taxa of fleshy Basidiomycetes. Data will be presented on several new species, a new genus, and new Thai distributions that suggest they are sister to most known members of their lineages. Are the montane forests of northern and central Thailand refugia for relictual taxa? Discussions of the following taxa will be presented: *Sparassis cystidiosa* sp. nov.; *Pterulicium xylogenum*; *Anamika indica*; *Russula zonata* sp. nov., seemingly intermediate between *Russula* and *Lactarius*; *Flegelomyces* gen. nov., allied with *Serpula* in the bolete clade; and others. In addition, information will be provided on research opportunities at a new facility, the Mushroom Research Centre, recently inaugurated in Mae Rim near Chiang Mai, northern Thailand. *Contributed Presentation*

*DETTMAN, JEREMY and TAYLOR, JOHN. Plant and Microbial Biology, Univ. California, Berkeley, CA, 94720 USA. jeremyd@uclink4.berkeley.edu **Microsatellite Evolution in *Neurospora*.**

Microsatellites have become one of the most popular classes of markers for population genetic analyses. Despite this fact, the evolutionary dynamics and mutational processes of microsatellites are still not fully understood. To address this issue, 4 unlinked microsatellites and their flanking regions were sequenced from 147 strains from 8 phylogenetic species of *Neurospora*. To elucidate the genealogical relationships among alleles, repeat number was mapped onto trees constructed from flanking sequence data. This allowed us to place the microsatellite mutations in the evolutionary context of the less rapidly evolving flanks. Mutational patterns differed among the 4 microsatellites, and between the two DNA regions. A significant relationship between maximum repeat number and variance in repeat number was found. Clear evidence of interspecific allelic homoplasy and microsatellite mutational saturation was observed, indicating these loci should not be used for inferring phylogenetic relationships among species. Within species and populations, frequency distributions of alleles were generally consistent with the stepwise mutational model proposed for microsatellites, confirming the usefulness of these loci for population-level analyses. Interpopulation relationships based on microsatellite-specific genetic distances were consistent with geographic differentiation. *Contributed Presentation*

DIGHTON, J.[1], TUGAY, T.[2], ZHDANOVA, N.[2], ZHELTONOZHSKY, V.[3], and McDERMOTT, P.[4] [1]Rutgers Univ. Pinelands Field Station, New Lisbon, NJ 08064 USA. [2]Inst. Microbiology and Virology, Natl Acad. Sci. of Ukraine, Kiev, Ukraine. [3]Inst. Nuclear Research, Natl Acad. Sci. of Ukraine, Kiev, Ukraine. [4]Rutgers Univ. Environment and Health Service, Piscataway, NJ 08854, USA. dighton@camden.rutgers.edu **The influence of ionizing radiation on directional growth of emergent hyphae from condiospores.**

Numerous micro-fungi have survived and persist in the soil and the reactor room of the nuclear power plant at Chernobyl since the explosion of that facility in the 1980s. Investigations into the ecology of these fungi at Chernobyl have shown that the effects of elevated levels of radioactivity have altered fungal community structure and may have influenced their physiology. We report findings from a comparative investigation of the influence of both gamma and beta radionuclide emissions of known activity on the directional growth of hyphae germinating from condiospores of a range of fungal species that were isolated in the neighborhood of, or at a distance from Chernobyl. Condiospores of *Cladosporium* and *Penicillum* isolates were germinated on agar or in aqueous media adjacent to a 1mm diameter collimated beam of radioactivity. The percentage germination, growth rate and direction of growth of the emerging hyphae were measured in the first 48h. Results are species and isolate dependent and show instances where the presence of radioactivity stimulated conidial germination and hyphal growth was significantly greater towards the source of radiation. *Contributed Presentation*

*DOERING, TAMARA, BOSE, INDRANI, ORY, JERAMIA, and REESE, AMY. Dept. Molecular Microbiology, Washington Univ. Medical School, Campus Box 8230, 660 South Euclid Avenue, St. Louis, MO 63110, USA. doering@borcim.wustl.edu **A yeast under cover: The capsule of *Cryptococcus neoformans*.**

Cryptococcus neoformans is an opportunistic fungal pathogen responsible for serious disease. Cryptococcosis is contracted by inhalation, and in the setting of immune compromise can spread throughout the body, with a particular tropism for the central nervous system. The devastating outcome of this infection is a meningoencephalitis, which is often fatal. The major virulence factor of *C. neoformans* is an elaborate polysaccharide capsule, which is involved in a variety of processes that help to thwart the host immune response. The capsule is composed of two polysaccharide structures that contain mannose, xylose, glucuronic acid, and galactose. The polysaccharides are shed copiously from growing cells and also form an extensive structure radiating outwards from the fungal cell wall. To better understand cryptococcal biology, and in particular capsule synthesis, we are employing biochemical, cell biological, molecular, and biophysical techniques. Among the processes we are examining are the provision of activated precursors for glycan synthetic reactions, the sugar transferase-mediated reactions themselves, and the attachment of capsule material to the outside of the fungal cell. Current work in each of these areas will be presented, as well as studies on the development of double stranded RNA interference (RNAi) as a useful tool in *C. neoformans*. *Symposium Presentation*

*DOUHAN, GREG and RIZZO, DAVID. Dept. Plant Pathology, Univ. California Davis, Davis, CA 95616 USA. gwdouhan@ucdavis.edu **Fine scale genetic structure analysis of *Cenococcum geophilum* reveals putative cryptic species.**

Cenococcum geophilum (*Cg*) is one of the most commonly encountered and widely distributed mycorrhizal fungal species. A significant amount of genetic and genotypic diversity has been detected in populations of *Cg*, despite the fact that this fungus is not thought to reproduce by meiotic or mitotic spores. Previous studies have concluded that a finer sampling scheme was needed to adequately

describe the genetic structure of *Cg*. Therefore, we chose to sample at a fine scale within a blue oak (*Quercus douglasii*) dominated California woodland. Three subpopulations of *Cg* were sampled within approximately 10 to 15 m of each other on a spatial scale of less than 4 square meters per subpopulation. Up to 18 soil samples were taken from each subpopulation and over 100 cultures were recovered from viable sclerotia. Amplified fragment length polymorphisms (AFLP) detected a substantial amount of diversity within and among each subpopulation. Genome-wide variability based on AFLP and preliminary phylogenetic analysis of the ITS region and a group I intron located between ITS 1 and the small subunit of rDNA of representative isolates from one subpopulation is consistent with cryptic species of *Cg* coexisting at a fine spatial scale. The hypothesis of cryptic species within *Cg* is being further tested based on AFLP and phylogenetic analyses of additional genetic loci. *Poster*

*DOUHAN, GREG and RIZZO, DAVID. Dept. Plant Pathology, Univ. California Davis, Davis, CA 95616 USA. gwdouhan@ucdavis.edu **Host-parasite relationships among bolete-infecting *Sepedonium* species.**

Some host specificity of the mycoparasite *Sepedonium microspermum* to the *Boletus chrysenteron* group has been observed. Our objectives were to test host specificity among *Sepedonium* spp. associated with boletes in California oak woodlands and to initiate studies on host-parasite coevolution. Bolete samples were collected from four locations separated by up to 640 km. *Sepedonium* was cultured and host tissue samples were taken for molecular identification. Based on AFLP analysis, four distinct *Sepedonium* clades were found. ITS regions of selected isolates from each group were sequenced and analyzed along with sequences from a previously published phylogeny. Two AFLP groups clustered with *S. microspermum* whereas the other two AFLP groups clustered with *S. chrysospermum*. ITS-RFLP and sequence analysis identified *B. dryophilus*, *B. chrysenteron*, and an unknown distantly related *Boletus* sp. as hosts. *S. microspermum* infected *B. dryophilus* and *B. chrysenteron*, whereas *S. chrysospermum* infected *B. chrysenteron* and the unknown *Boletus* sp.. *B. dryophilus* collected from distant locations were specific to one AFLP group of *S. microspermum*, indicating specificity within this species. However, due to a limited database for *Bolete* spp., host parasite coevolution studies within this system will not be possible until a *Boletes* phylogeny is in place. *Contributed Presentation*

*DYER, PAUL, LEE, HEATHER, MEAKIN, HELEN, MURTAGH, GARETH, and DICKINSON, MATTHEW. School of Life Sciences, Univ. Nottingham, Nottingham NG7 2RD, UK. Paul.Dyer@Nottingham.ac.uk **Phylogenetic analysis with "FreeTree;" a new programme for DNA fingerprint data.**

Various software programmes are available in the public and private domains for the phylogenetic analysis of molecular data obtained from single- and multi-locus investigations. Multi-locus approaches, using DNA fingerprinting methods such as RAPD and AFLP, offer advantages as phylogenetic trees may be based on data from loci throughout the genome and methods are often relatively cheap and easy to perform. However, there are very few programmes available for the analysis of fingerprint data that allow resampling to test robustness of trees. We now describe a programme "FreeTree" developed by Pavlicek, Hrda & Flegr (http://www.natur.cuni.cz/~flegr/freetree.htm) for the analysis of binary data (presence/absence of characters), and apply it for the first time to fungal data. The programme constructs trees according to distance-based methods (UPGMA or neighbour-joining), and allows use of a variety of similarity coefficients (e.g. Jaccard and Nei). Resulting tree topologies may be resampled directly for robustness using methods including bootstrapping and Jacknifing. Examples of the use of FreeTree to analyse RAPD and AFLP fingerprint data from studies involving toxigenic Aspergilli, the plant pathogen *Tapesia*, and lichen-forming fungi will be presented. Trees were also constructed using parsimony methods (PAUP) with similar results obtained to those from FreeTree. *Poster*

EBERHART, JOYCE, YOSHINAGA, ALOHA, and LUOMA, DANIEL. Dept. Forest Science, Oregon State Univ., Corvallis, Oregon 97331 USA. Joyce.Eberhart@orst.edu **Characterization of *Cortinarius* sporocarps using PCR/ RFLP.**

The Demonstration of Ecosystem Management Options project is designed to test the ecological effects of green-tree retention as an alternative to clear-cutting. Mushrooms and truffles were sampled over 3 years pre- and 3 years post-treatment in three study sites in the Oregon and Washington Cascades. Pre- and post-treatment soil cores were also collected and mycorrhizae were quantified. To test for treatment effects on biodiversity, it is necessary to identify collected specimens to species. The Cortinariaceae in our study area are poorly understood taxonomically. In order to better assess *Cortinarius* species diversity, we extracted DNA from 40 randomly selected collections from each of the three study sites. We used the primers ITS4 and ITS1F for PCR amplification and RFLPs were run on the resulting products. We found that the restriction enzymes Hae3 and Cfo were best for distinguishing RFLP species, although we also used Hinf1, Dpn2, and Rsa. Preliminary results show that there are dozens of *Cortinarius* species within the study area. With this randomized sub-sample method, we can estimate relative abundance of taxa and detect differences in diversity among treatments and study sites. Matches between the mushroom and mycorrhizae RFLP patterns were also found. These results will improve the accuracy of our assessment of treatment effects on the below-ground ecosystem. *Poster*

ENRIQUEZ, DIANA[1], *GONZALEZ, MARIA[2], HANLIN, RICHARD[3] and ULLOA, MIGUEL[2]. [1]Dept. Biologia Marina, Inst. Oceanologia, CITMA, Ciudad La Habana 12100 Cuba. [2]Dept. Botanica, Inst. Biologia, UNAM, Mexico DF 04510 Mexico. [3]Dept. Plant Pathology, Univ. Georgia, Athens GA30602 USA. mcgv@ibiologia.unam.mx **Marine fungi from Cuba.**

The marine fungal biota of Cuba remains unknown for the most part. The first collections of Cuban marine fungi were made by Hariot and Patouillard 99 years ago. Afterwards, subsequent interest in marine fungi was only sporadic. Recently, the first author made new collections from 12 Cuban beaches. In this work, the records from the literature have been merged with the new collections into a checklist of the marine fungi reported from Cuba. A total of 31 species are recorded from 14 localities. The most diverse group is the ascomycetes (25 spp.), followed by the mitosporic fungi (6 spp.). The seacoast of Province of Havana City on the Gulf of Mexico is the most studied in the country, whereas the Caribbean Coast is the least studied. The most frequently encountered ascomycetes are *Lindra marinera*, *Arenariomyces parvulus* and *Corollospora maritima*. Given the large amount of coastline in Cuba on the Caribbean Sea, Atlantic Ocean and Gulf of Mexico, many additional studies are needed to fully understand the mycodiversity of the country. *Poster*

ESTRADA-TORRES, ARTURO[1], GAITHER, THOMAS[2], MILLER, DENNIS[3], LADO, CARLOS[4], and *KELLER, HAROLD. [5] [1]Centro de Investigación en Ciencias Biológicas, Univ. Autónoma de Tlaxcala, Apdo. Postal 183. Tlaxcala 90000, México. [2]Dept. Biology, Slippery Rock Univ., Slippery Rock, PA 16507-1325 USA. [3]Dept. Molecular and Cell Biology F03.1, Univ. Texas at Dallas, Richardson, TX 75080 USA. [4]Real Jardín Botánico, Plaza de Murillo 2, 28014 Madrid, Spain. [5]Dept. Biology, Central Missouri State Univ., Warrensburg, MO 64093, USA. keller@cmsu1.cmsu.edu **The myxomycete genus *Schenella*: morphological and DNA sequence evidence for synonymy with the gasteromycete genus *Pyrenogaster*.**

Since its identification and description by Macbride in 1911, the genus *Schenella* has proven difficult to classify. Macbride placed it with the Myxomycetes but it was unclear with which myxomycete, if any, it should be grouped. Recent identification of abundant collections of *Schenella simplex* has allowed a re-evaluation of the classification of *Schenella* as a myxomycete. Morphological evidence based on light and scanning electron micrcoscopy of fresh field-collected specimens and the type specimen of Macbride, indicates that this taxon is a gasteromycete and not a myxomycete. Analysis of DNA sequences of the small subunit rRNA gene from both mitochondrial and nuclear DNA amplified by PCR from total DNA obtained from the freshly collected samples indicate that the genus *Schenella* is closely related to an anciently diverged, monophyletic group of fungi which includes several gasteromycete genera, including *Geastrum*, *Sphaerobolus*, and *Pseudocolus*. Further analysis and comparison of the morphological features of *Schenella* suggested that it might be synonymous with the gasteromycete genus *Pyrenogaster*. Preliminary morphological comparisons of collections authentically identified as *Pyrenogaster atrogleba* indicate that it is synonymous with *Schenella simplex*. *Poster*

*FALLAH, PAYAM, GALLUP, JANET, and SPERO, DAVID. Environmental Microbiology Laboratory, Inc., 10636 Scripps Summit Court, Suite 103, San Diego CA 92131 USA. stellipala@yahoo.com **Microfungi from indoor environments.**

In recent years considerable attention has been paid to fungi occurring in indoor environments. Many of these fungi are known to cause hypersensitivity responses in humans. Among these, the occurrence of fungal species in genera such as *Acremonium*, *Alternaria*, *Aspergillus*, *Aureobasidium*, *Cladosporium*, *Epicoccum*, *Fusarium*, *Penicillium*, *Stachybotrys*, and *Ulocladium* have been well documented. While these fungi are among the most commonly encountered taxa, a great majority of other noteworthy fungi occur in indoor environments and have received little or no attention. Moreover, the health significance of these fungi remains unknown. As a part of an ongoing investigation of microfungi in indoor environments, we are providing a preliminary list of fungal taxa, including common and uncommon genera, their substrata, and the means through which they were captured (e.g. bioaerosols, tapes, bulks, dusts, and culturable methods). Selected fungal taxa are illustrated. *Poster*

*FERTALA, JOANNA, and McCANN, MICHAEL. Biology Dept, Saint Josephs Univ., Philadelphia PA 19131 USA. ksnetsel@sju.edu **Sulfur metabolism and pathogenicity in *Ustilago maydis*.**

Ustilago maydis is a pathogenic fungus that causes disease in maize. Haploid cells grow vegetatively by budding but become filamentous in response to mating pheromones. Compatible mating filaments fuse and form an infectious filamentous dikaryon. We have isolated several mutants of *U. maydis* that are impaired in biosynthesis of sulfur-containing amino acids. Some are fed by either cysteine or methionine, and some only by methionine. Methionine-only auxotrophs are also impaired in mating and pathogenicity. The methionine auxotroph MIM114 was isolated as a mating impaired mutant. Feeding experiments showed that MIM114 is blocked in the production of homocysteine. MIM114 was complemented using a wild-type *U. maydis* plasmid library. The complementing plasmid contains a region with homology to the gene encoding homoserine O-acetyl transferase from several fungi. This enzyme catalyzes the conversion of homoserine to O-acetyl homoserine, a precursor of homocysteine. Based on several experiments, we conclude that *U. maydis* does not interconvert homocysteine and cysteine like *S. cerevisiae* does. Methionine-only auxotrophs are non-pathogenic because methionine is not available *in planta*. Auxotrophs fed by either cysteine or methionine are pathogenic, and can also be fed by sulfude; therefore we conclude that there is a source of reduced sulfur available *in planta*. *Poster*

*FINLAY, R.D.and ROSLING, A. Department of Forest Mycology and Pathology, SLU, SE-750 07 Uppsala Sweden. **Ectomycorrhizal fungi and their roles in metal tolerance and mineral weathering.**

Ectomycorrhizal fungi have direct access to a supply of energy-rich host assimilates which enables extensive mycelial production within both organic and mineral horizons of forest soils. Growth of these fungal mycelia and allocation of carbon compounds to their hyphal tips has important consequences for acquisition of base cations, tolerance of Al and heavy metals and weathering of different mineral substrates. Recent experimental evidence for these functions will be reviewed. Patterns of mycelial carbon allocation to different mineral substrates have been examined using electronic autoradiography and suggest that differential allocation of carbon to more easily weatherable substrates is possible. Physical evidence (SEM, AFM)of weathering interactions is more difficult to obtain and interpret in short term experiments but there is clear evidence of changed patterns of LMW organic acid production, and siderophore production from pure culture and microcosm experiments. Other evidence is available from PIXE analysis of elemental composition of ectomycorrhizal rhizomorphs grown in contact with different minerals, as well as from plant growth and nutrient uptake experiments. Recent experimental observations using these methods will be reviewed within the general context of biogeochemical cycling, carbon cycling and interactions with other microorganisms.

FOREMAN, P.K. [1], DEAN, R. [2], DUNN-COLEMAN, N.S. [1], GOEDEGEBUUR, F. [1], MITCHELL, T. [2], OLIVARES, H.A. [1], and *WARD, M. [1]. [1]Genencor International, Inc., 925 Page Mill Road, Palo Alto, CA 94304 USA. [2]Fungal Genomics Laboratory, North Carolina State Univ., Campus Box 7251, Raleigh, NC 2769 USA. mward@genencor.com **Discovery and regulation of biomass-degrading enzymes in *Trichoderma reesei*.**

Enzymatic digestion of biomass is an attractive and environmentally sensible approach for production of sugars suitable as an alternative to the use of petrochemicals in the production of chemicals and biofuel. The filamentous fungus *Trichoderma reesei* is a key host for the industrial production of the cellulolytic and hemi-cellulolytic enzymes used for biomass degradation. To identify new genes whose products may play a role in biomass degradation and to better understand their regulation, we sequenced the 5'-ends of approximately 5100 distinct *T. reesei*-derived cDNAs. Genes encoding several new putative endoglucanases, beta-glucosidases and hemicellulases were discovered. Oligonucleotide-based microarrays were constructed

to globally assay the expression levels all of the genes identified by sequencing. Transcriptional profiling was performed on wild type *T. reesei* and strains that have been selected for enhanced cellulase production. The consequences of growth on various carbon sources were assessed, along with the effects of growth in the presence of the potent cellulase inducer sophorose. These studies provide new and unexpected information that enhances our understanding of the transcriptional regulation of genes whose products are important for breakdown of lignocellulosic biomass. *Poster*

FOSTER, PETER. The Natural History Museum, London. **Modelling compositional heterogeneity.**

When the data that we analyze are compositionally heterogeneous, our analyses can be compromised because models in common use assume compositionally homogeneous data. Models that can accommodate compositional heterogeneity with few extra parameters are described, and tested in examples where the true tree is known with confidence. I focus on assessment of fit of the model to the data, in both ML and Bayesian frameworks. In the examples it is shown that when composition is not accommodated, then the model does not fit, and incorrect trees are found; but when composition is accommodated, the model then fits, and the known correct phylogenies are obtained. *Symposium presentation*.

*GADD, GEOFFREY[1], ADEYEMI, ADEMOLA[1], ALEXANDER, IAN[2], BURFORD, EUAN[1], MELVILLE, KARRIE[1], HILLIER, STEPHEN[3] and FOMINA, MARINA.[1] [1]Div. Environmental and Applied Biology, School of Life Sciences, Univ. Dundee, Dundee, DD1 4HN, Scotland, UK. [2] Dept. Plant and Soil Science, Univ. Aberdeen, Aberdeen, AB24 3UU, Scotland, UK. [3]Macaulay Institute, Craigiebuckler, Aberdeen, AB15 8QH, Scotland, UK. g.m.gadd@dundee.ac.uk **Metal and mineral transformations by fungi.**

Metals and their derivatives can interact with fungi in various ways depending on the metal species, organism and environment, while fungal metabolic activities also influence mobility. Certain mechanisms may mobilize metals, e.g. acidification and complexation, while immobilization can be effected by, e.g. sorption, transport and precipitation. We have found that the main mechanism of metal mobilization from metal minerals is a combination of acidification and ligand-promoted dissolution: if oxalic acid is produced the production of metal oxalates can occur. In addition, nucleation of crystalline material onto cell walls can result in the formation of biogenic microfabrics. Fungi may play such an important role in limestone and dolomite and we have direct evidence of mineralized hyphae with secondary carbonates. This contribution highlights the mechanisms by which free-living and symbiotic fungi interact with and transform metal-mineral species between soluble and insoluble forms, and their environmental significance. *Symposium Presentation*

GAITHER, THOMAS[1] and *KELLER, HAROLD[2] [1]Dept. Biology, Slippery Rock Univ., Slippery Rock, PA 16057 USA. [2] Dept. Biology, Central Missouri State Univ., Warrensburg, MO 64093 USA. keller@cmsu1.cmsu.edu **Light and scanning electron microscopy of the myxomycete species *Schenella microspora* and *S. simplex*: morphological evidence for a gastroid basidiomycete.**

Schenella simplex was described and illustrated as a new genus and species by Thomas H. Macbride in 1911. A single collection gathered in August of 1903 on a decaying pine log in the Yosemite Valley, California was designated as the holotype. In 1961, George W. Martin described a second species of *Schenella, S. microspora*, based on a single collection from Big Basin State Park, San Mateo County, California, 26 August 1957. Martin concluded that *Schenella* was a valid genus in the Stemonitaceae, closely allied to the genus *Amaurochaete*. Martin reinterpreted the morphology of this taxon as a pseudoaethalium with the sporangia arranged vertically much as in *Dictydiaethalium*. Holotypes of both *Schenella* species were examined with light and scanning electron microscopy. Observations with SEM confirmed the presence of simple capillitial threads twisted together to form vertical columns attached to the outer peridium and base of the fructification. These threads appeared septate. Spores were small, 3.0 to 6.0 micrometers in diameter, elliptical in shape, the surface roughened with flattened, disc-like areas, and a circular, recessed pore or scar at one end, unlike any known myxomycete spore; but identical to the spores of a gasteromycete, *Pyrenogaster atrogleba*. Additional specimens are needed of *Schenella =Pyrenogaster atrogleba*, from the type localities or nearby areas. *Poster*

*GARGAS, ANDREA and KRUEGER, DIRK Dept. Botany, Univ. Wisconsin, Madison, WI 53706. agargas@wisc.edu **Fungal communities and non-indigenous plant invasions.**

We are investigating the relationships between invasive plants and microbial communities, carrying the search for ecologically and phylogenetically significant soil and rhizosphere microbes to invasive plant systems. We ask whether colonizing invasive plants modulate the fungal communities in their rhizospheres as exemplified by PCR clones of ITS and SSU rDNA sequences obtained from rhizosphere and root samples. Our samples from south central Wisconsin include European buckthorn (*Rhamnus cathartica*) stands, and will extend to wetland mesocosms established to study Reed Canary Grass (*Phalaris arundinacea*) invasion. *Contributed Presentation*

*GEISER, DAVID, ABBAS, HAMED, DESJARDINS, ANNE, HACKETT, MARGARET, JUBA, JEAN, O'DONNELL, KERRY, ROYSE, JOHN, and TUNALI, BERNA. Dept. Plant Pathology, Pennsylvania State Univ., University Park, PA 16802 USA. dgeiser@psu.edu **Phylogenetic and biological species boundaries around *Fusarium proliferatum*.**

Fusarium proliferatum (mating population (MP-)D), *F. fujikuroi* (MP-C) and *F. globosum* are three closely related species in the Asian clade of the *Gibberella fujikuroi* species complex. Morphological analyses and mating tests do not always yield clear inferences for species identification in this group. To compare phylogenetic species boundaries with those defined by other means, portions of three loci, translation elongation factor 1-alpha (tef-1), beta-tubulin (benA) and the intergeneric spacer (IGS) region of the nuclear rRNA gene region, were sequenced in over 60 isolates previously identified as belonging to these species. The tef-1 and benA gene regions showed three clear clades corresponding to the species *F. proliferatum*, *F. fujikuroi* and *F. globosum*. The IGS sequences gave similar results, with three exceptions. Two isolates that had *F. proliferatum*-like tef-1 and benA alleles had *F. fujikuroi*-like IGS alleles, and a third had a *F. globosum*-like IGS allele. This could be explained by introgression, or by ancestral polymorphism. Two of these isolates were highly fertile in crosses with MP-D testers. These results showed good correspondence between species boundaries recognized using phylogenetic and other criteria, with some notable exceptions, underscoring the need for multiple loci in phylogenetic species recognition. *Contributed Presentation*

*GEML, JOZSEF, DAVIS, DONALD and GEISER, DAVID. Dept. Plant Pathology, Pennsylvania State Univ., University Park PA 16802 USA. jig5@psu.edu **What's in a name? New phylogenetic species of the artillery fungus (*Sphaerobolus*) revealed.**

The artillery fungus (*Sphaerobolus*) is a gasteromycete with a unique spore dispersal mechanism, ejecting a 1-mm diameter spore mass ("gleba") 6 m into the air toward the brightest light in its environment. In recent years, the artillery fungus has become a source of distress to homeowners, landscape mulch producers, and insurance companies due to the strong adhesion of the ejected spore mass to artificial surfaces (e.g. house siding, cars, windows etc.). Our goal was to elucidate the molecular evolution and systematics of the genus *Sphaerobolus*, to provide better understanding of the biology of the artillery fungus. We generated sequence data from multiple genes (EF 1-alpha, mtSSU, ITS, LSU) and analyzed them by maximum likelihood, maximum parsimony and distance methods. Our results show that the genus *Sphaerobolus* is monophyletic. However, there are at least three deeply divergent lineages in the genus. Beside two clades representing the two described species (*S. stellatus* [Tode] Pers. and *S. iowensis* Walker), a third lineage was revealed. Furthermore, at least half of the isolates in our collection grouped together in the *S. iowensis* clade, showing that this species is much more common than was previously thought based on the only two reported localities. *Poster*

* GILBERT, LUZ, KASUGA, TAKAO, TOWNSEND, JEFF, GLASS, LOUISE and TAYLOR, JOHN. Dept. Plant and Microbial Biology, U.C. Berkeley, Berkeley, Ca 94720 USA. lgilbert@uclink.berkeley.edu **Comparative genomics within the genus *Neurospora*.**

The value of global gene regulation studies using microarrays has been demonstrated for *E.coli*, yeast, *Arabidopsis* , and several other model organisms. However, the utility of microarrays to analyze ecological and population level questions has not yet been realized. Study of a simple eukaryote, the filamentous fungus *Neurospora* offers a unique opportunity to characterize the variability of global gene regulation within and between species. The genus *Neurospora* consists of five closely related conidiating species, indistinguishable by morphology, as well as several non-conidiating species. We have constructed a 70mer oligomer array for *Neurospora crassa* representing 3366 genes, approximately one third of the genome. To assess the effectiveness of our array for other members of the *Neurospora* genus, I have analyzed comparative genomic hybridizations for all five conidiating species of *Neurospora* as well as a few non-conidiating isolates. This technique uses genomic DNA as a substrate for labeling and hybridization to an oligo array, consequently avoiding the biases associated with transcription of mRNA. We can now determine gene coverage and estimate genome divergence among conidiating and non-conidiating *Neurospora* isolates by comparing the ratio of fluorescences between samples. *Poster*

*GORANOVA, GRETA, BINDER, MANFRED, and HIBBETT, DAVID. Biology Dept. Clark Univ., 950 Main Street, Worcester MA 01610 USA. mgoranova@clarku.edu **Molecular phylogenetics indicate that the corticioid genus *Dendrothele* is highly polyphyletic.**

The genus *Dendrothele* (Corticiaceae) includes morphologically reduced forms of bark inhabiting fungi, which produce tightly appressed crust-like fruiting bodies on stems and branches. Micromorphological characters in this group are surprisingly diverse. The objective of this study was to test the monophyly of *Dendrothele*. Nineteen *Dendrothele* isolates were sequenced and aligned to a dataset of representative homobasidiomycetes. We used isolates that contained at least three of the four nuclear and mitochondrial ribosomal DNA regions (nuc-ssu, nuc-lsu, mt-lsu, and mt-ssu) from 112 isolates for higher-level analyses, and nuc-lsu sequences from 214 isolates for a lower-level analysis. Our results inferred from maximum parsimony analyses suggest that *Dendrothele* is polyphyletic. *Dendrothele* species occur in as many as eleven lineages in the hymenochaetoid, russuloid, corticoid, and euagarics clades, indicating that convergent evolution of this unique corticioid form in combination with a specialized ecological habitat has occurred repeatedly. The type species of *Dendrothele*, *D. griseo-cana*, is placed in the Agaricales, in a clade basal to a group of marine fungi (*Nia*, *Halocyphina*, and *Calathella*) and their terrestrial, cyphelloid relatives. *Poster*

GORBUSHINA, ANNA. Geomicrobiology, ICBM, Oldenburg Univ., P.O.Box 2503, D-26111 Oldenburg, Germany. a.gorbushina@uni-oldenburg.de **Microcolonial fungi (MCF) and the biogeochemistry of life at the rock/atmosphere interface.**

Sub-aerial biofilms typically form on bare rock. They consist of 99% cell material and extracellular polymeric substances (EPS) metabolising at low water availability. Fungi represent an important part of the microbial community in these environments. Different cellular stress responses make MCF fit for survival under extremely changing irradiation, as well as water, energy sources and nutrient availability. Fungal adaptation patterns also change the underlying substrate. Sub-aerial biofilms produce surface discolorations (patina) consisting of organic compounds including polymers (EPS, melanins, carotenes etc) and of biominerals (carbonates, oxalates, oxides etc). Biogenic patina development has a chemical, mechanical, mineralogical and spectral impact on the transformation of rocks exposed to atmospheric conditions. Coloured patinas, which have been related exclusively to Fe and Mn minerals turn out to include numerous organic polymers and pigments (e.g. carotinoids, melanins and Maillard reaction products) firmly attached to the rock minerals and protected from degradation by the intimate organic-rock association. The pigments and other extracellular organic and mineral products produced by rock dwelling fungi change the reflection/adsorption pattern of sunlight and serve as UV-radiation protection screens of the rock associated microorganisms. *Symposium Presentation*

GOW, NEIL. Dept. Molecular and Cell Biology, Inst. Medical Sciences, Univ. Aberdeen, Aberdeen AB25 2ZD, UK. n.gow@abdn.ac.uk **Cell cycle and hyphal orientation in *Candida albicans*.**

Cell division of the hyphal form of the human pathogen *Candida albicans* is characterised by the formation of contiguous cell compartments bounded by septa. Following cytokinesis, apical cells of hyphae immediately re-enter the cell cycle. However, sub-apical cells are initially highly vacuolated and arrest in G1 phase until they resynthesise cytoplasm and then re-enter the cell cycle. This cell cycle arrest is extended in nitrogen poor environments. Hyphal growth may therefore be a response to nutrient stress. Hyphae of *C. albicans* exhibit directed turning responses in applied electrical fields (galvanotropism) and in response to topographical signals from the substratum (thigmotropism). We find that both orientation responses are attenuated by agents that block certain classes of calcium channels and in mutants in the CaCch1p/Mid1p calcium channel complex. Mutations in the Cph1 MAPK cascade and Efg1 Ras/cAMP dependent signalling pathways that are required for hypha induction, did not affect hyphal orientation responses. However, mutations in the PAK protein Cst20p, which interacts with the Cdc42p rho-type GTPase at sites of tip growth, attenuated hyphal turning. Therefore hypha orientation may be regulated by calcium uptake at sites of apical growth, which affects the assembly of the "polarosome" complex at bud and hyphal tips. *Symposium Presentation*

*GRAND, EDWARD, PETERSEN, RONALD, and HUGHES, KAREN. Dept. Botany, Univ. Tennessee, Knoxville, TN 37996-1100 USA. egrand@utk.edu **Phylogeography and systematics in the genus *Lentinus* (Basidiomycota).**

Many *Lentinus* spp. are globally distributed. In order to study species delimitations, we used a combination of morphological, biological, and phylogenetic species concepts. The congruence of these concepts was used to determine species boundaries and circumscriptions. Morphological species were determined using the methodology of Pegler. Biological species were determined by crossing single-basidiospore isolates (SBIs) from widely scattered geographic locations. Clamp formation implied biological conspecificity. Genetic species were ascertained using nrDNA ITS1-5.8S-ITS2 and mitochondrial COX3 sequences. Sequence homology was used as a measure of genetic relationship. We used these techniques for a genus-wide analysis, but we concentrated efforts on three species complexes, *Lentinus tigrinus*, *L. crinitus*, and *Panus rudis* (= *L. strigosus*). Based on the results of these experiments, attempts were made to correlate biogeographical patterns to the species distributions. Sequence analysis of the ITS1-5.8S-ITS2 and COX3 regions showed sufficient variability to allow separation of the species and to evaluate phylogeographic patterns among populations of the same species. *Contributed Presentation*

*GRIFFITH, GARETH[1], EASTON, G.L. [1], JONES, ANDREW[1], OSTLE, N. [2], and BOL, R.[3] [1]Inst. Biol. Sci., Univ. Wales Aberystwyth, Penglais, Aberystwyth, Ceredigion SY23 3DA, Wales. [2]Cntr. for Ecology & Hydrology, Merlewood Res. Sta., Grange-Over-Sands, Cumbria, LA11 6JU, England. [3]Inst. Grassland & Env. Research, N. Wyke Res. Sta., Devon, England, UK. GWG@aber.ac.UK **Autecology of *Hygrocybe* spp. in temperate grasslands.**

