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— In This Issue —

Cordyceps **1**
Canopy Soils **4**
MSA Business **5**
Abstracts **6**
Mycological News **40**
Mycologist's Bookshelf . . . **44**
Mycological Classifieds . . . **50**
Mycology On-Line **52**
Calender of Events **53**
Sustaining Members **55**

— Important Dates —

August 15 Deadline:
Inoculum 55(5)

July 17-21, 2004:
MSA-NAMA, Asheville, NC

July 30-Aug. 5, 2005:
MSA-MSJ, Hilo, HI

August 15-19, 2005:
International Congress on the Systematics and Ecology of Myxomycetes V

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Cordyceps Diversity and Its Preservation in Korea

By Jae-Mo Sung

Cordyceps are in general fungal species which produce mushroom-like fruit bodies on their insect hosts. They grow inside insects during winter and form fruit bodies in the summer. They infect living insects, invertebrates and other hypogeal *Elaphomyces* species, plant seeds and use their nutrient resources. They kill their hosts, form endosclerotium inside the host body and later produce stromata above the host body. There are about 300-400 *Cordyceps* species, which belong to Family Clavicipitaceae, Order Hypocreales of perithecial Ascomycetes (Kobayasi, 1941; Kobayasi and Shimizu, 1983; Mains, 1957, 1958; Petch, 1931, 1932, 1939, 1942; Shimizu 1994, 1997; Sung, 1996). In Korea, about 76 species of entomopathogenic fungi including *Cordyceps* species have been documented (Sung, 1996). Besides Korea, *Cordyceps* species are distributed all over the world including Nepal, China, Japan, America, etc. During my long experience, *Cordyceps* species are relatively more distributed in Korea with 4 distinct seasons, despite its small geographical area. *Cordyceps* and other entomopathogenic fungal species control insect populations as well as produce bio-active compounds useful for both human health and plant growth regulation.

Cordyceps species can survive in soil and infect insect hosts through integuments and grow inside respiratory and digestive tracts. They kill their hosts and grow inside them during winter in the form of endosclerotium, which help to preserve the shape of the host, and produce stromata the following year. Mostly, stromata are produced from mouth, thorax, head and abdominal portion of the hosts. At maturity, the apical portions of stromata produce ascospores and asexual spores (in case of asexual fungi) which again infect hosts in the summer and autumn after their release in nature.

Continued on following page

Dr. Jae-Mo Sung teaches students at a *Cordyceps* exhibition.

Cordyceps militaris

Cordyceps pentatomi

Fruiting bodies mostly form in the summer during warm temperature and high humidity in broad leaved forests. In Korea, distribution area and period of *Cordyceps* differs from species to species. In general, fruiting bodies are produced from late May to late October. Natural habitats of *Cordyceps* species depend upon their host type and population. Those *Cordyceps* species of which hosts are buried in soil are *C. militaris*, *C. kyushuensis*, *C. agriota*, *C. pruinosa* and *C. longissima*. *C. nutans*, *C. pentatomi*, *C. sphecocephala*, *C. tricentri*, *C. scarabaeicola*, *C. tuberculata* and *Paecilomyces tenuipes* are the species of which hosts are intermingled in the fallen leaves. Hosts of *C. nakazawai* and *C. nikkoensis* are buried inside tree trunk. *C. agriota*, *C. nigrella*, *Torrubiella neofusiformis*, *Hymenostilbe odonatae*, *Paecilomyces tenuipes* and *Metarhizium anisopliae* are usually found on tree leaves or fallen leaves.

Cordyceps longissima

For isolation of *Cordyceps* species, ascospores are better source than stromatal tissue. Ascospores are collected from mature stromata on water agar first. A small block of water agar containing discharged ascospores is then transferred to nutrient medium such as potato dextrose agar (PDA) or Sabouraud's dextrose (maltose) agar supplemented with yeast extract (SDAY, SMAY) and incubated at 25C. Air-dried specimens and isolates are preserved in Entomopathogenic Fungal Culture Collection (EFCC), Kangwon National University, Chuncheon, Korea.

Entomopathogenic Fungal Culture Collection (EFCC), Kangwon National University (www.mushtech.org) is supported by a grant to JRL from the Strategic National R&D Program through the Genetic Resources and Information Network Center funded by the Korean Ministry of Science and Technology of Korea. Its main objectives are to collect and preserve *Cordyceps* and other entomopathogenic fungal specimens and isolates from Korea and other parts of the world. Diverse collections of entomopathogenic fungi have been made from Korea and some parts of Nepal and other countries and are exchanged among research institutes for pure and scientific purposes. Besides specimens and isolates, a large number of about 14000 color slide pictures have been preserved in EFCC. Those materials have been used for publicity of *Cordyceps* and other entomopathogenic fungi among common people. *Cordyceps* exhibition is conducted every year in Insa-Dong, Central Seoul every year. Also, a *Cordyceps* museum has been established in Central Museum of Kangwon National University (www.ibfk.org).

I would like to request readers to visit website www.mushtech.org for more information regarding *Cordyceps* and entomopathogenic fungal species of Korea. Also, you can order *Cordyceps* isolates for pure and scientific research.

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Torrubiella neofusiformis

Hymenostilbe odonatae

Cordyceps nutans

Cordyceps pruinosa

Sampling Canopy Soils in New Zealand

By Steven L. Stephenson

One notable feature of tropical forests, particularly montane cloud forests in the Neotropics, is the abundance and diversity of vascular and nonvascular epiphytes. The larger branches and, to some extent, the trunks of the trees upon which these epiphytes occur typically have a mantle of dead organic matter (literally a "canopy soil") derived from decaying epiphytes, partially decomposed tree bark, insect frass, and intercepted litter. Trees in temperate rain forests on the southwestern coast of the South Island of New Zealand characteristically support communities of vascular epiphytes that are comparable to those of tropical forests, and the mantle of canopy soil associated with these epiphyte communities is often rather appreciable, sometimes achieving a thickness of more than 20 cm. It seems likely that such well-developed canopy soils would support a diverse assemblage of microorganisms, and the field component of a research project designed to characterize the mycetozoans, mycorrhizal fungi, zoosporic fungi and other microfungi found in the canopy soil microhabitat of these forests was carried out in a study area near Haast, New Zealand, during early March of 2004.Participants included **Steve Stephenson** and **Fred Spiegel** from the University of Arkansas, two of their undergraduate students (**Craig Chu** and **Natasha Jones**), **Randy Darrah** from Fairmont State University, **David Orlovich** and **Rob Daly** from the University of Otago in Dunedin, New Zealand, and **Suzy Draffin**, one of David's students (Fig. 1). As a result of the superb climbing ability of Rod Daly, it was possible to collect some samples from more than 20 m above the forest floor (Fig. 2).

Methods used to study the material collected during the March trip have included microscopic examination of field collected roots, primary isolation of microorganisms in the laboratory with standard culturing techniques used for the particular group being considered, and molecular characterization of microfungal biodiversity from DNA extracted from environmental samples. In addition to the research effort being carried out at the University of Arkansas and the University of Otago, some samples are being examined for zoosporic fungi by **Joyce Longcore** at the University of Maine.

The research in New Zealand was supported by a grant from the National Science Foundation. Additional information on the project is available on the University of Otago web site (www.botany.otago.ac.nz/mycology/).

Questions or comments should be sent to Steven L. Stephenson, Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville, AR 72701 or email at slsteph@uark.edu or wvmyxo@hotmail.com.

Fig. 1. (Above) Participants in the research project carried out in New Zealand. L to R: Steve Stephenson, Barbara Stephenson (Steve's wife), Craig Chu, Fred Spiegel, Natasha Jones, Rob Daly, Randy Darrah, Suzy Draffin, and David Orlovich.

Fig. 2. (Right) Rob Daly climbs a tree to collect samples of canopy soil from more than 20 m above the forest floor.

MSA Secretary Email Express

Email Polls

Council voted on the following email polls from February 1st to June 15th 2004.

E-Poll 2004-2: Council approved three amendments to the **MSA By-laws** to be included on the 2004 ballot. [All three motions were subsequently passed by the membership during the spring balloting. For complete revisions please see the MSA Society web site.]

1: Article IV (E): Addition of a new rotating committee on specific expertise, in the area of **Genetics and Cell BioloGy**.

2: Article IV (F) (5) Alterations to reflect the evolving responsibilities of the **Electronic Communication and Web Page Management Committee.**

3: Article IV-E-6-c: Addition of the administration of the Clark Rogerson Award and other appropriate awards to the **Research Awards Committee**.

E-Poll 2004-3: Dr. Donald Natvig was heartily approved as the new Editor-in-Chief of *Mycologia*, as recommended by the Search Committee, chaired by President-Elect, David **McLaughlin**.

E-Poll 2004-4: One new Honorary Member and five MSA Fellows were approved as recommended by the **Honorary Awards Committee**, chaired by Orson **Miller.** The recipients will be announced at the Annual Business Meeting in Asheville, North Carolina, July 2004.

E-Poll 2004-5: Council approved a motion to make the **Centraalbureau voor Schimmelcultures** an Honorary Member Institute of the Society and to present them with a plaque in honor of their centenary.

E-Poll 2004-6: A contribution of $500 was approved in support of the 1st International **Fungal Proteomics Symposium** organized by the Pacific Northwest National Laboratory to be held in Portland Oregon, October 2004.

E-Poll 2004-7: Following up on discussions at the Midyear Meeting, Executive Council approved a motion that the **MSA 2006** Annual Meeting be held with the American Phytopathological Society (APS) in Quebec City, July 29-Aug 6th.

E-Poll 2004-8: The recommendations for the Alexopoulos Award and the Weston Award were approved as put forward by the **Distinctions Awards Committee**, chaired by Greg **Mueller**. The recipients will be announced at the Annual Business Meeting in July.