Hygrocybe species are ubiquitous and colourful components of undisturbed, nutrient-poor grasslands in N. Europe. Through surveys of *Hygrocybe* spp. and of other macrofungi showing similar patterns of occurrence, a picture is emerging of the more important waxcap grassland sites, and of those species in greatest need of protection. As part of a UK-based Soil Biodiversity Programme (http://mwnta.nmw.ac.uk/soilbio/sourhope.htm), we monitored the effect of various management regimes on fruiting of *Hygrocybe* spp. Fine-scale mapping combined with genetic analysis (ISSR) is being used to measure the extent of individual genets, with species-specific PCR probes being used to establish the vertical location of mycelia. Analysis of the natural abundance of the stable isotopes in fruitbodies showed that grassland *Hygrocybe* spp. show significant depletion for ^{13}C(-28 to -30") and enrichment for ^{15}N(+12 to +20"), a pattern that sets them apart from most macrofungi previously examined. The other macrofungi associated with these undisturbed grasslands (e.g. Clavariaceae, Geoglossaceae) have similar isotope signatures despite being taxonomically unrelated. Experiments using plant litter enriched in ^{15}N are underway and will further clarify our understanding of the role of these fungi in nutrient cycling and explain why they are so adversely affected by many agricultural practices. *Contributed Presentation*

*GRUBISHA, LISA and BRUNS, THOMAS. Dept. Plant and Microbial Biology, Univ. California, Berkeley, CA 94720 USA. grubishl@nature.berkeley.edu **Analysis of population structure of island and mainland populations of *Rhizopogon occidentalis* using microsatelite loci.**

Local populations within a geographically larger population become genetically differentiated when gene flow is restricted among subpopulations. Spore dispersal in some fungi with forcibly discharged spores has been shown to occur at intercontinental, regional, or local scales. However, we know little about dispersal patterns in hypogeous fungi, whose spores are vectored by animals that consume them. *Rhizopogon occidentalis* is an ectomycorrhizal, hypogeous fungus that associates with pines. Endemic pine populations are located on two of the Channel Islands while along the California coast these pines form small, isolated populations and are essentially host islands for *R. occidentalis*. These physical and host islands provide a range of spatial scales to examine dispersal of *R. occidentalis*. We have collected population samples and are currently screening a library enriched for *R. occidentalis* microsatelite loci. One locus has been identified that corroborates data from single copy genes and the nrIGS that suggests limited dispersal among northern California and island populations. Our goal is to identify several additional microsatelite loci in order to examine fine scale population structure. *Contributed Presentation*

GUSSE, ADAM and VOLK, THOMAS. Dept. Biology, Univ. Wisconsin-LaCrosse, LaCrosse WI 54601 USA. adagusse@hotmail.com **A survey of wood-decay and other fungi from Kachemak Bay, AK.**

Besides the agarics and other large fleshy mushrooms, many fungal species in Alaska are under-collected and under-reported. This is especially true in the Aphyllphorales, an order of wood-inhabiting fungi that includes the polypores and the crust fungi. We collected wood-decay and other fungi to observe their diversity and distribution on the Kenai Peninsula of Alaska. This study will also add to the 754 species already catalogued in the *Fungi of Alaska* collection by Volk, Burdall, and Reynolds currently at the Forest Products Laboratory in Madison, WI. The Kachemak Bay area was chosen as the study site because of the increase in downed Sitka spruce (*Picea sitchensis*) and Lutz spruce (*Picea x lutzii*) due to a spruce bark beetle epidemic that has decimated over 1.4 million acres since 1989. Out of the approximately 300 specimens collected, over 120 species of fungi have been cataloged along with substrate and location of collection. Site descriptions and observations from the summer of 2002 in Kachemak Bay State Park and the Wynn Nature Center, both near Homer, further complement this list. This will increase the baseline data to assist in determining any possible connections between the fungal forest community and the spruce bark beetle epidemic. *Poster*

*HARKNESS, JENNIFER and ANDERSON, JAMES. Univ. Toronto, Dept Botany, Mississauga, Ontario, Canada L5L 1C6. jharknes@utm.utoronto.ca **Evolution of *Saccharomyces cerevisiae* in extreme environments.**

As a model for adaptation to extreme environments, we evolved artificial populations of *Saccharomyces cerevisiae* in high salinity (1 M NaCl) and high pH (8.0) environments. We chose these environments because (a) they are easy to maintain experimentally, (b) their immediate effects on genome-wide gene expression are known and (c) the relative fitness of each of the 4700+ viable gene knockout strains of *S. cerevisiae* in each of these enviroments has been measured. Replicate populations of five isogenic strains of *S. cerevisiae*, two haploid (*MAT*a, *MAT*alpha) and three diploid (*MAT*a/a, *MAT*/alpha, *MAT*alpha/alpha), propagated as batch cultures with daily transfer for over 500 generations in each of the two environments. The fitness of the evolved strains is now being compared to that of the progenitors. Any mutations of large effect on fitness will be identified and mapped. The effect of ploidy on the ability of populations to adapt to these environments will be measured. *Poster*

HARRIS, STEVEN. Plant Science Initiative, Univ. Nebraska, Lincoln, NE 68588-0660 USA. sharri1@unlnotes.unl.edu **Regulation of hyphal morphogenesis by a heterotrimeric G protein complex in *Aspergillus nidulans*.**

In *A. nidulans*, FadA and SfaD are the alpha and beta subunits, respectively, of a heterotrimeric G protein that promotes vegetative growth and represses development. FlbA is an RGS protein that down-regulates FadA signaling to allow initiation of development. Since a similar G protein controls chemotropic growth and morphogenesis during mating in budding yeast, we tested the possibility that the FadA pathway may regulate early aspects of hyphal morphogenesis in *A. nidulans*. Characteristic features of conidiospore germination in *A. nidulans* include a period of isotropic spore swelling followed by the establishment of hyphal polarity. Hyphae subsequently undergo septation and form branches. Compared to wildtype, *flbA* mutants form hyphae that are abnormally wide, display an aberrant branching pattern, and appear to contain increased levels of cell wall chitin. In contrast, *fadA* and *sfaD* mutants form hyphae that are notably thin, display a severe reduction in branching, and appear to contain less cell wall chitin. Moreover, whereas wildtype hyphae frequently meander, *fadA* and *sfaD* hyphae are remarkably straight. These observations suggest that signaling through the FadA heterotrimeric G protein pathway regulates multiple aspects of hyphal mophogenesis, including, the ability of hyphae to change growth direction in response to positional cues. *Contributed Presentation*

*HE, X.H., IDOL, T.W., HORWATH, W.R., BLEDSOE, C.S., and ZASOSKI, B.J. Univ. California, Davis, CA 95616 USA. huahe@ucdavis.edu **^{15}N transfer among pines, oaks, *Ceanothus* and grasses in a California oak woodland.**

We examined ^{15}N movement from a pine donor to adjacent trees and grasses in a CA oak woodland. Foothill pine acted as N-donor; N-receivers were foothill pine, blue oak or *Ceanothus*. We applied ^{15}NO3- solution to pine donor needles. For 4-wks after ^{15}N labeling, we collected weekly samples from trees & grasses between paired trees, & root tips from donor & receiver trees. At time-zero, leaf ^{15}N values were 2.4, 2.2, -0.12 & 2.5‰ in pines, oaks, *Ceanothus* & grasses. After 4-wks, leaf d^{15}N increased to 46‰ in donor pines & 5.7‰ in receiver pines; to 6.2, 3.7 & 8.1‰ in receiver oaks, *Ceanothus* & grasses. Root d^{15}N were 10, 14 & 13‰ for unlabeled pines, oaks & *Ceanothus*. After labeling, root d^{15}N increased to 29‰ in donor pines, to 21, 19 & 8.0‰ in receiver pines, oaks, *Ceanothus*. The amount & rate of ^{15}N transfer from donor tree roots to receiver tree roots & to grasses were similar regardless of the tree pair. Direct N transfer probably did not occur since not all tree pairs & grasses shared the same type of ecto- or AM mycorrhizae. The ^{15}N enrichment in adjacent grasses suggests ^{15}N from donor tree roots moved into the rhizosphere where taken up by receiver trees & grasses. The similarity of d^{15}N increase of receiver tree roots compared to their respective controls suggests that common mycorrhizal networks could play an important role in N distribution among plants. *Contributed Presentation*

*HEMMES, DON[1] and DESJARDIN, DENNIS[2]. [1]Biology Dept., Univ. Hawaii at Hilo, Hilo, HI 96720 USA. [2] Dept. Biology, San Francisco State Univ., 1600 Holloway Ave., San Francisco CA 94132 USA. hemmes@hawaii.edu **Puffballs of Hawaii.**

The number of puffballs, Lycoperdaceae, and stalked puffballs, Tulostomataceae, collected in the Hawaiian Islands has grown by a half dozen over the past year to a total of over twenty species. *Vascellum floridanum* is a common inhabitant of lawns and *Calvatia gigantea* and *Bovista plumbea* are found in pastures. *Battarraea phalloides*, *Battarraeoides diqueti*, *Disciseda verrucosa*, *Disciseda anomala* and a number of species of *Tulostoma* inhabit the drier, leeward sides of the islands from seashore to mountain top. *Lycoperdon perlatum* is basically found along trails in native rain forests growing on endemic tree ferns. *Mycenastrum corium* and a number of yet to be described species have been located in the desert botanical garden at Koko Head Crater on Oahu and other arid locations. In this presentation each species will be pictured and its distribution in the various vegetation zones of the islands will be described. *Poster*

*HENK, DANIEL and VILGALYS, RYTAS. Dept. Biology, Duke Univ., Durham, NC 27708 USA. dah@duke.edu **Mating system and genetic structure within colonies of *Septobasidium*.**

Fungi in the genus *Septobasidium* live symbiotically with scale insects. *Septobasidium* species form mats of hyphae around colonies of scale insects, and hyphae from multiple infected insects fuse to form a single fungal colony. However, infection is thought to occur when young scale insects are exposed to basidiospores, thus fungal colonies may be composed of multiple genetic individuals derived from numerous single spore infections of scale insects. Evidence from multiple loci show that a colony of *Septobasidium curtisii* is composed of a single dikaryotic individual and is likely to be the product of hetrothallic mating. Here we use DNA sequence data from single spore isolates and tissue isolates to examine the mating system and genetic composition of colonies in several *Septobasidium* species. Sequence data obtained from single spore isolates of *S. apiculatum, S. sinuosum,* and *S. fumigatum* show that colonies in these species are composed of dikaryotic individuals producing recombinant spores consistent with a heterothallic mating system. Another species, *S. psudopedicellatum* does not show a standard pattern of segregation in the loci sequenced from single spore isolates and may be pseudohomothallic. Sequence data from tissue isolates in these species is consistent with the hypothesis that each colony is composed of a single dikaryotic individual. *Poster*

*HERNANDEZ, JOSE and FARR, DAVID. USDA-ARS, Systematic Botany and Mycology Laboratory, Beltsville, MD 20705 USA. jose@nt.ars-grin.gov **An interactive identification system for species of *Ravenelia* (Uredinales) from Argentina and the USA.**

Species of the rust genus *Ravenelia* are found on legumes, especially in tropical and subtropical regions of the Americas, Africa and Asia. An interactive identification system (http://nt.ars-grin.gov/taxadescriptions/keys/RaveneliaIndex.cfm) was developed to provide users with a tool for identifying species of *Ravenelia*. It includes an interactive key, images, descriptions, distribution data, and additional information on nearly 50 species of *Ravenelia*. This web page is based on studies by the first author of the 18 species of *Ravenelia* that occur in Argentina. In addition, it includes work by Joe F. Hennen and George B. Cummins on species of *Ravenelia* in the USA. The characters in the interactive key are those that are of most value in delimiting the taxa. Additional taxa of *Ravenelia* from other geographic regions will be added until all species of *Ravenelia* are included. *Contributed Presentation*

HERRERA-GIRALDO, JOSE and *CANTRELL, SHARON. Science & Technology, Univ. del Turabo, P. O. Box 3030, Gurabo, P. R. 00778 USA. scantrel@suagm.edu **Isolation and characterization of endophytic fungi from leaves of the sea grape, *Coccoloba uvifera.***

Sea grapes occur in beaches in tropical areas and are used as ornamental shrub. The sea grape family includes species that occurs at different elevations and forest types. This makes the family a good

model to study the diversity of fungi along an elevation gradient and between natural and ornamental populations. We collected young leaves from two sites inside the university campus. The leaves were divided into 4 quadrants and twenty 5mm discs were cut from each. Ten randomly selected discs from each quadrant were placed into two media (Malt Extract and Rose Bengal Agar). The discs from three of the quadrants were surface sterilized using standard techniques. Pure cultures were isolated in MEA and PDA. A total of 52 isolates were obtained between the sites divided into 8 species. There was a 63% overlap and 37% complementarity between sites. The Sorensen Similarity Index between sites was 0.84. Most of the isolates are unidentifiable and were characterized using cultural characteristics. For four of the more common unidentifiable isolates the fatty acid methyl ester profile and the ITS sequence is being determined. Some of the isolates were identified as *Curvularia lunata*, *Nigrospora sphaerica*, *Trichocladium opacum*, *Pestalotiopsis* sp. and *Xylaria* sp.. This is the first report of endophytic fungi associated with the sea grapes. We will extend this study to natural populations. *Poster*

HEWITT, DAVID. Farlow Herbarium, Harvard Univ., 22 Divinity Ave., Cambridge, MA 02138, USA. dhewitt@oeb.harvard.edu **Development in the genus *Neolecta* is distinct from that of other discomycetes.**

The genus *Neolecta* comprises three species of clavate apotheciate ascomycetes. However, the currently accepted phylogeny of the ascomycetes does not place *Neolecta* with any other clavate apotheciate ascomycetes, nor with any other apotheciate ascomycetes (discomycetes). In fact, *Neolecta* is not even included in the Euascomycetes (the clade that includes all other ascoma forming ascomycetes). This phylogenetic placement is based on analysis of RNA polymerse II subunit, SSU and LSU. The exclusion of *Neolecta* from the Euascomycetes is also supported by morphological evidence, such as the lack of paraphyses and croziers. Ascomal development also differentiates *Neolecta* from other discomycetes. In *N. irregularis*, immature asci are found at the apex of the ascoma. More mature asci are found towards the base of the ascoma, at the margin of the hymenium. Thus, *N. irregularis* develops acropetally and centripetally. This is different from other discomycetes, which develop centrifugally; other clavate discomycetes develop basipetally and centrifugally. *Poster*

HICKEY, PATRICK and *READ, NICK. Fungal Cell Biology Group, Inst. Cell and Molecular Biology, Univ. Edinburgh, Rutherford Building, Edinburgh, EH9 3JH, UK. Nick@fungalcell.org **Biology of living fungi.**

A CD-ROM has been compiled with movies that illustrate key aspects of the cell biology of living filamentous fungi. The movies have been obtained using confocal microscopy and show time-lapse sequences and 3D-reconstructions of fungal cells stained with fluorescent dyes and/or expressing the green fluorescent protein (GFP). The aim of this CD-ROM is provide a valuable resource and powerful educational tool showing the dynamic nature of fungal cells. The target audience is anyone interested in fungal biology, and particularly students and those teaching mycology. The movies can be readily imported into Microsoft Powerpoint presentations. The CD-ROM can be purchased at minimal cost from from http://www.fungalcell.org. *Poster*

HOBBIE, ERIK. Univ. New Hampshire, Durham, NH 03824. erik.hobbie@unh.edu **Isotopic studies of carbon and nitrogen cycling by fungi in forest ecosystems.**

One promising tool to explore fungal functioning in soil or decaying wood, isotope ratio measurements, depends on most biochemical processes being faster for light isotopes (e.g., ^{14}N, ^{12}C) than for heavy isotopes (e.g., ^{15}N, ^{14}C, ^{13}C) (termed fractionation). Current research indicates several interesting patterns useful to continued studies of fungal functioning. For ectomycorrhizal fungi, both ^{15}N: ^{14}N ratios and radiocarbon (^{14}C) appear potentially useful as markers of organic nitrogen use, whereas ^{15}N: ^{14}N ratios in ectomycorrhizal plants correlate with carbon allocation to mycorrhizal fungi. Saprotrophic and ectomycorrhizal fungi generally differ in ^{15}N, ^{13}C, and ^{14}C content, suggesting that such measurements could determine mycorrhizal status in fungi of unknown life history strategies. Wood decay fungi primarily incorporate carbon derived from ^{13}C-enriched carbohydrates, with little or no incorporation of ^{13}C-depleted lignin. Fungal enrichment in ^{13}C relative to carbon substrates may correlate with microbial efficiency, with high enrichments on complex substrates such as wood, and low enrichments on simple substrates such as sugars. Continued improvements in our ability to interpret isotopic patterns in fungi will require detailed natural abundance and tracer (enriched) isotopic culture studies, coupled to models of fungal metabolism and isotopic fractionation. *Symposium Presentation*

*HOFSTETTER, VALERIE, KAUFF, FRANK and VILGALYS, RYTAS. Dept. Biology, Duke Univ., Durham NC 27708 USA. valh@duke.edu **Phylogeny of the *Lyophylleae* (Agaricales, Basidiomycetes): Systematic versus ecological transitions in Basidiomycota.**

To solve basal relationships within *Tricholomateae-Lyophylleae-Entolomataceae*, sequences of three protein-coding genes (RPB1, RPB2 and EF1-alpha) were used in a combined analysis with prior data. Phylogenetic analyses of combined data sets show *Lyophylleae* is monophyletic, including the four major clades recovered previously. *Hypsizygus* is also shown to be a sister group to the *Lyophylleae sensu strictu* and is paraphyletic/monophyletic with *Collybia tuberosa* and *Clitocybe connata*. The remaning *Tricholomateae* also form a monophyletic clade which is a sister group to the *Lyophylleae/Hypsizygus* clade. Phylogenetic reconstruction shows that siderophilous granulation has been lost at least twice during evolution, in *Ossicaulis* and in the *Tricholomateae*, with a progressive reappearance in *Hypsizygus/ Clitocybe connata*. As *Lyophylleae* and allies includes four of the major ecological types found in Basidiomycota (saprophyte, parasite, ectomycorrhizae and insect-related fungi), this group provides a phylogenetic framework to study evolution of major ecological transitions within Basidiomycota. To develop a model for ecological associations, ancestral characters have been reconstructed to determine if the ecological associations are stable or reversible; mutation rates are also being compared to see if these ecological transitions are associated with molecular accelerated evolution. *Contributed Presentation*

HORN, BRUCE. National Peanut Research Laboratory, USDA-ARS, Dawson GA 39842 USA. bhorn@nprl.usda.gov **Effect of soil density of *Aspergillus* species on invasion of peanut seeds.**

Soil is the source of primary inoculum for *Aspergillus flavus* and *A. parasiticus*, fungi that produce the highly carcinogenic aflatoxins in agricultural commodities. Aflatoxigenic fungi commonly invade peanut seeds during maturation and the highest concentrations of aflatoxins are found in insect-damaged seeds. A laboratory assay was developed in which sterile, viable peanut seeds were wounded and inoculated with different soils (n = 14) from cultivated and fallow fields and from forested land. Percent seed infection linearly regressed on soil population density was significant (P species in *Aspergillus* section *Flavi*: *A. flavus* L strain (coefficient of determination = 0.89), *A. flavus* S strain (0.82), *A. parasiticus* (0.36), *A. tamarii* (0.77), *A. caelatus*

(0.37) and *A. alliaceus* (0.87). Species from other sections in the genus, *A. niger* (0.76) and *A. terreus* (0.88), also showed significant linear regressions. Nearly all seeds became infected with *A. flavus* L strain at densities greater than 300 CFU/g soil. The density of aflatoxigenic fungi in soil may be a factor in determining the extent of aflatoxin contamination in peanuts. *Poster*

HORTON, THOMAS. Dept. Environmental and Forest Biology, SUNY-ESF, 350 Illick Hall, Syracuse, NY 13210 USA. trhorton@esf.edu **Occurrence of uni- and bi-nucleate spores in ectomycorrhizal Basidiomycetes: family and genus level trends.**

The role of ectomycorrhizal fungi (EMF) in the establishment of *Pinus contorta* under primary succession in the Oregon Dunes is being investigated. Here, DAPI stain was used to visualize the number of nuclei contained in EMF spores as a measure of the potential to produce heterokaryons from single spores. The observed proportions of binucleate spores were (mean (s.d.), number of sporocarps): Amanitaceae = 0.975 (0.007), 2; Boletaceae = 0.334 (0.410), 12; Cantherellacae = 0.0 (0.0), 3; Cortinariaceae = 0.982 (0.021), 23; Entelomataceae = 1.0 (0.0), 2; Rhizopogonaceae = .080 (0.254), 42; Russulaceae = 0.009 (0.017), 17; Thelephoraceae = 0.015 (0.021), 12; Tricholomataceae = 0.253 (0.426), 31. The high standard deviation seen in some families can be explained in part by generic patterns: Boletaceae, *Boletus* = 0.398 (0.422), 10; *Leccinum* = 0.15 (0.021), 2: Rhizopogonaceae, *Rhizopogon* = 0.001 (0.003), 10; *Suillus* = 0.156 (0.347), 12; *Chroogomphus* = 0.016 (0.015), 5; Tricholomatacae, *Tricholoma* = 0.006 (0.010), 23; *Laccaria* = 0.964 (0.026), 8. While these results do not indicate if any of the bi-nucleate spores were heterokaryotic, they do identify groups that form primarily uni-nucleate spores and are thus less likely to form a heterokaryon from a single spore dispersing to a primary successional zone. Taxonomic and ecological issues will be reviewed and discussed. *Poster*

*HOSAKA, KENTARO[1], COLGAN III, WESLEY[2], CASTELLANO, MICHAEL[3], and SPATAFORA, JOSEPH[1]. [1]Dept. Botany and Plant Pathology, Oregon State Univ., Corvallis, OR 97331 USA. [2]School Biological Sciences, Louisiana Tech Univ., Ruston, LA 71272 USA. [3]USDA - Forest Service, PNW Research Station, Corvallis, OR 97331 USA. hosakak@science.oregonstate.edu **Ordinal placement of *Hysterangium* and related taxa: phylogenetic support for recognizing the Hysterangiales.**

It is now clear that two orders of Homobasidiomycetes, Gomphales and Phallales, are closely related, forming a well supported clade. Although monophyly of Gomphales, including *Ramaria*, *Gomphus*, *Clavariadelphus*, and *Gautieria*, has been supported by previous phylogenetic analyses, support for monophyly of the Phallales was inconclusive. This uncertainty was largely due to the unstable grouping of the hypogeous taxa (e.g., *Hysterangium*) with the epigeous gasteroid fungi, collectively known as "stinkhorns". Subsequent phylogenetic analyses using DNA sequences of nuclear LSU rDNA, mitochondrial SSU rDNA, and ATP6 with an expanded sampling of *Hysterangium* and related taxa revealed that Phallales is not monophyletic. These results support the recognition of the order Hysterangiales, which contains several hypogeous genera including *Hysterangium*, *Protubera*, and *Gallacea*, from Phallales, which comprises the families Phallaceae and Clathraceae. Also, several unexpected relationships were found within the Hysterangiales clade, including the sister relationships of *Hysterangium* and the family Mesophelliaceae. We will present results from multigene phylogenetic analyses of Gomphales/Phallales/Hysterangiales clade based on parsimony and Bayesian methodologies, and we will discuss character and character state evolution of basidiomata. *Contributed Presentation*

*HUBERLI, DANIEL, HARNIK, TAMAR and GARBELOTTO, MATTEO. Dept. of ESPM-ES, Univ. California, Berkeley, CA 94720 USA. dhuberli@nature.berkeley.edu **Phenotypic variation among twelve AFLP genotypes of *Phytophthora ramorum* from California and Oregon.**

Phytophthora ramorum is a pathogen that has been isolated from dying *Quercus* spp. and other native plants to California and Oregon, as well as ornamental plants from nurseries and gardens in a number of European countries. Recent research has shown there is little genetic variation among twelve AFLP genotypes of *P. ramorum* isolated from different native plant hosts and *Rhododendron* sp. that were identified in California and Oregon. Morphological and pathological phenotypic variation was measured for twelve isolates with different AFLP profiles including: growth rates on V-8 and corn-meal agar at different temperatures, growth rates on agar amended with three effective control chemicals (unpublished data) at three concentrations, sporangia and chlamydospore size, and ability to form lesions on leaves of *Umbellularia californica* and stems of *Quercus agrifolia*. Significant variation was found among the isolates in some of the characters measured. Some isolates formed lesions more than two-fold larger on *Q. agrifolia* seedlings in comparison to other isolates. *Contributed Presentation*

*HUGHES, KAREN and PETERSEN, RONALD. Dept. Botany, Univ. Tennessee, Knoxville, TN 37996 USA khughes@utk.edu **Distributions and biogeography in *Lentinellus* (Russulales): phylogeographic signal in a generic phylogeny.**

In a forthcoming monograph of the genus *Lentinellus*, some species appear to be widely distributed. *Lentinellus castoreus*, while exhibiting wide morphological variation, is virtually cosmopolitan. Data suggest that this species may be Gondwanan in origin, possibly moving to the Northern Hemisphere via the Central American land bridge. *Lentinellus ursinus* is also morphologically variable but culture morphology and phylogenetic placement unite collections in a single clade. Some species complexes, such as those surrounding *L. novae-zealandiae* and *L. pulvinulus*, are limited to the Southern Hemisphere. Others are restricted to the Northern Hemisphere. *Contributed Presentation*

*HUGHES MONICA[1], WEIR, ALEX[1], GILLEN, BENJAMIN[1] and LESCHEN, RICHARD[2] [1]Dept. Environmental and Forest Biology, 350 Illick Hall, SUNY-ESF, Syracuse, NY 13210, USA. [2]Landcare Research, Mt. Albert Research Centre, Private Bag 92-170, Mt. Albert, Auckland, New Zealand. mohughes@syr.edu **Host specificity and sex biased parasitism of *Corethromyces* species (Laboulbeniales, Ascomycota) in New Zealand.**

Most Laboulbeniales, a diverse order of arthropod-associated fungi, display a high degree of host specificity. Some of these ectoparasites are further restricted in their growth to specific portions of the host integument or to one sex of host. Distribution, specificity phenomena, and sex bias in parasitism were investigated in recent collections of *Corethromyces* on Leiodidae (Coleoptera) from New Zealand. *Corethromyces bicolor* was found only on the North Island on *Mesocolon* only, while *Corethromyces* sp. nov. occurred equally on *Mesocolon* and *Paracatops* in both the North and South islands. The sexual transmission hypothesis was accepted for *C. bicolor* (p *C.* sp. nov. (p transmission of at least one of the fungi, males were more likely to be infected (p host sex was a significant predictor of the abundance of infection, with males more highly infected than females (poisson regr., p *C. bicolor*, p *C.* sp. nov.). Mate choice and the costs of sexual selection are proposed as explanations for the sex bias in parasitism, and similarities to other sexually transmitted diseases are discussed. *Poster*

*HUGHES MONICA[1], WEIR, ALEX[1], GILLEN, BENJAMIN[1], and ROSSI, WALTER[2]. [1]Dept. Environmental and Forest Biology, 350 Illick Hall, SUNY-ESF, Syracuse, New York, 13210, USA. [2]Dipt. Scienze Ambientali, Univ. dell Aquila, 67010 Coppito, L Aquila, Italy. mohughes@syr.edu ***Stigmatomyces*** **from New Zealand and New Caledonia: new records, new species, and two new host families.**

Stigmatomyces is a large genus of Laboulbeniales (Ascomycota) comprised of approximately 130 species and is associated exclusively with Diptera worldwide. Seven new records and three new species are described from New Zealand and New Caledonia. Two new host families are reported and a dichotomous key to *Stigmatomyces* species in the region is presented. *Poster*

*HUGHES, MONICA[1], WEIR, ALEX[1], LESCHEN, RICHARD[2], JUDD, CHRISTOPHER[1], and GILLEN, BENJAMIN. [1] [1]Dept. Environmental and Forest Biology, 350 Illick Hall, SUNY-ESF, Syracuse, New York 13210 USA. [2]Landcare Research, Mt. Albert Research Centre, Private Bag 92-170, Mt. Albert, Auckland, New Zealand. mohughes@syr.edu **Laboulbeniales from the subantarctic islands of New Zealand.**

Despite the endemicity and diversity of subantarctic Coleoptera and the high host-specificity of Laboulbeniales, only one species, *Rhachomyces kenodactyli* W. Rossi, has been reported from the region. Four new species (two each in Diphymyces and Laboulbenia) and five new records (*Cucujomyces phycophilus*, *Diphymyces penicillifer*, *Laboulbenia* sp. indet., *Rhachomyces* sp. indet., and *Teratomyces* sp. indet.) are reported, increasing the number of known subantarctic Laboulbeniales ten-fold. A relatively high percentage (12%) of subantarctic coleopteran species serve as hosts for Laboulbeniales, in contrast to lower host utilization rates in tropical (6-7%) and north temperate (9.5%) regions. The propensity for Laboulbeniales infections in aquatic habitats is generally high, and the larger proportion of intertidal coleopteran taxa in the subantarctic probably accounts for greater host utilization. Additionally, fungi on intertidal beetles are higher in both incidence and abundance than those on beetles in other habitats. The region has been well investigated, and it is likely that only a few species on Coleoptera remain undiscovered. Based upon host exploitation patterns from mainland New Zealand, we identify coleopteran taxa on which future discoveries of Laboulbeniales are likely. *Poster*

*INDERBITZIN, PATRIK, HARKNESS, JENNIFER and BERBEE, MARY L. Dept. Botany, #3529-6270 University Boulevard, Vancouver, B.C. Canada, V6T 1Z4. bhpatrik@mail.botany.ubc.ca **Evolution of mating type gene arrangement in the genus *Stemphylium* (Ascomycetes).**

In this study we are investigating the evolution of the mating type genes *MAT1-1* and *MAT1-2* in 114 isolates of the genus *Stemphylium*. The mating types were assessed with primer sets amplifying the diagnostic alpha and HMG boxes of the *MAT1-1* and *MAT1-2* genes respectively. In the closely related genus *Cochliobolus*, the occurrence of both mating type genes in one isolate is indicative of homothallism. In homothallic species of *Cochliobolus*, *MAT1-1* and *MAT1-2* are arranged in different ways. In *Stemphylium*, several species are known homothallics, including the type species of *Pleospora*, *S. herbarum*. *MAT1-1* and *MAT1-2* were found to be present in *S. herbarum*. The remaining isolates belonged to at least 18 other species. Some of these isolates contained only one mating type gene. The distribution of mating type genes and their arrangement was mapped onto phylogenetic trees inferred from *ITS*, partial *GPD* and *EF-1a* DNA sequences, as well as *ATP-GTP* intergenic spacer sequences. Phylogenetic trees were also constructed based on *MAT1-1* and *MAT1-2* sequences from representative isolates. It is generally thought that homothallism derived from heterothallism. To test this hypothesis, we used phylogenetic analyses to investigate whether heterothallism or homothallism was the ancestral state in *Stemphylium*, and how many times a switch from homothallism to heterothallism or vice versa occurred. *Contributed Presentation*

IVORS, KELLY, WILKINSON, CARLA, and GARBELOTTO, MATTEO. Dept. ESPM-ES, Univ. California, Berkeley, CA 94720 USA. kivors@nature.berkeley.edu **Nested TaqMan PCR for detection of *Phytophthora ramorum* in environmental plant samples.**

The detection and extent of *P. ramorum* colonization in host plant tissues was estimated with traditional PCR, followed by a round of real-time PCR utilizing TaqMan chemistry. Four specific PCR primers and a real-time probe were developed based on sequences of the internal transcribed spacer of nuclear rDNA of *P. ramorum*. The first set of primers (Phyto1 and Phyto4) was designed to amplify a 687 bp region of the ribosomal operon including portions of the ITS1 and ITS2, and entire 5.8S rDNA. The second set of primers (Pram5 and Pram6) and fluorogenic probe (Pram7) were designed to amplify a 74 bp fragment fully nested within the Phyto1-Phyto4 amplicon, using TaqMan chemistry. The protocol was applied to DNA dilutions of numerous *Phytophthora* spp., as well as artificially infected plant material and plant extracts from which cultures were and were not obtained. Using this nested approach, *P. ramorum* DNA could be detected without the need to run agarose gels or sequencing reactions. Amount of pathogen DNA was very low in some tissue and many plant extracts needed both rounds of amplification before indicating a positive result. The oligonucleotides designed in this study can be used as a rapid screening tool for the detection of *P. ramorum* in culture and environmental plant extracts without prior isolation and characterization of the organism by traditional microbiological methods. *Poster*

*IZZO, ANTONIO[1], MEYER, MARC[2], TRAPPE, JAMES[3], NORTH, MALCOLM[4], and BRUNS, THOMAS[1] [1]Plant and Microbial Biology Dept., Univ. California, Berkeley, CA, 94720-3102 USA, [2]Dept Wildlife, Fish, and Conservation Biology, Univ. California, Davis, CA 95616 USA [3]Dept Forest Science, Oregon State Univ., Corvalis, OR 97331 USA. [4]Ecology Depart., Univ. California, Davis, CA 95616 USA. aizzo@nature.berkeley.edu **Underground composition of ectomycorrhizal community of true fir (*Abies* spp.) relative to hypogeous fruiting taxa and those in small mammal diet in a mixed-conifer forest.**

Hypogeous fungi play important roles in the ecology of western coniferous forests. Studies of hypogeous sporocarps show impressive annual production rates and high levels of species richness. Despite this fact, in most underground ectomycorrhizal (ECM) community studies they seem to be less important on the roots, making up 0-5% of the species and no more than 15% of the root biomass. We took a directed effort to address this discrepancy and to develop an estimate of hypogeous contribution based on the belowground ECM community. In order to increase our ability and accuracy of identifying hypogeous ECM taxa, we compared DNA sequence data from the internally transcribed spacer (ITS) region of the rDNA amplified from three sources: 1) ECM root communities of true fir (*Abies concolor* and *Abies magnifica*) in a Sierra Nevada old growth mixed conifer forest; 2) scat samples collected from small mammals throughout the same study site; and 3) hypogeous sporocarps found throughout the

Sierra Nevada. Our results show that hypogeous taxa make up a minimum of 15-20% of the species and 25-40% of the dry root biomass on *Abies spp.* in this old growth forest. This value is much higher than has been reported in other ECM studies. We speculate that the difference is due in part to characteristics of the forest and to the directed sequence approach taken. *Contributed Presentation*

*JAIME, MARIA, ANDERSON, JAMES, and KOHN, LINDA. Univ. Toronto, Dept Botany, Mississauga, Ontario, Canada L5L 1C6. mjaime@ut,.utoronto.ca **Evolution of benomyl resistance.**

Development of fungicide resistance is now one of the major problems in plant disease control. Important factors contributing to the potential for evolution of resistance in the pathogen may include the availability and rates of mutations conveying resistance and their associated genetic mechanisms and fitness costs. As a model for fungicide resistance, we have evolved benomyl resistance in experimental populations of *Saccharomyces cerevisiae*, a rich system for forward and reverse genetics and functional genomics. Results of these experiments will be presented. These studies will be extended to experimental and field populations of two important plant pathogenic filamentous fungi, the genetically tractible *Botrytis cinerea* and its close relative, *Sclerotinia sclerotiorum*, in which field resistance has been observed. *Contributed Presentation*

*JAMES, TIMOTHY[1], KUES, U.[2], CULLEN, D.[3], and VILGALYS, R.[1] [1]Dept. Biology, Duke Univ., Durham, NC 27708 USA. [2]Inst. Forstbotanik, Georg-August-Univ. Gottingen, Gottingen, Germany. [3]Dept. Bacteriology, Univ. Wisconsin-Madison, Madison, Wisconsin 53706 USA. tyj2@duke.edu **The origins of unifactorial mating systems in *Coprinellus disseminatus* and *Phanerochaete chrysosporium* from bifactorial ancestors.**