New Members

The MSA extends a warm welcome to fourty-four new or returning members. From February through May the following candidates applied for MSA membership. New memberships will be formally approved by the Society at the Annual Business Meeting in Asheville, North Carolina, July 2004. *Australia*: **Teena Burgess**; *Canada*: **Young Lim**; *China*: **Wei Jiang-Chun**, **Xiao-Qing Zhang**, **Yi-Jian Yao**; *Costa Rica*: **Javier Brenes**; *Germany*: **Philomena M Bodensteiner**; *Japan*: **Richard P Shefferson**; *Korea*: **Yeonghan Han**, **Yunju Kim**; *South Africa*: **Emma Theodora Steenkamp**; *Turkey*: **Mustafa Isiloglu**; *United States*: **Chandalin M Bennett**, **Gregory M Bonito**, **Glenn Boyd**, **Ania Boyd**, **Catharine Catranis**, **Randy Darrah**, **Vanessa Maria De Souza Madchado**, **Greetchen M Diaz**, **Joseph Dumanov**, **Astrid Ferrer**, **Jennifer L Gillett**, **Ian Herriott**, **Rebecca Huskins**, **Ariunaa Jalsrai**, **Kevin Geoffrey Jones**, **Richard Kiyomoto**, **David S LeBauer**, **Erik Lilleskov**, **Darlene M Loprete**, **Keerthi Mandyam**, **Jordan Mayor**, **Nancy Mcclenny**, **Rachel S Novick**, **Ghulam Rabbani**, **Satyendra Nath Rajguru**, **Gail L Redberg**, **Megan K Romberg**, **Kimberley Smith**, **Monica Torres**, **Maho Uchida**, **Djibo Zanzot**.

Emeritus Candidates

Since my last report, one candidate, **Larry J. Littlefield,** has applied for Emeritus status which is conferred upon retired or retiring members who have at least 15 years good standing with the Society. Emeritus status will be formally approved by the general membership at the Annual Business Meeting in July.

Annual Report Requests

In preparation for the Annual Council Meeting requests for annual reports were sent out to all Committee Chairs and Representatives on June 6. These reports and other issues will be discussed at the Council Meeting to be held on Saturday, July 17th, in Asheville.

Respectfully submitted
Faye Murrin
MSA Secretary

MSA ABSTRACTS

*ABLER, R.A.B, AND MILLER, O.K., JR. Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg VA. 24061 **Ectomycorrhizal fungal diversity and colonization of naturally regenerated pine seedlings on a disturbed site in Floyd County, Virginia.**

The belowground ectomycorrhizal community colonizing *Pinus strobus* and *Pinus virginiana* seedlings on a roadcut fill site in Floyd County, Virginia was studied using morphotyping and DNA sequencing techniques. Sampling was performed on the fill site and the road embankment from which the fill was taken. The fill soil was characterized as having high acidity and no organic matter. Seedlings under one year old were sampled and the entire root systems examined for percent ectomycorrhizal colonization, number of morphotypes present, and number and identity of ectomycorrhizal taxa based on molecular analysis. Ectomycorrhizal colonization ranged from around 30 to 80 percent, with wide variation among samples. This suggests that ectomycorrhizal inoculum existed in patches on the disturbed soil. Twelve different ectomycorrhizal taxa were identified, with *Scleroderma* c.f. *citrinum* representing the dominant ectomycorrhizal mycobiont for both the road embankment and fill sites. Most of the identified ectomycorrhizal species were considered "early stage" or "multi-stage" fungi. Two ericoid mycobionts, *Hymenoscyphus* sp. and *Oidiodendron* sp. were putatively identified colonizing ectomycorrhizal hosts. This supports other studies suggesting that, contrary to traditional assumptions, ectomycorrhizal and ericoid mycobionts may be of the same taxonomic group.

*ABLER, R.A.B. AND MILLER, O.K., JR. Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, Virginia. 24061. **Inter- and intraspecific variation in copper and zinc tolerance among ectomycorrhizal fungi.**

Copper and zinc are micronutrients essential for fungal and plant growth, but, these metals are toxic at elevated concentrations. Increased metal concentrations may significantly reduce ectomycorrhizal growth and colonization of tree seedlings. Axenic screening of ectomycorrhizal isolates is an effective way to examine intrinsic fungal tolerance to a given metal or metals. Axenic tolerance was determined by colony growth on amended agar plates. *Suillus granulatus* and *Pisolithus tinctorius* were more tolerant to copper than *Paxillus involutus*, however none of the species showed growth past 100 ppm Cu. *Suillus granulatus* was most tolerant to zinc, followed by *Paxillus involutus* and finally *Pisolithus tinctorius*. Sectoring was observed on several plates containing colonies of *Suillus granulatus* strain VT 1990. Of the ten isolates tested (8 sectors, VT 1990 "parent strain", and VT 2176), one sector showed a higher tolerance for copper than VT 1990, VT 2176, and the other sectors. One isolate from nature, VT 2176, and three sectors (A, B, and D) did not grow well on agar amended with high levels of zinc. Inter-simple sequence repeat (ISSR) fingerprinting was performed to determine whether the morphologically distinct sectors differed genetically or whether the sectors were evidence of phenotypic plasticity within the fungus.

ADAMCIK, SLAVOMIR. Institute of Botany, Slovak Academy of Sciences, Dubravska cesta 14, SK-842 23, Bratislava, Slovakia. **Morphometric analysis in the genus *Russula*.**

A large number of prevailingly amateur mycologists has been interested in the genus *Russula*, because members of the genus produce relatively large and nice basidiocarps. This caused several problems in taxonomy and nomenclature of the genus. Uncertain interpretation of described characters and dubious taxonomic value of some prevailingly macromorphological characters are a part of these problems. A more precise system is proposed for better understanding of infraspecific and infrageneric variability of measured characters. Precise interpretation and measurement of micromorphological characters, such as spore ornamentation and shape and size of terminal cells of generative hyphae in the pileipellis, should allow using new and more stable characters for delimitation of taxa. Use of scales for qualitative characters enables comparison of average values of measurements with statistical analyses. Afterwards, it is possible to perform numerical analysis of measured characters, a method that is practically unknown in classical mycology, but is frequently used for comparison of DNA fragments. Use of numerical analyses will be demonstrated on particular examples.

*AIME, M.C.[1] AND PASTOR-CORRALES, M.A.[2] [1]Systematic Botany and Mycology Laboratory, [2]Vegetable Laboratory, USDA-ARS, Beltsville, MD 20705. **Host gene pool specialization in *Uromyces appendiculatus*, the common bean rust.**

We explored genotypic diversity in a global collection of isolates of *Uromyces appendiculatus*, causal agent of rust of common bean, using both molecular markers and virulence assays. For virulence analysis we used a set of 12 common bean *Phaseolus vulgaris* differential cultivars, six each from the Andean and the Middle American bean gene pools. Genotypic diversity was examined with alpha 1 elongation factor sequences and ISSR analyses. Phenotypic and genotypic results were congruent and revealed the existence of two distinct groups of pathogen isolates that corresponded to the Andean and Middle American gene pools of the common bean host. These results also revealed that the *U. appendiculatus* Andean gene pool is less diverse and has greater host-specificity compared to the Middle American gene pool. A molecular assay has been developed to rapidly identify the group to which isolates of *U. appendiculatus* belong.

*AKERS, BRIAN P., OVREBO, CLARK L. St. Andrews Presbyterian College, Laurinburg, NC 28352; Department of Biology, University of Central Oklahoma, Edmond, OK 73034. ***Leucoagaricus bivelatus*, a new volvate lepiotoid species from Panama.**

A new lepiotoid species, *Leucoagaricus bivelatus*, is described from Barro Colorado Island, Panama. It is one of the few species of lepiotoid fungi to possess a well-developed universal veil. In addition to free lamellae and partial veil, both characteristic of lepiotoid fungi, this fungus has a distinct volva which forms by dehiscence of the universal veil. Other distinguishing features of the fungus include a radially fibrillose, bluish black pileus surface, off-white, non-staining lamellae and stipe, and rather broad cheilocystidia. *Leucoagaricus bivelatus* is most closely related to *L. volvatus* Bon & Caballero. *Leucoagaricus bivelatus* differs by having larger basidiospores and wider cheilocystidia.

*ANDERSON, JENNIFER L.[1], CHEN, WEIDONG[2], BEEVER, JON[3], SHEARER, CAROL A.[1]. [1]Dept. of Plant Biology, University of Illinois at Urbana-Champaign, Urbana IL 61801. [2]USDA-ARS, Washington State University, Pullman WA 99164. [3]Dept. of Animal Science, University of Illinois at Urbana-Champaign, Urbana IL 61801. ***Tetracladium marchalianum*: sex, space, and time.**

Aquatic hyphomycetes contribute to energy flow and nutrient spiraling in rivers by making energy and fixed carbon in autumn-shed leaves available to aquatic invertebrates. These fungi are haploid, predominantly or exclusively asexual, have restricted dispersal abilities, and experience yearly population bottlenecks as the amount of available substrate decreases in late summer; four factors that may limit the ability of populations of aquatic hyphomycetes to acquire and maintain genetic diversity. *Tetracladium marchalianum*is used in this study to answer three questions pertaining to the natural histories and evolutionary potential of these ecologically important fungi. 1) Is genetic recombination contributing to genotypic diversity of this fungus? 2) How is genotypic diversity distributed among populations of this fungus? 3) Is genotypic diversity changing over time as population size rises and falls seasonally? To answer these questions, eight polymorphic microsatellite loci were identified for *T. marchalianum*and used to obtain multilocus haplotypes for use in population genetic analyses. AFLP analyses are currently underway to supplement the microsatellite data. Research to date reveals no evidence for genetic recombination for this species, high genotypic diversity within populations, and population differentiation only among the most distant populations studied.