The mating system of most homobasidiomycetes is bifactorial, controlled by two incompatibility loci (the *A* and *B* mating-type loci). Of the remaining species, as many as 25% have a mating system determined by a single locus (unifactorial mating system). Unifactorial species are scattered throughout the phylogeny of homobasidiomycetes, suggesting multiple derivations of the unfactorial system from bifactorial ancestry. Using genetic crosses and DNA sequences of the mating-type loci, we explore the origins of the unifactorial mating systems of two unrelated species, *C. disseminatus* and *P. chrysosporium*. Our analyses suggest that in both fungi, genes similar to the *A* mating-type genes of bifactorial species (encoding homeodomain transcription factors) determine the mating-types of individuals. DNA sequences very similar to those of the *B* mating-type genes, encoding both pheromones and pheromone receptors in bifactorial species, are also present, but these genes are unlinked to the mating-type locus in these two species and, moreover, are not polymorphic. One plausible explanation for the origin of the unifactorial mating systems of these two species is that the *B* mating-type genes have mutated to a self-compatible combination of pheromone/receptor within a haploid individual, causing loss of mating-type discrimination at this locus. *Contributed Presentation*

*JEDD, GREGORY[1], YUAN, P.[2], KUNCHITHIPADAM, S.[2], and CHUA, N-H.[1] [1]Lab of Plant Molecular Biology, Rockefeller Univ., New York, NY 10021 USA. [2]Dept. Biological Science, National Univ. Singapore, 117543. jeddg@imap.rockefeller.edu **Structure, function and origin of the Woronin body crystal lattice.**

The Woronin body is an osmophilic organelle specific to filamentous ascomycetes (Euascomycetes). The HEX-1 protein is necessary and sufficient for formation of the Woronin body core and a *hex-1* mutant exhibits protoplasmic bleeding following cell lysis. In addition, HEX-1 utilizes a C-terminal peroxisome-targeting signal (PTS-1). Thus, Woronin bodies are fungal peroxisomes that function to seal the septal pore. The crystal structure of HEX-1 reveals three intermolecular interfaces that promote HEX-1 self-assembly. HEX-1 assembly defective mutants produce aberrant Woronin bodies that possess a soluble non-crystalline core and these mutants also fail to complement a *Neurospora hex-1* deletion, revealing a functional requirement for the HEX-1 protein lattice. In addition to sharing sequence homology, the tertiary structure of HEX-1 is remarkably similar to that of eukaryotic translation initiation factor 5A (*eIF-5A* is found throughout archaea and eukaryotes). However, amino acid residues required for HEX-1 self-assembly and peroxisomal targeting are absent in eIF-5A. These observations suggest that *hex-1* evolved via gene duplication of an ancestral *eIF-5a* followed by the acquisition of new functions. Current efforts are focusing on the diversity and phylogenetic distribution of *hex-1* with the aim of understanding the timing and mechanism of these evolutionary events. *Symposium Presentation*

*JEEWON, RAJESH[1], HYDE, KEVIN[1], and LIEW, EDWARD[2] [1]Centre for Research in Fungal Diversity, Dept. Ecology & Biodiversity, Univ. Hong Kong, Pokfulam Rd, Hong Kong, SAR, P R China. [2]School of Land, Water & Crop Sciences, McMillan Building A05, Univ. Sydney, NSW 2006, Australia. rajeshjeewon@yahoo.com **Molecular phylogenetics of *Pestalotiopsis*.**

Phylogenetic analyses on partial rDNA gene sequences were conducted to evaluate the utility of morphological characters used in the taxonomy of *Pestalotiopsis* and allied genera. Results based on 28S rDNA sequences showed that *Bartalinia*, *Pestalotiopsis*, *Seimatosporium* and *Seiridium* represent distinct monophyletic groups while *Truncatella* is paraphyletic. Characters such as pigmentation and septation of median cells, number and position of appendages are useful for generic delineation. Molecular data also supports the association of these coelomycetous fungi with the ascomycetous Amphisphaeriaceae. There is, however, insufficient evidence to restrict the Amphisphaeriaceae to *Pestalotiopsis*-like anamorphs. Analyses based on the ITS and 5.8S regions to infer phylogenies at the species level revealed 3 taxonomic groups congruent with morphology-based schemes. Pigmentation of median cells and appendage tip morphology should be given high taxonomic weightings whereas spore and appendage dimensions are morphologically important at lower taxonomic levels. Phenotypic characters such as spore shape and number of appendages are unreliable for species delineation. Further analyses also showed that species isolated from same and different hosts are phylogenetically related based on morphology rather than host. Therefore, species nomenclature associated with host names is highly inaccurate. *Contributed Presentation*

*JIMENEZ-GASCO, MARIA and GEISER, DAVID. Dept. Plant Pathology, Pennsylvania State Univ. University Park, PA 16802 USA. jimenez-gasco@psu.edu **Killing *Fusarium moniliforme*: correct identification of Fusarium Research Center culture collection accessions using molecular phylogenetics.**

The species name *Fusarium moniliforme* has been applied to at least eight biological species, and more than fifty phylogenetic species, leading taxonomists to recommend its abandonment. Unfortunately, the name is still in wide usage, and over 3000 isolates are accessioned in the Fusarium Research Center (FRC) culture collection under the name *F. moniliforme*. To correct this, we analyzed 500 diverse isolates from the Fusarium Research Center culture collection accessioned as *F.*

moniliforme, using DNA sequencing of a portion of the translation elongation factor 1-alpha (tef-1) gene. Isolates were found to belong exclusively to the *Gibberella fujikuroi* species complex, almost all of them in the African and Asian clades, representing at least fifteen already characterized species and a number of new candidate species. More isolates were found that belonged to *F. verticillioides*, the species most often associated with the name as *F. moniliforme*, than any other species, but they did not represent a majority. The growing tef-1 database proved to be an outstanding tool for quick and accurate species identification. *Contributed Presentation*

*JOHANNESSON, HANNA[1] and STENLID, JAN.[2] [1]Dept Plant and Microbial Biology, UC Berkeley, Berkeley CA 94720 USA. [2]Dept Forest Mycology and Pathology, Swedish Univ. Agricultural Sciences, Inst. Forest Mycology and Pathology, Uppsala, Sweden. hjohanne@nature.berkeley.edu **Nuclear reassortment between vegetative mycelia in natural populations of the basidiomycete *Heterobasidion annosum*.**

Somatic incompatibility (SI) in the basidiomycete *Heterobasidion annosum* is controlled at a series of three to four multiallelic discrete loci. Previous laboratory studies have indicated that SI reactions are not an absolute block to nuclear exchange between unrelated heterokaryotic strains of *H. annosum*, and in this study we present evidence for nuclear reassortment between vegetative mycelia in natural populations of the species. By using six highly variable microsatellite markers we genotyped single nuclei obtained from 20 somatically incompatible strains of *H. annosum* originating from a single stump of *Picea abies*. We found that 28 nuclei compose the 20 heterokaryotic genotypes found in the stump. Accordingly, the heterokaryons were not composed of unique nuclei; 10 of the nuclei were found in more than one heterokaryotic mycelia from the same stump. Furthermore, in one of the heterokaryotic mycelia we verified the coexistence of four different nuclear haplotypes. All heterokaryotic single-conidial mycelia from that mycelium were somatically compatible, indicating we had found a natural chimera of genetically distinct mycelia sharing alleles at the vegetative incompatibility loci. Taken together, the results strongly suggest that nuclear reassortment occur between mycelia of *H. annosum* in nature. *Contributed Presentation*

JOHNSON, ALEXANDER. **Cellular and Molecular Biology of Mating in *Candida albicans.***

Although long considered asexual, the fungal pathogen *C. albicans* was recently shown to undergo sexual mating. The mating process is elaborate, first involving a "phenotypic switch" from the white phase to the opaque phase followed by the action of mating pheromones and receptors. Because *C. albicans* is diploid, the mating products are tetraploid. Certain growth conditions induce efficient, random loss of chromosomes from these tetraploids. The products of this chromosome loss are typically diploid, or very close to diploid, in DNA content. If they inherit the appropriate MTL (mating-type like) loci, these diploid products are themselves mating competent. Thus an efficient parasexual cycle can be performed in *C. albicans*, one that leads to the reassortment of genetic material in this organism. This parasexual cycle-consisting of mating followed by chromosome loss-can be used in the laboratory for simple genetic manipulations in *C. albicans.* Symposium Presentation

JONESON, SUZANNE. Dept. Biology, Univ. Washington, Box 355325, Seattle WA, 98195-5325 USA. joneson@u.washington.edu **A molecular phylogeny of the *Ramalina almquistii* species complex.**

Plastic morphology and limited range information have confounded the taxonomy of many lichenized fungal genera, including *Ramalina*. One example is the *R. almquistii* complex, which includes three putative members found growing on coastal rocks, cliffs, and land of the greater northern Pacific Ocean and Bering Sea regions. Historically the species were separated by morphology, habit and geography, however these characters often overlap. To determine if more than one species is included in this complex, as well as to determine the most closely related taxa, a phylogeny was constructed based on ITS and beta-tubulin sequences using Maximum Parsimony and Maximum Likelihood analysis. Seventeen species of *Ramalina* were surveyed from throughout the genus. A combined dataset tree shows no variation within the *R. almquistii* complex, or support for more than one species. Instead, a group of closely related taxa highlights new questions of habitat preference, species pairs and biogeography of circumboreal and local members of this genus. *Contributed Presentation*

*KAUFF, FRANK[1], BUEDEL, BURKHARD[2] and LUTZONI, FRANCOIS.[1] [1]Duke Univ., Dept. Biology, Box 90338, Durham, NC-27708 USA. [2]Univ. Kaiserslautern, FB Biologie, Abt. Allgemeine Botanik, Postfach 3049, 67653 Kaiserslautern, Germany. fkauff@duke.edu **Ascoma ontogeny and apothecial anatomy in the Gyalectaceae (Ostropales, Ascomycetes) and the restoration of the Coenogoniaceae.**

The family Gyalectaceae, shown recently to be part of the Ostropales s.l., comprises mostly crustose species with characteristic urceolate apothecia. It also includes filamentous species of *Coenogonium* (including *Dimerella*) which exhibit an apothecial anatomy different from the remaining genera of the family. To establish a stable circumscription of the Gyalectaceae and to investigate relationships and delimitation of the genera currently included in the family, we analyzed the apothecial ontogeny and the anatomy of the adult fruiting bodies and compared the results to molecular analyses of the nuclear rDNA small and large subunits. All investigated taxa share a common type of hemiangiocarpous ascoma ontogeny, but both the actual apothecial development and the resulting anatomy of the adult ascomata are variable and characteristic for distinct subgroups. Three different ontogenetic types can be distinguished: (1) the genus *Coenogonium* with its unique development and anatomy is raised to the family level as a second family within the Gyalectales, and (2) *Belonia* and *Cryptolechia* have an ascoma ontogeny that differs from (3) the remaining Gyalectaceae. The morphological results are supported by molecular studies and underline the importance of ontogenetic evidence in phylogeny and taxonomy of ascomycetes. *Contributed Presentation*

*KEIRLE, MATTHEW[1], HEMMES, DON [2], and DESJARDIN, DENNIS[1]. [1]Dept. Biology, San Francisco State Univ., San Francisco, CA 94132 USA. [2]Dept. Biology, Univ. Hawaii at Hilo, Hilo, HI 96720 USA. mkeirle@sfsu.edu **Taxonomic analyses of Hawaiian members of the *Coprinus cordisporus*/*C. cardiasporus* complex based on ITS sequence data.**

The ecological and morphological features traditionally used to distinguish *Coprinus cordisporus* from *C. cardiasporus* (sect. Vestiti) appear to be inconsistent and overlapping among the Hawaiian collections in this group. Molecular sequence data (ITS region) obtained from numerous Hawaiian collections and additional material from Europe representing the *Coprinus cordisporus*/*C. cardiasporus* complex and related taxa are analyzed to investigate taxonomic relationships. The potential conspecificity of *Coprinus cordisporus*

and *C. cardiasporus* is examined, as well as the usefulness of morphological and ecological characters in delimiting species within the complex. Molecular phylogenies of the coprini based on nLSU-rDNA sequence data have placed other members of sect. Vestiti in the *Coprinopsis* clade. However, *C. cordisporus* appeared as either sister to *Coprinellus curtus* (Hopple & Vilgalys, 1999), or on a separate branch but still distinctly within the *Coprinellus*/*Psathyrella* clade (Moncalvo et. al., 2003). The ITS data presented here support inclusion of the *Coprinus cordisporus*/*C. cardiasporus* complex in the genus *Coprinellus*. *Poster*

*KELLER, HAROLD and SNELL, KENNETH. Dept. Biology, Central Missouri State Univ., Warrensburg, MO 64093 USA. keller@cmsu1.cmsu.edu **Cryptogam tree canopy biodiversity in the Great Smoky Mountains National Park.**

The Great Smoky Mountains National Park has over 40,000 hectares of old-growth forest in eastern United States. The All Taxa Biodiversity Inventory program aims to inventory all life forms in the Park. This tree canopy biodiversity study represents the first comprehensive inventory of cryptogams (myxomycetes, macrofungi, mosses, liverworts, lichens, and ferns) in the Park. A student research team climbed a total of 240 trees representing 35 different tree species during two three-week periods the summer of calendar years 2000 and 2001. Using the double rope climbing technique students scaled the tree canopy to heights of 40 meters. Preliminary results suggest that the myxomycetes are the only group of tree canopy organisms with some species that are restricted to the bark and epiphytes of living trees. There were 95 myxomycete species harvested mostly from moist chamber cultures derived from bark samples taken from the tree canopy, including 52 new records for the Park. A new species of *Diachea* was restricted to heights above 6 meters. This is the first upper tree canopy species documented for the Myxomycetes. This research project was funded by the National Science Foundation, Division of Environmental Biology, Biotic Surveys and Inventories Program, Award DEB-0079058 and Discover Life in America Awards 2001-26 and 2002-17. *Poster*

*KENNEDY, PETER [1] and BRUNS, THOMAS[2] [1]Dept. Integrative Biology, and [2]Dept. Plant and Microbial Biology, Berkeley, CA 94720 USA. pkennedy@socrates.berkeley.edu **Changes in ectomycorrhizal colonization, community structure and diversity associated with *Pseudotsuga menziesii* across a forest-grassland ecotone in coastal California.**

Determining how the mycorrhizal community changes along environmental ecotones may be important to understanding patterns in host plant distribution. In this bioassay study, we examined how ectomycorrhizal (ECM) colonization and community structure associated with Douglas fir (*Pseudotsuga menziesii*) seedlings changed across a forest-grassland ecotone in coastal California. Seedlings were planted into soils collected from five distances across the ecotone (10 m in the forest, 1 m in the forest, 1 m in the grassland, 10 m in the grassland, and 60 m in the grassland) at two sites and grown in the greenhouse for 9 months. There were significant decreases in ECM colonization in the grassland soils compared to forest soils, however, colonization also varied across sites. Species richness decreased moving away from the forest edge in addition to a shift in ECM community composition. These results suggest the ECM community changes across the ecotone in ways that may affect Douglas fir distributions. *Contributed Presentation*

*KERRIGAN, RICHARD, VELCKO, ANTHONY, JR., THOMAS, JUEL, McGRADY, JACKIE, and WACH, MARK. Sylvan Research, 198 Nolte Dr., Kittanning, PA, 16201 USA. kerrigan@penn.com **Multiple LTR-retrotransposons of the cultivated basidiomycete *Agaricus bisporus*.**

Screening of cosmid libraries of *Agaricus bisporus* (Lange) Imbach has revealed a diverse array of LTR-retrotransposons, often with affinities to *gypsy* or *copia* elements. Based on the deduced amino acid sequences of ORFs corresponding to *gag* and *pol* genes, at least eight distinct LTR-retrotransposons, either fragmentary or intact, are present in the genome of this mushroom. These elements are often present in high copy numbers and appear to be dispersed throughout the genome. It is common to find multiple elements represented within relatively short segments of chromosomal DNA. Fragments of elements also commonly disrupt the organization of other elements, making reconstruction of full-length sequences challenging. Although we have no direct evidence for active transposition, some retroelements are associated with occasional alterations of the genome, based on data from Southern hybridizations to genomic DNA. *Contributed Presentation*

*KIM, JAE-JIN[1], KIM, SEONG HWAN[1], BREUIL, COLETTE[1], and KIM, GYU-HYEOK.[2] [1] Dept. Wood Science, Univ. British Columbia, Vancouver, BC V6T 1Z4, Canada. [2]Div. Environmental Science & Ecological Engineering, Korea Univ., Seoul 136-701, Korea. jaekim@interchange.ubc.ca **A new *Ophiostoma* species isolated from radiata pine logs.**

A new *Ophiostoma* species causing sapstain has been isolated from radiata pine (*Pinus radiata* D. Don) logs both in New Zealand and imported to Korea. Its morphological and genetic characters are described. This species produces dark perithecia with neck and hyaline one-celled reniform ascospores. Mating tests on pine wood wafers show that it is a sexually compatible heterothallic species with two mating types. It is also tolerant to the antibiotic cycloheximide. The new *Ophiostoma* species can be distinguished from other *Ophiostoma* species by differences in its unique anamorph features: it has a *Leptographium* anamorph with mononematous and erect-synnematous conidiophores that have not been reported in known *Leptographium* anamorphs. When the new species grows on malt extract agar, its colony color is colorless at a young stage but turns greenish black at late growing stages, its mycelia are mostly immersed, and its growth rate is about 2.7 mm in diameter per a day at 25°C. We have sequenced and compared its ITS and 28S rDNA to determine the phylogenetic position of this species. It is most closely related to *Ophiostoma leptographioides*. *Poster*

*KIM, JAE-JIN, LEE, SANGWON and BREUIL, COLETTE. Dept. Wood Science, Univ. British Columbia, Vancouver, B.C. V6T 1Z4, Canada. jaekim@interchange.ubc.ca **Ophiostomatoid and basidiomycete fungi isolated from mountain pine beetle-infested lodgepole pine.**

To understand the diversity of Ophiostomatoid and basidiomycete fungi in mountain pine beetle-infested lodgepole pine, a preliminary survey was conducted at Kamloops and Williams Lake, British Columbia between October 2002 and March 2003. Samplings were performed with the beetle-infested pine trees at three different infestation stages that show green, red, and gray tree colors, respectively. In Ophiostomatoid fungi, a total of 11 species were identified. *Ophiostoma clavigerum*, *O. montium*, *Ceratocystiopsis minuta*-like, and *C. minuta-bicolor* were commonly present across the three different infestation stages. *O. olivaceum*, *O. sparsum*-like, and *Petosum fragrans* were found only at red stage. *O. minus* and

Hyalorhinocladiella sp. were isolated only at gray stage. *Leptographium terebrantis* was found from both red and gray stages. No significant difference in species distribution was found between the two sampled sites. In basidiomycetes, around 10 different species were found including *Bjerkandera adusta*, *Sistotrema brinkmanii*, *Stereum sanguinolentum*, *Trichatum abietinum*, and unknown species. *S. brinkmanii* and two unknown species were the three major species. The only species found at all different infestation stages were *Sistotrema* sp. and an unknown species. In contrast to Ophiostomatoid species, the distribution of basidiomycete species was very different between the two sampled sites. *Poster*

KLICH, MAREN. USDA-ARS Southern Regional Research Center, 1100 Robert E. Lee Blvd, New Orleans LA 70124 USA. mklich@srrc.ars.usda.gov **Characteristics of aflatoxin-producing fungi outside of *Aspergillus* section *Flavi*.**

Most aspergilli that produce aflatoxin are members of *Aspergillus* section *Flavi*. Several species that do not have the characteristics of that section have been found to produce aflatoxin, including: *A. ochraceoroseus*, *A. taiensis* and *Emericella venezuelensis*. Recently we have found that a strain of *Em. astellata* also produces aflatoxin. Morphologically, the two *Aspergillus* species are similar to members of section *Circumdati*. The *Emericella* species are slow-growing members of that genus and possess ascospores with large flanges. All of these species were isolated in equatorial zones. The two *Aspergillus* isolates were both from the same forest soils in the Ivory Coast. *Em. venezuelensis* was found in soil in Venezuela and the *Em. astellata* isolate was from *Ilex* leaves in the Galapagos Islands. Interestingly, in spite of their tropical origins, none of these isolates grew at 37°C. *Poster*

KOTLOVA, EKATERINA[1] and GORBUSHINA*, ANNA[2]. [1]Komarov Botanical Inst., Prof. Popov St. 2, St. Petersburg, Russia. [2]Carl von Ossietzky Univ., P. O. Box 2503, 26111 Oldenburg, Germany. a.gorbushina@uni-oldenburg.de **Adaptive responses of rock inhabiting microcolonial ascomycetes to de- and rehydration.**

Rock-dwelling microcolonial fungi (MCF) are highly adapted to environmental stress. Their protective mechanisms include slow meristematic growth, protective cell envelopes, internal and external water-binding compounds. MCF also possess mycosporines - UV-absorbing compounds, common in survival structures. Effects of slow or fast desiccation and subsequent rehydration on ultrastructure and lipid composition of a marble isolate *Phaeococcomyces* sp. was investigated. Abundant intracellular lipid droplets and recolonization of old cells were observed. The reserve lipid compounds were predominantly triacylglycerols, sterol esters and free fatty acids. The content of all reserve lipids was practically doubled during fast desiccation, while slow dehydration induced a considerable decrease in their amount. After rewetting the amount of reserve lipids reverted to the initial concentration. On the contrary, the amount of membrane lipids (phosphatidylcholines, phosphatidylethanolamines, sterols) remained unchangeable during dehydration. Such stability of membrane components during desiccation might be due to the use of reserve lipids both for energy production/water supply, as well as for membrane lipid synthesis. It was proved that highly stress-tolerant microcolonial fungi also have an effective biochemical membrane repair mechanism in response to de- and rehydration. *Poster*

LEBOGANG, LESEDI, *TAYLOR, JOANNE and MASWABI, TUDUETSO. Dept. Biological Sciences, Univ. Botswana, Private Bag UB 00704, Gaborone, Botswana. taylor@mopipi.ub.bw **Fungal biodiversity in several aquatic habitats in Botswana.**

Botswana is a landlocked, arid country in southern Africa, characterised by grasslands, Thorn and Kalahari bushveld, and Mopane woodlands. Aquatic habitats consist of three river systems in the north and east, the Okavango Delta and a system of intermittently flooded salt pans. No studies have been undertaken on aquatic fungi in Botswana and few studies have been carried out in the region. Several rivers and dams with permanent water, in east and south-eastern Botswana were sampled for aquatic fungi. Fifty submerged wood samples were collected from each site and incubated to encourage fruiting body development. Physical parameters of the water, such as oxygen level, temperature and pH, were measured. Biodiversity was low with between 16 - 48% of samples yielding fungal taxa, mainly colonised by single species. *Nais aquatica* was the most frequently encountered species (15% of samples) and occurred at all sites. Other common taxa included *Kirschsteiniothelia elasteroascus* and species of *Halosarpheia*, *Zopfiella*, *Ophioceras* and unidentified coelomycetes. Similarity of species composition was measured using Sorensen's index of similarity, which indicated that there was little overlap of species between sites with distinct species assemblages occurring at each site. Several novel fungi were recorded and lignocellulolytic activities of all of the fungi were tested. *Poster*

*LEE, JIN, KIM, CHANG M., PARK, JAE and JUNG, HACK. School Biological Sciences, Seoul National Univ., Seoul 151-747, Korea. minervas@snu.ac.kr **Fungal diversity in *Taxus cuspidata* community soil.**

Fungal diversity was examined in yew (*Taxus cuspidata*) community soil. Yew is famous for producing an anti-cancer drug taxol and, in Korea, inhabits in a mountain ridge area over 1300 m high in altitude near the top of the Pirobong Peak in Sobaeksan National Park. To elucidate the diversity and ecological role of fungi associated with the yew community, soil samples were collected from around the roots of yew trees and total DNA was prepared using a soil DNA extraction kit. PCR amplification was performed and small subunit ribosomal RNA gene libraries were constructed for 150 clones. Different clone types were confirmed from analysis of amplified ribosomal DNA restriction analysis (ARDRA) patterns. Fifty-four phylotypes were identified and then sequenced. Phylogenetic analyses were conducted for their sequences along with some related taxa and representative members of Kingdom Fungi. They were distributed all over fungal divisions: 2 in Chytridiomycota, 11 in Zygomycota, 30 in Ascomycota, and 11 in Basidiomycota. On the other hand, analyses of cultured soil samples developed only 7 different types of fungi, which were 2 in Zygomycota, 3 in Ascomycota, and 2 in Basidiomycota. As expected, some phylotypes were identified as members of arbuscular mycorrhizal fungi (AMF) that have obligate biotrophic nature and constitute an important component of forest ecosystems. *Poster*

*LEE, HEATHER[1], AL-SHEIKH, HASHEM[1], LOUNDS, CHRIS[1], MONTIEL,MARIA[1], DICKINSON, MATT[2], BRAKHAGE, AXEL[3], and ARCHER, DAVID. [1] [1]School Life and Environmental Sciences, Univ. Nottingham, Nottingham NG7 2RD, UK. [2]School Biosciences, Univ. Nottingham, Sutton Bonington Campus LE12 5RD, UK. [3]Inst. Microbiology, Univ. Hannover, D-30167 Hannover, Germany. heather.lee@nottingham.ac.uk **DNA methylation in biotechnologically and medically important fungi.**

DNA methylation is an epigenetic mechanism found in many eukaryotic genomes, with the dual roles of gene regulation and protection of the genome. Apart from detailed work in *Ascobolus*

immersus and *Neurospora crassa* , few studies have been conducted on DNA methylation in fungi, and until recently it was believed not to be present in *Aspergillus* species. We have used the amplified polymorphism technique (AFLP), with enzymes sensitive to methylated cytosine, to show that DNA methylation is present in the *A. flavi* complex, *A. niger*, *A. fumigatus* and the zygomycete, *Mortierella alpina*. We have also shown that in some cases DNA methylation changes with nutritional stress. Two DNA fragments isolated from AFLPs of *A. oryzae* and *A. parasiticus* have been cloned, sequenced and databases searched for homologs. Fragment MS-2 (81bp) has similarity to a region upstream of the *Neurospora* ALG11 protein that is a putative glycosyltransferase. Fragment MS-6 (152bp) has similarity with the heavy metal tolerance protein in *Schizosaccharomyces pombe*, which is an ATP-binding-type membrane protein. Expression of these genes in *A. flavi* species has been shown to vary with nutritional conditions or between species by reverse transcriptase-PCR. *Poster*

LEE, SEONJU[1] and CROUS, PEDRO[2]. [1]Dept. Plant Pathology, Univ. Stellenbosch, P. Bag X1, Matieland 7602, South Africa. [2]Centraalbureau voor Schimmelcultures, Fungal Biodiversity Ctr, Uppsalaan 8, 3584 CT Utrecht, The Netherlands. slee@maties.sun.ac.za **Biodiversity of saprobic microfungi in fynbos of the Cape Floral Kingdom of South Africa.**

The Cape Floral Kingdom (CFK), is located at the southern and south-western tip of South Africa, and represents the world's smallest and most diverse plant kingdom. Fynbos is the dominant vegetation type of the CFK and has winter rain, summer drought and periodic fire. Although the word comes from the Dutch "ëfijnboschí" describing the narrow-leaved bushes, fynbos also supports broad-leaved bushes like members of the Proteaceae (protea) and wiry, reed-like restioids. Despite its unique ecological attributes, no focused research has been directed towards understanding the fungal mycota occurring in fynbos, although some studies on the pathogens of proteas have indicated it to be highly diverse and unique. This study was therefore initiated in anticipation of a similar degree of diversity in saprobic fungi. Monocotyledonous restios and dicotyledonous proteas were chosen due to their high endemic ratio in fynbos, accessibility and tissue types favoured by saprobic fungi. Leaf and twig litter and senescent flowerheads of proteas, and culm litter of restios were collected over a three-year-period, and approximately 1200 saprobic fungi were isolated. Preliminary findings have revealed a mycota that includes several known, but also many unknown species. Details are provided as to the distribution and incidence of fungal taxa associated with the different host plants and substrates. *Contributed Presentation*

LILLESKOV, ERIK. USDA-Forest Service, North Central Research Station, Houghton, MI 49931 USA. elilleskov@fs.fed.us **Effects of changing global patterns of atmospheric N deposition on mycorrhizal fungal biodiversity: what do we know so far?**

Anthropogenic N fixation rates now exceed natural fixation, leading to regional increases in N deposition of up to two orders of magnitude. In Europe, where N deposition rates are highest, there has been a large decline in sporocarp production by ectomycorrhizal fungi, with certain taxonomic groups declining more rapidly than others. Atmospheric N deposition has emerged as the most likely causal agent in this decline. The same genus-specific declines have been seen in response to experimental N additions and over N deposition gradients, as have been seen in affected regions of Europe, strongly supporting the role of N deposition in European sporocarp decline. Sporocarp production and diversity is more sensitive to short-term N inputs than root-level diversity. However, root-level diversity does decline significantly in response to long-term N inputs, at least in oligotrophic boreal coniferous forests. It also appears that arbuscular mycorrhizal fungal diversity may be sensitive to long-term N inputs. Europe, North America, and East Asia are expected to have the highest levels of N inputs over the next decades, and should be areas of intensive research and monitoring for effects of N deposition on mycorrhizal fungal diversity. Future research efforts should also focus on understanding the functional consequences of these declines in biodiversity. *Symposium Presentation*

*LIN, XIAORONG, and MOMANY, MICHELLE. Dept. Plant Biology, Univ. Georgia, Athens, GA 30602 USA. xrlin@plantbio.uga.edu **Abnormal hyphal branching mutants *ahbA1* and *ahbB1* in *Aspergillus nidulans*.**

Branching is a process that generates new tip growth and is a key characteristic in filamentous fungi. It is important for mycelial development, reproduction and pathogenity. To understand the mechanisms of branch initiation and the relationship between vegetative hyphal branching and conidiophore development, two *Aspergillus nidulans* temperature sensitive (ts-) abnormal hyphal branching mutants *ahbA1* and *ahbB1* have been characterized. At restrictive temperature, the *ahbA1* mutant shows a hypobranching phenotype and defective nuclear division and nuclear morphology. The *ahbB1* mutant shows a hyperbranching phenotype. The *ahbB1* mutant is Calcofluor resistant and osomotically remediated, suggesting a defect in cell wall integrity. Both *ahbA1* and *ahbB1* mutants show abnormal conidiophore development during asexual reproduction at restrictive temperature, although viable spores are produced. Study of the *ahbA1* and *ahbB1* mutants should give insights into branch initiation, the relationship between hyphal branching and the cell wall integrity and the relationship between vegetative hyphal branch initiation and reproductive cell type differentiation during conidiophore development. *Contributed Presentation*

LIU, BO and LEE, JULIE Section Plant Biology, UC-Davis, Davis, CA 95616 USA. bliu@ucdavis.edu **Microtubules and septation in *Aspergillus*.**

Aspergillus nidulans is useful for studying spatial and temporal regulation of septation. After conidial germination, the first septum is made at the basal end of the germ tube after three mitoses. This septation event is known to be dependent on microtubules. We have found that in the absence of the activity of the microtubule motor cytoplasmic dynein, the first septum was made toward the apical end of the germ tube rendering an anucleate apical cell. We have determined that cytoplasmic dynein is dynamically present at the septation site. Future work will be devoted to testing whether motor(s) contribute to the transport of septation machinery. Temporal activation of septation involves a kinase cascade in fungi. The MOB1 protein is an evolutionarily conserved kinase-binding protein in this cascade. We have cloned the *Anmob1* gene in *A. nidulans*. A deletion mutation of *Anmob1* abolished septation, but surprisingly was not lethal. A functional GFP-AnMOB1 fusion localized to the spindle pole body during interphase, and also to the septation site at later stages of cell division. When the microtubule drug benomyl was applied to the culture medium, GFP-AnMOB1 first disappeared from the septation site, and later from the spindle pole body as well. Future work will be devoted to understanding whether microtubule motors contribute to the motility of septation signaling molecules. *Symposium Presentation*

*LIU, MIAO and HODGE, KATHIE. Dept. Plant Pathology, Cornell Univ., Ithaca NY 14853 USA. ml276@cornell.edu **Phylogenetic relationships of *Aschersonia aleyrodis* and related species based on nuclear large subunit ribosomal DNA sequences.**

The entomopathogenic fungi in the genus *Aschersonia* (teleomorph: *Hypocrella*) commonly infect whiteflies and scale insects in tropical areas. *Aschersonia aleyrodis* has been developed as a biocontrol agent, and other species show similar promise. Previous taxonomic studies have described species in this genus based solely on morphological characters, which has led to many uncertainties in delimiting taxa, especially for morphologically similar species. Molecular phylogenetic analyses were carried out for thirty isolates of seven *Aschersonia* species using the rDNA LSU region. Parsimony analysis revealed four major clades which are generally concordant with morphological species delimitation. However, isolates identified as *Aschersonia goldiana* are shown to be evolutionarily disparate. We tested T. Petch's subgeneric concepts, in which two subgenera are defined based on the host and the presence or absence of paraphyses. Our data suggest that the latter character is homoplasious; in the resulting trees Petch's subgenera do not form monophyletic groups. *Poster*

LIU, YAJUAN, *HODSON, MATTHEW, and HALL, BENJAMIN. Dept. Biology, Univ. Washington, Seattle WA 98195 USA. matthod@u.washington.edu **Molecular phylogeny of fungi based on RPB1 and RPB2 protein sequences.**

Over the past two decades, evolutionary relationships among major groups of fungi have primarily been investigated using rDNA sequences. There remain considerable uncertainties in the resulting phylogenies. We have developed and exploited two molecular markers, RPB1 and RPB2, to achieve a more complete view of evolutionary relationships among major groups of fungi. The highly conserved nuclear genes RPB1 and RPB2 encode the largest and the second largest subunits of RNA polymerase II, respectively. Representatives of the major groups in four fungal phyla were sampled. The protein sequences of RPB1, RPB2, and the combined dataset (about 1800 amino acids in length) were analyzed using both maximum parsimony and Bayesian inference. Overall, RPB1 and RPB2 provided excellent phylogenetic resolution, revealing several new relationships that have strong statistical support. Our major conclusions are that the Ascomycota and Basidiomycota are sister groups, the Zygomycota (including representatives of Trichomycetes and Zygomycetes) are monophyletic, and the Chytridiomycota are paraphyletic and the basal group of fungi. We will discuss the ways in which the phylogeny we infer from RNA Polymerase II subunit sequences differs from those presented earlier, based upon rDNA sequences. *Poster*

LOBUGLIO, KATHERINE F. and PFISTER, DONALD H. Farlow Herbarium, Harvard Univ., Cambridge MA 02138 USA. klobuglio@oeb.harvard.edu **Phylogenetic relationships within the Orbiliaceae.**

Phylogenetic relationships among species of the Discomycete family Orbiliaceae are being assessed from sequence data of the Large Subunit rDNA and RNA Polymerase II Subunit genes. Preliminary analysis of the sequence data indicates that the nematode trapping *Orbilia* species form a well-supported clade, distinct from the non-nematode trapping *Orbilia* species. In some cases among the non-nematode trapping *Orbilia* species, teleomorphs with similar anamorphs are each otherís closest relatives. Significant variation exists among isolates of the cosmopolitan species *Orbilia delicatula*. The consideration of *Orbilia inflatula* as a distinct genus, *Hyalorbilia*, is supported by the sequence data. *Poster*

*LODGE, D. JEAN[1], SANTANA, MIRNA[2], and LEBOW, PATTI[3]. [1]USDA-Forest Service, Forest Products Laboratory, Luquillo PR 00773-1377 USA. [2]Smithsonian Tropical Research Inst. (BCI), Box 2072, Balboa, Ancon, Panama. [3]USDA-Forest Service, Forest Products Laboratory, One Gifford Pinchot Dr., Madison WI 53726 USA. Email djlodge@caribe.net **Relationship of host preference in fungi to rates of leaf decomposition in Puerto Rico.**

Microfungi are differentially abundant in decomposing leaf species. We used 10 dominant microfungi and gamma irradiated litter of 5 leaf species in a microcosm experiment to test if decomposition differed depending on phylogenetic relatedness or similarities in litter quality (lignin, N and P) between the source of the fungal isolate and the substratum. A basidiomycete, *Melanotus eccentricus*, survived irradiation in some microcosms and decomposed leaves faster than microfungi. A significant interaction was found between fungi and leaf species. After variation from the basidiomycete was removed, a marginally significant (P=0.0523) difference in decomposition was found between fungal dominants from leaves of the same plant species or family as the substratum vs. leaves from different plant families that had contrasting qualities. No differences were found between fungal dominants from leaves of the same plant species or family vs those from different families that had similar litter quality (P=0.562), or between fungi from leaves of different families than the substratum that had similar vs contrasting litter qualities (P=0.588). The data on microfungi suggests preferences for related hosts, which contributes to species diversity, affects decomposition rates. A generalist delignifying basidiomycete, however, had a stronger effect on leaf decomposition than microfungi. *Contributed Presentation*

LOPRETE, DARLENE[1], HOGGARD, TIMOTHY[2], MARUTHUR, MARIO[2], and *HILL, TERRY[2] [1]Dept. Chemistry, and [2]Dept Biology, Rhodes College, Memphis TN 38112 USA. hill@rhodes.edu **Genetic complementation of Calcofluor hypersensitivity in a *calC* strain of *Aspergillus nidulans*.**

The cell wall plays important roles in defining cell shape and mediating interactions between a fungal cell and its environment. It is a dynamic organelle, assembled in situ from exported precursors and developmentally modified during growth and reproduction. The architectural relationships between the numerous polysaccharides and glycoproteins of the wall are incompletely known, as are the steps by which the complex fabric of the wall is assembled and modified. We have identified several mutant strains of the filamentous fungus *Aspergillus nidulans*, containing defective alleles causing hypersensitivity to the chitin synthase inhibitor Calcofluor White (CFW). CFW hypersensitivity has been tied to cell wall defects in the yeast system (e.g., M. Lussier et al., 1997, Genetics 147: 435-450). Using a plasmid genomic DNA library ("AMA NotI", Osherov and May, 2000, Genetics 155: 647-656), we have cloned a genomic DNA fragment, which complements the defective phenotype of one mutation (designated *calC*), which is blocked in conidium germination in the presence of low levels of CFW. The plasmid has been randomly transposon-mutagenized to disable individual candidate genomic ORFs; sequencing and retransformations of the *calC* strain with plasmid subtypes bearing specific insertional inactivations are underway to identify the ORF responsible for this phenotypic rescue. *Poster*

LOWRY, DAVID, FISHER, KAREN, and * ROBERSON, ROBERT. Dept. Plant Biology, Box 871601, Arizona State Univ., Tempe, AZ 85287-1601 USA. Robert.Roberson@asu.edu **Functional necessity of the cytoskeleton during cleavage membrane development and zoosporogenesis in *Allomyces macrogynus*.**

Cleavage membrane development and cytokinesis were examined in

zoosporangia of *Allomyces macrogynus* treated with cytoskeletal inhibitors and compared to zoosporogenesis under control conditions. Developing membranes were visualized in living zoosporangia with laser scanning confocal microscopy using the lipophilic membrane dye FM4-64. Under control conditions, cleavage membranes developed in four discrete stages, ultimately interconnecting to delimit the cytoplasm into polygonal uninucleate domains of near uniform size. Disruption of microtubules did not impede the normal four-stage development of cleavage membranes and cytokinesis occurred with only minor detectable anomalies, though zoospores lacked flagella. Disruption of actin microfilaments did not inhibit membrane formation, but blocked nuclear migration and significantly disrupted membrane alignment and cytoplasmic delimitation. This resulted in masses of membrane that remained primarily in cortical regions of the zoosporangia, as did nuclei, throughout zoosporogenesis. These results show that in *Allomyces* zoosporangia a functional actin microfilament cytoskeleton is required for proper alignment of cleavage elements and cytokinesis while microtubules play a less significant role. *Contributed Presentation*

*LUMBSCH, THORSTEN, and SCHMITT, IMKE. Dept. Botany, Field Museum, 1400 S. Lake Shore Drive, Chicago, IL 60605 USA. tlumbsch@fmnh.org **Phylogenetic relationships of lichen-forming disco- and pyrenomycetes.**

The phylogenetic relationships of lichen-forming ascomycetes forming apothecia or perithecia were examined using sequence data of the nulear LSU rDNA and the mitochondrial SSU rDNA. Taxa of the pyrenomcete orders Pyrenulales, Trichotheliales, and Verrucariales and the discomycete orders Agyriales, Lecanorales s.lat., Ostroaples s.lat., and Pertusariales were included in this study. The combined data set was analyzed using a Bayesian approach. The study concentrated on the inference of basal parts of Lecanoromycetes phylogeny and their relationships to pyrenocarpous ascomycetes. It is shown that lichen-forming discomycetes are not related to non-lichenized discomycetes that are currently classified in Leotiomycetes and Pezizomycetes. The lichenized pyrenomycetes are also not related to the Sordariomycetes, but belong in Chaetothriomycetes. The evolution of ascoma-types in lichen-forming ascomycetes is discussed in this phylogenetic context. *Contributed Presentation*

*LUOMA, DANIEL[1], EBERHART, JOYCE[1], and ABBOTT, R. [2] [1]Dept. Forest Science, Oregon State Univ., Corvallis OR 97331, USA. [2]Diamond Lake Ranger District, Umpqua National Forest, Roseburg, OR 97470, USA. luomad@fsl.orst.edu **Effects of spore inoculum on the ectomycorrhiza diversity of Douglas-fir seedlings.**

Ectomycorrhiza diversity helps stabilize below-ground processes after disturbance. In addition, EM diversity can increase tree's competitive abilities. Nursery grown seedlings often have low EM diversity and the EM species may be poorly adapted to out-planting sites. Harsh sites tend to have low EM inoculum potential. Hence, applying spore inoculum of EM species that vigorously colonize roots may increase growth and survival of out-planted stock. In a pilot project, we experimentally address two questions: 1) Does spore inoculation at the time of out-planting affect survival and growth? 2) Do the inoculated fungi affect EM diversity? During out-planting, we inoculated *Pseudotusga* seedlings with *Rhizopogon* spores. Preliminary results suggest that *Rhizopogon* EM increased on some sites. To improve statistics, replication will be increased from 5 to10 in future studies. Regardless of growth response, successful inoculation of out-planted seedlings has the potential to impact the broader soil ecosystem. Because the EM species that may be established via inoculation are aggressive colonists, they have the potential to alter the biodiversity of ectomycorrhizal fungi on a wide scale. The knowledge gained by this study will allow forest managers to improve planning for reforestation projects and may be particularly valuable when considering ecosystem management and restoration projects. *Contributed Presentation*

MAGGIO-HALL, L., WILSON, R.A. and *KELLER, N.P. Dept. Plant Pathology, Univ. Wisconsin-Madison, 1630 Linden Dr., Madison, WI 53706 USA. npk@plantpath.wisc.edu **Pathways for polyketides in *Aspergillus nidulans*.**

The *Aspergillus* mycotoxins, aflatoxin (AF) and sterigmatocystin (ST), are polyketides assembled from acetyl-coenzyme A units. We are interested in how the acetyl-CoA pool is made available for polyketides. Here we present evidence that the peroxisome plays a role in the synthesis of ST and AF. We have found that *Aspergillus* delta 12 desaturase mutants show signs of peroxisomal proliferation, accumulate oleic acid, overexpress beta-oxidation and ST/AF biosynthetic genes and make substantially more ST/AF than wild type strains. Oleic acid growth medium supports a similar phenotype in wild type strains. Disruption of *A. nidulans fox2*, the gene encoding the multifunctional beta-oxidation protein which generates acetyl-CoA units in the peroxisome, results in a strain unable to grow on oleic acid as the sole carbon source and crippled in the ability to synthesize ST. Finally, microscopic studies showed that the ST/AF precursor norsolorinic acid (NOR) accumulates in the peroxisomes. Since NOR is generated from a ST/AF specific fatty acid synthase (FAS) - polyketide synthase (PKS) complex, it is possible that these acetyl-CoA-requiring steps occur in the peroxisome. We are currently exploring the subcellular localization of the FAS and PKS, and analyzing the effect of mutations that alter carbon flow into and/or out of the peroxisome on the synthesis of ST. *Symposium Presentation*

*MARRA, ROBERT[1], CORTESI, PAOLO[2], BISSEGGER, MARTIN[1], and MILGROOM, MICHAEL[1]. [1]Dept. Plant Pathology, Cornell Univ., Ithaca, New York 14853, [2]Ist. Patologia Vegetale, Univ. degli Studi di Milano, Milan, Italy. r.marra@duke.edu **Mixed mating in natural populations of the chestnut blight pathogen, *Cryphonectria parasitica*.**

The chestnut blight pathogen, *Cryphonectria parasitica*, is a haploid ascomycete that was previously shown to have a mixed mating system in one population in USA. In this report, we show that mixtures of selfing and outcrossing occur in 10 additional populations of *C. parasitica* sampled from Japan, Italy, Switzerland and USA. Progeny arrays from each population were assayed for segregation at vegetative incompatibility (*vic*) and DNA fingerprinting loci. Outcrossing rates were estimated as the proportion of progeny arrays showing segregation at one or more loci, corrected by the probability of nondetection of outcrossing. Outcrossing estimates varied from 0.74 to 0.97, with the lowest rates consistently detected in USA populations (0.74 - 0.78). Five populations (four in USA and one in Italy) had outcrossing rates significantly less than 1, supporting the conclusion that these populations exhibit mixed mating. The underlying causes of variation in outcrossing rates among populations of *C. parasitica* are not known, but we speculate that outcrossing is a function of ecological, demographic and genetic factors. *Contributed Presentation*

*MARRA, ROBERT[1], HUANG, JOHNNY[1], NIELSEN, KIRSTEN[1], FUNG, EULA[2], HEITMAN, JOSEPH[1], VILGALYS, RYTAS[2], and MITCHELL, THOMAS[1]. [1]Dept. Molecular Genetics and Microbiology, Duke Univ. Medical Center, Durham, NC 27710 USA. [2]Dept. Biology, Duke Univ., Durham, NC 27710 USA. [3]Stanford Genome Technology Center, Stanford, CA 94304 USA. r.marra@duke.edu **Mapping the genome of *Cryptococcus neoformans* var. *neoformans*.**

Cryptococcus neoformans is a pathogenic yeast that can cause life-threatening infections in the central nervous systems of immunocompromised and other patients. A dimorphic basidiomycete, the dikaryotic filamentous form originates from sexual fusion between *MATalpha* and *MATa* cells. We crossed the *MATalpha* strain B3501 and the *MATa* strain B3502 to produce 94 basidiospores, which were used to generate a genetic linkage map of the *C. neoformans* genome. The map is based principally on two classes of polymorphic markers: restriction fragment length polymorphisms (RFLPs) and microsatellites. To identify candidate polymorphisms, we used the *C. neoformans* genome sequence database (Stanford Genome Technology Center) and identified 66 polymorphic microsatellites and over 250 RFLPs. Nearly all markers showed normal segregation ratios. Linkage mapping was done with JoinMap 3.0 (Plant Research International, Wageningen, The Netherlands), using recombination thresholds of 35% and LOD score thresholds of 6.0. The majority of markers resolved into10 large and several smaller linkage groups. Correspondence between linkage groups and chromosomes was established by hybridization of marker-based probes to CHEF blots. The linkage map is proving an essential tool to genome sequence assembly and a powerful approach to investigating the genetics of clinically relevant complex traits. *Contributed Presentation*

*MATA, JUAN, HUGHES, KAREN, and PETERSEN, RONALD. Univ. Tennessee, Dept. Botany, 437 Hesler Biology Bldg., Knoxville 37996-1100 USA. jmata@utk.edu **Infrageneric taxonomy of *Gymnopus* (Agaricales).**

Currently, the genus *Gymnopus* is divided into four sections based on morphology. A phylogenetic analysis was carried out to test whether these sections were supported by molecular data. Sequences from the ITS nrDNA region were obtained from specimens representing these sections and a phylogenetic tree was generated. Data in that tree agree with sectional status of *Gymnopus*, *Levipedes*, and *Vestipedes* all of which include their type species. New sections are proposed for phylogenetically segregate clades, justified also by morphological characteristics. *Poster*

McGUIRE, CRISTINA, *MARRA, ROBERT, and MILGROOM, MICHAEL. Dept. Plant Pathology, Cornell Univ., Ithaca, New York 14853 USA. r.marra@duke.edu **Mating-type heterokaryosis as a mechanism for self-fertilization in the chestnut blight pathogen, *Cryphonectria parasitica*.**

Selfing in ascomycetes typically requires the involvement of both alleles (idiomorphs) of the mating-type (*MAT*) locus. While this appears to be true for some selfing in *Cryphonectria parasitica* as well, the mechanisms by which *C. parasitica* selfs are unlike those of other ascomycetes. In most cases of selfing in *C. parasitica*, the segregation of both mating types among the progeny demonstrates the presence of both *MAT* idiomorphs in the parent. Self-fertile laboratory isolates (including ascospore isolates) and field isolates were shown to be heterokaryons, as they resolved into uninucleate, single-spore (conidia) isolates of both mating types. We also resolved *MAT* heterokaryons in single-conidial isolates from hyphal tip isolates, demonstrating conclusively that they came from heterokaryotic mycelium. The progeny from four perithecia that resulted from selfing did not segregate for mating type, suggesting that *C. parasitica* has an alternative mechanism of selfing that does not require both mating types. However, this alternative mechanism is less common. These two results together indicate that the mating system of *C. parasitica* is unlike any other previously described in ascomycetes. *Contributed Presentation*

McGUIRE, SARAH LEA. Millsaps College, 1701 N. State St., Jackson, MS USA mcguisl@millsaps.edu **The Cell Cycle in *Aspergillus nidulans*.**

Many of the *Aspergillus nidulans* cell cycle mutants originally identified by Ron Morris encode key components of the cell cycle regulatory machinery. The *nim* mutants have led to a greater understanding of the events that occur at the G2-M transition, and include *nimA*, which is required for mitotic entry parallel to the activity of the p34cdc2 kinase. The *bim* mutants led to the identification of proteins involved in mitotic exit, including two proteins later identified as part of the Anaphase Promoting Complex (APC). Extragenic suppressor analyses of these mutants have resulted in the identification of genes that have aided in the elucidation of how the various pathways function and how they potentially interact. Suppressors of *nimX*, *nimO*, and *nimT* mutants have implicated the roles of these proteins in the DNA damage response (*nimX*, *nimT*) and DNA replication (*nimO*). Suppressors of *nimA* mutants are nuclear pore complex proteins, suggesting that NIMA is involved in regulating the entry of mitotic proteins through the nuclear pore complex. Together, these works provide a more comprehensive understanding of the biology of the cell cycle in *Aspergillus nidulans* and a foundation for a wide variety of future studies. *Symposium Presentation*

*McLENON, TERESITA[1] and MONCALVO, JEAN-MARC.[2] [1]Univ. Toronto, Dept. of Botany, Toronto ON M5S 3B2 CANADA. [2]Royal Ontario Museum, Center for Biodiversity and Conservation Biology, Toronto ON M5S 2C6 CANADA. terri.mclenon@utoronto.ca **The basidiomycete community in a hemlock-dominated plot in a southern Ontario temperate forest.**

We determined the above-ground diversity of basidiomycetes in a 625m^2 hemlock-dominated plot by sampling fruiting bodies and identifying them using morphological characters. The internal transcribed spacer region (ITS) of nuclear-encoded ribosomal DNA was sequenced and added to a database. We also examined the below-ground diversity of root-tip fungi. The ITS region and the 5' end of the nuclear large ribosomal subunit (nLSU) gene were sequenced and compared to existing sequence databases to determine the identity and phylogenetic affinities of the root tip fungi in relation to the fruiting bodies. 283 collections of 95 species from 47 genera were made during 20 collection visits. Preliminary results indicate three ecological groups: 16 ectomycorrhizal genera, 13 saprophytic on wood, and 18 being variable with substrate and found on litter, wood or soil. The most commonly collected genera were *Cortinarius*, *Entoloma*, *Inocybe*, *Lactarius*, *Mycena*, and *Tricholoma*. Four different diversity estimators suggest that there are at least 140-170 species present. Preliminary comparison indicates that there are 17 genera including 7 species that are found associated with Eastern Hemlock in this study and Western Hemlock from previous studies. Preliminary results of the fruiting body and root tip fungi identified will also be presented. *Contributed Presentation*

*MEDING, MERCER and ZASOSKI, R.J. Land, Air, and Water Resources, Univ. California, Davis, Davis, CA 95616 USA. smmeding@ucdavis.edu **Transfer of ^{15}Nitrate and Rare Element Analogs of Phosphorous, Potassium, and Calcium through Common Mycorrhizal Networks for Grass and Forb Species of the Sierra Foothills of California.**

Arbuscular mycorrhizal fungi infect the majority of plant species found within the savannah/oak woodland ecosystem of the California Sierra Foothills. These fungi have the potential to form underground networks that link the roots of individual plants and/or species of plants. A common mycorrhizal network (CMN) may function as an efficient transport mechanism for the movement of nutrients between plants. An experiment was conducted, as part of an on-going study, to examine the transfer of macronutrients between plants restricted to mycelial connections. Nutrient labels applied to the foliage of donor plants were then analyzed for detection in the foliage of receiver plants. In order to examine the potential movement for an array of plant macronutrients through a CMN, a stable isotope and rare element nutrient analogs were used as tracers. ^{15}Nitrate was used to trace nitrogen movement. Arsenic, cesium, rubidium, and strontium were used as tracers for phosphorous, potassium, and calcium respectively. Treatments included separated monocots, dicots, and a mixture of grass and forb species common to a California Sierra Foothill research site. The treatments were set up to encompass two levels of plant biocomplexity. *Contributed Presentation*

*MIADLIKOWSKA, JOLANTA, ARNOLD, ELIZABETH, HOFSTETTER, VALERIE and LUTZONI, FRANCOIS. Dept. Biology, Duke Univ., Durham, NC 27707-0338 USA. jolantam@duke.edu **Endolichenic fungi: Morphological and molecular diversity of fungi from surface-sterilized lichens of the genus *Peltigera* in a temperate and tropical forest.**

Only lichenicolous fungi with visible reproductive structures have been studied previously. Therefore, the potential for fungi to grow asymptomatically within lichen thalli remains mostly unexplored. We used a gradient of surface sterilization to examine fungal communities upon and within the lichen genus *Peltigera* (*P.* cf. *polydactylon*, southeastern USA; *P. dolichorhiza* s.l., Costa Rica). From two thalli per species, two 2 square cm pieces were subjected to washing in water, or in water followed by 0.5% sodium hypochlorite and 70% ethanol. Thallus pieces were pressed lightly against 2% malt extract agar (MEA) to harvest viable fungi from external surfaces, and then were cut into small pieces and transferred to 2% MEA plates to harvest all cultivable fungi in and on the thallus. From all isolates and treated thallus pieces, the entire ITS nrDNA was sequenced and used to identify taxa. We compared species richness as estimated by culturing and cloning under different degrees of surface sterilization, and used our library of isolates to distinguish among fungi that appeared within or upon treated thalli. We will discuss abundance, diversity, and species composition of fungi occurring in and on the selected *Peltigera* species, giving special attention to fungi living asymptomatically within thalli (endolichenic) subjected to the most rigorous sterilization treatment.

*MILLER, STEVEN[1] and HENKEL, TERRY[2]. [1]Dept. Botany, Univ. Wyoming, Laramie, WY 82071 USA. [2] Dept. Biological Sciences, Humboldt State Univ., Arcata, CA 95521 USA. fungi@uwyo.edu **Biology and molecular ecology of subiculate *Lactarius* species from Guyana.**

To date four species of *Lactarius* that produce basidiomata from well developed subiculae have been collected from the Pakaraima mountains of Guyana. Three of these, *L. panuoides, L. multiceps* and *L. brunella* are pleurotoid. An additional undescribed species is centrally stipitate from a short stipe. Depending on the species, the subiculum can vary in size from several square centimeters to nearly 1000 square meters, and can cover rocks, soil, roots, saplings and tree trunks. Although all of these species have been shown to form ectomycorrhizae, several appear to be detrimental to recruitment of saplings, with many dead or dying saplings observed covered by the subiculum. A plaque-like slime phase has been found in association with at least two of these fungi, and molecular techniques have shown that this is an early stage in development of the subiculum. The subiculae in *L. panuoides* and *L. brunella* are extensive and thick, measuring up to 15-20 cm deep. The inner portions of the subiculum appear to be well humified material and outer layers indicate a coexistence or competition with algae and bryophytes. A visual tour of these fungi, along with descriptive data, molecular documentation of their phylogeny, ectomycorrhizal status and life-history will be presented. *Contributed Presentation*

*MILLER, STEVEN[1], ROBERTS, PETER[2], and WATLING, ROY[3]. [1]Dept. Botany, Univ Wyoming, Laramie, WY 82071 USA. [2]Royal Botanic Gardens, Kew, England. [3]Royal Botanic Gardens, Edinburgh, Scotland. fungi@uwyo.edu **Comparative biogeography of the Russulaceae: mycofloras of west Africa and the Guiana Highlands of South America.**

South America and Africa, once united by the supercontinent Pangea, share many similarities in geologic history, paleofloras and faunas, and modern plant and animal biogeography. Ectomycorrhizal leguminous host trees such as *Brachystegia* and *Gilbertiodendron* in Africa and *Dicymbe* in South America are interesting disjuncts. While several genera of saprotrophic macrofungi, including *Thamnomyces* and *Polydiscidium*, are known to be disjuncts between South America and Africa, little is known regarding the distribution and similarities in ectomycorrhizal fungi associated with leguminous hosts. Collections of Russulaceae members in the genera *Russula* and *Lactarius*, collected during multiyear expeditions to Korup National Park in Cameroon, west Africa, and the Guiana Highlands of western Guyana, were used in this study. The fungi were identified to species and the floras compared directly at the subgenus, section and subsection levels. ITS sequence data were used to construct phylogenies for each genus and to assess biogeographic connectedness. Annulate species of *Russula* in the section *Heterophyllae* and members of the subgenus *Plinthogali* of *Lactarius* are well represented in both regions. Results from cladistic biogeography, sequence analysis and ordination methodologies will be presented. Other interesting ectomycorrhizal disjuncts will be briefly discussed. *Contributed Presentation*

*MORGENSTERN, INGO and HIBBETT, DAVID. Dept. Biology, Clark Univ., Worcester MA 01610 USA. IMorgenstern@clarku.edu **Evolutionary diversity of manganese dependent peroxidase genes in ligninolytic homobasidiomycetes.**

White rot homobasidiomycetes use an array of different enzymes including extracellular peroxidases to degrade lignin. Most focus has been applied so far on lignin peroxidases (LiP) and manganese dependent peroxidases (MnP), which occur in a number of closely related isoforms. In *Phanerochaete chrysosporium*, three different MnP isozymes (MnP1-MnP3) have been described and their encoding genes been characterized. We have been studying the evolutionary diversity of these structurally related genes in saprotrophic homobasidiomycetes using molecular tools. The pattern of occurrence of ligninolytic enzymes may reflect the phylogenetic relationships of ligninolytic fungal lineages. Phylogenetic analyses of published MnP sequences suggests that gene duplication has occurred

repeatedly in homobasidiomycete phylogeny. Since the MnP system is thought to be evolutionary younger compared with LiP, the former genes may better reflect more recent changes in phylogeny. We are currently developing primers for PCR amplification of MnP genes from diverse homobasidiomycetes, with the goal of understanding the evolution of this ecologically important gene family. *Poster*

*MOSER, A. M., PETERSEN, C., TUGAW, H., BERNINGHAUSEN, H., and SOUTHWORTH, D. Dept. Biology, Southern Oregon Univ., Ashland, OR 97520 USA. southworth@sou.edu **Mycorrhizas on *Quercus garryana* on serpentine soils.**

Serpentine soils are known for paucity of vegetation and for a high proportion of endemic species. The soils are relatively high in magnesium, iron and other heavy metals, but low in fertility. Oregon white oaks (*Quercus garryana*) are not primarily found on serpentine, but do occur on scattered sites. We wanted to determine whether the mycorrhizal status of these trees was similar to that on the Agate desert in southwest Oregon. The Agate Desert is an alluvial fan capped with a shallow layer of clay loam over cemented hard pan and is characterized by patterned ground with mounds and vernal pools. We hypothesized that mycorrhizas on serpentine would be less abundant and less diverse - parallel to the situation with green plants above ground. We sampled oak roots at three serpentine sites in Oregon. We morphotyped mycorrhizas and used molecular techniques to distinguish among morphotypes, to compare mycorrhizal tips to fungal fruitbodies, and to sequence portions of fungal DNA. Ectomycorrhizal diversity was greater on oak roots in serpentine soils than on the Agate desert suggesting that lack of fertility in serpentine soils promotes mycorrhizal formation and that heavy metals in serpentine soils do not inhibit mycorrhizal growth. Research funded by National Science Foundation Grant DEB-9981337 through the Biocomplexity Program and Research at Undergraduate Institutions. *Poster*

*MULLANEY, EDWARD and DALY, CATHERINE. SRRC USDA-ARS, New Orleans, LA 70124 USA. emul@srrc.ars.usda.gov **Conserved structural features of a putative histidine acid phosphatase encoded by a *Neurospora crassa* gene.**

Several fungal phytases have been identified as being histidine acid phosphatases (HAP). This group of enzymes has a conserved amino acid sequence, RHGXRXP, previously identified as its catalytic active site. A hypothetical protein identified from the *Neurospora crassa* sequencing project, Locus NCU06351.1, has this characteristic active site motif, plus several other structural components that suggest that this protein is analogous to *Aspergillus niger* phytase. *A. niger* phytase, a HAP, is commercially marketed as an animal feed additive and has been extensively studied. All the principal components of both the active site and the substrate specificity site are present in this Neurospora protein. Further analysis of the DNA sequence of NCU06351.1 suggests both a different 5' end and the presence of an intron. These findings increase the similarity between this *N. crassa* and the *A. niger* phytase gene. It also appears that all the cysteine residues necessary for the five disulfide bridges in *A. niger* phytase are present in NCU06351.1. Isolation and characterization of this *N. crassa* enzyme will refine our understanding of other structurally important features of the phytase molecule. *Poster*

*MUNKACSI, ANDY[1], PAN, JEAN[2], and MAY, GEORGIANA[1,2] [1]Dept. Plant Biology, and [2]Dept. Ecology, Evolution, and Behavior, Univ. Minnesota, St. Paul, MN 55108 USA. munk0009@tc.umn.edu **Origin and migration of *Ustilago maydis*.**

Morphological, molecular, palynological, and archeological evidence indicate that maize was domesticated from one of the teosintes 6,000-9,000 years ago in southern Mexico. The migration of maize to the United States and South America is well documented, while migration of the maize- and teosinte-specific pathogen, *Ustilago maydis*, is not known. Using phylogenetic analyses of DNA sequence data from five protein-coding genes, we predict the geographical location of the ancestral *U. maydis* population and whether it was on maize or a teosinte. We describe the genetic structure of *U. maydis* populations in the United States, Mexico, and South America with single nucleotide and microsatellite length polymorphisms. Preliminary determination of whether the migration of *U. maydis* is the same as that of maize will be reported. *Contributed Presentation*

MURRIN, F. Dept. Biology, Memorial Univ., St. Johns, NL, Canada, A1B 3X9. fmurrin@mun.ca **The epigeous, ectomycorrhizal basidiomycete community in balsam fir dominated, coastal boreal forest, Newfoundland.**

Terra Nova National Park is Canada's most easterly national park and it protects remnants of the ancient Appalachian Mountains alongside the Atlantic coast. In the Park, stands of balsam fir (*Abies balsamea*) are being replaced by black spruce (*Picea mariana*) as a result of natural and anthropogenic activities, decreasing biodiversity within the boreal forest. Our long-term goal is the quantitative assessment of disturbance on mature and disturbed Balsam Fir ectomycorrhizal communities and on forest structure. Because so little is known about the fungi of the area, our first focus has been a general inventory. During a three-year period, 2000-2002, we visited a total of ten sites and made approximately 900 collections. Over seventy species of mushrooms were identified which were associated with balsam fir and which belong to genera known to form ectomycorrhizal associations. Species of the genera *Cortinarius, Russula, Lactarius* and *Amanita* were most commonly collected in each of the three years. We present here a summary of our findings, along with species descriptions and a regional key to the ectomycorrhizal mushrooms associated with balsam fir. This work gives a strong basis for future quantitative studies on disturbance effects in the Park, and also represents baseline biodiversity data for mushrooms of Terra Nova National Park. *Poster*

NALIM, F.A.[1], SAMUELS, G.J.[2], WIJESUNDERA, R.L.[3], and *GEISER, D.M.[1] [1]Dept. Plant Pathology, Penn State Univ., University Park, PA 16802 USA. [2]Systematic Botany and Mycology Lab., USDA-ARS, Beltsville, MD. 20705 USA. [3]Faculty of Science, Univ. Colombo, Colombo 3, Sri Lanka. fan106@psu.edu **Biogeography of the *Fusarium solani* species complex: sampling in the Southern Hemisphere.**

The *Fusarium solani* species complex is a highly diverse, cosmopolitan group of species lineages with some biogeographic structure. We investigated the phylogenetics of *F. solani* isolates obtained from non-agricultural soils and perithecia from primary forests in Sri Lanka and other places of Gondwanic origin. Pure cultures of members of the complex were obtained from soil, and from ascospores taken from the perithecial samples. Parts of the translation elongation factor 1-alpha (tef) gene, the nuclear large subunit gene, and the internal transcribed spacer regions (ITS) of the nuclear ribosomal RNA gene were sequenced in over 30 of the isolates. All of the isolates from Sri Lanka were found to be members of newly identified clades in the *Fusarium solani* species complex, with soil-derived and ascospore isolates forming separate lineages. Correlations between phylogeny and biogeography will be discussed. *Contributed Presentation*

*NGUYEN, DIEM, IZZO, ANTONIO, and BRUNS, THOMAS. Plant and Microbial Biology Dept., Univ. California, Berkeley, CA, 94720 USA. aizzo@nature.berkeley.edu **Spore bank spatial structure across a Sierra Nevada mixed-conifer forest.**

Spores and resistant propagules act as the primary ectomycorrhizal inoculum for seedlings in the absence of an active mycelial network. In forests where disturbances such as fire are common, spatial structure in the spore bank composition could affect seedling establishment across the forest. While the distribution of the spores that seedlings see appears to be uniform in studies, this has not been implicitly tested. To test for spore bank spatial structure and estimate its diversity, we performed bioassays of soils collected across 54 plots across approximately 36 hectares of Sierra Nevada mixed-conifer forest using seed from the native *Pinus jeffreyii* and *Abies concolor*. The spores that germinated and colonized the roots were characterized both by morphotypes and molecular-based techniques (PCR and RFLP of ITS region of rDNA). Though there are at least twenty different RFLP types of *P. jeffreyii* colonizers, three taxa appear to be frequent and widespread spatially across the forest. These data suggest that although the spore bank is relatively species-rich, there is little detectable spatial structure across the forest for *P. jeffreyi* seedlings. Preliminary results suggest that *A. concolor* may see a different spore bank community altogether. The results will be discussed relative to the active ectomycorrhizal root community and the characteristics of this forest. *Contributed Presentation*

*NGUYEN, NHU, SUH, SUNG-OUI, and BLACKWELL, MEREDITH. Dept. Biological Sciences, Louisiana State Univ., Baton Rouge, LA 70803 USA. ssuh@lsu.edu **Effect of starvation of basidiocarp-feeding beetles on suspected yeast endosymbionts.**

Yeasts were routinely isolated from the gut of basidiocarp-feeding beetles in this study. An experiment was performed to determine the effect of beetle starvation on the gut yeasts. Two species of tenebrionid beetles (*Neomida bicornis* and an unidentified species) were collected from *Fomitella supina* and *Inonotus ludovicianus*, respectively and kept in sterile Petri plates with sterile water but no food until they were dissected over a period of eleven days. The beetles were dissected at two-day intervals and the gut contents, plated on acidified YM agar. After three days of incubation at 25°C the colonies were counted and each morphologically distinct colony was identified by LSU rDNA sequence. One yeast type predominated in the cultures and was the only yeast present after several days. The number of gut yeasts isolated decreased dramatically to none after nine days for *Neomida bicornis* and eleven for the unidentified tenebrionid. Failure to isolate yeasts from controls indicated that the yeasts probably were restricted to the beetle gut. *Poster*

*NIEVES-RIVERA, ANGEL[1], STEPHENSON, STEVEN [2], and WRIGLEY DE BASANTA, DIANA[3]. [1]Dept. Marine Sciences, Univ. Puerto Rico, Mayaguez, PR 00681-9013 USA. [2]Dept. Biology, Fairmont State College, Fairmont, WV 26554 USA. [3]The American School of Madrid, Apartado 80, 28080 Madrid, Spain. anieves@coqui.net **Living and dead lianas as a special microhabitat for myxomycetes in tropical forests.**

Decaying coarse woody debris, dead leaves and various other types of plant litter, and the bark surface of living trees are generally considered as the primary microhabitats for myxomycetes (plasmodial slime molds). However, these organisms also can be found in a number of other special microhabitats. In tropical forests, one example of such a microhabitat is represented by the surface of living and dead lianas. During the 2002 field seasons, samples of lianas were collected from (1) study sites at several localities in eastern, central and southwestern Puerto Rico, (2) a site approximately 45 km north of the city of Iquitos in eastern Peru, and (3) a number of sites in northern Queensland, Australia. Fifty-nine of the 68 (87%) moist chamber cultures prepared with these samples yielded some evidence (either plasmodia or fruiting bodies) of myxomycetes, and at least 27 species representing 13 genera were identified. This total included a number of species (e.g., *Arcyria cinerea*, *Diderma hemisphaericum*, *Didymium iridis*, *Didymium squamulosum*, *Physarum compressum*, and *Physarum pusillum*) that are common in other types of aerial microhabitats in tropical forests as well as several other species (e.g., *Ceratiomyxa fruticulosa*, *Stemonitis fusca* var. *nigrescens*, and *Willkommlangea reticulata*) not usually recorded from such microhabitats. *Poster*

*NIEVES-RIVERA, ANGEL[1], TATTAR, TERRY[2], RYVARDEN, LEIF[3], ZAIDI, BAQAR[1], LODGE, D. JEAN[4], and WILLIAMS, JR., ERNEST[1]. [1]Dept. of Marine Sciences, Univ. Puerto Rico, Mayaguez PR 00681-9013 USA. [2]Dept. Microbiology, Univ. Massachusetts, Amherst, MA 01003-5720 USA. [3]Botany Dept., Univ. Oslo, Blindern, Oslo, N-0316 Norway. [4]USDA-Forest Service, Forest Products Laboratory, Luquillo, PR 00773 USA. anieves@coqui.net **Lignicolous basidiomycetes in mangroves of Puerto Rico.**