*ANNIS, SEANNA L. AND STUBBS, CONNIE S. Dept. of Biological Sciences, University of Maine, Orono ME 04469**. Fungi associated with leaves and their involvement in leaf spot diseases of lowbush blueberry in Maine.**

Estimates of leaf spot diseases in lowbush blueberry (*Vaccinium angustifolium*) fields were made from 1999 to 2002 in Maine. Samples of leaves, some showing signs of leaf spot symptoms, were surface sterilized and the fungi associated with the leaves identified. The incidence of leaf spot in crop bearing fields did not vary significantly over the study suggesting that weather conditions may not have a strong effect on this disease complex since 2000 and 2001 were severe drought years in Maine. For 5 fields examined over 4 years, the average incidence of leaf spot in the crop bearing years (2000 and 2002) was significantly higher than in nonbearing years (1999 and 2001). *Alternaria, Aureobasidium*, and *Cladosporium* were commonly isolated from leaves. Only 11 of the 24 fungi most frequently identified from infected leaves in 1999 were also identified from leaves in 2000 and/or 2001 suggesting that there is a complex of fungi that colonize the leaves, but the prevalence of a particular genus varies between years.

Continued on following page

*ARNOLD, A. ELIZABETH, SARVATE, SNEHAL, AND LUTZONI, FRANÇOIS. Department of Biology, Duke University, Durham, NC 27708. **Diversity and specificity of endophytic fungi associated with representatives of major plant lineages.**

We surveyed fungal endophytes associated with eight species representing major lineages of land plants (ferns and allies, conifers, and angiosperms) in North Carolina, USA, with the goal of understanding broad-scale patterns of endophyte diversity, species composition, and culturability. We isolated 998 endophytic fungi from three individuals/species (*Huperzia*, Lycopodiaceae, 47 isolates; *Equisetum*, Equisetaceae, 18 isolates; *Polystichum*, Dryopteridaceae, 57 isolates; *Juniperus virginiana*, Cupressaceae, 119 isolates; *Pinus taeda*, Pinaceae, 138 isolates; *Arundinaria gigantea*, Poaceae, 123 isolates; *Magnolia grandiflora*, Magnoliaceae, 196 isolates; *Acer barbatum*, Aceraceae, 106 isolates), with infections observed in 27-100% of tissue segments. Examination of nrDNA data (ITS) for 218 unique morphotypes indicated that although some fungal groups occurred in all host species (e.g., Xylariaceae), endophyte abundance and diversity, and the species composition of dominant endophytes, differed among plant lineages. Direct PCR for three focal host taxa (*Equisetum, Pinus*, and *Magnolia*) indicated a higher infection rate and altered conclusions regarding endophyte species composition, but did not significantly increase inferred diversity. Overall genotypic diversity of endophytes was high in all host species, suggesting a remarkable richness of endophytes yet to be discovered.

BACON, CHARLES W. USDA, ARS, Russell Research Center, Athens, GA 30604 USA. **Indirect actions: mycotoxins and the drive toward mutualisms.**

Grasses are considered to have originated as understory plants in forests, and from this origin the family developed key characteristics that allowed species to reach a climax association in open habitats. This diversity is due in part to the symbiotic relationship with grazing animals, especially ruminants, the developments of the perennial habit, unique intercalary meristem, and the absence of poisonous secondary metabolites. However, fungi are notorious for their production of poisonous secondary compounds, which can served important functions to grasses. The fungi of concern belong to a relatively small grouping of species within the Clavicipitaceae, and include species of the tribes Balansieae and Clavicipiteae. This group of fungi shares a common feature in being systemically associated with grasses, sedges and rushes as obligate biotrophic parasites. The association of these two groups of fungi with grasses results in the accumulation of several classes of toxic fungal metabolites that are describes as defensive. However, these metabolites may have other roles that may be both physiologically and ecologically relevant. This defensive mutualism is presented as a model, along with mycotoxins in general, with apparent inter- and intraspecific competition and ecological outcomes described for specific symbioses.

*BAHLMANN, LIESCHEN[1], WINGFIELD, MICHAEL[1], MYBURG, ALEXANDER A[1], DESJARDINS, ANNE E.[2], GORDON, TOM R.[3], WINGFIELD, BRENDA D[1]. [1]Dept. of Genetics, Forestry and Agricultural Biotechnology Inst., University of Pretoria, Pretoria, [2]Mycotoxin Research Unit, U.S. Dept. of Agriculture, Peoria, IL 61604, [3]Department of Plant Pathology, University of California, Davis, CA 95616. A**FLP genetic linkage maps of *Fusarium circinatum* (mating population H) and *Fusarium subglutinans* (mating population E).**

The *Gibberella fujikuroi* complex includes nine different mating populations or biological species (A-I). A genetic ap is available for *F. verticillioides* (mating population A). In a recent study, a cross between between *F. circinatum* and *F. subglutinans* (mating population H and E) was reported and we have used this cross for genetic linkage mapping of the two species. Two parental framework maps containing 227 and 242 amplified fragment length polymorphism (AFLP) markers, respectively were constructed using 94 randomly selected ascospore progeny. A total of 12 major linkage groups were identified for both parents of the cross. The linkage groups ranged in size from 30 to 170 cM. The mating type (*MAT-1* and *MAT-2*) genes, the histone (H3) gene and 469 accessory AFLP markers were placed in the framework maps. Forty-seven percent of all markers displayed transmission ratio distortion at alpha = 0.05, suggesting large-scale preferential transmission of parental alleles into the hybrid genetic background. To the best of our knowledge, this is the first study where a hybrid cross between two *Fusarium* spp. has been used to construct a genetic map for this group of fungi. These maps will provide powerful tools to study the genetic architecture of interspecific differentiation and pathogenicity in the two parental genomes.

*BATES, SCOTT T.[1], WOJCIECHOWSKI, MARTIN F.[1], ROBERSON, ROBERT W.[1] AND DESJARDIN, DENNIS E.[2] [1]School of Life Sciences, Arizona State University, Tempe, AZ 85287, [2]Department of Biology, San Francisco State University, San Francisco, CA 94132. **Arizona members of the Geastraceae and Lycoperdaceae (Basidiomycota, Fungi): monography, phylogeny and spore ultrastructure.**

Within Arizona there is a diverse assemblage of biotic communities that support an equally diverse mycota. In an effort to record this fungal biodiversity, a monograph was produced documenting numerous taxa in the Geastraceae and Lycoperdaceae that are present in the state. In addition to various widely distributed species, rare or understudied species, such as *Holocotylon brandegeeanum*, are reported from the state for the first time. As part of a larger study, internal transcribed spacer (ITS 1 and 2, including 5.8S) regions of the nuclear ribosomal RNA gene were sequenced. Sequence data were used in phylogenic analyses to assist in clarifying the taxonomic position of some taxa. Basidiospore morphology was also examined ultrastructurally using field-emission scanning electron microscopy. Spore ultrastructure and additional morphology characters were then analyzed in conjunction with the molecular phylogenies produced to determine synapomorphies. Once discovered, synapomorphies can be used in defining monophyletic taxa, thus producing a more robust and phylogenetically based taxonomy for these families of fungi. In addition to contributing to taxonomic understanding, the monograph will aid in establishing baseline data for fungal diversity in Arizona.

*BAUCOM, DEANA L., BRUHN, JOHANN N., MIHAIL, JEANNE D., AND GASSMANN, WALTER. University of Missouri, 108 Waters Hall Columbia, Mo 65211. **Using PCR-RFLP to identify species of *Armillaria* in Missouri Ozark mountains.**

Armillaria root disease has been associated with oak decline in the Ozark Mountains of Southern Missouri. Population arrangement of *Armillaria* species differing in virulence on oak may be affecting the spatial structure of the forest. Studying these interactions requires an accurate and efficient method for identification of fungal isolates at both the species and individual (i.e., genet) level. Previously collected *Armillaria* isolates were identified as *A. mellea*, *A. tabescens*, and *A. gallica* using diploid and haploid mating tests. Although mating tests are accurate, they are also time consuming. For quicker and more efficient identification, PCR-RFLP profiling was applied for identification of isolates collected in 2002. Amplification of the intergenic spacer region (IGS1) with subsequent restriction by Alu I identified 71 of the 141 isolates as *A. mellea*, *A. tabescens*, or *A. gallica*. A new restriction pattern was found for 25 of the 141 isolates. The PCR-RFLP results will allow evaluation of the spatial distribution of *Armillaria* species, including the new pattern isolates. Characterization of all isolates to the genet level will further contribute to our understanding of the interactions among *Armillaria* species shaping forest structure by permitting us to associate genet territories with spatial patterns of forest decline.

*BEARD, CHARLES E. AND ADLER, PETER H. Entomology, Soils, and Plant Sciences, Clemson University, Clemson SC 29634. **Geographic distribution of the trichomycete genus *Harpella*.**

Harpella spp. occur commonly and exclusively in black flies Diptera: Simuliidae) worldwide. The fungi grow in the midgut attached to the peritrophic matrix (gut lining). We were interested in the worldwide distribution of the predominant species, *Harpella melusinae*, and areas of sympatry with less prevalent species (i.e., *H. leptosa*, *H. meridianalis*, and *H. tica*). Emphasis was placed on poorly collected areas such as the northern and southern extremes of host distribution, continental areas (e.g., Africa), and previously unsampled islands. We found *H. melusinae* as far north as 69°15'N and in Africa (continental record). We also found examples on oceanic islands (Iceland and Madagascar) and areas difficult to access such as the former USSR. North and South America have five species, whereas the rest of the world has only *H. melusinae*. The ranges of the species of *Harpella* overlap in the Rocky Mountains of North America, the southwestern United States, Mexico, and many areas of South America. We speculate that *H. melusinae* is a complex of unresolved cryptic species based on its widespread distribution and subtle morphological variation compared with the restricted distribution of other *Harpella* spp.