Manglicolous (mangrove-loving) fungi have been extensively studied worldwide, but little is known about mangrove mycobiota on most Caribbean islands including Puerto Rico. Lignicolous basidiomycetes were surveyed in four sites on the southwestern coast of Puerto Rico. Basidiomycetes were collected from April 2001 through April 2002. Thirteen species were identified: *Coriolopsis* sp., *Dacryopinax spathularia*, *Hexagonia hydnoides*, *Gloeophyllum striatum*, *Lentinus* cf. *crinitus*, *Marasmiellus* sp., *Phellinus* sp., *Pycnoporus sanguineus*, *Schizophyllum commune*, *Stereum* cf. *bicolor*, *Trametes* cf. *elegans*, *Trichaptum* aff. *biformis*, and *Tyromyces* cf. *chioneus*. In the Boqueron Wildlife Refuge, *Tyromyces* cf. *chioneus* was found on substrata subject to immersion once or twice a year by brackish water (salinity ± 14 ppt). The most common species were *Dacryopinax spathularia*, *Gloeophyllum striatum*, *Schizophyllum commune*, and *Trichaptum* aff. *biformis*. The Polyporaceae/Coriolaceae had the greatest number of species in Puerto Rican mangrove forests. The preferred substratum was decomposing *Rhizophora mangle*. All specimens collected grew above the tide line in upper portions of trees (> 0.5 to 30 m). Basidiomycetes appear to be important mangrove wood decomposers in Puerto Rico and are more diverse than previously recorded. *Poster*

*NORVELL, LORELEI[1], PILZ, DAVID[2], DANELL, ERIC[3], and MOLINA, RANDY[4]. [1]Pacific Northwest Mycology Service, Portland, OR 97229-1309 USA. [2]Forest Science, Oregon State Univ., Corvallis, OR 97331-5752 USA. [3]Museum of Evolution, Uppsala Univ., Uppsala, Sweden. [4]USDA Forest Service, PNW Research Station, Forestry Sciences Lab, Corvallis, OR 97331-4401 USA. llnorvell@pnw-ms.com **Ecology and management of commercially harvested chanterelle mushrooms.**

The "chanterelle" mushroom harvest, now a multimillion dollar industry in the Pacific Northwest, is the subject of a recent USDA-FS research handbook by Pilz, Norvell, Danell, & Molina (2003). The authors provide a comprehensive synthesis of information on chanterelles, craterelles, and other edible cantharelloid mushrooms for scientists, forest managers, commercial harvesters, and recreational mushroom pickers. A comprehensive bibliography of scientific papers

and field guides accompanies an overview of all chanterelle species, international chanterelle markets, chanterelle biology, and advances in chanterelle cultivation. Field keys to chanterelles and look-alikes are provided for the generalist. Pacific Northwest species discussed in detail include *Cantharellus formosus* (Pacific golden chanterelle — and the Oregon state mushroom), *C. cibarius* var. *roseocanus* (rainbow chanterelle), *C. subalbidus* (white chanterelle), *Craterellus cornucopioides* (horn of plenty), *Cr. "neotubaeformis"* (winter craterelle), *Gomphus clavatus* (pig's ears), and *Polyozellus multiplex* (blue chanterelle). Results from recent scientific investigations are outlined with regional forest management issues addressed. Suggestions are made for future research and monitoring needed to sustain this prized forest resource. *Poster*

OLLER, ANNA. Dept. Biology, Central Missouri State Univ., Warrensburg, MO 64093 USA. oller@cmsu1.cmsu.edu
***Aureobasidium pullulans* (Deuteromycota): Molecular characterization using the polymerase chain reaction.**

The polymorphic fungus *Aureobasidium pullulans* inhabits environmental ecosystems, such as apple tree leaves and salt marshes, and man-made habitats such as ventilation ducts and walls of buildings. The fungus has been implicated in opportunistic infections of the respiratory and urinary tracts, as well as allergies. Determination of the morphological stages involved in plant and animal cell adherence are being pursued. The development of a rapid molecular technique to determine fungal disease in humans will enhance patient therapies. Genomic DNA from normal and mutated *Aureobasidium pullulans* strains, as well as *Aspergillus niger, Candida albicans, Mucor ruoxii, Nocardia asteroides, Penicillium notatum, Rhizopus nigricans,* and *Saccharomyces cerevisiae,* was isolated using standard protocols. A random amplified polymorphic DNA (RAPD) primer was used in the polymerase chain reaction (PCR) and results were observed via electrophoresis and photographed. *Aureobasidium pullulans* showed a distinct banding pattern different from any of the other fungi. Further PCR analyses of the fungal results will be presented. *Poster*

*O'REILLY, BERNADETTE and VOLK, THOMAS. Dept. Biology, Univ. Wisconsin-La Crosse, La Crosse, WI 54601 USA. oreilly.bern@students.uwlax.edu **Time-lapse and epifluorescence microscopy of hyphal interactions of *Armillaria* with its pathogen *Entoloma abortivum*.**

Armillaria is a common fungal root rot tree pathogen that produces abundant fruiting bodies (honey mushrooms) and rhizomorphs. This fungus, in turn, has a fungal pathogen *Entoloma abortivum.* Until very recently the pathogenesis was thought to occur in the other direction. We now know that *E. abortivum* has the potential to act as a biological control agent. However, little is known about how *E. abortivum* parasitizes *Armillaria*. Is it physically controlling *Armillaria* by wrapping around it? Are cell contents being removed from *Armillaria*? Are *Entoloma* hyphae invading *Armillaria* hyphae? Since the hyphae of the two species are very difficult to distinguish from one another, we used a vital fluorescent dye (DAPI) to label one of the species. The drawback of this method is that because DAPI is light sensitive, its fluorescence can be viewed only once. To get around this problem, time-lapse photographs were taken on colonies that did not contain the dye. Once the interaction was observed, DAPI was added to one species, and the hyphae were viewed using an episcopic-fluorescence microscope. Combined with the time-lapse photography, this dye allowed us to distinguish between *Armillaria* and *Entoloma* hyphae when they merged in a divided Petri dish. Photographs revealing the physical interactions of the two species will be presented. *Poster*

*OVERTON, BARRIE[1], STEWART, E. L.[1], and SAMUELS, GARY[2]. [1]Dept. Plant Pathology, Pennsylvania State Univ., State College PA 16802 USA. [2]USDA-ARS, SBML, 10300 Baltimore Ave., Beltsville MD 20705 USA. beo102@psu.edu **Systematics of *Hypocrea* with effuse stromata and anamorphs in *Trichoderma* Section *Hypocreanum*.**

Hypocrea that have effused stromata and anamorphs referable to *Trichoderma* section *Hypocreanum* Bissett are the focus of my dissertation research. It has commonly been accepted that species in section *Hypocreanum* share plesiomorphic characters and that the grouping of these forms is not monophyletic. Previously published molecular results by our laboratory have indicated that taxa with *Hypocreanum* anamorphs form a monophyletic group, the limits of which are not known. The objectives of my disseration were to (1) determine whether *Hypocrea* with effuse stromata and anamorphs in section *Hypocreanum* form a monophyletic lineage; and (2)identify species of *Hypocrea* using phylogenetic species recognition. Morphological data, partial sequences from 3 regions; ITS1-5.8S-ITS2, tef-1 alpha, and RPB2 were generated and analyzed. *Hypocrea* with effused stromata containing pseudoparenchymatous tissue and anamorphs referable to *Trichoderma* section *Hypocreanum* form a monophyletic lineage. *Hypocrea* with hyphal stromata and *Hypocreanum* anamorphs, such as *H. avellanea* are not derived within the *Hypocreanum* clade. Data generated from RPB2 and the large exon of tef-1 alpha provided greater species level variation and better alignments than ITS. Phylogenetic species recognition provided a unique opportunity to solve nomenclatural problems surrounding the application of the name *H. citrina*. *Contributed Presentation*

*PAN, JEAN and CLAY, KEITH. Dept. Biology, Indiana University, Bloomington, IN 47405 USA. jepan@umn.edu ***Epichloe glyceriae* infection and carbon translocation in the grass *Glyceria striata*.**

Physiological integration, or resource translocation, is the movement of resources from one part of a clonal plant to another part. Changes in resource translocation patterns may affect clonal growth patterns and ramet establishment. We have shown that infection by the fungus *Epichloe glyceriae* causes greater clonal growth in its host *Glyceria striata*. Because *Epichloe* relies completely on *Glyceria* for resources, fungal infection is likely to alter resource translocation and clonal growth patterns. To test this hypothesis, we compared the growth of intact and severed stolons and carbon distribution within stolons. Biomass did not differ between intact and severed stolons, regardless of host infection status. Intact stolons had more daughter ramets than severed stolons in disinfected plants, but the number of daughter ramets did not differ between intact and severed stolons of infected plants. Carbon distribution patterns, as determined from 14^{o}C, indicated that assimilate movement was more extensive for infected stolons. The labeled leaf retained more assimilate in disinfected stolons. Overall, we found that pathogen infection changed physiology and resource movement. However, these data suggest that changes in carbon sink dynamics were not responsible for differences in host growth pattern and that *Epichloe* infection was not a substantial carbon drain on host plants. *Contributed Presentation*

*PARRENT, J.L., MORRIS,W.F. and VILGALYS, R. Box 90338, Durham, NC 27708 USA. jlp13@duke.edu **Ectomycorrhizal fungal community response to chronic nitrogen addition at Harvard Forest, MA.**

Anthropogenic N deposition alters soil chemistry and enhances N availability in naturally N-limited temperate forests. Changes to the

soil chemical environment and to the supply and demand of nutrients may profoundly affect EMF communities upon which trees normally depend for mobilization of limiting nutrients. Although N deposition rates in forests of northeastern USA are among the world's highest, this study is the first to investigate how EMF communities in this geographic region respond to chronic N fertilization. My study site is located in Harvard Forest, MA, and is part of a 15 yr Chronic N addition experiment. Roots were collected from control and N-amended (5 g N/m2/yr) red pine stands. EMF species were identified using ITS sequences. Dominant EMF associates at Harvard forest include *Piloderma, Russula, Lactarius, Tylopilus*, and *Clavulina* species. Significant results from this study suggest 1) community diversity declines with N addition, and 2) community structure differs between the two stands, with strong differences in relative proportions of EMF species observed between the two stands including those species with the highest relative frequencies. Additional experiments are needed to determine the ecological mechanisms responsible for EMF community shifts, and ultimately to predict how forests will respond as N concentrations in these ecosystems increase. *Poster*

*PEEVER, TOBIN [1], SALIMATH, SHANMUKH[1], SU, GUOPING[1], KAISER WALTER[2] and MUEHLBAUER, FRED[3]. [1]Dept. Plant Pathology, Washington State Univ., Pullman, WA, USA. [2]USDA-ARS, Western Regional Plant Introduction Station. [3]USDA-ARS Grain Legume Genetics and Physiology Unit, Washington State Univ., Pullman, WA, USA. tpeever@wsu.edu **Historical and contemporary population structure of *Ascochyta rabiei* (teleomorph: *Didymella rabiei*) in the US Pacific Northwest.**

The historical and contemporary population genetic structure of *Ascochyta rabiei*, the causal agent of Ascochyta blight of chickpea, in the US Pacific Northwest (PNW) was determined using genetically characterized sequence-tagged microsatellite (STMS) and mating type markers. Data from three historical samples of the fungus indicated that a single genotype of *A. rabiei* (*MAT1-1*) was introduced into the PNW in 1983 and was responsible for the first report of Ascochyta blight of chickpea in the United States. Several additional STMS alleles and the alternate mating type allele (*MAT1-2*) were detected in a sample from the same location in 1984. In samples from 1987, many additional genotypes were detected and all the STMS alleles currently found in the PNW were present. Contemporary subpopulations (sampled in 2000) were moderately genetically differentiated suggesting some restriction on gene flow among subpopulations and/or genetic drift within subpopulations. Subpopulations present at the USDA-ARS resistance screening nursery were significantly differentiated from those in commercial chickpea fields. The widespread occurrence of the sexual stage of the fungus (*Didymella rabiei*) and the results of multilocus gametic disequilibrium and mating type ratio tests indicate that the fungus is randomly mating in the PNW. *Contributed Presentation*

*PERRY, BRIAN, HANSEN, KAREN, and PFISTER, DONALD. Harvard Univ. Herbaria, 22 Divinity Ave., Cambridge MA 02138 USA. bperry@oeb.harvard.edu **Phylogenetic relationships in the Pyronemataceae.**

Of the families of the Pezizales, the Pyronemataceae (including Otideaceae) remains the least well studied. The family has been considered a default family for pezizalean taxa with uninucleate spores and iodine negative asci, which lack distinguishing anatomical characters by which they can be assigned to other families. Standard treatments of the Pyronemataceae include taxa with a wide diversity of both morphological features and nutritional modes. Recent molecular phylogenetic studies indicate that the Pyronemataceae is part of a lineage composed of Sarcosomataceae, Sarcoscyphaceae, Ascodesmidaceae, and Glaziellacae. The goal of this investigation is to generate a multiple gene phylogeny of the Pyronemataceae and closely related taxa using sequence data from three unlinked nuclear loci (large subunit rDNA, RNA polymerase II and beta-tubulin) to resolve relationships of the family and genera, and infer evolutionary patterns of morphological, cytological and ecological characters. Initial results based on the nuclear large subunit rDNA sequence data will be presented and discussed. *Poster*

*PETERSON, KRISTIN and PFISTER, DONALD. Dept. Organismic & Evolutionary Biology, Harvard Univ., 22 Divinity Ave., Cambridge, MA 02138 USA. kpeterson@oeb.harvard.edu **Molecular phylogeny of *Cyttaria* (Cyttariales, Ascomycota).**

Species of *Cyttaria* are obligately parasitic on species of *Nothofagus* (the southern beech). *Cyttaria* species have a unique morphology that provides little insight into their phylogenetic affinities. Their morphology, habit, and association with hosts that have a Gondwanan distribution and well preserved fossil record have inspired many hypotheses regarding the origin and radiation of *Cyttaria* species. We are in the process of sequencing nuclear ribosomal DNA to elucidate these events. The genus *Cyttaria* seems to be closely related to a group that includes certain Erysiphales, Helotiales, and Rhytismatales species. Within *Cyttaria*, we have found that there are three lineages: species of two lineages exclusively parasitize members of *Nothofagus* subgenus *Nothofagus*, while species of the third lineage exclusively parasitize members of *Nothofagus* subgenus *Lophozonia*. Subgenus *Nothofagus* is found only in South America (Argentina and Chile); subgenus *Lophozonia* is found there as well as in Australasia (Australia, Tasmania, and New Zealand). Our evidence so far indicates that two cospeciation events between host and parasite produced a non-monophyletic South American *Cyttaria* species grade and a monophyletic Australasian species clade. In other instances, extinction and speciation of the parasite, but not the host, seem to explain the modern distribution of *Cyttaria* species. *Poster*

*PETERSEN, RONALD and HUGHES, KAREN. Botany Dept., Univ. Tennessee, Knoxville, TN 37996 USA. repete@utk.edu ***Lentinellus* (Russulales): recognition of North Temperate agaricoid taxa.**

Traditionally, the name *Lentinellus omphalodes* has been used to represent a stipitate, agaricoid taxon, thought to be distributed across the North Temperate Zone. Results from sexual compatibility experiments and a phylogenetic reconstruction based on ITS sequences, show that several species must be accepted. Four widely distributed taxa, *L. micheneri*, *L. subaustralis*, *L. flabelliformis* and *L. tridentinus*, are illustrated and their geographic ranges described. Other similar but less widely distributed taxa are mentioned. *Contributed Presentation*

PETERSON, STEPHEN. National Center for Agricultural Utilization Research, USAD - Agricultural Research Service, 1815 North University Street, Peoria, Illinois 61604 USA. peterssw@ncaur.usda.gov **Multi-locus phylogenetic analysis of *Aspergillus* section *Circumdati*.**

Peterson (2000) analyzed relationships in the "*A. ochraceus* group" (Raper & Fennell, 1965) using a short segment of large subunit rDNA. On the basis of that analysis, several species were removed from the section and some potential synonymies were detected. To determine if these closely related isolates are separate phylogenetic species, additional sequences were obtained from the ITS region,

mitochondrial small subunit rDNA, the calmodulin gene, and translation elongation factor 1 alpha. Included in one lsu rDNA clade were isolates of *A. ostianus, A. petrakii, A. melleus*, and *A. ochraceus*. In multi-locus analysis, *A. ochraceus* and *A. petrakii* isolates are indistinguishable, and thus synonymy is supported. The distinctions of *A. ochraceus, A. ostianus* and *A. melleus* are substantiated by the congruence of trees from multiple loci. *A. insulicola* and *A. ochraceopetaliformis*, with identical lsu rDNA sequences, show single base differences at each of the additional loci, and these taxa are retained tentatively as distinct species; additional isolates of these are needed to clarify their relationship. *A. bridgeri* and *A. sclerotiorum* were identical in lsu rDNA but differ at other loci suggesting that these are sister species. Two isolates *phenotypically* identified as *A. bridgeri* are genetically distinct and may represent undescribed species. *Poster*

*PHILLIPS, ANITA. 10801 University Boulevard, Manassas, VA 20110 USA. phillips@atcc.org **Special Collections at the American Type Culture Collection.**

The American Type Culture Collection is a global nonprofit bioresource center that provides biological products, technical services, and educational programs to industry, government, and academic organizations around the world. ATCC Special Collections represent collaborations with top research institutions to provide valuable research tools to the scientific community. Each collection has a distinct emphasis in the type of materials it offers: a focus on one field or application; a spectrum of materials from one source; unique or exclusive availability. Institutions participating in forming Special Collections benefit from ATCC's unique capabilities in custom storage and distribution services for their valuable materials. Advantages to partnership with ATCC include: ATCC scientists as Co-Principal Investigators on grant proposals offering the service of ATCC's professional grant writing staff; ATCC biologists can work on research projects or subcontracts written into grant proposals; ATCC scientists can contribute expertise in systematics and phylogenetics for a wide diversity of organisms; ATCC can safely protect and preserve organisms that are particularly difficult to maintain in culture, and resupply these organisms to the investigator; ATCC can distribute cultures and DNA with the legal and regulatory framework to protect patented organisms; ATCC can distribute cultures and DNA with the legal and regulatory framework to protect the ownership rights of foreign nations. *Poster*

PLUMRIDGE, ANDREW[1], WATSON, ADRIAN[1], LOWE, KENNETH[1], HESSE, STEPHAN[2], STRATFORD, MALCOLM[3], and ARCHER, DAVID[1] [1]School of Life and Environmental Sciences, Univ. Nottingham, Nottingham, NG7 2RD, UK. [2]Dept. Biophysics, Wageningen Univ., Dreijenlaan 3, 6703 HA Wageningen, the Netherlands. [3]Microbiology Dept., Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, Uk. plxap@nottingham.ac.uk **Weak acid stress in *Aspergillus niger*.**

Weak acid preservatives, such as sorbic or benzoic acids, together with the acidulant, acetic acid, are used to protect food against microbial spoilage. Unfortunately, some filamentous fungi, including *A. niger*, are extremely tolerant to weak acids. Thus, the effects of sorbic, benzoic or acetic acid at pH 4.0 on spore germination and mycelial growth by *A. niger* have been studied. Sorbic and benzoic acid (at 3.0 mM) effectively delayed both the onset of spore germination and subsequent mycelial growth, although cell yields after 96 hours of incubation were comparable to controls. Acetic acid at 3.0 mM had no inhibitory activity against either spore germination or subsequent mycelial growth. Both sorbic and benzoic acid, but not acetic acid, at 3.0 mM, completely inhibited the growth of *A. niger* when a mycelial inoculum was used. Studies using different spore inoculum sizes showed that the minimum inhibitory concentration of weak acids increased as the size of the spore inoculum increased. These results show that sorbic and benzoic acids have growth-inhibitory effects on *A. niger* that are influenced by the size and type of the inoculum. In addition, NMR is being used to measure the impact of weak acids on intracellular pH. *Poster*

*PORRAS-ALFARO, ANDREA and BAYMAN, PAUL. Dept. Biologia, Univ. de Puerto Rico-Rio Piedras, PO Box 23360, San Juan, PR 00931 USA. re026983@rrpac.upr.clu.edu **Specificity of *Vanilla planifolia* and *V. poitaei* for mycorrhizal fungi.**

Vanilla is an orchid of great commercial importance, but as in other tropical orchids, not much is known about its associations with mycorrhizal fungi. The hypothesis is that different species have the same mycorrhizal fungi and similar patterns of infection. Roots of adult plants were collected from forests in Puerto Rico. Frequency of mycorrhizal infection and the appearance of pelotons were compared among different species of *Vanilla*. Fungi were identified by sequencing the nuclear ribosomal ITS. Levels of mycorrhizal infection varied greatly among roots and plants. Roots of *Vanilla planifolia* and *V. poitae*i had similar frequencies of mycorrhizal zones along the length of the roots, but transverse sections had higher densities of pelotons in *V. poitaei* than in *V. planifolia*. Most of the pelotons observed in both species of *Vanilla* were degraded. *Tulasnella* was the most common genus found. In contrast, previous studies have shown that *Ceratobasidium* is the most common mycorrhizal fungus in epiphytic orchids in Puerto Rico. Previous research on the importance of mycorrhizal fungi for orchids has focused on seed germination; not much is known about their importance for adult plants. Identifying the fungi and their specificity is essential for understanding the functional basis of the relationship. *Poster*

*RAJA, HUZEFA and SHEARER, CAROL. Dept. Plant Biology, Univ. Illinois at Urbana-Champaign, 505 South Goodwin Avenue, Urbana, IL 61801 USA. raja@life.uiuc.edu **Freshwater lignicolous meiosporic and mitosporic euascomycetes from the Great Smoky Mountains National Park.**

As part of the All-Taxa Biotic Inventory of the Great Smoky Mountains National Park, we are investigating the freshwater lignicolous meiosporic and mitosporic euascomycetes. Submerged wood was collected in July 2002 and January 2003 from freshwater habitats at elevations ranging from 1000 to 4000 ft. Samples were incubated in moist chambers and examined periodically for the presence of fruiting bodies. Thirty meiosporic, and twenty- two mitosporic euascomycetes have been reported thus far. *Helicoon gigantisporum*, *Helicosporium gigasporum*, *Pachyella depressa*, and *Torrentispora fibrosa* are reported from North America for the first time. *Cyanoannulus petersenii*, a new genus and species in the Annulatascaceae is reported. *Annulatascus triseptatus*, *Acrogenospora sphaerocephala*, *Pseudoproboscispora caudae-suis*, *Sporoschisma saccardoi*, and *Submersisphaeria aquatica* were the most frequently collected species. Results suggest that species composition in the Great Smoky Mountains is similar to that found in the Austral/Asian tropics and subtropics. A possible historic biogeographic connection with the Austral/Asian continent is discussed, and new and noteworthy species are illustrated. *Poster*

*READ, NICK[1], KALKMAN, ERIC[1], ATKINSON, HELEN[1], HICKEY, PATRICK[1], and ROBERSON ROBERT[2] [1]Fungal Cell Biology Group, Inst. Cell and Molecular Biology, Univ. Edinburgh, Edinburgh, EH9 3JH, UK. [2]Dept. Botany, Arizona State Univ., Tempe, Arizona 85287 USA. Nick@fungalcell.org **Endocytosis in filamentous fungi.**

Endocytosis has been well characterized in budding yeast and animal cells, and to a lesser extent in plant cells. In contrast, much less is known about this process in filamentous fungi although it is likely to have important roles in membrane recycling, membrane degradation, and the uptake of signal molecules. This presentation will provide evidence from studies on *Neurospora crassa* and *Magnaporthe grisea* which support the occurrence of endocytosis in filamentous fungi. This evidence is: (1) Membrane-selective markers of endocytosis (FM1-43 and FM4-64) are internalized. (2) Markers of fluid-phase endocytosis (Lucifer Yellow and FITC-dextran) are internalized. (3) Internalization of endocytosis markers is active and not by diffusion because it is reversibly inhibited by azide or cold treatment. The best candidate for endocytic vesicles are actin-coated microvesicles called filasomes. (4) Internalization of FM4-64 is actin-mediated because it is inhibited by Cytochalasin D. (5) The *Neurospora* genome encodes a complex endocytic protein machinery. *Poster*

*READ, NICK[1], ZELTER, A.[1], KOZLOVA-ZWINDERMAN, O.[1], NELSON, G.[1], BENCINA, M.[2], COLLIS, A.J.[1], and ALTENBACH, K.[1] [1]Fungal Cell Biology Group, Inst. Cell and Molecular Biology, Univ. Edinburgh, Rutherford Building, Edinburgh, EH9 3JH, UK. [2]Laboratory for Biotchnology and Industrial Mycology, National Inst. Chemistry, Hajdrihova 19, SI-1000 Ljubljana, Slovenia. Nick@fungalcell.org
Measuring the calcium message in *Neurospora* and *Aspergillus*.

We have made a thorough BLAST analysis of the calcium-signalling proteins encoded in the *Neurospora crassa* genome. Our results indicate that *Neurospora* possesses a complex calcium signalling machinery with interesting differences when compared with that in animals and plants. We have developed the aequorin method as an easy and routine method for calcium measurement in living hyphae. High levels of aequorin expression were obtained in *Neurospora* and *Aspergillus* by codon optimisation of the aequorin gene. We have found a range of external stimuli (e.g. mechanical perturbation and hypoosmotic shock) produce transients in cytosolic free calcium with unique signatures, which are highly reproducible and robust under a wide range of environmental conditions. This is consistent with the idea that each calcium signature encodes unique signal transduction information, which can be decoded to produce specific cellular responses. An analysis of cross-talk between calcium and cAMP signalling has indicated that calcium channels are regulated by cAMP-mediated, protein kinase A (PKA)-dependent phosphorylation. Our results further suggest that PKA-dependent phosphorylation increases cytosolic fee calcium to induce a polar to apolar shift in hyphal morphology. Recent results with imaging calcium in living cells expressing calcium-sensitive cameleon FRET probes will also be described. *Symposium Presentation*

ROBERSON, ROBERT. Dept. Plant Biology, Box 871601, Arizona State Univ., Tempe, AZ 85287-1601 USA. Robert.Roberson@asu.edu
The many faces of the Spitzenkorper: towards understanding structure and function.

Filamentous fungi have evolved one of the most efficient means of polarized growth through the generation of hyphae. 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. As noted by G. W. Gooday, "For the fungal hypha, life is at the apex." Indeed, cytological studies, and more recently molecular studies, of hyphal tip growth have placed great emphasis on the apical structure known as the Spitzenkorper. The Spitzenkorper appears to have evolved only in the filamentous fungi where it is present in all members of the Basidiomycota and Ascomycota, except for the yeasts. Among the lower fungi, Spitzenkorper have been identified only in *Allomyces* (Chytridiomycota). Though progress is being made in better understanding the cell and molecular biology of the Spitzenkorper, its precise function(s) in hyphal growth remains an important unanswered question. In this presentation, the state-of-the-knowledge concerning Spitzenkorper biology will be reviewed. New data revealing the three-dimensional organization of structurally and biochemically important components obtained using transmission electron microscopy, immunoelectron microscopy and electron tomography will be presented and discussed. *Symposium Presentation*

ROCA, GABRIELA[1], JACOBSON, DAVID[2], HICKEY, PATRICK[1], ARLT, JOCHEN[1], GLASS, LOUISE[2] and *READ, NICK[1] [1]Inst. Cell and Molecular Biology/COSMIC, Univ., Edinburgh UK. [2]Dept. Plant and Microbial Biology, Univ. California, Berkeley, CA, USA. Nick@fungalcell.org **Hyphal fusion in *Neurospora crassa*.**

Mycelial morphogenesis consists of three integrated processes: hyphal tip extension, branching and fusion. Of these hyphal fusion (anastomosis) is the least understood and is the focus of this presentation. Hyphal fusion, by networking hyphae, is important for intrahyphal communication, translocation of water and nutrients, and general homeostasis within a colony. It is also important for parasexuality and self/non-self recognition between fungal individuals. Using live-cell imaging with confocal microscopy, we have analysed the process of hyphal fusion in growing colonies of *Neurospora crassa* stained with the membrane-selective dyes, FM4-64 and FM1-43, and with a strain of *N. crassa* expressing nuclear-targeted GFP. Time-lapse imaging has illustrated the dynamics of hyphal growth, branching and fusion during the pre-contact, contact and post-contact stages in mature colonies and between young germlings. Live-cell imaging is also being used to characterize a number of mutants which are unable to undergo hyphal fusion. Finally, we have developed a novel experimental technique that allows whole conidial germlings to be captured with laser tweezers and to be moved relative to other cells. This non-invasive experimental approach is being used to demonstrate the production of chemoattractant signal molecules that diffuse between cells. *Poster*

*ROMAINE, PETER, SCHLAGNHAUFER, CARL and STONE, MICHELLE. Dept. Plant Pathology, Pennsylvania State Univ., University Park PA16802 USA. cpr2@psu.edu ***Agrobacterium*-mediated transfer of DNA to fruiting body tissue of *Agaricus bisporus*.**

We have devised a highly effective gene transfer method for the button mushroom, *Agaricus bisporus*, involving *Agrobacterium*-mediated delivery of DNA to fruiting body tissue. Transformation was carried out using bacterial strain AGL-1 carrying binary plasmid vector pBHg. pBHg contains the hygromycin resistance (*hph*) gene controlled by the *A. bisporus* glyceraldehyde 3-phosphate dehydrogenase gene promoter and situated between the *Agrobacterium* T-DNA border sequences. Transformation efficiencies (TE's) of 40-100%, measured by the fraction of the tissue pieces expressing the *hph* gene, were obtained by pre-induction of the bacterium with acetosyringone for 2 to 3 hr at 24°C and co-cultivation of the bacterium and fruiting

body tissue for 3 to 4 days at 18-26°C. For co-cultivation, higher TE's were obtained using the gill tissue (ca. 67%) rather than the spongy tissue (ca. 38%) of fruiting bodies. TE's of ca. 90% were observed using gill or spongy tissue of a sporeless strain. Transformed colonies developed on a hygromycin-amended selection medium after 7 to 28 days of incubation. Southern blot analysis revealed that ca. 75% of the transformants contained one copy of the *hph* gene integrated randomly in the genome. Our method represents a facile tool for introducing genes into *A. bisporus*, and might be applicable to other fungi bearing fleshy fruiting bodies. *Poster*

*RYDHOLM, CARLA[1], MITCHELL, THOMAS[2], and VILGALYS, RYTAS[1]. [1]Dept. Biology, and [2]Dept. Molecular Genetics and Microbiology, Duke Univ., Durham NC 27708. clr@duke.edu **Is local adaptation present in the pan-global pathogenic mold *Aspergillus fumigatus*?**

Aspergillus fumigatus is a ubiquitous, ascomycete mold. This species exists on all continents, grows at temperatures ranging from 10 to 55°C, and persists as both a soil saprobe and an opportunistic pathogen of immunocompromised patients. Surprisingly, little information is known about the evolutionary processes and recent evolutionary history of this highly successful pathogenic species. Local adaptation is expected as *A. fumigatus* occupies a multitude of varied and extreme environments, and is haploid. Selective sweeps may occur which result in populations with limited genetic variation that are very different from other populations. However, other characteristics such as its highly dispersive airborne conidia, asexual nature and limited genetic variation indicate that *A. fumigatus* could be a recently emerged "homogeneous" clone. This study used SNPs and AFLP markers to examine multiple strains from geographically and ecologically diverse sites for evidence of a locally adapted versus a homogeneous clonal population structure. A global sampling of environmental and clinical strains was also analyzed in a phylogeographical framework. These preliminary results establish the basis for further experimental approaches to investigate the evolution, adaptability, and success of the species *A. fumigatus*. *Poster*

*RYDHOLM, CARLA[1], MITCHELL, THOMAS, MONCALVO, JEAN MARC[2], and VILGALYS, RYTAS[1]. [1]Dept. Biology, Duke University, Durham, NC 27708 USA. [2]Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, and Dept. Botany, Univ. Toronto, Toronto ON Canada. **Concordance between phylogenetic and biological species for the red polypore genus *Pycnoporus*.**

Pycnoporus is a globally distributed genus of red polypores. On the basis of intersterility tests and morphological evidence, Nobles and Frew (1962) concluded that three biological species are present in this group, and that each species has a distinctive, albeit broad, distribution range. The three species have intergrading morphological characters and overlapping distributions. We used molecular phylogenies for two loci to test for evidence of gene flow and to estimate divergence times. Ninety geographically diverse strains of *Pycnoporus*, including reference strains from Nobles' and Frew's work were sequenced at the rDNA ITS locus, and a smaller subset at the EF1-alpha gene region. Both gene phylogenies agree with Nobles' and Frew's delimitation of three main groups. Statistically significant evidence for limited gene flow and several instances of genetic recombination between *P. sanguineus* and *P. coccineus* suggest that recent hybridization has occurred within this species complex. *Contributed Presentation*

SAENZ, GREGORY[1], JACOBSON, DAVID[2], POWELL, AMY[1], DVORACHEK, WILLIAM[1] and NATVIG, DONALD[1]. [1]Dept. Biology, Univ. New Mexico, Albuquerque NM 87131 USA. [2]Dept. Biological Sciences, Stanford Univ., Stanford CA 94305 USA. dnatvig@unm.edu **Multiple phylogenetic and reproductive groups among pseudohomothallic isolates identified as *Neurospora tetrasperma*.**

Isolates of *Neurospora* with four ascospores per ascus are heterokaryotic for mating type (*mat A + mat a*) and are therefore self-fertile. This life cycle, termed pseudohomothallism, is in contrast with that of truly heterothallic species in the genus, which produce eight single-mating-type ascospores. Pseudohomothallic isolates form a monophyletic group and invariably are designated *N. tetrasperma*. Our previous work demonstrated that *N. tetrasperma* at least occasionally outcrosses in nature. The current study began as an attempt to assess the level of outcrossing employing isolates from a single 5-ha field in Louisiana. Results suggest, however, that the 14 isolates examined represent three separate phylogenetic groups rather than a single population of interbreeding individuals, a conclusion strongly supported by analysis of three separate genes, *frq*, *sod-2*, and *pdx-2*. In laboratory crosses, one of the three lineages was reproductively isolated, while the other two were part of a single reproductive group, which also included isolates from other sites. Moreover, reproductive isolation was observed between the two most closely related lineages. The results indicate that *N. tetrasperma sensu lato* actually includes multiple phylogenetic and biological species and that phylogenetic differentiation can precede the development of genetic barriers to sexual reproduction. *Poster*

SCHERRER, SANDRA[1], RAMOS, CHRISTINE[2], and *MAY, GEORGIANA[2]. [1]ETH, Switzerland; [2]Dept. of Ecology, Evolution, and Behavior, Univ. Minnesota, St. Paul, MN55108 USA. gmay@tc.umn.edu **Variation and recombination at the *Ustilago maydis b* locus.**

How are a large number of alleles generated and maintained at the *b* locus in populations of *Ustilago maydis*? Sequence was generated across the hyper-variable region of mating alleles from North and South America, as well as Mexico and subjected to several molecular evolutionary analyses. The results demonstrate that most functional alleles have evolved only once, however, we also obtained evidence of historical recombination events in this region. Because the hypervariable region is known to encode mating specificity, recombination events could potentially result in novel mating specificities. The biogeographic distribution of mating alleles and the resulting model for the evolutionary history of this locus will be presented. *Contributed Presentation*

*SCHMIT, JOHN PAUL[1], SHEARER, C.A. [1], FRISCHER, M.E. [2], FOY, TARA[2], DANFORTH, J.M. [2] and WALTERS T.L. [2]. [1]Univ. Illinois, Urbana-Champaign, IL 61801 USA. [2]Skidaway Inst. Oceanography, Savannah, GA 31411 USA. **Fungal and bacterial abundance, diversity, and response to nutrient enrichment in mangrove forests.**

Due to the involvement of microbial communities in nutrient cycling, bacterial and fungal assemblages likely both reflect and control nutrient cycling in mangrove ecosystems. As part of an effort to elucidate interactions involved in nutrient cycling and stability in mangroves, the abundance and species richness of bacterial and fungal communities was investigated in mangrove peat sediments and leaf and wood litter. Studies were conducted on a mangrove island located off of Belize, in conjunction with a long-

term nutrient fertilization experiment (addition of either NO_3 or PO_4 to mangrove trees). Fungal diversity and abundance in peat sediments did not change with depth (to 30 cm). Species richness and abundance of fungi was significantly higher at the shoreline at the mangrove-ocean interface. Although bacterial abundance did not change with depth, there was a noticeable change in bacterial species with depth. Impact of fertilization on fungi and bacteria was minimal in peat sediments, although N fertilization did have a non-significant positive impact on fungal diversity and abundance. Fungal diversity and abundance was highest on freshly fallen leaves, whereas bacterial abundance increased as the leaf decayed. Wood from the areas fertilized with phosphorus supported a more diverse fungal community, whereas nitrogen fertilizer had little effect on fungi inhabiting wood. *Contributed Presentation*

*SCHOCH, CONRAD[1], YODER, OLEN[2], AIST, JAMES[3], ROBBERTSE, B., and TURGEON, GILLIAN[3]. [1]Dept. Botany and Plant Pathology, Oregon State Univ., Corvallis OR 97331 USA. [2]Diversa Corporation, 4955 Directors Place, San Diego, CA 92121 USA. [1]Dept. Plant Pathology, Cornell Univ., Ithaca NY 14653 USA. conrad.schoch@science.oregonstate.edu **Kinesin phylogenomic profiles in representative ascomycetes.**

Availability of fungal genomic sequences has enabled comprehensive comparisons of gene taxonomies. This process allows functional prediction of unknown proteins and enables discovery of novel taxon-specific proteins. To investigate the evolution of genes involved in fungal growth, we extracted complete inventories of kinesin related motor proteins from three phytopathogenic filamentous ascomycetes, *Botryotinia fuckeliana*, *Cochliobolus heterostrophus* and *Gibberella moniliformis*. These protein sequences were compared with those of the filamentous saprophyte, *Neurospora crassa* and the yeasts *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*, enabling comparisons between kinesin profiles and life style variations. We found a constant set of 10 kinesins in the filamentous fungal species, compared with smaller sets in the yeasts. The filamentous fungal kinesins fell into nine subfamilies when compared with well-characterized kinesins from other eukaryotes. These associations were investigated by disruption of the motor domains in 10 different *C. heterostrophus* kinesins. Although most mutants had no obvious defects, two strains without functional protein orthologs for conventional kinesin and *Caenorhabditis elegans* Unc-104 had restricted growth. A straight hyphal growth phenotype with abnormal branching was also observed for a protein closely related to human Kid. *Contributed Presentation*

*SCHWECKE, TORSTEN, GOETTLING, KIRSTEN, LEE, MIN-HI, and VON DOEHREN, HANS. Dept. Biochemistry and Molecular Biology, Inst. Chemistry, Technical Univ., Franklinstr. 29, 10587 Berlin, Germany. ts789@gmx.de **A nonribosomal peptide synthetase involved in siderophore biosynthesis in *Schizosaccharomyces pombe*.**

The genome sequence of the fission yeast *Schizosaccharomyces pombe* has recently been completed. The largest open reading frame encodes a protein with a deduced Mr of 560 kDa. This protein displays high sequence similarity to nonribosomal peptide synthetases (NRPSs), in particular to those responsible in fungi for the formation of siderophores, low molecular weight compounds with high affinity to Fe3+. We have undertaken detailed analyses of the NRPS, both *in silico* and *in vivo* and will report on the biosynthetic mechanism as well as the possible function of its product. *Contributed Presentation*

*SCHWECKE, TORSTEN, NEUHOF, TORSTEN, REIBER, KATHRIN, GOETTLING, KIRSTEN, LEE, MIN-HI and VON DOEHREN, HANS. Dept. of Biochemistry and Molecular Biology, Institute of Chemistry, Technical University, Franklinstr. 29, 10587 Berlin, Germany. doehren@chem.tu-berlin.de **Fungal NRPS systems.**

A survey will be given on nonribosomal peptide production in fungi, and compared to well-characterized prokaroytic production systems. The discussion on the evolution of these unique modular systems will be illustrated with penicillin and cephalosporin biosynthetic clusters in Ascomycetes. Unique fungal modules and their organization will be analysed by exploiting the biosynthesis of siderophores. Finally routes to biodiversity by natural combinatorial biology are demonstrated on peptaibols, the unique linear peptides originating from the largest fungal genes and enzymes. *Poster*

*SCHWEIGKOFLER, WOLFGANG and GARBELOTTO, MATTEO. ESPM, UC Berkeley, Berkeley CA 94720 USA. wolfgang@nature.berkeley.edu **Detection of the black stain fungus *Leptographium wageneri* var. *wageneri* from insect hosts using direct DNA amplification.**

Leptograpium wageneri var. wageneri is the causal agent of black stain root disease, a vascular wilt which seriously affects ponderosa pine (*Pinus ponderosa*) in Northern California, the Pacific Northwest and British Columbia. Spread of the disease is thought to be vectored by root feeding beetles of the genus *Hylastes* (Scolytidae), but all isolations attempts so far have failed. We developed a specific primer pair based on the ITS-region to amplify *L. wageneri* DNA directly from whole DNA extracts of the insect vectors. So far, fungal DNA was detected from six different beetle species collected during spring 2001 and 2002 using Lindgren funnel traps. Extractions from a single insect specimen can be used for a successful reaction. Sequencing of the amplified DNA fragment revealed its origin from *L. wageneri*. Further experiments are on-going to quantify the spore numbers vectored by the insects. These results show the power of PCR-aided diagnosis. *Poster*

*SCHWEIGKOFLER, WOLFGANG and GARBELOTTO, MATTEO. ESPM, UC Berkeley, Berkeley CA 94720 USA. wolfgang@nature.berkeley.edu **Detection and quantification of *Fusarium circinatum*, the causal agent of pine pitch canker, using a novel real time (RT)-PCR approach combined with a simple spore trapping method.**

Monterey pine (*Pinus radiata*), native to California and Northern Mexico, is planted for timber production worldwide on several millions of hectares. A major threat for Monterey pine production is pine pitch canker, caused by *Fusarium circinatum*. We established a novel trapping approach using filter papers in combination with a fast molecular method to detect the presence of the inoculum well before symptoms may appear on standing trees, or on material that is commercially transported. The test is based on the specific primer pair CIRC1A-CIRC4A, which amplifies a 360 bp DNA fragment in the Intergenic Spacer Region (IGS) of *F. circinatum*. Real-time (RT)-PCR was used to calculate the starting copy numbers of target sequences (= fungal spores) present in each reaction by comparing the threshold cycle (Ct) of unknown spore samples to the Ct values of previously established standards with known amounts of DNA and spores, respectively. *F. circinatum* DNA was quantified over four orders of magnitude with a detection limit of 10 pg per reaction. The filter paper-method allows for prolonged spore sampling in the field

compared to traditional traps using Petri dishes with selective medium. In addition, the mating type of *F. circinatum* spores obtained from the spore traps was determined. All samples from California analyzed so far belonged to MAT-1. *Poster*

*SEYMOUR, FABIAN, DICKINSON, MATTHEW, CRITTENDEN, PETER, AND DYER, PAUL. School of Life and Environmental Sciences, University Park, Univ. Nottingham, Nottingham, NG7 2RD, UK fabian.seymour@nottingham.ac.uk
Breeding systems in the lichen-forming genus *Cladonia*.

The majority of lichen species produce ascomata containing sexually derived ascospores, whereas only a minority forms symbiotic vegetative propagules. Sex in lichenised fungi has been assumed to equate with outcrossing, but recent evidence using DNA fingerprinting methods has demonstrated homothallism (selfing) in the crustose lichens *Graphis scripta* and *Ochrolechia parella*. In further studies, we are examining the breeding systems in species of the lichen-forming fungal genus *Cladonia* that exhibit contrasting ecological lifestyles. Specimens of *C. floerkeana*, *C. portentosa* and *C. galendezii* were collected from single locations (from Derbyshire, England; Caithness, Scotland; and Adelaide Island, Antarctica, respectively), with replicate thalli collected at spots more than 10 metres apart. Three fruiting bodies from each thallus were excised and each used to generate eight single-spore sibling progeny. These were subcultured for molecular analysis using RAPD-PCR and AFLP analyses. Results of ongoing studies will be presented indicating whether these contrasting *Cladonia* species exhibit selfing or outcrossing breeding systems. *Poster*

*SHA, YU and KAMINSKYJ, SUSAN. Dept. Biology, Univ. Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada. yus661@duke.usask.ca **Molecular and confocal characterization of the *Aspergillus nidulans* morphogenetic locus *hypA*.**

Aspergillus nidulans hypA affects hyphal morphogenesis by promoting tip growth and suppressing growth behind the tip. The temperature sensitive alleles, *hypA1* and *hypA6*, have the same structural gene mutation although they were selected from different 4-NQO mutagenized collections. Both strains had statistically similar restrictive phenotypes given the same nutritional background. Previously reported differences between these two alleles appear to have been due to *pabaA6* in one of the stains being compared. The *hypA* orthologue in *Saccharomyces cerevisiae, TRS120,* encodes a putative regulatory subunit in the TRAPP II complex that mediates Golgi traffic. *TRS120* is essential in *S. cerevisiae*, but *hypA* is dispensible in *A. nidulans*, although knockout mutants grow poorly. Confocal microscope examination of germlings grown at 42°C and stained with FM4-64 showed that both strains had weak endomembrane polarity and no obvious Spitzenkörper, which is required for polarized hyphal growth. In contrast, their microtubule cytoskeletons as examined in GFP-tagged alpha-tubulin *hypA1* and *hypA6* strains had a sparse but normal arrangement. *Contributed Presentation*

*SHAW, BRIAN[1] and MOMANY, MICHELLE[2]. [1]Program for the Biology of Filamentous Fungi, Dept. Plant Pathology and Microbiology, Texas A&M Univ., 2132 TAMU, College Station, Texas 77845, USA. Dept. Plant Biology, Univ.Georgia, Athens, GA, 30602 USA. bshaw@plantbio.uga.edu **Function of *swoA* and *swoF* genes in *Aspergillus nidulans* polar growth.**

A. nidulans swollen cell (*swo*) mutants *swoA* and *swoF* are aberrant in polarized growth when incubated at restrictive temperature. Both gene products are involved in protein modification. The *swoA* mutant grows only isotropically producing giant >50 micrometer diameter round cells with no germ tube. SwoA is a protein mannosyl transferase responsible for the first step in protein O-glycosylation. The *swoF* mutant can send out a polarized germ tube but after 10 micrometers of growth the tip ceases extension and begins to swell. SwoF is an N-myristoyl transferase responsible for attaching a 14 carbon fatty acid, myristate, to the N-terminus of a small subset of proteins, thereby increasing the affinity of the substrate to membranes. Strategies to identify the targets of these protein modifications will be discussed, including a 2D proteomics approach comparing total protein from wild type and *swoF* cells. Progress in mutant screens to identify additional swollen cell mutants will be discussed. To date at least six new single locus *swo* mutants have been identified. *Symposium Presentation*

*SILLIKER, MARGARET, TIU, ALPHONSE, and SMITH, BRENDA. Dept. Biological Sciences, DePaul Univ., Chicago IL 60614 USA. msillike@depaul.edu **Small mitochondrial DNA molecules of the plasmodial slime mold *Didymium iridis* contain mitochondrial gene sequences.**

Previously we reported on the presence of mitochondrial plasmids in *Didymium iridis* (Myxomycota, Order Physarales) and verified their cellular location by *in situ* hybridization. However, these molecules may be more properly termed sub-genomic mitochondrial DNA molecules as a preliminary sequencing project has identified sequences with high similarity to typical mitochondrial genes. On one small molecule we found sequences showing 81-91% similarity with *Physarum polycephalum* (Order Physarales) genes *nad5*, *nad7*, *cox2*, and *cox3*. While plant mitochondrial genomes show extensive recombination with the production of sub-genomic molecules, it is not a common feature of fungal or protozoan mitochondrial genomes. A linear mitochondrial plasmid found in *P. polycephalum*, that promotes mitochondrial fusion and mtDNA recombination, has been found to recombine with the mitochondrial genome of that organism, but in a site-specific manner. We have previously shown by hybridization that the *Physarum* plasmid is not homologous to *D. iridis* mitochondrial DNA or its small molecules. With completion of the sequence we will determine whether these sequences could potentially code for complete transcripts, or produce substrates for trans-splicing, however, the presence of RNA editing in *Didymium* will require further experiments to verify the role of these small mitochondrial molecules. *Poster*

*SIME, A.D.[1] and HEINSOHN, P.[2] [1]Aerobiology Laboratories, Inc. 245 Roosevelt Ave, Redwood City, CA 94061-2367 USA. [2]Microbios, 1517 Palmetto Ave, Ste. 2 Pacifica, CA 94044 USA. aeromycology@sbcglobal.net **A comparative analysis of analytical methodologies utilized in the generation of non-culturable inertial-impaction bioaerosol data for environmental mycology.**

The use of inertial impaction devices for the detection and identification of non-culturable fungi has become commonplace in the industrial hygiene profession in recent years. We collected spore trap air samples using a high volume pump and Zefon Air-O-Cell cassettes and submitted them for EMLAP laboratory analysis consisting of direct microscopy after histological staining. We then determined the effect upon the calculated number of spores per fungal taxon/cubic meter of air by changing the following dependent variables: 1) the type of objective lens used; 2) the field diameter of the microscope oculars; 3) the number of traverses counted when viewing the deposition trace; and 4) the sampling time and flow rate. We report on several

commonly used microscopes, and the changes in the calculated spore counts depending on the microscope optical set employed, and finally, the interpretation of the different data using published criteria.

*SMITH, MATTHEW, DOUHAN, GREG, and RIZZO, DAVID. Dept. Plant Pathology, Univ. Califoria, Davis, CA 95616 USA. mesmith@ucdavis.edu **A comparison between the fungal community found on ectomycorrhizal roots and the fungal community found as fruiting bodies in a mature stand of Blue Oak (*Quercus douglasii*).**

Few studies of ectomycorrhizal (EM) community ecology have examined xeric, *Quercus* -dominated woodlands and savannas, despite the abundance of these vegetation types in the Northern Hemisphere. In this study we compare the EM community from roots under a mature stand of blue oak with EM fruiting bodies from the surrounding forest. We collected epigeous, hypogeous, and resupinate EM fruiting bodies from a 500x500m plot. Specimens were identified based on morphology and ITS sequences. In March 2003 EM roots were sampled from a 32x32m hierarchical grid. DNA was extracted from 100 bulked EM roots per core. The ITS region and part of the ribosomal large subunit will be amplified and cloned; then 30 clones will be sequenced using ITS-1F. Sequences of root tips were compared with a sequence database from fruiting bodies. Among epigeous fungi, *Cortinarius*, *Lactarius*, and *Russula* were among the most commonly collected, while *Genea* and *Tuber* were among the most common hypogeous fungi. Preliminary sequence results from root tips indicate that ascomycetous fungi and fungi that produce hypogeous fruiting bodies will be most common on roots. *Contributed Presentation*

*SNETSELAAR, KAREN, CARRE JR., CARLOS, and McCANN, MICHAEL. Biology Dept., Saint Josephs Univ., 5600 City Av, Philadelphia PA 19131 USA. ksnetsel@sju.edu **Nuclear condition in *Ustilago maydis* filaments and teliospores.**

Ustilago maydis causes corn smut disease of maize. Infection is preceded by mating of compatible cells that locate each other by a pheromone system, arrest in G2 phase of the cell cycle, and fuse to form a dikaryon. Nuclei are arrested in G2 until the dikaryon enters the host tissue. Hyphae are multinucleate early in the infection process, but later regularly septate dikaryotic hyphae are observed. As in other basidiomycetes, the dikaryon is long-lived. In the smut fungi, the dikaryotic phase ends with the production of melanized teliospores with diploid nuclei. Previous studies indicated that in *U. maydis* nuclei fuse prior to development of large masses of teliospores. This suggests that the diploid nuclei might undergo mitosis prior to teliospore formation. Nuclear fusion and teliospore development occur inside tissues of the host plant and are accompanied by the production of large quantities of mucilaginous material, making these processes difficult to study with conventional histological methods. We have combined DAPI staining with a strain of *U. maydis* that produces tubulin labeled with GFP to show the presence of spindles and elongated nuclei in sporulating hyphae. Nuclear cycle events are correlated with developmental stages of the host-pathogen interaction in *U. maydis*. *Contributed Presentation*

SOLL, DAVID. Dept. Biological Sciences, 302 BBE, Univ. Iowa, Iowa City, IA 52242 USA. **The cell biology of *Candida albicans* switching.**

Johnson and co-workers first demonstrated that engineered *MTL*-hemizygous strains of *C. albicans* acquired the capacity to switch from white to opaque, and that opaque facilitated mating. These conclusions were then generalized to natural strains. In addition, the mating process in *C. albicans* was observed and reconstructed for the first time employing continuous videomicroscopy, three-dimensional reconstruction of cells, and fluorescence microscopy. Because mating depends on the opaque phenotype but the opaque phenotype is unstable at physiological temperature, we hypothesized that mating may occur outside the body. Skin appeared to be a reasonable location. It will be demonstrated that skin greatly facilitates mating, and that the cytological stages of mating are similar to that *in vitro*, but not identical. Finally, the role of selective adhesins in the mating process will be discussed. In particular, data will be presented that a major *C. albicans* adhesin is selectively expressed on the wall of the a/a shmoo and conjugation tube, that it is restricted to that part of the conjugation bridge contributed by the a/a parent cell, and that the location of the first daughter bud is restricted to that portion of the conjugation bridge harboring the adhesin. Expression of this adhesin is mating type-specific, switching regulated and induced by alpha-pheromone. *Symposium Presentation*

*SOUTHWORTH, DARLENE, PETERSEN, CAROLYN, TUGAW, HEATHER, and BERNINGHAUSEN, HAROLD. Southern Oregon Univ., Ashland, OR 97520 USA. southworth@sou.edu **Hypogeous fungi associated with *Quercus garryana* in southwest Oregon.**

Hypogeous fungi are found in diverse dry habitats as an adaptation to seasonal drought, e.g., with eucalypts in Australia and with conifers (Douglas fir and ponderosa pine) in the Pacific Northwest. Oregon white oak (*Quercus garryana*) also occurs in seasonally dry habitats and is mycorrhizal. Our primary site was Whetstone Savanna Preserve, a part of the Agate Desert in southwest Oregon. The Agate Desert, with 48 cm annual precipitation, is an alluvial fan capped with a shallow layer of clay loam over cemented hardpan and characterized by patterned ground with vernal pools. In three years of collecting, we found hypogeous fungi only in spring (April-May). Genera include the Ascomycetes *Tuber*, *Peziza*, and *Genea*, and the Basidiomycetes *Zelleromyces* and *Elasmomyces*. DNA was extracted from fruitbodies and from ectomycorrhizal tips, amplified by PCR and cut with restriction enzymes. RFLPs of mycorrhizas match several *Tuber* species -probably undescribed ones - and *Peziza quercicola*. Pocket gophers (*Thomomys* sp.) are abundant on site. These findings raise the question of the importance of small mammals in dispersal of hypogeous fungi in oak habitats and their role in mycorrhizal inoculation of oak seedlings. This research was funded by National Science Foundation Grant DEB-9981337 through the "Biocomplexity Program and Research at Undergraduate Institutions" program. *Contributed Presentation*

*STADLER, MARC[1], HELLWIG, VERONIKA[1], JU, YU-MING[2] and ROGERS, JACK[3]. Bayer Health Care, Pharma Research, POB 101709, D-42096 Wuppertal, Germany. [2]Inst. Botany, Academia Sinica, Nangkang, Taipei 11529, Taiwan. [3]Dept. Plant Pathology, Washington State Univ., Pullman, WA 99164 USA. marc.stadler@t-online.de **Affinities of *Entonaema*, *Pulveria* and *Rhopalostroma* to other Xylariaceae as deduced from chemotaxonomical studies.**

Entonaema, *Pulveria* and *Rhopalostroma* are included in the Xylariaceae, albeit the latter two genera have lost the ability to actively discharge ascospores. All three genera are believed to be related to *Hypoxylon* and *Daldinia* because of their rather similar teleomorphic and anamorphic characters. A HPLC-based secondary metabolite profiling study was conducted as to confirm these findings. Because the characteristic metabolites remained stable even in specimens collected 100 years ago, this method proved valuable to establish conspecificity of type materials with recently collected

specimens. Stromata of *Entonaema* spp. contained mitorubrin and other metabolites of *Hypoxylon*, while their metabolite profiles in culture resembled those of *Daldinia*. Stromata of *Rh. indicum* contained large amounts of binaphthyls, which are prevailing in *Daldinia* and *Hypoxylon p.p. P. porrecta* also contained binaphthlys. In addition, macrocarpones (recently found in *H. macrocarpum*) and cytochalasin-like chaetoglobosins were encountered in this species. Hence, chemotaxonomic characters reflected the adaptive radiation of Xylariaceae. Possible correlations between the evolution of morphological/anatomical characters and these findings are discussed. HPLC profiles of additional *Hypoxylon* spp. are compared with those of the aforementioned genera. The anamorphs of *E. cinnabarina* and *Rh. indicum* are described. *Contributed Presentation*

*STADLER, MARC and HELLWIG, VERONIKA. Bayer Health Care, PH-R EU ET Natural Products Research, P.O.B. 101709, D-42196 Wuppertal, Germany. marc.stadler@t-online.de **Bioactive secondary metabolites of *Pochonia* and other invertebrate-associated Ascomycetes.**

Pochonins are antiviral and antiparasitic resorcylic acid lactones structurally related to monorden from the invertebrate-associated clavicipitaceous fungus *Pochonia chlamydosporia*. Their production was studied by HPLC-UV/Vis and HPLC-MS methodology in over 100 cultures of *Pochonia* species and allied genera previously included in *Verticillium* sect. *Prostrata*. Concurrently, morphological characters and PCR-based data of these fungi were compared. The results supported the generic segregation by Gams & Zare (Nova Hedw. 72:329-337, 2001) as pochonins were found to occur exclusively in *Pochonia* spp., and their production appeared to be a rather constant feature of *P. chlamydosporia* and *P. rubescens*. Secondary metabolite profiles in strains of allied genera differed from those encountered in *Pochonia. P. suchlasporia* and *P. bulbillosa* clustered into several chemotypes. The sequences of the ITS nrDNA in several strains of *P. suchlasporia* were found identical, in spite of striking differences in their metabolite profiles. Minisatellite PCR fingerprinting was found useful to segregate *Pochonia* at species and strain level, pointing toward the existence of further, cryptic species. The isolation, identification and biological activities, as well as possible chemotaxonomical importance and ecological functions of pochonins and other metabolites of these fungi are discussed. *Symposium Presentation*

*STADLER, MARC[1], PERSOH, EREK[2], and TRIEBEL, DAGMAR[3]. [1]Bayer Health Care, POB 101709, D-42096 Wuppertal, Germany. [2]Univ. Bayreuth, Lehrstuhl fuer Pflanzensystematik, Universitaetsstr. 30 - NW I, D-95440 Bayreuth, Germany. [3]Botanische Staatsammlung Muenchen, Dept. Mycology, Menzinger Str. 67, D-80638 Muenchen, Germany. marc.stadler@t-online.de **A comparison of ITS-nrDNA data of Xylariales with emphasis on Xylariaceae with nodulisporium-like anamorphs.**

The ITS nrDNA sequences of several European species of *Hypoxylon* and allied members of Xylariaceae were aligned with those of ca. 350 Xylariales from GenBank. Phylogenetic analyses basically revealed the major families of the Xylariales as monophyletic groups. Albeit the current generic concepts within the Xylariaceae were not fully resolved, the main Xylariaceae lineages with geniculosporium-like (e.g., *Entoleuca, Kretschmaria, Nemania, Rosellinia, Xylaria*) and nodulisporium-like conidial stages (*Biscogniauxia/Camillea*, and *Daldinia/Entonaema/Hypoxylon/Rhopalostroma*, respectively) were emphasised. *Daldinia* and *Entonaema* appeared closely related, while *Hypoxylon* split into several unresolved clades and therefore a monophyletic origin of the genus could neither be confirmed nor rejected. However, the species of *Hypoxylon* clustered in several well- supported groups, which are not completely in accordance with the current classification. The results are discussed with respect to morphological and chemotaxonomical characters and compared with previously published phylogenetic studies of the Xylariaceae. *Poster*

*SUH, SUNG-OUI[1], MCHUGH, JOSEPH[2], and BLACKWELL, MEREDITH[1]. [1]Dept. Biological Sciences, Louisiana State Univ., Baton Rouge, LA 70803 USA. [2]Dept. Entomology, Univ. Georgia, Athens, Georgia 30602 USA. ssuh@lsu.edu **One to 42 taxa: Expansion of the *Candida tanzawaensis* yeast clade from basidiocarp-feeding beetles.**

A major clade of yeasts (Saccharomycetes) from the gut of basidiocarp-feeding beetles (Coleoptera) has been recognized based on LSU rDNA sequence comparisons. Almost 30% of 650 yeast isolates from the beetles formed a well-supported clade that included *Candida tanzawaensis*, the only clade member known at the time the study was begun. The yeasts were isolated from twelve families of beetles of which Tenebrionidae and Erotylidae were most commonly sampled. The yeasts comprised 42 genotypes based on unique sequences of the D1/D2 loop of LSU rDNA. Repeated isolation of certain genotypes from the same beetle species at different times and places indicated strong host specificity. Sexual reproduction was not observed in any of the yeasts. Based on comparisons of LSU rDNA sequences by BLAST searches and of almost 100 morphological and physiological traits, most of the yeasts in the clade are undescribed species. The *C. tanzawaensis* clade is the largest of several clades of insect-associated diversity that we have discovered among the Saccharomycetes. *Contributed Presentation*

*SUNG, GI-HO, and SPATAFORA, JOSEPH. Dept. Botany and Plant Pathology, Oregon State Univ., Corvallis OR 97331 USA. sungg@science.oregonstate.edu **Systematics of *Cordyceps sensu stricto*.**

The genus *Cordyceps* includes over 300 described species of pathogens that infect arthropods and fungi. In subgeneric classifications, *Cordyceps* species have been separated into four subgenera largely based on ascospore morphology and orientation of perithecia in stromata. Previous phylogenetic analyses of the family Clavicipitaceae, which were based on a four-gene regions including the nuclear SSU and LSU rDNA, beta-tubulin, and elongation factor 1-alpha, have rejected the monophyly of genus *Cordyceps* and have separated the Clavicipitaceae into three clades. In this study, we focus on the systematics of the *Cordyceps* sensu stricto clade, which includes the type species *C. militaris*, with the goal of testing and refining the traditional generic and subgeneric classification system of the genus. The *Cordyceps* s.s. clade includes members of *C.* subg. *Ophiocordyceps*, *C.* subg. *Eucordyceps*, *C.* subg. *Bolacordyceps*, and the genus *Torrubiella*. Our results indicate that the morphological characters, which are used in the subgeneric classification, are not indicative of the phylogenetic relationships based on the DNA data. In addition to teleomorphic taxa, several anamorphic genera (e.g., *Lecanicillium, Beauveria, Paecilomyces*, etc.) are also interspersed among *Cordyceps* and *Torrubiella* species in this clade. The taxonomy and morphological evolution of *Cordyceps* s. s. will be discussed. *Contributed Presentation*

*SWENSON, WILLIAM, and ALLEN, MICHAEL. Center for Conservation Biology, Dept. Plant Pathology, UC Riverside, Riverside, CA 92507 USA. willsw@citrus.ucr.edu **Exploring the ecological stoichiometry of mycorrhizal interactions.**

Mycorrhizal fungi associated with a single plant may belong to diverse taxonomic and functional groups. Each variety of fungus may exhibit a unique profile of interactions with its plant symbiont: differing in relative capacity to make phosphorous, water, nitrogen, and other nutrients available to the plant—requiring correspondingly different quantities of photosynthate in exchange. As a consequence, the simultaneous infection of a plant host by multiple species of mycorrhizal fungi will be a complex set of interacting relationships. Complex interactions of this kind can have results that are nonintuitive and difficult to predict. We employ a theoretical model based on the ecological stoichiometry of nutrient exchange between plant, fungus, and soil to develop predictions about the effects of multiple mycorrhizal interactions in time and space. Understanding the complexity of these relationships should help to understand the ecological and evolutionary significance of the relationship between function and diversity in mycorrhizal systems. *Poster*

*THOMPSON, THERESE and BLANCHARD, ROBERT. Dept. Plant Biology, Univ. New Hampshire, Durham NH 03824 USA. rb@cisunix.unh.edu **Isolating decay basidiomycetes from organic and mineral soil horizons using selective media and red maple/white pine wood baits.**

In an attempt to determine if decay basidiomycete fungi form a bridge between felled decaying wood and the contiguous soil horizons, as a means of transporting nutrients used in the decay process, techniques for efficient isolations were developed. Spodic soil horizons in a red maple-beech-balsam fir forest at six sites in the Bartlett Experimental Forest, New Hampshire, were classified and evaluated. Fungi from these soils were isolated by a variety of techniques including 1)French square jar baits using red maple and white pine wood, 2)soil pit baits using red maple wood, and 3)direct plating, all on selective media previously reported (*Proc. 7th Int. Cong. Plant Pathol., 3: 3.7.10, 1998*). DNA sequencing results of unknown non-fruiting fungal cultures showed that all isolates from the jar and soil pit bait cultures were basidiomycetes. Sequence identification of the direct soil cultures showed 79% of them to be basidiomycetes. *Poster*

*THOMPSON, THERESE[1], BLANCHARD, ROBERT[1], and THORN, GREG[2]. [1]Dept. Plant Biology, Univ. New Hampshire, Durham NH 03824, [1]Dept. Plant Sciences, Univ. Western Ontario, London, Ont., Canada N6A 5B7. rb@cisunix.unh.edu **A hyphal bridge between mineral soil and decaying coarse woody debris.**

Basidiomycetes are known to translocate various nutrients, and we have hypothesized that they tap the mineral soil for nutrients utilized in the decay of coarse woody debris on the forest floor. In order to determine if a hyphal bridge exists between felled decaying wood and contiguous soil horizons, putative basidiomycetes were isolated from these substrates at research sites in Bartlett Experimental Forest, New Hampshire. Unknown fungal cultures from mineral soil, organic soil, bole wood, and basidiocarp fruiting bodies on wood were identified by sequencing of ITS-1 and ITS-2 regions of nuclear rDNA. By comparing DNA sequences of organisms from different substrates, one organism, *Hypholoma capnoides*, a basidiomycete that causes a white rot of wood, was identified in all substrates. Additional DNA markers are being used to determine if these isolates represent the same individual organism or clone. Results suggest that this fungus does form a hyphal bridge from mineral soil to the decaying woody debris. If this can be shown for other decay fungi, it may have implications for calculated nutrient budgets within forest ecosystems and how we manage our forests. *Contributed Presentation*

TLALKA, M., DARRAH, P.R., WATKINSON, S.C. and *FRICKER, M.D. Dept. Plant Sciences, Univ. Oxford, South Parks Road, Oxford, OX1 3RB, UK. mark.fricker@plants.ox.ac.uk I**maging pulsatile amino acid translocation in basidiomycetes.**

Cord-forming woodland basidiomycete fungi form extensive, interconnected mycelial networks that efficiently scavenge nitrogen. The N-dynamics of the ^{14}C-labelled amino-acid analogue, alpha-aminoisobutyrate (^{14}C-AIB) was imaged in *Phanerochaete velutina* growing across scintillation screens using a photon-counting camera. The signal oscillated with a temperature-dependent period of 16 h for both the assimilatory hyphae in the inoculum and the foraging hyphae, but with complementary profiles. Pulses were asymmetric, switching between an exponential decay phase and the next rising phase. There were no obvious pulses in growth. In baited networks, transport switched between different parts of the colony and distinct domains pulsing with different phases were observed. Some of the features of the oscillations were simulated using a model of amino-acid transport that included both vacuolar uptake, and release once a vacuolar concentration threshold was exceeded. To characterise the role of the vacuole in transport further, vacuole connectivity was assessed using FRAP and confocal imaging of hyphae loaded with Oregon Green. Rapid equilibration of vacuolar contents occurred through highly dynamic inter-vacuolar tubular connections. The effect of these connections on net flux was estimated from an *in silico* simulation of diffusive movement through a series of interconnected vacuoles. *Contributed Presentation*

*TRAPPE, MATTHEW[1] and SPATAFORA, JOSEPH[2] [1]Dept. Environmental Sciences, Oregon State Univ., Corvallis, OR 97331 USA. [2]Dept. Botany and Plant Pathology, Oregon State Univ., Corvallis, OR 97331 USA. trappem@onid.orst.edu **Biogeography of the *Craterellus tubaeformis* species complex inferred from rDNA LSU sequence analysis.**

The biogeography of the *Craterellus tubaeformis* species complex is poorly understood. *Craterellus tubaeformis* sensu lato is present around the northern hemisphere but previous studies indicated the likelihood of several distinct species. We analyzed sequences of the 28S LSU rDNA from specimens of *C. tubaeformis* representing a variety of longitudes, with data from other closely related taxa. Preliminary results indicate that the *C. tubaeformis* complex falls into at least two distinct geographic groups: a western North American group and an eastern North American/European/eastern Asian group. It is probable that there are still more genetically distinct populations: An unexpected, but poorly supported, clade grouped a *Craterellus* cf. *tubaeformis* collection from Nepal with a *Craterellus aurora* from Norway and a *Pseudocraterellus sinuata* from Mississippi; and a collection from southern China resembling *C. tubaeformis* in stature appears more closely related to members of the genus *Cantharellus*. Additional analyses will concentrate on a more intensive sampling of *C. tubaeformis* from more regions of the Northern Hemisphere and the detection of additional clades of *C. tubaeformis*-like species. *Contributed Presentation*

*TRUDELL, STEVEN and EDMONDS, ROBERT. Division of Ecosystem Sciences, College of Forest Resources, Box 352100, Univ. Washington, Seattle, WA 98195-2100 USA. mycecol@u.washington.edu **Macrofungal community structure reflects contrasting moisture and nitrogen levels in two old-growth conifer forests.**

The ecology of forest macrofungi and the reasons for their high diversity are not well understood, despite their global ecological importance. During an investigation of nitrogen cycling in two climatically contrasting old-growth conifer forests, we characterized the epigeous macrofungal communities by collecting sporocarps. Despite a high similarity in the tree species in the two forests, the macrofungal communities are very different. At the drier, nitrogen-poor Deer Park area, the mycota is heavily dominated by ectomycorrhizal genera such as *Cortinarius*, *Hydnellum*, *Sarcodon*, *Tricholoma*, and *Suillus*. At the wetter, higher-nitrogen Hoh Valley, the mycota is characterized by different ectomycorrhizal genera, such as *Amanita*, *Boletus*, *Inocybe*, and *Phaeocollybia*, and saprotrophic fungi account for a greater proportion of the community. Species richness is very similar at the two areas, but sporocarp production is much higher at Deer Park. To a first approximation, these community differences can be explained by differences in moisture and nitrogen abundance between the two areas. Among the ectomycorrhizal fungi, mycelial morphology, carbon allocation, and ability to utilize organic nitrogen appear to be important in determining the macrofungal diversity and community structure at the sites. *Contributed Presentation*

*TURNER, ELIZABETH and TAYLOR, JOHN. Dept. Plant and Microbial Biology, Univ. California, Berkeley, CA 94720. eturner@nature.berkeley.edu **Marker development for a study of the genetic basis of reproductive isolation in *Neurospora*.**

The genetic basis of postmating reproductive isolation between some outcrossing *Neurospora* species is being investigated. Two taxa pairs at different stages of divergence have been selected. One pair is *N. crassa* and *N. intermedia*, reciprocally monophyletic species that can be crossed in the lab but that do not hybridize in nature despite having broadly overlapping geographic ranges and apparently identical ecological requirements. The second taxa pair is the core *N. crassa* clade and a group of *N. crassa*-like individuals from Tamil Nadu state, India, which show incomplete phylogenetic and reproductive isolation and may provide an example of incipient speciation in *Neurospora*. To lay the groundwork for quantitative trait locus (QTL) studies of the genetic architecture of reproductive isolation in these two taxa pairs, two high density (approach has yielded numerous polymorphisms. Twenty-two, two-b.p.-selective primer pairs were tested in each parent. Five of these primer pairs yielded >20 fragments (range 23-57, mean 40.7) that were specific to only one parent in a given taxa pair. Experiments are underway to determine marker segregation in populations of f1 strains generated in the lab for the QTL studies, and to construct linkage maps for the two taxa pairs. *Poster*

TURNER, GOEFFREY. Dept. Molecular Biology and Biotechnology, University of Sheffield, Sheffield S10 2TN UK. **Identification of genes controlling hyphal branching and morphology in *Aspergillus nidulans*.**

Morphological variants, including hyperbranching strains, can arise spontaneously during industrial fermentations of filamentous fungi. To learn more about genes controlling such morphological changes, we have tried several approaches at gene identification using the model genetic system *A. nidulans*. These included screening of a set of ts mutants for a hyperbranching phenotype and gene cloning by complementation, random integration of a transforming vector, and testing the function of homologues of genes which are associated with changes in morphology and polarity in other fungal species. For this purpose, *Saccharomyces cerevisiae* provides the most detailed understanding to date of polar growth. All of the approaches were relatively time consuming because of the technical limitations associated with *A. nidulans*. The advent of whole genome sequencing offers new opportunities for a more systematic and rapid approach to analysis of gene function, though there is a need for new tools. We have experimented with a PCR based method for promoter exchange, using the *alcA* promoter as the best currently available conditional promoter in *A. nidulans*, to eliminate the need for vector construction. So far, we have tested the system successfully on homologues of *N. crassa cot-1* and *S. cerevisiae STE20* and *BEM1*.