*BENNETT, REBECCA S.[1]KRUPINSKY, JOE M.[2], MILGROOM, MICHAEL G.[1] AND BERGSTROM, GARY C.[1] [1]Dept. of Plant Pathology, Cornell University, Ithaca NY 14853. [2]USDA-ARS, Northern Great Plains Research Lab, Mandan, ND 58554. **A comparison of *Stagonospora nodorum***

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from wild grasses and wheat in North Dakota and implications for the *Stagonospora nodorum* blotch pathosystem.

While *Stagonospora nodorum* (Berk.) Castellani & Germano has been reported on many grass species, the inoculum contribution of wild and weedy grasses to epidemics on wheat is unknown. Previous work in North Dakota found evidence for host specialization: isolates of *S. nodorum* from wild grasses were less virulent on wheat than isolates derived from wheat, and vice-versa. Using AFLP markers, we examined the genetic relationship between previously characterized wheat-derived and grass-derived isolates and tested for population differentiation. Several potential sources of inoculum for *Stagonospora nodorum* blotch epidemics on wheat have been identified - wheat debris, infected seed, and alternate gramineous hosts - but, the relative importance of each is generally unknown. Our comparison should elucidate the potential importance of alternate hosts.

*BENNETT, REBECCA S.[1], MILGROOM, MICHAEL G.[1], CUNFER, BARRY M.[2], AND BERGSTROM, GARY C.[1]. [1]Dept. of Plant Pathology, Cornell University, Ithaca NY 14853 . [2]Dept. of Plant Pathology, University of Georgia, Griffin GA 30223. T**he relative contributions of seedborne and windborne inoculum to foliar epidemics of *Phaeosphaeria nodorum*.**

Population genetic and epidemiological data, when examined separately, have resulted in different hypotheses about the predominant source of inoculum in the *Phaeosphaeria nodorum* - wheat pathosystem, i.e., sexually-derived, windborne ascospores versus asexual, seedborne inoculum, respectively. We are addressing these competing hypotheses by using a mark-recapture experiment in which seedborne isolates of *P. nodorum* can be identified by rare alleles. We planted infected wheat seed in experimental plots and sampled *P. nodorum* throughout the growing season. If inoculum comes primarily from seed, we expect to find that isolates collected have the same rare alleles as in our released isolates. If the inoculum is coming primarily from immigrant, windborne ascospores, we expect to find that isolates collected from different experimental plots are genetically similar to each other but distinct from the released isolates. We will present preliminary results from sampling foliar isolates of *P. nodorum* early and midway through the growing season.

*BERBEE, MARY L.[1], ADAIR, SOLVEIG E.[1], JAMES, TIM Y.[2], LONGCORE, JOYCE E.[3], STAJICH, JASON[4], VILGALYS, RYTAS[2]. [1]Dept. of Botany, University of British Columbia, V6T 1Z4, Canada, [2]Dept. of Biology, Duke University, Durham, NC 27708, [3]Biological Sciences, University of Maine, Orono, ME 04469-5722, [4]Dept. of Molecular Genetics and Microbiology, Duke University, Durham, NC 27708. **Expressed sequence libraries from *Batrachochytrium dendrobatidis* and *Mortierella verticillata*.**

We made cDNA libraries of *Batrachochytrium dendrobatidis* (Chytridiomycota) and *Mortierella verticillata* (a zygomyete) as steps towards the goals of characterizing fungal metabolic capabilities and of developing genes as phylogenetic markers for the basal fungi. We have over 750 sequences from each library and are in the process of analyzing the results. Many of the highly expressed, repeatedly encountered sequences were related to protein synthesis or protein turnover. For example, from *M. verticillata*, 20 of the expressed sequences coded for elongation factor 1alpha. In both fungal libraries, numerous cDNA clones coded for ribosomal proteins and translation factors. Other moderately to highly expressed genes coded for actins, tubulins, heat shock proteins, and enzymes of primary metabolism. Both fungal libraries contain chitin synthases, enzymes involved in ergosterol production, and septins (related to cell cycle control in animals and fungi and contributing to regulation of cell shape and septation in fungi). The *M. verticillata* library contains homologues to laccases (involved in lignin breakdown in basidiomycetes) and both libraries included proteases and chitinases. Indicating that both fungal species were synthesizing diverse proteins, about 60% of the sequences represented genes that were found only once in each library.

*BERGEMANN, SARAH E., KORDESCH, NICHOLAS C., MESHRIY, MATTHEW G., GARBELOTTO, MATTEO. University of California, Berkeley, ESPM-ES, 151 Hilgard Hall, Berkeley, CA 94720. **Real-time quantification of genomic DNA from ectomycorrhizal fungi associated with tanoak (*Lithocarpus densiflorus*) using TaqMan PCR assays.**

A reliable and robust method for measuring the biomass of ectmycorrhizal fungi is an important step in investigating the extent of the mycorrhizal mycelium. So far, accurate quantification of ectomycorrhizal fungi has been difficult due to the intrinsic limitations of conventional techniques. TaqMan PCR assays have been shown to be a sensitive assay for detection and quantification of genomic DNA from environmental samples. In this study, TaqMan primers and probes were developed to assess the extent of ectomycorrhizal colonization in soil and root tips of tanaoks. PCR primers and hybridization probes were designed for the 28S rRNA for genes of fungal species or groups including *Amanita* spp., *Cenococcum geophilum*, *Lactarius* spp., *Russula* spp., *Sebacina* spp., and Thelephoroid taxa. To check for specificity, the primer and probe combinations were applied to DNA dilutions of all known ectomycorrhizal taxa occuring across plots. Our results indicate that up to 1 femtogram of DNA may be detected in soil and root samples. The TaqMan probes and primer sets designed in this study can be used as a rapid screening tool for the detection and quantification of ectomycorrhizal fungi from genomic extracts.

*BERGEMANN, SARAH E.[1], DOUHAN, GREG W.[2] AND MILLER, STEVEN L.[3] [1]ESPM - Ecosystem Sciences, University of California, Berkeley, 151 Hilgard Hall, Berkeley CA 94720. [2]Dept. of Plant Pathology, University of California, Davis, Davis CA 95616. [3]Botany Dept. 3165, 1000 E University Ave, Laramie WY 82071. **Population structure and cryptic speciation in the *Russula brevipes* complex**.

Russula brevipes is a common ectomycorrhizal basidiomycete associated with many hosts in North America. The goals of this project are to examine the distribution, dispersal and genetic diversity in *R. brevipes* at disparate geographic scales. High estimates of genetic structure in populations from western North America suggest that this ubiquitous "species" is composed of a variety of cryptic taxa. To determine the genetic diversity of lineages, the mt *atp*6 gene region was sequenced from over 250 sporocarps found in association with 8 hosts in western North America. Five genetically divergent lineages were detected which likely represent reproductively isolated species. Lineages varied in abundance and geographic distribution. Low levels of genetic differentiation were found based on the analysis of 6 microsatellite loci between populations separated by 200–700 m, with more substantial genetic differentiation between populations sampled at >1000 m. These results suggest substantial gene flow at local scales but much less at regional levels, reflecting short dispersal distances. Our finding that *R. brevipes sensu latu* contains genetically distinct and geographically restricted lineages suggests that diversification has been structured in part by the operation of terrestrial barriers to gene flow rather than host associations.

*BHUVANESWARI, S., UDAYA, PRAKASH, N.K. AND VITTAL, P.B.R. 408, Centre for Advanced Studies in Botany, University of Madras, Guindy Campus, Chennai 600 025, INDIA. **A study on airborne thermophilic fungi in the residence of asthmatics**.

A survey on airborne thermophilic fungi in the residence of asthmatics in Chennai city, India was conducted using 2-stage Andersen viable sampler. Altogether 100 asthmatic residences were chosen for the study. Living room, kitchen, bedroom and offsite of the residence were studied for the presence of airborne thermophilic fungi. Altogether 19 species belonging to 16 genera were isolated. Among the environments studied, an average of 77.6 cfu/m^3 of air was recorded from bedroom followed by living room with 69.5 cfu/m3 of air and kitchen recorded 61.6 cfu/m^3 of air. However, the offsite environment recorded 66.6 cfu/m^3 of air. Among the fungi isolated, *Aspergillus fumigatus* was dominant in all the sites followed by *Thermomyces lanuginosus* and *Mucor pusillus*. The results of this investigation will be discussed in detail.

BININDA-EMONDS, OLAF R.P. Lehrstuhl fuer Tierzucht, Technical University of Munich, 85354 Freising, Germany. **Supertrees, supermatrices, and phyloinformatics**.

Supertree construction is an approach to phylogenetic inference where source trees, rather than the character data underlying those trees, are combined to build a larger, more comprehensive phylogeny. It thus involves a tradeoff between an inherent loss of information and the ability to combine all available phylogenetic hypotheses to achieve a more complete phylogeny. To date, the lack of sufficient compatible character data for most groups has justified this tradeoff. By combining source trees from the literature, supertrees have produced complete phylogenetic estimates of very large clades that have yet to be approached using conventional phylogenetic techniques. However, the growing wealth of sequence data means that comparable taxonomic coverage for many groups will soon be achievable using supermatrix approaches. But, rather than fade away, I argue that supertrees will still play an essential, but altered role in phyloinformatics for the efficient analysis of large sequence matrices. Under a divide-and-conquer framework, the single large supermatrix is broken down into many smaller and computationally simpler subproblems for analysis. The

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global answer is then obtained by combining the results of the subproblems as a supertree. Thus, the compatible strengths of the supertree and supermatrix approaches will prove invaluable in our attempts to reconstruct the Tree of Life.

*BINDER, MANFRED[1], HIBBETT, DAVID S.[1], LARSSON, KARL-HENRIK[2], LARSSON, ELLEN[2], LANGER, EWALD[3], AND LANGER, GITTA[3]. [1]Biology Department, Clark University, 950 Main Street, Worcester MA 01610; [2]Göeteborg University, Botanical Institute, Box 461, 405 30 Göeteborg, Sweden; [3]Universitaet Kassel, Naturwissenschaften, Institut fuer Biologie, FG Oekologie, Heinrich-Plett-Str. 40, D-34123 Kassel, Germany. **The phylogenetic distribution of resupinate forms in the homobasidiomycetes.**

Phylogenetic relationships of resupinate homobasidiomycetes in the Corticiaceae *s. lat.* and other families were studied using rDNA sequences from a broad sample of resupinate and nonresupinate taxa. This study draws together a large body of data from recent phylogenetic analyses of resupinate homobasidiomycetes and adds 158 new sequences from 76 species. Two datasets were assembled, a core dataset of 142 species, each of which is represented by four rDNA regions (mt- and nuc- ssu and lsu), and a full dataset of 656 species, most of which were represented only by nuclear large subunit rDNA sequences. Both datasets were analysed using heuristic methods with bootstrapping; the full dataset was also analysed with the Parsimony Ratchet, using equal character weights and six-parameter weighted parsimony. Analyses of both datasets supported monophyly of the 8 major clades of homobasidiomycetes recognised by Hibbett & Thorn, as well as independent lineages corresponding to the *Gloeophyllum* clade, corticioid clade, and *Jaapia argillacea*. Analyses of the full dataset resolved two additional groups, the athelioid clade and trechisporoid clade, which were recognised by K.-H. Larsson et al. Resupinate forms occur in each of the 12 major clades of homobasidiomycetes. The euagarics clade, which is by far the largest clade in the homobasidiomycetes, has the smallest fraction of resupinate species.

*BLACK, DAWN R. AND BROWN, KIM J. Department of Environmental and Plant Biology, 317 Porter Hall, Ohio University, Athens, OH 45701. **Aboveground diversity of ectomycorrhizal fungi in managed oak-hickory forests of Southeastern Ohio.**

Oaks (*Quercus* spp.) form obligate symbioses with ectomycorrhizal fungi (EMF). Various management strategies are currently being considered for oak regeneration, especially the use of prescribed fire and thinning. However, the effect of these practices on EMF is not well understood. Consequently, our research investigates the following questions in managed oak-hickory forests in unglaciated southeastern Ohio: (i) what is the species richness of EMF in oak forests, (ii) how do thinning and burning practices affect the EMF community structure within a given landscape position? Sporocarps of EMF were collected and identified from July to November 2003. A total of 55 EMF taxa have been identified at our study site, 20 of which are commonly associated with oaks. *Russula, Amanita*, and *Lactarius* were the best represented EMF genera aboveground, with 12, 10 and 9 species, respectively. The greatest number of EMF taxa were found in the control (28 species) and prescribed fire treatments (24 species), whereas both thinning treatments (thin and thin plus fire) had fewer EMF species (15 and 8, respectively). Increased light on the forest floor appears to alter EMF communities, especially when accompanied by fire (increased albedo and decreased moisture). Future studies will assess EMF diversity through morphotyping and molecular analysis of ectomycorrhizal root tips.

BLACKWELL, MEREDITH[1], AND GILBERTSON, ROBERT L.[2] [1]Dept. of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803. [2]Department of Plant Pathology, University of Arizona, Tucson, AZ 85721. **George Cummins at 100.**

CURRICULUM VITAE: George Baker Cummins, born 29 August 1904. PUBLICATIONS: From Montana discomycetes from Flathead National Forest, Papers Mich. Acad. Sci. 11:105-115 (1930) [see Abbott and Currah (1997) *Mycotaxon* 62: 1-125] to Cummins and Hiratsuka's *Illustrated Genera of Rust Fungi*, (AKA Grandson of Illustrated Genera, 2003). PROFESSIONAL SPECIALITY: Taxonomy and biology of the rust fungi of the world. Studied and published concerning the rust fungi of the Philippines, New Guinea, continental China, the Himalaya, central and western Africa, and North and South America. Special emphasis has been given to the rust diseases of cereals and grasses (see under books). PUBLICATIONS: Approximately 117 refereed papers, 8 books (Purdue); 17 papers, 4 books (University of Arizona). SERVICE TO MSA: Charter Member (1932); all offices, President (1948); Life Member (1967); Distinguished Mycologist (1981).

*BLACKWELL, WILL H., POWELL, MARTHA J., LETCHER, PETER M. AND LOPEZ-BAUTISTA, JUAN M. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa AL 35487. **Chytridiomycota of Marr's Spring, Alabama: subhabitats and implications for studies of freshwater fungal ecology.**

Chytridiomycota (chytrids) are inhabitants of freshwater and soil environments, typically detected indirectly by baiting samples with pollen and other refractive substrates. In baited cultures from aquatic habitats, the exact source of origin of these microscopic fungi is often ambiguous, complicated by asymmetric sampling of specialized sub-habitats. Certain benthic and periphytonous sub-habitats may be sampled less commonly than is the plankton. Marr's Spring and contiguous pond, an historic site on the University of Alabama campus, encompassed a number of specialized micro-habitats, including: algal coatings on submerged leaf detritus; biofilms on leaves, stems and roots of living aquatic plants; and algal coverings of floating and submerged plant parts. Leaf and root tissues of selected aquatic plants were also sampled. Chytrids were observed directly in material collected from these sub-habitats, and certain chytrids exhibited specific relationships with host organisms or particular substrates. Ecological studies of aquatic habitats may underestimate fungal diversity and biomass, partly because probes for fungi, such as ergosterol concentration, will not detect chytrids. Development of specific detection methods would enhance research and understanding of these aquatic fungi.

*BODENSTEINER, PHILOMENA[1], BINDER, MANFRED[2], MONCALVO, JEAN-MARC[3], AGERER, REINHARD[1], AND HIBBETT, DAVID S.[2] [1]Dept. Biology I LMU Munich, Biodiv. Research: Syst. Mycology, 67 Menzinger St., Munich 80638, Germany; [2]Biology Dept., Clark University, 950 Main St., Worcester, MA 01610; [3]Centre for Biodiv. and Conserv. Biology, Royal Ontario Museum, 100 Queen's Park, Toronto, Ontario M5S 2C6, Canada. **Phylogenetic diversity of cyphelloid forms in the euagarics clade.**

Besides conspicuous macrofungi, the homobasidiomycetes also includes the so-called cyphelloid fungi that produce minute, cup- or tube-shaped fruiting bodies with smooth hymenium. Most of the relatively few taxonomically informative characters for cyphelloid forms are derived from spore morphology and anatomy of surface hyphae. Cyphelloid fungi include ca. 120 well-characterized species in 40 genera. The first study that focused the phylogenetic placements of cyphelloid fungi within the homobasidiomycetes included 71 sequences (nuc-lsu and 5.8S rDNA) from 41 cyphelloid samples, representing 26 species in 16 genera. Phylogenetic analyses (parsimony and maximum likelihood) were performed on one data set with 209 samples represented by nuc-lsu rDNA sequences and a subset of 38 samples represented by nuc-lsu and 5.8S rDNA sequences. Consistent with anatomical evidence, the results indicate that cyphelloid fungi represent a polyphyletic group of species that have been derived multiple times from within the euagarics clade. Unconstrained tree topologies suggest that there have been about 10-12 origins of cyphelloid forms, but evaluation of constrained topologies with the S-H test indicates that there may have been as few as 8-9. Whatever their number, the independent origins of cyphelloid forms represent striking cases of parallel evolutionary reduction.

*BONITO, GREGORY AND VILGALYS, RYTAS. Duke University, Durham NC. **Microbial Succession During Composting Municipal Organic Waste.**

Composting organic matter is a microbial process resulting from the work of a succession of microbial communities. Bacteria and fungi are especially critical to the decomposition processes, and exhibit wide range of enzymatic capabilities. Early composting research used culture dependent methods and found the initial mesophilic phase to be dominated by bacteria and fungi, which are rapidly replaced by thermophilic bacteria as compost temperatures increase to over 60 ^{0}C; during the final curing phase temperatures decrease and mesophilic bacteria and fungi reemerge. Although these basic biotic trends are known, there is still a lack of understanding of the specific biology involved in this process, and how this biology changes with changing physical parameters. For this study, we combine the use of culture dependent and independent methods to determine the structure and succession of saprotrophic fungal communities in composting municipal organic waste, and perform phylogenetic analysis to determine the evolutionary relationships between these organisms. An understanding of the synecology and specific fungi involved in composting, and their phylogenetic relationships, will aid our understanding of biodegradation and in ecological applications using these organisms for *in situ* bioremediation and organic waste management.

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MSA ABSTRACTS

BRUNS, THOMAS, D. University of California, Berkeley, CA. **Rethinking the rust life-cycle and host jumps from a phylogenetic, molecular, and ecological perspective**.

Phylogenetic studies in the rusts have made it clear that the simple co-evolutionary explanation for the pattern of host associations is wrong, as is the primitive rust/primitive host assumption. Recent work by Roy (Evolution 55: 41-53) has shown that host expansion within a family of related hosts appears to be driven primarily by co-occurrence of species rather than their phylogenetic relationships. However, such ecological opportunity, though necessary, is probably not sufficient to explain the broader pattern of host jumping between families. Any theory that tries to explain the pattern needs to account for the following: 1) Major host jumps to new families of hosts are rare. but appear to be punctuated in time; 2) Host jumps within a particular rust lineage are often asymmetric; occurring more frequently in either the spermatial/aecial stage or the uredinial/telial stage; 3) Some hosts have been colonized by multiple unrelated lineages of rusts. 4) Some rusts are highly promiscuous and colonized hosts in many families. Models that incorporate unique features of the rust life cycle and molecular mechanisms of plant disease resistance will be explored in the talk.