*VELLINGA, ELSE and BRUNS, THOMAS. Dept. Plant and Microbial Biology, Univ. California at Berkeley, Berkeley CA 94720 USA. vellinga@uclink.berkeley.edu **Lepiotaceous fungi (Agaricaceae) in a changing world.**

Lepiotaceous fungi are generally saprotrophic forest floor dwellers. They occur worldwide, with many representatives in the tropics, but only a few are found in deserts and in arctic-alpine areas. Most taxa are agaricoid, but a small number of secotioid forms exist as adaptations to drought. How will these species react to changes in the environment? The present distribution and understanding of their ecology indicate the following: A warmer climate will increase the number of *Leucoagaricus* and *Leucocoprinus* species in temperate areas, as these genera are now abundant in the (sub)tropics and absent from arctic and alpine environments. Desertification will mean that drought resistant species, like *Endoptychum agaricoides*, will expand, and the many fragile species may perish. Coloured, thick-walledspores with a germ pore, confer a real advantage in the dispersal, survival and colonization processes, as is shown by the wide occurrence of *Chlorophyllum molybdites*. However, many species lack these characters, are rare and have a local distribution. Many European Red Data Lists include *Lepiota* species. Rarity, and the fact that many species share the same ecology and grow together in small areas, makes them especially vulnerable to habitat destruction. Increasing nitrogen deposition and urbanization will make some common weedy species, like *Lepiota cristata*, yet more abundant. *Contributed Presentation*

*VOTH, PETER[1], LOCKHART, BEN[2], and MAY, GEORGIANA.[1] [1]Dept. Plant Biology, and [2]Dept. Plant Pathology, Univ. Minnesota, St. Paul MN55108. voth0016@umn.edu **Migration and geneflow in the *Ustilago maydis* virus.**

Ustilago maydis infects vegetative and reproductive tissues of maize and the teosintes. Infecting *U. maydis* is the *Ustilago maydis* virus (UMV), a double-stranded RNA virus that encodes the production of a "killer" toxin within the host fungal cell. The proteinaceous UMV toxin is lethal to susceptible *U. maydis* individuals and can inhibit mating between compatible *U. maydis* individuals. UMV is only transmitted through cytoplasmic fusion during mating of compatible *U. maydis* individuals. *U. maydis* individuals are protected from the virus through nuclear resistance or cytoplasmic immunity. The interactions between UMV and *U. maydis* may affect the reproductive biology of *U. maydis* and subsequently the population genetic structure of UMV. The aim of the current study is to use sequence analysis to characterize the population genetic structure of UMV throughout the Western Hemisphere. I used immuno-capture RT-

PCR to amplify and sequence a 500bp region of the capsid gene from North and South American UMV. The data suggests there are no biogeographical trends in the population structure of UMV, which contrasts the population structure of the host, *U. maydis*, based on analysis of neutral markers. Comparisons of geneaologies of the capsid and RNA dependent RNA polymerase (RdRp) will allow for further inferences to be made about the levels of migration and gene flow in UMV populations. *Contributed Presentation*

*WANG, ZHENG, BINDER, MANFRED, and HIBBETT, DAVID. Dept. Biology, Clark Univ., 950 Main Street, Worcester, MA 01610 USA. ***Sparsitubus*, an unusual cyphelloid-like polypore from China, is the sister group of the Ganodermataceae.**

Sparsitubus is a monotypic genus found in east Asia that has a bizarre cyphelloid-like hymenophore. The position of *Sparsitubus* in the Polyporaceae has been suggested previously based on morphological characters. We are using molecular data from several loci to study the relationships of *Sparsitubus* to other homobasidiomycetes. Preliminary analyses suggest that *Sparsitubus* is in the sister group of the Ganodermataceae, and is closely related to certain resupinate polypores of Grammotheleaceae. Fruiting body forms, hyphal systems, and basidiospore morphology range from simple to complex in this clade. We are performing ancestral state reconstructions on molecular phylogenies to understand patterns of evolution leading to this unusual fungus.

*WARNER, RACHEL[1], OTROSINA, WILLIAM[2], and GARBELOTTO, MATTEO[1]. Dept. Environmental Science, Policy, and Management - Ecosystem Sciences, Univ. California, Berkeley, Berkeley, CA 94720 USA. [2]Forest Sciences Laboratory, USDA Forest Service, Athens, GA 30602 USA. rwarner@nature.berkeley.edu **Phylogenetic analysis of *Heterobasidion annosum* from regions in North America.**

The forest pathogen, *Heterobasidion annosum*, is widely distributed in northern temperate forests. We investigated phylogenetic relationships of *H. annosum* populations from three regions: Canada, California and the East Coast of the United States, including SP hybrid, S and P intersterility groups. In a preliminary study, two regions of DNA were PCR-amplified from 56 individuals from 12 sites: an intron of the mitochondrial large rRNA gene and part of the nuclear gene, Elongation factor 1-alpha. Products were sequenced and used to construct phylogentic trees for both loci using maximum parsimony and bootstrap methods. Initial results suggest: 1) East Coast and Canadian populations are not phylogenetically distinguishable, 2) East Coast and Canadian populations group in clades separate from Northern California, and 3) Two samples from a Canadian site have a mitochondrial intron sequence identical to two from a Southern Californian site. Elongation factor 1-alpha sequences of these Canadian individuals do not group in the Southern California clade. Such divergent mitochondrial and nuclear gene phylogenies indicate possible reticulation. Further nuclear and mitochondrial genes will be sequenced to clarify phylogenetic relationships of *H. annosum* populations in these regions. Additional sites and more individuals from current sites will also be included. *Poster*

*WESTMORELAND, SEAN[1], VOLK, THOMAS[1], and HOPKINS, SUSAN[2]. [1]Dept. of Biology, Univ. Wisconsin-La Crosse, La Crosse, WI 54601 USA. [2]New Jersey Mycological Society, Old Wick, NJ 08858 USA. Antedon@centurytel.net **Morphological, molecular, and musical studies in *Hydnellum* (Basidiomycota, Thelephoraceae), reinforced with a new method - Chemosystematics with HPLC using Mass Spec (CHUMS).**

Hydnellum is a genus of stipitate hydnaceous fungi that can be recognized by their brown, ornamented basidiospores, leathery texture, and indeterminate, mycorrhizal growth habit. Although previous taxonomic works have been useful, there are many disagreements between authors as to the correct delimitation and placement of *Hydnellum* species. For this reason, a re-examination of the species with modern taxonomic methods is warranted. We have undertaken morphological, molecular, and chemical (pigment) studies of *Hydnellum* species. Eighty-seven collections were examined morphologically, and 36 collections were analyzed by comparing ITS sequences. Fifteen collections were studied with CHUMS, Chemosystematics with High performance liquid chromatography (HPLC), Using Mass Spectroscopy, to compare species using the presence or absence of chemical compounds. A total of 54 compounds were analyzed to construct a chemical "sequence," similar to a nucleotide sequence, with each compound being analogous to one nucleotide position on the DNA. From this sequence we are able to produce phylogenies to show relatedness of species. All three lines of evidence, morphological, chemical, and DNA were used to determine a final taxonomic placement of 15 *Hydnellum* species. Another original song about *Hydnellum* will be presented. *Contributed Presentation*

*WHITE, MERLIN[1], LICHTWARDT, ROBERT[1], GUARDIA VALLE, LAIA[2], and STRONGMAN, DOUGLAS[3]. [1]Univ. Kansas, Dept. Ecol. and Evol. Biology, Lawrence, KS 66045 USA. [2]Unitat de Botanica, Dept. Biologia Animal, Biologia Vegetal i Ecologia, Univ. Autonoma de Barcelona, 08193-Bellaterra, Spain. [3]Dept. Biology, St. Mary's Univ., Halifax, NS, B3H 3C3, Canada. trichos@ku.edu ***Orphella* — an unusual gut fungus associated with stoneflies.**

The gut fungi (Trichomycetes) are obligate symbionts of various Arthropoda. The traditional, morphologically-based classification system has included three fungal orders (Eccrinales, Asellariales and Harpellales). Sequence data are providing insights into the natural associations of the members of this class, which will necessitate an eventual reclassification. Members of the Harpellales are unique in the possession of asexual trichospores and conical zygospores (where the sexual process has been observed). However, the asexual spores of *Orphella* are released as dissemination units. The dissemination units mature distally and form clusters that may be seen as sporulating heads extending beyond the anus of their stonefly (Plecoptera) host. Zygospores have never been reported for *Orphella*. Nonetheless, on a morphological basis, this genus has been recognized as being an unusual harpellid. Additionally, based on rDNA sequence data obtained to date, *Orphella* falls outside an otherwise monophyletic clade of Harpellales, more closely allied with the Kickxellales. Our current efforts have been focused on collecting more samples of *Orphella* (in North America and Europe) and putative closely related taxa to expand the molecular data set used to infer the phylogeny of the group. *Orphella* has been found only in the Northern Hemisphere and the biogeographical implications are discussed. *Poster*

*WILSON, ANDY[1] and DESJARDIN, DENNIS[2]. [1]Dept. Biology, Clark Univ., Worcester MA 01610 USA. [1]Dept. Biology, San Francisico State Univ., San Francisco CA 94132 USA. anwilson@clarku.edu **A phylogenetic analysis of the *Gymnopus/Marasmiellus* complex using nuclear large subunit sequence data.**

The *Gymnopus/Marasmiellus* complex consists of many species whose taxonomic placement has been controversial. A broad study of the phylogeny of the Agaricales was done by Moncalvo et. al. (2002), who referred to this complex as the lentinuloid group. In their study,

the majority of genera in the *Gymnopus/Marasmiellus* complex appear to be non-monophyletic. This study uses an expanded sampling of the *Gymnopus/Marasmiellus* clade along with a thorough phylogenetic analysis to address the relationships of this group. Species chosen for this study represent several subgeneric sections from 10 genera of the *Gymnopus/Marasmiellus* complex, including *Gymnopus, Marasmius, Marasmiellus, Tetrapyrgos, Campanella, Micromphale, Rhodocollybia, Callistosporium, Lentinula,* and *Trogia*. Sequence data from 25S nuclear ribosomal DNA was collected from selected specimens and combined with sequences gathered from Genbank. Parsimony, maximum likelihood and Bayesian analyses are being used to analyze the phylogeny and test the monophyly of the genera presented in this study. *Poster*

WOLL, MATT, COLLOPY, PATRICK, and ROYSE, DANIEL. Dept. Plant Pathology, Pennsylvania State Univ., University Park, PA 16803 USA. djr4@psu.edu **DNA sequence determination of host and parasite of the lobster mushroom.**

The lobster mushroom (named because of red outer crust) is the result of a parasite, *Hypomyces lactifluorum*, colonizing an unknown basidiomycete host. Presumed hosts are species belonging to the *Russula* and *Lactarius* genera. Lobster mushroom specimens were collected in Centre County, Pennsylvania and internal transcribed spacers 1 and 2 and 5.8 S regions of the nuclear ribosomal DNA transcriptional unit were PCR-amplified (primers ITS1AF and ALRO) for both host and parasite. Amplification products were purified and sequenced using the Applied Biosystems Big Dye Terminator. In order to determine the closest match to any known fungi, resulting sequences were edited and subjected to BLASTnr searches in NCBI nucleotide databases. The closest match for parasite and host was *Cordyceps heteropoda* (order Hypocreales) and *Russula delica*, respectively. This is the first report of *Russula delica* as a host species for *Hyphomyces lactifluorum*. *Poster*

YANG, YI and KAMINSKYJ, SUSAN. Dept. Biology, Univ. Saskatchewan, 112 Science Place, Saskatoon, Saskatchewan, Canada S7N 5E2. yiy345@duke.usask.ca **Cloning and characterization of the *Aspergillus nidulans* morphogenetic locus, *hypB*.**

Aspergillus nidulans hyphae produce tubular cells by localized exocytosis. Temperature sensitive *A. nidulans* strains define five genes, *hypA1-hypE2*, that cause hyphal morphogenesis defects at 42°C. *hypA* is orthologous to *Saccharomyces TRS120*, which mediates Golgi transit. The *hypB5* restrictive phenotype resembles that of *hypA1*: wide hyphae, and short basal cells. A *hypA1, hypB5* double mutant was impaired for growth at 28°C, suggesting these genes have related roles, but neither was epistatic at 37°C suggesting they function in different pathways. *hypB5* was cloned using the *A. nidulans* pRG3-*AMA1* genomic library, and subcloned to a 5kb *Kpn*I fragment, pYY2. pYY2 was disrupted and sequenced by Tn1000 insertion. The *hypB* genomic sequence is 2106 bp and *in silico* analysis predicts it to have one intron. *hypB* encodes a putative 392 amino acid protein, with a predicted weight of 43.9kD. *hypB* is 38% identical to the full length *Saccharomyces SEC7*, and 80.6% identical in the *Sec7* domain, which is highly conserved from yeasts to mammals. *Saccharomyces SEC7* encodes a guanyl nucleotide exchange factor, and is involved in Golgi biogenesis. pYY2 with Tn1000 insertions into the predicted Sec7 domain in *hypB* could not complement a *hypB5* mutant strain, suggesting that this gene is essential for function. *Contributed Presentation*

*ZHANG, NING[1], GEISER, DAVID[1], and O'DONNELL, KERRY[2]. [1]Dept. Plant Pathology, Pennsylvania State Univ., University Park, PA 16802 USA. [2]NCAUR, USDA-ARS, 1815 N. University St., Peoria IL 61604 USA. nzhang@psu.edu **An elongation factor database of the *Fusarium solani* species complex.**

A portion of the translation elongation factor 1-alpha (EF1-alpha) gene was sequenced for over 300 *F. solani* isolates from various geographic locations and substrates. A number of new lineages were identified from the neighbor-joining tree, which do not group with any known mating populations (MP I through VII), suggesting that there are more species in the *F. solani* complex than previously recognized. For 224 isolates, mating type was determined by using the polymerase chain reaction. Among them, 139 isolates were mating type MAT1-1 and 85 were MAT1-2. In most lineages, both mating types were present, suggesting the potential for an active sexual stage. In order to apply phylogenetic species concept to the *F. solani* complex, multiple loci were analyzed for a subset of isolates. In addition to the EF-1 alpha gene, we also sequenced mating type idiomorphs (MAT), the internal transcribed spacer regions of the nuclear rRNA genes (ITS) and the large subunit (LSU) of the nuclear ribosomal RNA gene. The results show strong support for clades corresponding to known mating populations, in addition to a number of new lineages. Overall, the *F. solani* complex was found to contain a tremendous amount of phylogenetic diversity. *Contributed Presentation*

*ZHENG, WANG., BINDER, MANRED and HIBBETT, DAVID, 950 Main Street, Worcester, MA 01610. zwang@clarku.edu ***Sparsitubus*, an unusual cyphelloid-like polypore from China, is the sister group of the Ganodermataceae.**

Sparsitubus , is a monotypic genus found in east Asia that has a bizarre cyphelloid-like hymenophore. The position of *Sparsitubus* , the Polyporaceae has been suggested previously based on morphological characters. We are using molecular data from several loci to study the relationships of *Sparsitubus* , to other homobasidiomycetes. Preliminary analyses suggest that *Sparsitubus* , is in the sister group of the Ganodermataceae, and is closely related to certain resupinate polypores of Grammotheleaceae. Fruiting body forms, hyphal systems, and basidiospore morphology range from simple to complex in this clade. We are performing ancestral state reconstructions on molecular phylogenies to understand patterns of evolution leading to this unusual fungus. *Poster*

*ZITOMER, NICHOLAS[1], VOLK, THOMAS[1], and ROTT, MARC[2]. [1]Dept. Biology, and [2]Dept. Microbiology, UW-La Crosse, La Crosse WI 54601 USA. nzitomer79@msn.com **Isolation and characterization of antimicrobial substances from fruiting bodies of macrofungi.**

Fungi are known to produce a variety of bioactive metabolites, including many pharmaceutically useful compounds such as penicillins, cephalosporins, and cyclosporins. The majority of these compounds have been isolated from deuteromycetes or non-fruiting mycelia from other groups of fungi. This project widens the scope of the search for new compounds from fungi by focusing on the fruiting bodies. Fleshy fruiting bodies from numerous fungi were collected, with emphasis on sampling those that are persistent in nature. Also of interest were those fungi that cannot yet be grown in the laboratory, such as the obligate mychorrizal fungi and plant pathogens. After identification, our approach was to extract the

basidiomata with methylene chloride and to test these extracts using anti-bacterial and anti-*Candida* bioassays (a standard disk diffusion method). After 12 to 18 hours of growth, the plates were observed for zones of inhibition around the disks. Once promising extracts were identified, the bioactive compounds were purified and further characterized using chromatographic methods, mass spectrometry and nuclear magnetic resonance. We present our preliminary findings of such compounds.
Contributed Presentation

Additional Abstracts are on page 63 of this issue of Inoculum

MYCOLOGICAL NEWS

Fungi Book for Children

A book entitled "Fungi" in a new series of Ranger Rick books called "Exploring Our World" introduces and explores key earth, life and physical science and geography concepts for children in grades 3 to 5. They are beautiful books filled with photographs and printed in magazine size, as well as a big book size, which can be shared at the front of a classroom. Two-page vignettes include stories under the topical headings of Animal, Vegetable, or What?; Tour of the Kingdom; Natures Recycler; Partners with Fungi; Fungal Foes, Fungal Friends; Exploring for Fungi and a Glossary. The color images range from chanterelles on the front cover, coral fungi, lichens, bird's nest fungi and many others. Mycologists are highlighted as scientists who study fungi as part of the Tour of the Kingdom.

The story on pages 16 and 17 entitled "Exploring for Fungi" features **Melissa Skrabal** using the double rope climbing technique to collect lichens high in the tree tops in the Great Smoky Mountains National Park. A color image of a new species of *Diachea* highlights its discovery in the tree canopy by Melissa. This *Diachea* has a peridiadal surface covering the sporangium with a stunning iridescence which glistens like gold. This is an example of a woman doing fieldwork in the tree canopy which requires strength, agility, and athleticism to scale the heights of champion-sized trees. Melissa represents a role model for other young girls to follow in her footsteps. A panoramic view of the forested terrain typical of the Great Smoky Mountains National Park was taken by Damon Lesmeister from the top of a white pine at about 30 meters. James Murray took the photograph of Melissa Skrabal collecting lichens. Kenneth Snell took the photograph of the new species of *Diachea*. The Great Smoky Mountains National Park is highlighted as a temperate biosphere with high species diversity for plants, animals, and fungi.

For more information about tree canopy biodiversity in the Great Smoky Mountains National Park contact Harold W. Keller, Department of Biology, Central Missouri State University, Warrensburg, MO 64093; < **keller@cmsu1.cmsu.edu** >.

Carson M.K. (2003) Fungi. Newbridge Educational Publishing, New York, New York.

-- Harold W. Keller
keller@cmsu1.cmsu.edu

Fungal Diversity Press

Fungal Diversity Press is a non profit publishing venture in the Department of Ecology & Biodiversity at The University of Hong Kong. The aim of the press is to facilitate the publication of mycological text and use any proceeds from sales to fund research in fungal biodiversity in the Asian region. Fungal Diversity Press was initiated in 1998 as it was felt that there was a need for a new journal to publish the outcomes of fungal diversity research. The first publication was the International Journal *Fungal Diversity*. This is now in it 13th Volume and is receiving submissions from all over the world. Because of the difficulty in publishing fungal monographs and books, the press introduced a new series, the *Fungal Diversity Research Series*. The first 7 books in this series were "in house", but in 2002 the series began to accept external monographs for publication and published "Smut Fungi of New Zealand" in association with Landcare Research and "The genus *Mycena* in South-Eastern Australia with ABRS". Fungal Diversity Press welcomes other monograph or book submissions to consider for publication.

Any funds from book sales are being used to publish further books and promote the study of mycology in the Asian region. Fungal Diversity Press will fund a workshop in Fungal Taxonomy in Chiang Mai University, Thailand in July 2003. We therefore urge you to support "the press" in its future endeavors and encourage you to submit articles, monographs and books to Fungal Diversity press for publication and consider purchasing the book that are published.

-- K.D. Hyde
http://www.hku.hk/ecolgy/mycology/FDP.html

Lichen Collection at the University of Michigan

The University of Michigan Fungus Collection has assumed responsibility for curating the MICH lichen collection. Requests for loans should be addressed to: Fungus Collection, Herbarium, 3600 Varsity Stores, Ann Arbor, MI 48108-2287, USA.

-- Robert Fogel
rfogel@umich.edu

News About MSA Members . . . .

Cathie Aime Joins USDA-ARS in Beltsville, MD

Dr. Mary Catherine "Cathie" Aime has recently joined the USDA-ARS Systematic Botany and Mycology Laboratory/ U.S. National Fungus Collections in Beltsville, MD. She will lead a research program on the molecular systematics of rust fungi with emphasis on species of *Phakopsora* and other rusts of agricultural and horticultural importance. In 2001 Dr. Aime received her Ph.D. from Virginia Polytechnic Institute in Blacksburg, VA with Dr. Orson Miller working on the systematics of *Crepidotus* (Crepidotaceae, Agaricales). She also conducted the molecular systematic aspects of research on the Gomphidiaceae with Dr. Miller. While working on her dissertation she travelled throughout the American topics and Japan collecting macrofungi. After receiving her Ph.D. she worked as a research associate with Dr. Lorna Casselton In Oxford, England, studying the genetics of *Coprinopsis cinerea.* The mycologists at Beltsville are pleased to welcome Dr. Aime to their group.

Dr. Mary Catherine "Cathie" Aime

Dr. Cathie Aime's new address: Systematic Botany and Mycology Laboratory, USDA-ARS, Rm. 304, B011A, 10300 Baltimore Ave., Beltsville, MD 20705, 301-504-5364 (office line, no direct line yet), FAX 301-504-5810, email: cathie@nt.ars-grin.gov

-- Amy Y. Rossman
amy@nt.ars-grin.gov

Rebecca Belling Abler Named Teaching Assistant of the Year at Virginia Polytechnic Institute and State University

Rebecca Belling Abler was named Teaching Assistant of the Year in March for the entire University (Virginia Polytechnic Institute and State University) for 2003. Virginia Tech has over 800 teaching assistants so this is a very great honor for our Department of Biology as well as for the Mycology Lab. Becky is completing her dissertation research and should receive her PhD degree in the next academic year. She is carrying out research on the effects of heavy metals on ectomycorrhizal function. She has taught Introductory Biology, Microbiology, and Mycology labs and last fall did both lecture and lab in Introductory Mycology.

***– Orson K. Miller Jr.,* PhD**
orsonk@frontiernet.net

Regional Mycology Conferences

Midwest Regional Mycology Meeting?

The University of Wisconsin - Botany Dept. Mycologists are thinking of an annual Midwest regional mycology meeting in the tradition of the MASMC on the East Coast. It should serve as an opportunity for undergraduate and graduate students, as well as postdocs, to present their research. In addition, it could be seen as a Deep Hypha spin-off, and may lead to regional research projects. It should be fun and low-key/ low-cost, and could perhaps happen this fall 2003 or next spring (2004).

We are interested in hearing from people across the Northern Plains, around the Great Lakes, and also the central Canadian provinces. Working name for the idea: **MiCoMyco-Get** (MidContinental Mycology-Get-Together). Contact: **dirkkrueger@wisc.edu**.

***-- Dirk Krueger,* PhD**
dirkkrueger@wiscmail.wisc.edu

Where Has MASMC Gone?

The Middle Atlantic States Mycology Conference (MASMC) in an informal spring meeting that offers mycologists from the eastern seaboard a chance to meet in a less formal venue than those stuffy national and international meetings.

You may be wondering, what's up with MASMC this spring? In spite of a very successful meeting last year with over 75 attendees at the Beltsville USDA Mycology Lab, no one volunteered to host this year's meeting. So, after 22 years of meeting every spring, MASMC is taking a little vacation, but it will be back next year!

MASMC is usually held in spring, often coinciding with the peak of the local morel season. The first conference was organized in 1979 by Jerry Motta at the Univ. of Maryland, with subsequent meetings held in Blacksburg, Durham, and Athens,. We are currently looking for a lab to host MASMC for 2004, (possibly in Pennsylvania). If you would like to host MASMC for 2004, or know someone who would, please contact **R. Vilgalys** (**fungi@duke.edu**). We hope to see you all next year!

-- Rytas Vilgalys
fungi@duke.edu

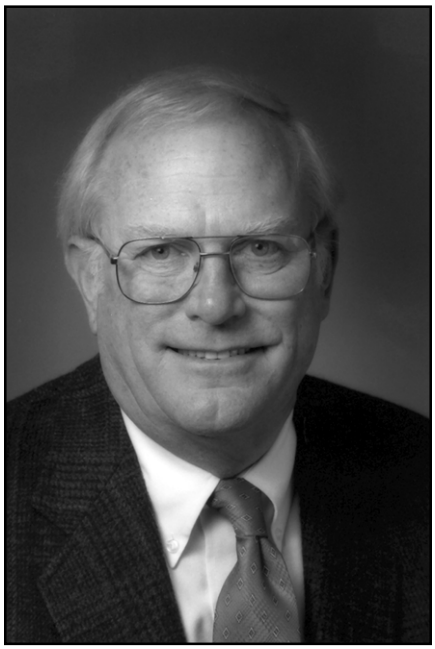
Obituaries . . . .

William Louis Culberson

It is with great sadness that I report the death of William Louis Culberson, Hugo L. Blomquist Professor Emeritus of Botany at Duke University. Dr. Culberson was one of the greatest lichenologists of his time, and a long-time member of MSA. He died on February 8, 2003, after a short battle with cancer.

Born April 5, 1929, in Indianapolis, he attended the University of Cincinnati (B.S.), the Universite de Paris (M.S.), the University of Wisconsin (Ph.D.), and Harvard University (postdoc) before coming to Duke in 1955.

In addition to MSA, Dr. Culberson was also a member and past-president of the Botanical Society of America, and the American Bryological and Lichenological Society. During his career, he served as an editor, or editor-in-chief, for eight botanical journals. His enthusiasm for horticulture rivaled his mycological interests: he was Director of the Sarah P. Duke Gardens (Duke University) for 20 years, and, at the time



William Louis Culberson

of his death, he was the Grants Director for the Stanley Smith Horticultural Trust.

Dr. Culberson authored over 100 papers in lichenology, including many with his wife, Chicita. Together, they explored the nature and significance of lichen chemotypes, and pioneering the field of lichen chemosystematics. Unlike some lichenologists, Dr. Culberson was ever-mindful that lichens were fungi, and his and Chicita's classic, meticulous experiments on lichen mycobiont cultures remains the best research on that subject to date. In addition to his research, Dr. Culberson was a great teacher, and served as advisor for two M.S. and eight Ph.D. students (including myself). He was a treasured advisor, colleague and friend, and he is greatly missed.

-- Scott LaGreca
Farlow Herbarium of Cryptogamic Botany

Colin Booth

Colin Booth, former Assistant Director of the CMI at Kew, died on April 9, following a brief illness. He was 78. He is survived by his wife Doeothy. You should send your condolences to her at Mrs Doeothy Booth, The Old Rectory, Batcombe, UK.

***-- Roger D. Goos,* PhD**
Rgoos@URI.EDU

First Circular for the XVII International Botanical Congress

This is to announce the availability of the First Circular for the XVII International Botanical Congress to be held **18 to 23 July 2005 in Vienna, Austria** (nomenclature sessions 13 to 16 July). The First Circular and additional general information are available on the congress website < **http://www.ibc2005.ac.at/** >. Specific details or clarifications can be obtained through e-mail from the Secretary-General: < **office@ibc2005.ac.at** >. Please download the pre-registration form contained in the First Circular, fill in the requested information, and return the form (preferably electronically) to:

Dr. **Josef Greimler**
Secretary-General, IBC 2005
Institute of Botany, Univ. of Vienna
Rennweg 14
A-1030 Vienna, Austria
office@ibc2005.ac.at
+43-1-4277-54123 (phone)
+43-1-4277-9541 (fax)

Please take notice of the **deadline for proposals for symposia is 30 September 2003**. The Second Circular will be distributed in the summer of 2004.

***– Josef Greimler,* PhD**
office@ibc2005.ac.at

***– Meredith Blackwell,* PhD**
mblackwell@lsu.edu

Mycena spinosissima, *one of the many cool mycenoid fungi encountered in Southeast Asia. (Photo by Dennis*

MYCOLOGICAL CLASSIFIEDS

Read the Classified for announcements of courses, books for sale, employment, positions available, and mycological goods and services offered or needed.

International Volunteer Program Seeks Mushroom Growers

My name is **Kristina Gribovskaja**, and I work for CNFA (Citizens Network for Foreign Affairs), a non-profit organization in Washington, DC that >promotes agricultural development in developing countries. I am writing to introduce you to our international agriculture volunteer program. We are currently working with mushroom growers in Belarus and Ukraine (countries located in the western part of the former Soviet Union) and are seeking U.S. mushroom growers as volunteers for this project. Please send me an email if you would like more information or monthly updates.

The CNFA Agribusiness Volunteer Program sends volunteers from the US agricultural sector on three-week overseas assignments. We cover the costs of the assignments (including but not limited to airplane tickets, lodging, meals, and transportation), and provide a translator. We also make all logistical arrangements in preparation for the trip (tickets, visas, hotel reservations, etc). Since these are volunteer assignments, CNFA does not pay any consulting fees or honorariums. The volunteer donates his/her time and skills. Participation in this program is open only to US citizens who currently reside in the US.

The following two mushroom assignments are in **Belarus**:

1. **Mushroom Production**: Teach the owner and employees of a small private mushroom production company the advanced techniques of Oyster mushroom production and production management. Help them develop a mushroom production plan.
2. **Mushroom Marketing**: Work with the owner of a small private Oyster mushroom production company and help him assess his current marketing policy and determine the business' strengths, weaknesses, opportunities and threats of breaking into new markets. Help the company develop a marketing plan.

The following mushroom assignment is in **Ukraine**:

1. **Business Planning for Mushroom Processing** (for white button and oyster mushrooms): Work with the owners of a small private mushroom production company in western Ukraine to teach them the components of a business plan for mushroom processing and distribution, how to collect the information, how to evaluate the capital budgeting decisions and calculate start-up costs and operating expenses. Help the company develop a business plan for a small-scale processing enterprise within the company.

We also have other agriculture volunteer assignments available, from Strategic Planning, Financial Management and Wholesale Market Development to Beekeeping, Vegetable Marketing, and Animal Health Improvement to *In-Vitro* Production of flower, strawberry and grape rootstocks. Please email me if you would like a complete listing or more information on the mushroom assignments.

– Kristina Gribovskaja
Kgribovskaja@cnfa.org
Program Coordinator, CNFA
1111 19th St., NW
Suite 900
Washington, DC 20036
1-888-872-2632 (toll-free)
202-296-3920 (phone)
202-296-3948 (fax)
www.cnfa.org

Mycotaxon, Mycologia, Transactions of the BMC and *Mycological Research* For Sale

Anyone interested in purchasing the following issue of *Mycotaxon*, *Mycologia, Transactions of the British Mycological Society* and *Mycological Research* should contact **Roger Goos**. The issue for sale include:

Transactions of the British Mycological Society:
Vol. 43 (1960) to Vol. 91 (1989)

Mycological Research
Vol 92 (1999) to Vol. 106 (2002)

Mycotaxon
Vol 1 to Vol. 46 (1993)

Mycologia
Vol. 36 (1944) Bound
Vol. 38 (1946) Complete, unbound
Vol. 40 (1949) to Vol. 46 (1954) Complete, unbound
Vol. 47 (1955) Missing No. 6. Unbound
Vol 48 (1956) to Vol. 58 (1966) complete, unbound
Vol. 59 (1967) Missing No. 2.

Spare parts -- *Mycologia*:
Vol. 43 (1961) Nos. 1, 3, 4, 5, 6.
Vol. 44 (1952) Nos. 1, 2, 6.
Vol. 45 (1953) Nos. 1 and 4.
Vol. 46 (1954). No. 6.
Vol. 48, Complete, unbd..
Vol. 50 (1958) No. 2.
Vol. 71 (1979) No. 1.