*BUSHLEY, KATHRYN E. AND TURGEON, B. Gillian. Cornell University, Dept. of Plant Pathology, Ithaca, NY 14853. **Conservation of non ribosomal peptide synthetases in closely related *Cochliobolus* species.**

Previous studies suggest that members of the class of large proteins known as non-ribosomal peptide synthetases (NPSs), responsible for production of secondary metabolites, have a highly discontinuous distribution in the genomes of filamentous ascomycetes. We are investigating diversity and evolutionary history of NPSs among closely related taxa, using three *Cochliobolus* species as subjects (*C. heterostrophus, C. carbonum* and *C. victoriae*. For this, core conserved domains from 26 adenylation (AMP) domains extracted from 11 NPS genes identified in *C. heterostrophus* (Lee et al, submitted) were used to design degenerate primers for amplification of AMP domains from *C. carbonum* and *C. victoriae*. Preliminary results suggest that the set of *C. heterostrophus* AMP domains is largely conserved in the two related species and that recombination has a role in generating diversity.

*CAMPBELL, JINX AND SHEARER, CAROL A. Dept of Plant Biology, UIUC, 265 Morrill Hall, 505 S. Goodwin Ave, Urbana, IL, 61801. **Molecular systematics of the Halosphaeriaceae: continued.**

This study was undertaken to evaluate the phylogeny of several genera in Halosphaeriaceae with a set of similar ascus characteristics (*Aniptodera*-type) that differs from those of the majority of genera in the family. The asci of *Aniptodera*, *Neptunella, Phaeonectriella* and *Lignincola tropica* are persistent to semi persistent, have an apical thickening and pore, and the cytoplasm is retracted below the ascus apex (asci of the type species of *Lignincola, L. laevis*, do not have an *Aniptodera*-type ascus). Phylogenetic analyses of 18S and 28S rDNA sequence data were used to examine patterns of ascus character evolution. The *Aniptodera*-type ascus is polyphyletic within Halosphaeriaceae: *Aniptodera, Neptunella, Phaeonectriella* and *L. tropica* are distributed in separate clades throughout Halosphaeriaceae and do not group with each other. This demonstrates that, for the taxa studied, ascus characters alone are not taxonomically informative.

*CARRE JR., CARLOS, MCCANN, MICHAEL AND SNETSELAAR, KAREN. Saint Josephs University, Philadelphia PA 19131. **Inducing *Ustilago maydis* infection structures.**

Ustilago maydis is a basidiomycete that causes smut disease in maize. The fungus is dimorphic; it can grow by budding (nonpathogenic phase) or by filaments (pathogenic phase). The filamentous stage begins when pairs of compatible haploid cells respond to pheromone by producing mating filaments that elongate toward each other and fuse. The resulting dikaryotic infection filament forms a non-melanized appressorium over elongating host epidermal cells to begin the obligately parasitic phase of the life cycle. Little is known about this early stage of infection in *U. maydis*, largely because appressoria form only over certain epidermal cells, and they have not been induced except on living plants. We used various physical and chemical inducers in attempts to produce infection structures in vitro. Several factors, including hydrophobic surfaces and ethylene, induced adhesion of cells and promoted formation of mating and infection filaments. Appressorium-like structures formed occasionally on collodion membranes supplemented with mineral oil, but no attempts to penetrate the surfaces were observed. Replicas of leaf surfaces induced adhesion as well as formation of filament projections previously observed only in planta, but, again, development stopped short of attempts to penetrate surfaces. Appressorium maturation in *U. maydis* may require multiple stimuli.

CASTELLANO, MICHAEL A. USDA Forest Service, PNW Research Station, 3200 Jefferson Way, Corvallis, OR 97331. **Assessing rare macrofungi across the landscape: A case study from the Northwest Forest Plan in the western United States.**

The Northwest Forest Plan encompasses a large physical area (24.5 million acres) in western United States. It includes a mandate to survey and manage for a large number of organisms (189 macrofungal species) that occur on US Forest Service and Bureau of Land Management lands in western Oregon, Washington and Northwestern California. One requirement of the program is to survey strategically across the landscape for all species. The goals of these surveys were to contribute information on the degree of rarity, distribution, and habitat of all species encountered. A stratified random sample of 750 plots revealed numerous new locations of many species. A brief synopsis of survey design and preliminary results to date will be presented.

*CELIO, G.J., DENTINGER, B.C., PADAMSEE, M., AND MCLAUGHLIN, D.J. Dept. of Plant Biology, University of Minnesota, St. Paul MN 55108. **Characterizing structural evolution in the fungi: the AFTOL non-molecular database**.

One goal of the Assembling the Fungal Tree of Life Project is to create a database of selected ultrastructural characters from published and new data. Ultrastructure reveals details that are not visible at the light microscope level and may unmask homoplasious characters. Improved fixation techniques such as freeze substitution warrant the re-examination of many species. Characters are dynamic and vary with the age of the cell and developmental stage of the organism. Challenges involved in constructing a structural database include: 1, evaluating the quality of published data and their documentation; 2, selecting characters and providing complete character descriptions; 3, determining the taxonomic level and degree of phylogenetic utility of a character; and 4, assessing the significance of character location and development. Phylogenetic studies combining structural and molecular data can provide reciprocal illumination when evaluating the evolutionary significance of ultrastructural characters, with hypotheses based on one data set being evaluated using the other. Initial analyses of septal characters illustrate the challenges and evolutionary significance of ultrastructural details.

*CHA, JOO YOUNG[1], CRIPPS, CATHY[2] AND MILLER, STEVEN[1]. [1]Dept. Botany, Univ. Wyoming, Laramie, WY 82071. [2]Dept. Plant Sciences & Plant Pathology, Montana State Univ., Bozeman, MT 59717. ***Russula* of the western United States (III): *Russula* in quaking aspen *(Populus tremuloides)* forests.**

The genus *Russula* forms a conspicuous and important mushroom element in forest and arctic-alpine ecosystems. They contribute significantly to fungal biomass, are important dietary elements for insects and animals, and many species are harvested world-wide for human consumption. Quaking aspen has the widest distribution of any tree in North America and is second in world distribution to the closely related *P. tremula* L. from Europe. Quaking aspen is a source of wood fiber for particleboard, forage for livestock, protection of watersheds, and is prized for its esthetic value. Quaking aspen makes an important contribution to biodiversity in montane and subalpine forests, as many organisms depend on the unique and varied habitat provided by quaking aspen stands. Although putative associations of individual species of ectomycorrhizal fungi and quaking aspen are reported in field guides and taxonomic journal articles, the mycorrhizal flora of quaking aspen in the western United States has not been the focus of much study. Members of the genus *Russula* collected from quaking aspen forests were identified to species and the macro- and microscopical characteristics compared. ITS sequence data were used to confirm identification and infrageneric placement for each species. Results from relationships between aspen and *Russula* will be discussed.

*CHA, JOO YOUNG[1], CRIPPS, CATHY[2], AND MILLER, STEVEN[1]. [1]Dept. Botany, Univ. Wyoming, Laramie, WY 82071; [2]Dept. Plant Sciences & Plant Pathology, Montana State Univ., Bozeman, MT 59717. **Snowbank mushrooms of the Rocky Mountains.**

Snowbanks linger long into spring and summer in heavily timbered areas of the high Rocky Mountains. A unique guild of macrofungi, apparently only found in western North America, occurs in close association with slowly retreating high-elevation snowbanks and their meltwaters. The fungi have been

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termed "snowbank fungi" by mycologists because of the constancy of their fruiting habitat. The snowbank fungi are more dependent on snowmelt than rain for their moisture. A majority of the snowbank fungi are thought to be endemic to western North America, and are primarily reported from the Rocky Mountain and the Cascade ranges. The snowbank fungi are a taxonomically and ecologically diverse group of mushrooms, and include both basidiomycetes and ascomycetes adapted to this unique microclimate. Their mode of nutrition includes mycorrrhizal, saprotrophic and pathogenic species important in forest systems. At present, their taxonomy, ecology, and distribution is not completely known. Snowbank mushrooms were collected from high elevation sites in Montana and Wyoming, and identified to species. Approximately thirty species were encountered. These results will enrich the list of snowbank species. Their ecological aspects will be discussed.

CHAMBERS, JAMES G., *POWELL, MARTHA J., AND LETCHER, PETER M. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487. **Variation in the C1 helix region of LSU rRNA as a tool to indicate relationships among chytrids**.

The use of secondary structural variation within highly variable regions of rRNA is explored as a tool to understand relationships among closely related chytrids. In a combined analysis of small subunit (SSU) and large subunit (LSU) nuclear rDNA sequences, members of the Chytridiales grouped into two well supported clades. The overall secondary SSU structure of the chytrid taxa studied differed little from that of the *Saccharomyces cerevisiae* SSU rRNA model (Van de Peer et al. 1997). The main regions of variation were in helices E23_1, E23_2, and E23_5. In contrast, the secondary structure of LSU differed significantly from that of the yeast model (De Rijk et al. 1999). Much of this variation was situated within the C1 helix region of the molecule, and much of the size difference was attributed to the helix C1_3 expansion segment. Comparison of secondary structural similarities and differences within the C1_3 helix of LSU are valuable in indicating relationships among closely related chytrid taxa.

*CHANG, LI-PING, TRUJILLO, MONICA, HUCUL, JOHN A., SINGH, MAYA P. AND GREENSTEIN, MICHAEL. Wyeth Research, Pearl River, NY. **A Simple and Efficient Method for Extracting Genomic DNA From Filamentous Fungi.**

Taxonomic dereplication of fungal isolates is an important step in a microbial natural products discovery program focused on distinct and diverse cultures for fermentation and screening. Sequences of the internal transcribed spacer (ITS) region are commonly used to resolve the taxonomic difference between morphologically related isolates. While experimenting with various known methods for the isolation of fungal genomic DNA, we developed a rapid, simple, and reliable method using culture colonies from a fresh agar plate and DMSO as the sole solvent. This one-tube one-solvent DNA extraction method was used for 136 fungal isolates belonging to various taxa. The extracted DNA samples were used as templates in polymerase chain reactions (PCRs). A universal pair of primers for the ITS region, *ITS1* and *ITS4*, was used to amplify the region to confirm the quality of the extracted DNA. Over 90% of the DNA samples showed a clear band of PCR product corresponding to the ITS region. The PCR products were isolated and sequenced. Comparison of the ITS sequences enabled us to rapidly dereplicate fungal cultures to be used for screening. The isolated DNA was also used to successfully amplify ketosynthase domains from putative polyketide biosynthetic pathways using primer sets designed from conserved ketosynthase regions. The sequence of the amplified fragments can help to predict the types of secondary metabolites produced by the fungi.

*CHARLTON, NIKKI D.[1], TAVANTZIS, STELLOS M.[2] AND CUBETA, MARC A.[1] [1]Dept. of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7616, [2]Dept. of Biological Sciences, University of Maine, Orono, ME 04469-5722. **The presence of the M2 dsRNA mycovirus in field populations of *Rhizoctonia solani* anastomosis group 3.**

Rhizoctonia canker and black scurf of potato are caused by *Thanatephorus cucumeris* (anamorph = *Rhizoctonia solani* anastomosis group 3 (AG-3) and occurs wherever potatoes are grown. Five double-stranded RNA (dsRNA) mycoviruses have been identified in *R. solani*AG-3 and are thought to be associated with the disease producing capacity of the fungus. A 3.6 kb dsRNA mycovirus (M2) has been associated with reduced virulence in previous research. A sample of 78 isolates of *R. solani* AG-3 was examined to determine the occurrence of the M2 dsRNA using reverse transcription PCR (RT-PCR). The M2 dsRNA was present in 42 of the 78 field isolates. Field studies have been conducted to better understand the effect of the M2 dsRNA mycovirus on the biology of the fungus in terms of aggressiveness on potato stems and stolons, and the production of sclerotia on potato tubers. A range of aggressiveness on stems and stolons and sclerotial production was observed among a sub-sample of 16 isolates. The genetic relatedness of M2 mycovirus sequences from field isolates of *R. solani*AG-3 will be examined to determine their association with aggressiveness.

*CHAVERRI, PRISCILA[1] AND VILCHEZ, BRAULIO.[2] [1]Dept. of Plant Pathology, Cornell University, Ithaca, NY 14853. [2]Dept. Forest Engineering, Instituto Tecnologico de Costa Rica, Cartago, Costa Rica. **Hypocrealean fungi and forest succession in a tropical forest.**

A pilot study was done in a tropical lowland rainforest in Costa Rica to measure the diversity of hypocrealean fungi in different stages of forest succession. Species richness and abundance of hypocrealean fungi were measured in three forest stands that were 2, 18 and 25 years, and in an old growth stand. Every anamorph and teleomorph spore-bearing structure within each plot was collected and identified. The greatest species diversity was found in the 2-year-old stand. However, measures of individual families or genera yielded varied outcomes. For example, a high abundance of Nectriaceae was found in the 2-year-old stand; whereas, Clavicipitaceae species were abundant in the old growth stand. Further, saprophytic species were abundant in the 2-year-old forest, yet almost absent in the old growth forest. This contrasted with entomopathogenic fungi, which had greater diversity in the old growth stand compared to the 2-year-old stand. This study attempts to elucidate the relationship between forest succession and biodiversity of hypocrealean fungi.

*CHEN, WEIDONG[1], SHARMA, KAMAL D.[1] AND WHEELER, MICHEAL H.[2] [1]USDA-ARS, 303 Johnson Hall, Washington State University, Pullman, WA 99164, and [2]USDA-ARS, College Station, TX 77840. **Demonstration of the 1,8-dihydroxynaphthalene melanin pathway in *Ascochyta rabiei*.**

Ascochyta rabiI, the causal agent of Ascochyta blight of chickpea, produces melanin as exhibited in black pycnidia and black pseudothecia in culture and in infected plants. Since different types of melanin have been reported in fungi, we used two spontaneous albino mutants of *A. rabiei*, deficient in melanin production, to determine if wild types of the fungus synthesize 1,8 dihydroxynaphthalene (DHN) melanin. Three lines of evidence were obtained to suggest that *A. rabiei* uses the DHN-pathway for melanin biosynthesis: 1) two specific inhibitors of the DHN-melanin pathway, pyroquilon and tricyclazole, inhibited melanin production by wild-type *A. rabiI* in culture; 2) a precursor in the DHN-pathway, scytalone, restored melanin production in the albino mutants of *A. rabiI*; and 3) transcripts of an intermediate enzyme of the DHN-pathway, scytalone dehydratase, were detected in cDNAs from pycnidial spores of *A. rabiei* by using reverse-transcription PCR. In contrast to wild types, the albino mutants were not pathogenic on chickpea plants, suggesting that melanin is a virulence factor in the disease.

*CLARK, TRAVIS A. AND ANDERSON, JAMES B. Department of Botany, University of Toronto, Mississauga, ON L5L 1C6, Canada. **Ploidy determines response to selection in long-term cultures of *Schizophyllum commune*.**

While many eukaryotic organisms exist as diploids, with two sets of gametic genomes in one nucleus, most basidiomycetes exist as dikaryons in which the two genomes exist in separate, physically paired nuclei that synchronously divide during growth. To determine if haploid monokaryons and dikaryons adapt to novel environments under natural selection, we serially transferred replicate lines of each ploidy state on minimal medium for ~13,000 generations. Dikaryons responded to selection with increases in growth rate, while monokaryons did not. To determine if the haploid components of the dikaryon adapt reciprocally to one another's presence over time, we recovered the intact haploid components of dikaryons at different time points (without meiosis) and mated them with nuclei of different evolutionary histories. We found evidence for co-adaptation between nuclei in one dikaryotic line, a dominant deleterious mutation in one nucleus was followed by a compensatory mutation in the other nucleus; the mutant nuclei that evolved together had the best overall fitness. In other lines, nuclei had equal or higher fitness when paired with nuclei of other histories, indicating a heterozygote advantage. Episodic somatic recombination was found in the dikaryotic lines. Experiments are underway to test if the adaptive potential of the dikaryon is greater than that of the isogenic diploid.

*COX, CYMON J. AND KAUFF, FRANK. Duke University Durham, NC 27708. **Of Snakes and Mushrooms: The use of (Bio)Python in the AFTOL project**.

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MSA ABSTRACTS

The NSF funded Assembling the Fungal Tree of Life (AFTOL) project seeks to enhance our understanding of the evolutionary history of Fungi. The project is based in five laboratories in four Universities with worldwide participation. The aim of the project is to sample 1500+ species of fungi for 8 genetic loci, plus a subset of taxa for a suite of morphological and ultrastructural characters, to estimate the phylogenetic relationships and diversity in the Fungi. To facilitate the collection and dissemination of molecular data to (and from) the laboratories and public, a custom-made web-based application and a suite of accessory applications have been written to provide storage and automated analysis. These applications are written in the Python programming language and often use modules provided by the BioPython project. The web-based database interface is built upon the Zope application server, itself a Python application, and provides secure, real-time access to project data and analyses. Custom-made Python applications provide a through-flow of data from the sequencing facility to the database, and to automated sequence quality checking, BLAST analysis, contiguous assembly, multiple sequence alignment, and phylogenetic analysis. The AFTOL database/bioinformatics project uses only Open Source Software.

*CRIPPS, CATHY L. AND EDDINGTON, LESLIE. Plant Sciences & Plant Pathology Dept., Montana State University, Bozeman, MT 59717. **Ectomycorrhizal and AM associations of vascular plants in the Rocky Mountain alpine zone: adding to the arctic-alpine knowledge base.**

The arctic-alpine biome covers almost one tenth of the earth's land, and includes low latitude tundra and mountain tops above treeline. A review suggests AM fungi are common in the alpine and low arctic, scarce in the high arctic, with a few woody genera such as *Salix, Dryas,* and *Betula* hosting a diversity of arctic-alpine macromycetes across the entire biome. Our work in the Rocky Mountain alpine zone from the Beartooth Plateau at 3300 m and 450 N to the San Juan Mountains at 3600 m at 380 N, supports this pattern. Over 80 species of ectomycorrhizal fungi occur with 7 plant taxa, including *Salix reticulata, S. arctica, S. planifolia, S. glauca, Dryas octopetala, Betula glandulosa* (rare), and *Polygonum viviparum*. The most common genera in Agaricales are *Cortinarius* (primarily *Telemonia*), *Inocybe, Hebeloma, Entoloma, Laccaria, Amanita*, and epigeous Russulales. Most species are known from other arctic-alpine regions. For the 44 non-woody alpine plant species (in 20 families) examined, 25 hosted AM fungi, 4 ericaceous-arbutoid fungi, and 17 were not mycorrhizal, although many hosted non-mycorrhizal fungi. The patchy distribution of mycorrhizal types associated with large-scale perennial vegetation mosaics suggests that microbial functioning is not uniform across tundra landscapes, since various types mycorrhizal types access different nutrient sources.

*CZEDERPILTZ, DANIEL L.L. AND BANIK, MARK T. USDA-FS Forest Products Laboratory, One Gifford Pinchot Dr., Madison WI 53726-2398. **Root associated fungi in an aspen dominated ecosystem in northern Wisconsin**.