***– Roger Goos*, PhD**
Rgoos@uriacc.uri.edu
401-874-2630

Mold Testing and Identification Services

Identification and contamination control for food technology, spawn technology, plant diseases, and insectaries. ASTM & Mil-Spec testing for aerospace, controlled environments and environmental engineering. 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.pioneer.net/~microbe/abbeylab.html**.

***-- Steven E. Carpenter*, PhD**
microbe@pioneer.net

Positions Available . . . .

Undergraduate and Graduate Students Needed for Tree Canopy Biodiversity Research Project in the Great Smoky Mountains National Park

The objectives of this research project are to complete the first comprehensive survey and inventory of tree canopy biodiversity for cryptogams (Myxomycetes, macrofungi, mosses, liverworts, lichens, ferns), and, added later, tardigrades, insects, and molluscs in the Great Smoky Mountains National Park (GSMNP); to collect these targeted groups of organisms above three meters on a vertical transect to the tree tops; to assemble a multidisciplinary research team of experts who will collect, identify and curate this diverse group of organisms; to compare the assemblages of tree canopy targeted organisms with those of ground sites; to search for species new to science in all of the targeted groups of organisms; to involve volunteers, park interns, undergraduate and graduate students, and project personnel in park interpretive exhibitions, news media coverage (print and television), and publication of articles in popular magazines that will send a powerful conservation message for biodiversity.

Previously eight student climbers participated in this project. Most of these students have graduated and are attending graduate schools. Students inquire about learning how to climb trees but the double rope climbing method requires strength and agility to master. Tremendous upper body and arm strength are required to ascend the rope. Once in the tree canopy maneuvering over limbs and advancing to higher canopy levels requires special athletic skills. Climbing to heights of 30 meters is risky so training is provided and safety is emphasized. Students are involved in an adventure phase (two three week field trips), laboratory phase (one to two years), and publication phase as part of this project. All students enroll in Special Problems in Biology, keep a daily diary of their experiences, and are given writing assignments upon return to Central Missouri State University.

Limited financial support is available through several grants. Graduate assistantships are available based on academic credentials and availability of funds. If you know of a student that would be enthusiastic in this project as part of their undergraduate or master's degrees please contact me at the address given below.

Please contact: Professor Harold W. Keller, Ph.D., Department of Biology, 118 W.C. Morris Building, Central Missouri State University, Warrensburg, MO 64093, telephone 660-543-4823; fax 660-543-4355; e-mail keller@cmsu1.cmsu.edu.

-- Harold W. Keller
keller@cmsu1.cmsu.edu

Postdoctoral Position -- USDA Agricultural Research Service, Davis, CA

A two-year postdoctoral position is available starting June 2003 for a motivated candidate who is interested in the population structure of Basidiomycetes. This research is expected to lead to an improved understanding of variation in population structure of *Armillaria mellea* at different geographic scales (several kilometers versus several thousand kilometers). Research will focus on developing molecular markers for characterization of a collection of diploid individuals gathered from throughout the state of California, using these markers to infer relationships among individual genotypes, and estimating population genetics parameters (size of a breeding population, gene flow among subpopulations, etc.). Research will be conducted at the Department of Plant Pathology, University of California, Davis and at the Oakville Experimental Station, Napa, CA. A Ph.D. in mycology or a related scientific discipline is required. Applicant must have practical knowledge of population genetics, experience with molecular techniques, and skill in conducting research using appropriate experimental design, techniques, and software. Salary is $40,239 - $50,970, depending on experience.

Send letter of interest, CV, and contact information for three references to:

-- Kendra Baumgartner
USDA-ARS
Department of Plant Pathology
University of California
One Shields Avenue
Davis, CA 95616
phone 530-754-7461
fax 530-754-7195
kbaumgartner@ucdavis.edu

Australian National University Faculty of Science School of Botany and Zoology Lecturer in Plant-Microbial Interactions (Level B) Reference No: BOZO 1582

The School of Botany and Zoology in the Faculty of Science is seeking to attract an outstanding Lecturer (Level B)/ Researcher to fill a full-time position in plant-microbial interactions, particularly in the field of evolutionary and molecular ecology, population and evolutionary genetics, systematics and biogeography. An interest in mycology would be an advantage. The successful applicant will be involved in developing, organising and contributing to undergraduate units in biology, in supervision of honours and graduate students, and also will be expected to develop a strong independent

(Continued next page)

research program. The position is available from 1 July 2003.

Enquiries to Dr **Mike Crisp**, Head, School of Botany & Zoology, tel: (61 2) 6125 2866 or email **Head.BoZo@anu.edu.au**. Additional information regarding the School may be obtained from the internet address **http://www.anu.edu.au/BoZo/**.

Selection documentation, should be obtained before applying from **Madeleine Haag**, tel: (61 2 61252866); fax: (61 2 61255573), email <**Madeleine.Haag@anu.edu.au**> or from ANU web at **< http://www.anu.edu.au/hr/jobs/bozo1582.pdf** >.

Information on how to apply may be obtained from the ANU Web page **<http://www.anu.edu.au/hr/jobs >** or by telephoning/emailing the contact.

Closing Date: 12 May, 2003.

-- Rytas Vilgalys
fungi@duke.edu

Courses and Workshops . . . .

Advanced Mycology: Fungi and Their Associates
August 26-31, 2003

Do you long for a field biology experience? Check out the field course "Advanced Mycology: Fungi and Their Associates," to be offered as an Eagle Hill Seminar at the Humboldt Field Research Institute, Steuben, Maine, August 26-31, 2003 < **http://www.eaglehill.us/msmycolo.html** >.

- A week-long seminar designed for students with a basic knowledge of fungi
- Studies include field and microscopic examination, biology of fungi and their associates in specialized habitats
- Field collected material and independent projects emphasized

Instructors:

Dr. **Donald H. Pfister**, Asa Gray Professor of Systematic Botany at Harvard University, Director of the Harvard University Herbaria and Curator of the Farlow Reference Library and Herbarium of Cryptogamic Botany. He teaches mycology and lichenology at Harvard. He also has designed a course for non-science majors on the Biology of Trees and Forests. His research involves the systematics, phylogeny, and biology of a group of Ascomycota, the Discomycetes.

Dr. **Meredith Blackwell**, Boyd Professor at Louisiana State University. She teaches courses in mycology and the biology of fungi. She has been interested in many different groups of fungi, primarily those associated with insects. Current research in her laboratory involves the discovery and investigation of the basis for the associations of more than 200 undescribed species of yeasts that live in the gut of beetles. She coauthored with CJ Alexopoulos and CW Mims the current edition of Introductory Mycology.

***– Meredith Blackwell,* PhD**
mblackwell@lsu.edu

-- Donald H. Pfister, PhD
dpfister@oeb.harvard.edu

Field Mycology at Raquette Lake in the Adirondacks
July 19 to August 1, 2003

This two week course in Field Mycology will be taught at the Huntington Camp facility of the Outdoor Education Center at Raquette Lake, a campus owned and operated by the State University of New York, College at Cortland. The course will emphasize field-work and laboratory techniques used in identifying macrofungi. Skills involving microscopic preparations, evaluation of histochemical reactions and proper tissue sectioning will be developed. Lecture and laboratory topics will cover the morphology, ecology, taxonomy and economic importance of the macrofungi. Students will also learn how to make scientifically accurate and valuable voucher specimens.

Raquette Lake is in the heart of New York State's 2.5 million acre Adirondack Forest Preserve. Huntington Camp, originally dubbed Camp Pine Knot by its creator, William West Durant, was the first of the Great Camps of the Adirondacks, and much of that old architecture is still present in the buildings that make up the campus. The facility is considered a State Historical site today, even though it is solely used for educational purposes by SUNY – College at Cortland. The Adirondack Forest Preserve has large tracks of wilderness and Camp Huntington sits at the edge of one of these large tracks. One can literally walk out the door of the laboratory and be in the forest in

Dr. Tim Baroni, Instructor

a matter of minutes. The mature forests and bogs are lush and diverse, and the corresponding diversity of fleshy fungi is high. Three semester hours of graduate credit or advanced undergraduate credit

MYCOLOGICAL CLASSIFIEDS *concl'd*

(Field Mycology -- Adirondacks con't)

are available from SUNY – College at Cortland. Tuition is based on resident vs. non-resident and graduate vs. undergraduate status. The cost of lodging and meals is $345.00. For additional information contact Dr. **Timothy J. Baroni**, Department of Biological Sciences, PO Box 2000, State University of New York – College at Cortland, Cortland, NY 13045. telephone: 607-753-2725. Email: **BaroniTJ@Cortland.edu**.

Diseases and Other Pests of Forest Trees in the Southern Appalachian Mountains
Highlands Biological Station, Highlands, NC
August 4-16, 2003

You will arrive on August 3 and the course begins on August 4.

[*Note:* This conflicts with the Annual APS Meeting in Charlotte, NC.]

Coordinator:

Dr. **Rich Baird**, Mississippi State Univ.

Instructors:

Dr. **Mark Windham**, University of Tennessee
Mr. **John Knighten**, Forest Health Unit, USFS (retired)
Dr. **Steven Jeffers**, Clemson University
Dr. **Jay Stipes**, Virginia Tech (retired)
Dr. **Alan Henn**, Mississippi State Univ.

The Southern Appalachian Mountains comprises a rich and diverse community of forest tree species and woody shrubs. Within this region, Highlands is located in the Blue Ridge Mountains which is near the Great Smoky Mountains National Park. The course will be taught in these and surrounding forest ecosystem and will include lectures, laboratory activities and field trips. Field trips will include moderate hiking on and off the Appalachian Trail. During the course, many forest diseases (biotic) will be discussed with emphasis on pathogen ecology, epidemiology, physiology, taxonomy, their transmission or dissemination mechanisms, and associated pests (e.g. insects and nematodes). Important diseases of the forest community will be reviewed such as dogwood anthracnose, beech bark disease, rusts of conifers, and chestnut blight. In addition, the newly emerging forest tree and woody plants pathogen, *Phytophthora ramorum*, will be discussed concerning it potential impact to the eastern forest system. Methods for identification of important pathogens such as *Phytophthora* spp. will be reviewed and several sessions will focus on the identification (keys and descriptions) of the fungal pathogens and wood decay fungi. Abiotic factors such as pollution, mechanical damage from humans and environment (e.g. ice damage) will be covered and their long-term impact on forest trees and woody vegetation community. Field trips to observe these types of forest pest damage will be arranged throughout the southern range. During the course, students will also learn to establish field impact plots and to determine the extent of damage and disease progression (epidemiology) associated with biotic and abiotic problems using GPS equipment. Associated mycorrhizal associations of fungi and forest trees will be covered if appropriate. Please refer to the following for last years activities **<http://www.msstate.edu/courses/rh131/forest.path/index.html>**.

For additonal information, contact Rich Baird.

***-- Richard Baird,* PhD**
662-325-9661
rbaird@plantpath.msstate.edu

THE MYCOLOGIST'S BOOKSHELF

In this issue we feature books received from February through April 2003, and list previously featured books received since April 2002. I am still working to clear the backlog of books for review that I have received and will be contacting you if you have requested books to review over the last several months. Thanks to all who have written to request a book to review and to suggest books for the bookshelf. Have patience, I have all your e-mails and will be working to answer your requests.

John Zak, *BOOK REVIEW EDITOR Email at* **john.zak@ ttu.edu**

BOOKS AND PUBLICATIONS RECEIVED FEBRUARY THROUGH APRIL 2003

None Received

PREVIOUSLY LISTED BOOKS FROM APRIL 2002

- **The *Amanita caesarea*-Complex**. Bibliotecheca Mycologica No 187. 2001. G Guzman and F Ramirez-Guillen. J Cramer in der Gebruder Borntraeger Verlagsbuchhandlung, D-14129, Berlin, Germany, 66pp. Price: Unknown. *Reviewer needed*.
- **Basic Biotechnology**, 2nd edition. 2001. C Ratledge and B Kristiansen (eds.), Cambridge University Press, The Eddinburgh Building, Cambridge CB2 2RU, UK, 568 pp. Price: $45 US. *Review needed*.
- ***Candida* and Candidiasis**. 2001. RA Calderone (ed). ASM Press. PO Box 605, Herdon, VA 2017, books@asmusa.org, 472 pp. Price: $100 US. *Review needed*.
- **Cell Biology of Plant and Fungal Tip Growth.** 2001. A Geitmann, M Cresti, and I B Heath (eds). NATO Science Series I. Life and Behavioural Sciences, IOS Press, Nieuwe Hemweg 6B, 1013 BG Amsterdam, Netherlands, www.iospress.nl, 241pp. Price: unknown. *Review needed*.
- **Dictionary of the Fungi, 9th edition.** 2001. PM Kirk, PF Cannon, JC David, and JA Stalpers (eds.). CABI Bioscience, Bakeham Lane, Egham, Surrey, TW20 9TY, UK, www.cabi.org, 655 pp. Price not confirmed. *Review in progress*.
- **Dictyostelium: Evolution, Cell Bioilogy, and the Development of Multicellularity.** 2001. RH Kessin and J Franke, Cambridge University Press, The Edinburgh Building, Cambridge CB2 2RU, UK. Price : $90.00 US. *Review in Inoculum 53(2): 18-19.*
- **A Dictionary of Plant Pathology** 2nd edition**.** 2001. P Holliday. Cambridge University Press, The Edinburgh Building, Cambridge CB2 2RU, UK, www.cambridge.org, 536pp. Price: Hardback - $120 US, Paperback - $45 US. *Review needed*.
- **Fungi in Marine Environments**. Fungal Diversity Research Series 7. 2002. KD Hyde (ed), Fungal Diversity Press, Center for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Pokfulam Road, Hong Kong, kdhyde@hkucc.hku.hk. 397 pp. No price provided. *Review needed*.
- **Fungal Pathogenesis: Principles and Clinical Applications**. 2002. RA Calderone, and RL Cihlar (eds.). Marcel Dekker, Inc., 270n Madison Ave., New York, NY. 10016, http://www.dekker.com, 762 pp. Price: $195 US. *Review in progress.*
- **Fungi as Biocontrol Agents: Progress, Problems, and Potential**. 2001. T Butt, C Jackson, and N Magan (eds.). CABI Bioscience, Bakeham Lane, Egham, Surrey, TW20 9TY, UK. 416 pp. Price not confirmed. *Review in progress.*
- **Fungi in Bioremediation**. 2001. GM Gadd (ed.), Cambridge University Press, The Edinburgh Building, Cambridge CB2 2RU, UK, www.cambridge.org. Price: $120 US. *Review in process.*
- **Fungi in Marine Environments**. Fungal Diversity Research Series 7. 2002. KD Hyde (ed), Fungal Diversity Press, Center for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Pokfulam Road, Hong Kong, kdhyde@hkucc.hku.hk. 397 pp. No price provided. *Review needed*.
- ***Fusarium*: Paul Nelson Memorial Symposium**. 2001. BA Summerell, JF Leslie, D Backhouse, WL Bryden, and LW Burgess (eds.), APS Press, 3340 Pilot Knob Road, St. Paul MN 55121-2097, www.shopapspress.org, 408 pp. $59 US. *Review needed*.
- **The Genus *Mycena* in South-Eastern Australia.** 2003. CA Grurinovic. , Fungal Diversity Press, Center for Research in Fungal Diversity, Department of Ecology and Biodiversity, The University of Hong Kong, Hong Kong SAR, China, www.hku.hk/ecology/mycology/FDP.html, 329pp. *Review needed.*
- **Guide to Yeast Genetics and Molecular and Cell Biology**. Vols 350 and 350. 2002. C Guthrie and GR Fink (eds), Published by Academic Press, csterv.ap@,elsevier.com 664pp, Vol. 351 776pp. Price: $79.95 US each. *Review needed*.
- ***Leptographium* Species: Tree Pathogens, Insect Associates, and Agents of Blue-Stain**. 2002. K Jacobs and MJ Wingfield, APS Press, 3340 Pilot Knob Road, St. Paul MN 55121-2097, www.shopapspress.org, 224 pp. $69 US. *Review needed.*
- **Lichens of Antarctica and South Georgia: A Guide to their Identification and Ecology.** Studies in Polar Research. 2001. DO Ovstedal and RL Lewis-Smith. Cambridge University Press, The Edinburgh Building, Cambridge CB2 2RU, UK, www.cambridge.org, 411pp. Price: $100 US. *Reviewed in Inoculum 53(4):20 – 21.*
- **Lichens of North America**. 2001. IM Brodo, SD Sharnoff, and S Sharnoff. Yale University Press, P.O.Box 209040, New Haven, CT 06520, 795pp. Price: $70 US. *Review in progress.*
- **Microorganisms in Home and Indoor Work Environments**. 2001. B Flannigan, RA Samson, and JD Miller (eds.), Taylor& Francis, 11 New Fetter Lane, London EC4P 4EE, 490 pp. Price: Unknown. *Review in progress.*
- **Molecular Biology of Fungal Development**. (Mycology Series/15). 2002. HD Osiewacz, Marcel Dekker, Inc. Cimarron Road, PO Box 5005,

THE MYCOLOGIST'S BOOKSHELF *concl'd*

Monticello, NY 12701-5185, bookorders@dekker.com, 608 pp. $195 US. Book *requested from publisher*.

- **Molecular and Cellular Biology of Filamentous Fungi**. 2001. N Talbot (ed). Oxford University Press, Great Claredon Street, Oxford OX2 6DP, UK. www.oup.co.uk.pas, see Practical Approaches Series for additional information, 267pp. price: $115 US. *Review needed.*
- **A Monograph of *Bionectria* (Ascomycota, Hypocreales, Bionectriaceae) and its *Clonostachys* Anamorphs**, (Studies in Mycology 46). 2001. H-J Schroers, Centraalbureau voor Schimmelcultures, PO Box 85167,Fungal Biodiversity Center, Utrecht, The Netherlands, www.cbs.knaw.nl. Price: 20,000 Euro. *Review needed*.
- **Mr. Bloomfield's Orchard: The Mysertious World of Mushrooms, Molds, and Mycologists**. 2002. N. Money. Oxford University Press, 198Madison Ave., New York, NY 10016-4314. www.oup.com. 208 pp. $26 US. *Review in Inoculum: 54:17-18.*
- **Mushrooms of CapCod and the National Seashore**. 2001. AR Bessette, AE Bessette, and WJ Neill. Syracuse University Press, 621 Skytop Rd, Suite 110, Syracuse, NY 13244-5290, sumweb.syr.edu/su_press/, 174pp. Price: Hardback - $60 US, Paper - $27 US. *Review needed.*
- **Mushrooms of Hawai'I: An Identification Guide**. 2002. DE Hemmes and DE Desjardin, Ten Speed Press, Berkeley, CA 94707, sarahg@tenspeed.com, 224 pp. Price: $40 US. *Review in Inoculum 54*: 18.
- **Mushrooms of Nepal**. 2000. MKAdhikari, Published by: KS Adhikari, O Laurence (Mycosphere), E Sano and G Kawi, Mailing address: 21/835 Adhikari Niwas, Alka Basti, Lainchour, Behind British Embassy, GPO Box no. 841, Kathmandu, Nepal, e_sano@ d2.dion.ne.jp. 236pp. Price: $43.00 includes shipping. *Review needed*.
- **The Mycota Vol VII A & B, Systematics and Evolution**. 2001. DJ McLaughlin, EG McLaughlin, and PA Lempke (eds.). Springer-Verlag New York, Inc., PO Box 19386, Newark, NJ 07195-9386, service@springer-ny.com, Part A 366 pp, Part B 259 pp. Price: Part A is $215 US, Part B is $159 US. *Review needed.*
- **Mycotoxin Protocols. Methods in Molecular Biology Vol. 157.** 2000. MW Truckess, AE Pohland (eds.). Humana Press Inc: 999 Riverview Drive, Suite 208, Totowa, NJ 07512 USA. 244 pp. *Review needed.*
- **Nomenmyx. A Nomenclatural TaxaBase of Myxomycetes**. Vol 16 in the Series Cuadernos de Trabajo de Flora Micológica Ibérica. 2001. C Lado. Consejo Superior de Investigaciones Cientificas, Real Jardin Botanico, Plaza de Murillo, 2-28014 Madrid, Spain. lado@ma-rjb.csic.es, 219 pp. $15.63 US. *Review needed*.
- **The Rainbow Beneath my Feet: A Mushroom Dyer's Field Guide**. 2001. AR Bessette and AE Bessette. Syracuse University Press, 621 Skytop Rd, Suite 110, Syracuse, NY 13244-5290, sumweb.syr.edu/su_press/, 176pp. Price: Unknown. *Review needed.*
- **A Revision of the Species Described in *Phyllosticta***. 2002. HA vander Aa and S Vanev. Publisher: Centraalbureau voor Schimmelcultures, www.cbs.knaw.nil. 510pp. Price: • 50,000. *Review needed.*
- **Pathogenic Fungi in Humans and Animals**, 2nd edition. Mycology Series Volume 16. 2003. DH Howard. Published by Marcel Dekker, www.dekker.com. 790pp. Price: $225 US. *Review needed*.
- **Slayers, Saviors, Servants, and Sex: An Expose of the Kingdom Fungi**. 2001. D Moore. Springer Verlag Customer Service, PO Box 2485, Secaucus, NJ 07096, orders@springer-ny.com. Price not confirmed. *Reviewed in Inoculum 54:7-18.*
- **Stem Rust of Wheat: From Ancient Enemy to Modern Foe**. 2001. PD Peterson, APS Press, 3340 Pilot Knob Road, St. Paul MN 55121-2097, www.shopapspress.org, 168 pp. $69 US. *Review requested*.
- **Taxonomy and Pathology of *Cylindrocladium* (*Calonectria*) and Allied Genera**. 2002. PW Crous. APS Press, 3340 Pilot Knob Road, St. Paul MN 55121-2097, www.shopapspress.org, 294 pp. $69 US. *Review needed*.
- **Tropical Mycology: Volume 1. Macromycetes**. 2001. R Watling (ed). CABI Bioscience, Bakeham Lane, Egham, Surrey, TW20 9TY, UK. 208 pp. Price not confirmed. *Review needed.*
- **Tropical Mycology. Volume 2 Micromycetes**. 2002. R Watling, JC Frankland, AM Ainsworth, S Isaac, and CH Robinson (eds), CABI Publishing, CABI International, Wallingford, Oxon OX10 8DE, UK, www.cabi-publishing.org, 203pp. Price: $75.00 US. *Review needed.*

CALENDAR OF EVENTS

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

2003 (May 25-29). **International Society for Human and Animal Mycology.**
San Antonio, TEXAS
Heather Drew
Imedex®®, Inc.
770.751.7332
www.imedex.com
http://www.isham.org

2003 (July 26 - 31). **2003 MSA Annual Meeting.**
Asilomar, CALIFORNIA
Tom Bruns
510-642-7987
boletus@socrates.berkeley.edu
http://msafungi.org
http://www.asilomarcenter.com/

2003 (August 10-15). **Fourth International Conference on Mycorrhizae (ICOM 4)**
DETAILS: *Inoculum* 53(4):19.
Montréal, QUÉBEC
Yolande Dalpé
ECORC / AAC
Ottawa K1A OC6 Canada
613-759-1381 (phone)
dalpey@em.agr.ca
http://www.congresbcu.com/icom4

2003 (August 17-23). **Fourth International Symbiosis Congress.**
DETAILS: *Inoculum* 53(3):61
Halifax, NOVA SCOTIA
David Richardson
902-420-5493 (phone)
david.Richardson@stmarys.ca
http://people.bu.edu/dzook/

2003 (September 22-27). **14th Congress of European Mycologists.**
Yalta, Crimea, UKRAINE
XIV CEM Secretariat
Department of Mycology
M. G. Kholodny Institute of Botany
Tereshchenkivska Steet 2
UA-01601 Kiev, Ukraine
xivcem@symbiosis.kiev.ua
http://www.biodiversity.ac.psiweb.com/14cem

2003 (September 28 - October 4). **21st foray of the European Cortinarius Society/ 21es Journées européennes du Cortinaire.**
Podbanské, SLOVAKIA
Slovak Mycological Society
Institute of Botany
Dúbravská 14
SK-842 23 Bratislava, Slovakia
botumyko@savba.sk
http://www.jec-cortinarius.org and/or
http://fungi.sav.sk/jec21

2003 (October 15-17). **VIII Congreso Nacional de Micologia (8th Mexican Mycological Conference).**
DETAILS: *Inoculum* 54(2):12.
UAEM, Toluca, MEXICO
Mexican Mycological Society
Cristina Burrola Aguilar
Facultad de Ciencias, UAEM
Instituto Literario No. 100, C.P. 50000
Toluca, Mexico
Tel/Fax. 017222965553, 54 & 56
cba@uaemex.mx
http://www.tap-ecosur.edu.mx/smdm/8cnm.htm

2004 (March 14-17). **ISMS XVIth International Congress.**
DETAILS: *Inoculum* 54(1):10
Miami, FLORIDA
Laura Phelps
American Muchroom Institure
One Massachusetts Avenue, NW
Washington, DC 20001 USA
202.842.4344 (phone)
202.842.2345 (Fax)
http://www.americanmushroom.org/isms.htm

2004. **MSA Annual Meeting.**
Asheville, NORTH CAROLINA

2005 (July 18-23). **XVII International Botanical Congress**
DETAILS: *Inoculum* 54(3):54
Vienna, AUSTRIA
Dr. Josef Greimler
Secretary-General, IBC 2005
Institute of Botany, Univ. of Vienna
Rennweg 14
A-1030 Vienna, Austria
office@ibc2005.ac.at
+43-1-4277-54123 (phone)
+43-1-4277-9541 (fax)
office@ibc2005.ac.at
http://www.ibc2005.ac.at/

MYCOLOGY ON-LINE

Pyrenomycetes for Southwestern France
http://pyrenomycetes.free.fr

This site is devoted to the Pyrenomycetes (Ascomycota) collected by **Françcoise Candoussau**, **Jacques Fournier** and **Jean Françcois Magni** in southwestern France. The aim of the authors is to present photographs of fungi that have been previously not or rarely illustrated, along with descriptions based on the material they collected and interactive and dichotomous keys.

It started at the end of February 2003 with the xylariaceous genera allied to *Hypoxylon*. The authors hope it will enable "advanced" amateurs to improve their knowledge of these tiny but fascinating fungi.

– Jacques Fournier
jacques.fournier@club-internet.fr

MYCOLOGY ON-LINE *con't*

CABI Bioscience Databases
http://www.indexfungorum.org/

CABI Bioscience (incorporating IMI) maintain a number of internationally important databases. Here you can search, on-line, a number of these databases.

The world database of fungal names (**IndexFungorum; a.k.a. funindex**) contains over 345,000 names of fungi (including yeast, lichens, chromistan fungi, protozoan fungi and fossil forms) at species level and below. It has been derived from a number of published lists including Saccardo's Sylloge Fungorum (contributed by SBML, USDA), Petrak's Lists, Saccardo's Omissions, Lamb's Index, Zahlbruckner's Catalogue of Lichens (comprehensive for names at species level only but with an increasing number of names of infraspecific taxa) and CABI's Index of Fungi. A new collaboration between Centraalbureau voor Schimmelcultures (CBS) and CABI Bioscience will see a significant increase in the information content in Index Fungorum.

A name record will usually have a reference to an entry in one of the bibliographic catalogues cited above and, in addition, more recent records from the Index of Fungi will have the full citation from the source publication (excluding those from the last 5 years). Author citations conform with the Brummitt & Powell standard (now searchable on line through IPNI), or are indicated '{?}' thus. Many records include information on taxonomic synonymy and publication details derived from numerous acknowledged sources. You may search the database by either the species name or the specific epithet.

The **Bibliography of Systematic Mycology** provided a survey of the literature encompassing the biodiversity, classification, distribution, evolution, identification, nomenclature, phylogeny, systematics and taxonomy of fungi (including those groups traditionally treated as fungi but now better classified in other kingdoms). The printed BSM provides full bibliographic details of relevant literature from books, conference proceedings, monographs and serials arranged under broad taxonomic categories, with author and generic indexes, and is published twice a year, cumulating into a volume over five years. Some 1500-2000 items per annum give comprehensive cover of both the pure and applied systematic mycological literature, from the level of kingdom right down to population. A back-file of these records covering the period from 1986 is now searchable on-line using genus or author names.

The **Dictionary of the Fungi** (currently 9th edition) published by CABI Publishing also contains the current consensus on the fungal taxonomic hierarchy to the rank of genus. Here you may search the database for the status of generic names, or walk down the hierarchy from the rank of Kingdom. The entries for each genus generally include authors and place of publication together with the type species and other data.

A recent addition is the database of **family names** which includes authors, place of publication and type genus. This database will eventually be expanded to include all supra-familial ranks.

CABI Bioscience is coordinating the fungal component of the **Species2000** project; for more information regarding this global initiative visit their website. Here you may search a small but growing number of taxonomically complete datasets - **global species databases**.

MYCOLOGY ON-LINE DIRECTORY

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

ASCOMYCOTA – NEW CLASSIFICATION (51-5)
http://194.131.255.3/cabipages/Names/FundicNew.asp

ASOCIACION LATINOAMERICANA DE MICOLOGIA (51-5)
http://www.ecologia.edu.mx/alm/

AUSTRALASIAN MYCOLOGICAL SOCIETY WEBSITE FOR INTRODUCTORY FUNGAL BIOLOGY (53-4)
http://bugs.bio.usyd.edu.au/mycology/default.htm

AUTHORS OF FUNGAL NAMES (54-2)
http://www.indexfungorum.org/AuthorsOfFungalNames.htm

BIBLIOGRAPHY OF SYSTEMATIC MYCOLOGY (51-6)
http://194.131.255.3/cabipages/BSM/bsm.htm

BRITISH MYCOLOGICAL SOCIETY (54-1)
http://britmycolsoc.org.uk

CABI BIOSCIENCE DATABASES (54-3)
http://www.indexfungorum.org/

EUROPEAN POWDERY MILDEWS (52-2)
http://.nt.ars-grin.gov

FUNGA VERACRUZANA (53-6)
http://www.uv.mx/institutos/forest/hongos/funga-vera/index.html

HADRIANUS JUNIUS STINKHORNS (52-2)
http://www.collectivesource.com/hadrianus

IMC7 (51-3)
http://lsb380.plbio.lsu.edu/ima/index.htm

ING (INDEX NOMINUM GENERICORUM) DATABASE (52-5)
http://rathbun.si.edu/botany/ing/ingForm.cfm

INTERACTIVE CATALOGUE OF AUSTRALIAN FUNGI (52-1)
http://www.rbgmelb.org.au/fungi/

MYCOLOGY ON-LINE *concl'd*

INTERACTIVE KEY, DESCRIPTIONS & ILLUSTRATIONS FOR *HYPOMYCES* (52-6)
http://nt.ars-grin.gov/taxadescriptions/hypomyces/

MSA BULLETIN BOARD (51-5)
http://msafungi.org/bulletinboard/

MYCOLOGIA ON-LINE (53-3, page 18)
http://www.mycologia.org

MYCOLOGICAL PROGRESS (52-3)
http://www.botanik.biologie.uni-muenchen.de/botsyst/mycpro.html

MYCOSEARCH WEB DIRECTORY/SEARCH ENGINE (51-5)
http://www.mycosearch.com

MUSHROOM WORLD [NEW KOREAN/ENGLISH SITE IN 2001] (51-6)
www.mushworld.com

NAMA POISON CASE REGISTRY (51-4)
http://www.sph.umich.edu/~kwcee/mpcr

PATHOGENIC FUNGI FROM SOUTH AFRICA (52-4, page 29)
http://nt.ars-grin.gov/fungaldatabases/southafrica
or **http://www.saspp.co.za/**

PLANT-ASSOCIATED FUNGI OF BRAZIL (54-2)
http://nt.ars-grin.gov
(Select Search Fungal Databases, option 3, Host-Fungus Distributions)

PYRENOMYCETES FOR SOUTHWESTERN FRANCE (54-3)
http://pyrenomycetes.free.fr

SYSTEMATICS OF THE SAPROLEGNIACEAE (53-4)
http://www.ilumina-dlib.org

WEB MSA (51-6)
http://msafungi.org

ADDITIONAL MSA ABSTRACTS

BERUBE, J.A[1]., STEFANI, F.O.P, PIERCEY-NORMORE, M.D.[2], GUILLAUMIN, J.J.[3] and HAMELIN R.C.[1] [1]Canadian Forest Service, 1055 du PEPS, P.O. Box 3800, Ste-Foy, QC, G1V 4C7 Canada. [2]Dept Botany, Univ. Manitoba, Winnipeg, MB, R3T2N2, Canada. [3]INRA Centre de Clermont-Ferrand, UMR 234 Breset, F-63039, Clermont Ferrand, France. **Phylogeny of the genus *Armillaria* from five continents using coding genes.**

The genus *Armillaria* has been studied extensively to determine its evolutionary history in relation to virulence, hosts and distribution. Known patterns of phylogenetic evolution of this genus is only based on nuclear ribosomal ITS sequence which yields poor resolution among some species. To improve resolution between species, we sequenced and analyzed selected coding genes, including actin, beta-tubulin and G3PD, and compared with published ITS phylogeny. Phylogenetic patterns of more than 30 species of *Armillaria* from North America, Europe, Africa, Asia, Australia and South America will be presented in relation to distribution, morphology, hosts and virulence.

*ROBINSON, CLARE H., SAUNDERS, PHILIP W. and MADAN, NANETTE J. Dept. Life Sciences, King's College, University of London, Franklin-Wilkins Building, 150 Stamford Street, London SE1 9NN, UK. **Does simulated N deposition affect saprotrophic fungal biodiversity at a high Arctic site?**

N is particularly scarce in Arctic soils, but inputs of pollutant N are large in comparison with the amount recycled from dead organic matter, a process predominantly driven by decomposer fungi. The diversity of such fungi is likely to be sensitive to N additions but the nature of any effects in high Arctic soils is unknown. The aims of the study were to determine (1) the effects of N (with and without P) enrichment on the diversity of soil microfungi in a high Arctic polar semi-desert ecosystem, and (2) the changes in this diversity over the summer season. P was added because it may limit plant and fungal response to N in this ecosystem. The field-site at Ny-Aalesund, Svalbard (78 degrees N) was set up in June 2000, with factorial combinations of three rates of N and two of P. Soil samples were collected in late June and in early August 2001 from both bare mineral soil areas and under patches of Dryas octopetala. Soil fungi were isolated and a numerical measure of community diversity was calculated. The number of fungal species isolated was low, ranging from 2 to 8 per treatment per sampling per soil. The fungal assemblages isolated from the organic soils were usually more diverse than those of the mineral ones, and fungal diversity was generally greater in early August than in late June. The relationship between increased N and fungal diversity will be discussed.

inoculum

The Newsletter of the Mycological Society of America

Supplement to Mycologia
Volume 54, No. 3
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Inoculum is published six times a year and mailed with *Mycologia*, the Society's journal. Submit copy to the Editor as email (in the body, MS Word or WordPerfect attachment in 10pt Tms Rmn font), on disk (MS-Word 6.0,WordPerfect, *.tif. *.jpg), or hard copy. Line drawings and sharp glossy photos are welcome. The Editor reserves the right to edit copy submitted in accordance with the policies of *Inoculum* and the Council of the Mycological Society of America.

Donald G. Ruch, Editor
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Muncie, IN 47306-0440
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