To determine the fungi associated with roots in an aspen (*Populus tremuloides* and *P. grandidentata*) dominated ecosystem, two sites, "Willow " and "Fern", were sampled in northern Wisconsin. At each site 13, 3 cm dia. x 20 cm deep soil cores were collected at 5 m intervals along a transect. Each core was divided into a top and a bottom sample at an approximate depth of 10 cm, yielding 52 samples. In total, 454 root tips from Willow and 467 root tips from Fern were washed and individually excised. DNA was extracted from each root tip and the ITS region amplified using primers ITS4 and ITS1F. PCR products were sequenced and a putative identification was assigned based on comparison to GenBank sequences. For both sites, the bottom samples contained about half as many root tips as the top samples. Approximately 36% of the top root tips and 25 % of the bottom root tips yielded sequences. Fourteen unique taxa were identified at Willow, 33 at Fern, and 16 were present at both sites. Twenty of the taxa belonged to the ascomycotina, 42 belonged to the basidiomycotina, and one was of unknown affiliation. Thelephoraceous taxa were present in 35 samples and were represented by 14 taxa. Russuloids were present in 28 samples and were represented by nine taxa. *Phialophora* and *Lactarius* affiliated taxa were the third most common, each represented by three taxa in nine samples.

*CZEDERPILTZ, DANIEL L.L.[1] AND STENLID, JAN[2] [1]USDA-FS Forest Products Laboratory, One Gifford Pinchot Dr., Madison WI 53726-2398. [2]Swedish University of Agricultural Sciences, Dept. of Forest Mycology & Pathology, Box 7026, SE-750 07 Uppsala, Sweden. **Determining fungal succession in *Picea abies* logs using direct analysis of community rDNA sequences, culturing, and fruiting bodies.**

In order to investigate pathways of fungal succession in *Picea abies* (Norway spruce) logs, 24 one-meter logs were placed at two boreal sites in Sweden. Eight of the logs were initially inoculated with a brown-rot fungus (*Fomitopsis pinicola*), eight with a white rot fungus (*Resinicium bicolor*), and eight left as controls. The fungal community was sampled after seven years by collecting fruiting bodies, by culturing wood samples, and by analyzing sequences of rDNA extracted directly from wood samples. Macroscopic fruiting bodies were collected in the field, and then each log was divided into three sections after the bark was removed. Thirty-two wood samples for culturing were taken from four different cross-sectional faces within each log. Isolates were identified using sequencing and morphology, and were tested for vegetative compatibility. Thirty-six additional samples were drilled from the interior of each log and used for DNA extraction. The ITS region was amplified using fungal specific primers, followed by cloning and sequencing. Preliminary results indicate that direct sequence analysis and culturing identified the largest number of species per log, while collection of fruiting bodies identified the least. Although most sequences could be identified using databases of known species, some sequences had ITS1 and ITS2 regions with no significant similarity to known sequences.

*DARRAH, RANDY G. AND STEPHENSON, STEVEN L. University of Arkansas, Fayetteville, AR 72701. **Slime mold TWIG collection survey during ATBI High Country Quest.**

The High Country Quest was an ATBI sponsored project to bring many of the participating taxonomic working groups (TWIG) together to survey the high elevations of the Great Smoky Mountains National Park. Efforts were made to collect material and specimens for eumycetozoans. Field-based collections were made by experts, interested amateurs and volunteers during the event. International scientists from India, England, Costa Rica, Lithuania, and the Ukraine also participated in the survey. The Quest offered an educational opportunity for all participants to compare and discuss findings and methods. The records obtained during the High Country Quest will be added to the ATBI database as well as those being developed for the global biodiversity inventory project.

*DAWLEY, MICHAEL, SEMINACK, MICHAEL, MCCANN, MICHAEL, AND SNETSELAAR, KAREN. Biology Department, Saint Josephs University. **Characterizing a Co-enzyme A synthesis gene from *Ustilago maydis*.**

Ustilago maydis is a dimorphic basidiomycete fungal pathogen of corn, which can grow vegetatively by budding or by filamentous cells. A temperature sensitive mutant of *U. maydis* was isolated (TS87) that is unable to grow at 34C, although cells survive at that temperature. TS87 cells also have an interesting double-budded phenotype at 34C. Microdensitometry analysis of nuclear DNA content showed that these cells have arrested in the G2 phase of the cell cycle. TS87 was complemented using a wild-type genomic DNA library. A genomic insert was found that restored growth in TS 87 at 34C. The insert contained an ORF that would produce a polypeptide with very similar sequence to the c-terminal half of the bifunctional enzyme, Dfp from *Escherichia coli*, that catalyzes the first two steps in Co-enzyme A synthesis. Interestingly, TS mutants in dfp slowly stop DNA synthesis at the non-permissive temperature. When the sequence of the insert was compared to genes from fungi, regions of high similarity were found in genes encoding CoaB, the 4'-phosphopantothenoyl-cysteine synthase enzyme that performs the second step in Co-enzymeA biosynthesis. This suggests that the mutation in TS87 is in the gene that encodes for the CoaB protein, which catalyzes the second step in CoA biosynthesis.

*DEAN, A., MITCHELL, T., BROWN, D., DONOFRIO, N., AND OH, Y. North Carolina State University, 840 Main Campus Drive Raleigh, NC 27606. **Global gene expression during infection development of *Magnaporthe grisea*.**

Rice blast, caused by the fungus *Magnaporthe grisea*, is historically the most devastating disease of rice and is a major threat to global food security. Like many fungal pathogens, *M. grisea* elaborates a specialized cell, an appressorium, to attach to and penetrate the underlying plant tissues. To further dissect the molecular mechanisms regulating appressorium formation, we have embarked on a whole genome approach. The 6X draft shotgun assembly, the more than 30,000 ESTs, and the MPSS and LongSAGE data available for *M. grisea* were used to identify more than 13,000 candidate ORFs. In collaboration with Agilent Technologies, we have used these ORFs to design an oligo-based microarray. The array also contains ~7,000 rice defense related elements and is publicly available. These arrays are being used to identify and measure both pathogen and host gene expression during the early stages of the infection process. All results are collected in a centralized database called MGOS (www.mgosdb.org) that allows researchers to query the data. Results from gene

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expression during appressorium formation as well as during starvation, conditions that may mimic the environment at the plant interface, will be discussed.

*DEL PRADO, RUTH AND LUMBSCH, THORSTEN. Dept. of Botany, Field Museum of Natural History. 1400 S. Lake Shore Drive, Chicago, IL 60605. **Phylogeny of pyrenocarpous lichens: combining ascoma development and molecular data.**

The evolution of ascomata, especially perithecia and perithecioid forms in lichen-forming ascomycetes is studied using ontogenetical and molecular methods. As a basis for this, the phylogenetic relationships of some major groups of lichen-forming ascomycetes, such as Pyrenulales, Trichotheliales, Verrucariales, Arthopyreniaceae, and the non-lichenized Chaetothyriales were investigated using sequence data of the nuclear LSU rDNA and the mitochondrial SSU rDNA. The lichenized pyrenomycetes basically fall into three groups: 1) the Arthopyreniaceae with bitunicate asci and strictly ascolocular ascoma development belong to the Dothideomycetes s. str., 2) some families, such as Thelenellaceae and Trichoteliales with unitunicate asci and ascohymenial ascoma development are derived independently within the usually discocarpous Lecanoromycetes, and 3) taxa with bitunicate asci, but ascohymenial development, including Pyrenulales, Verrucariales, and numerous lichenicolous fungi, belong to Chaetothyriomycetes. The last group is closely related to the non-lichenized Chaetothyriales. This raises the question of the type of ascoma development in this order. Based on the molecularly inferred phylogeny, the ontogeny of ascoma types was also studied in these groups to reach a better understanding of the evolution of the fruiting bodies in lichen-forming fungi and related non-lichenized taxa.

DICKMAN, M.B. University of Nebraska, Department of Plant Pathology, Lincoln NE 68583. **Appressorium development in *Colletotrichum trifolii*.**

A growing body of evidence indicates that signals released from both the plant and pathogen are crucial in determining the course of a parasitic relationship. Signal exchange following "recognition" events determines the outcome of a given interaction. It is not surprising that host molecules or surface architecture can be sensed by fungal pathogens, triggering specific developmental processes that promote disease development. When *Collectotrichum trifolii*, which causes alfalfa anthracnose, contacts host plant surfaces, as the case with a number of fungi, specialized infection structures (appressoria) are produced that facilitate penetration of the plant cuticle. Recognition of this hydrophobic host surface must be sensed by the fungus, initiating the appropriate signaling, pathway(s) for pathogenic development. Using a variety of approaches, we have islolated genes associated with appressorium development including, cyclic AMP dependent protein kinase (PKA), calmodulin (CAM), Ras and lipid activated protein kinase (LIPK). Using antisense, over expression and gene disruption approaches, the role of these genes for pathogenic development have been established. Our results, which will be presented, indicate that *C. trifolii* is able to sense and use host surface chemistry to induce a protein kinase-mediated pathway required for appressorium development.

DIEZMANN, STEPHANIE. Dept. of Molecular Genetics and Microbiology, Duke University Medical Center, Box 3568, Durham, NC 27701. **Phylogeny and evolution of Candida and related taxa: a multigenic analysis.**

The order Saccharomycetales encompasses disparate genera with a variety of life styles, including opportunistic human pathogenic yeasts, plant pathogens and commensals of both animals and plants. From 36 strains representing five of the eleven families in the order Saccharomycetales, DNA sequences of six nuclear genes were analysed using maximum likelihood and Bayesian phylogenetic methods. Three major lineages were significantly supported. One clade comprised only human pathogenic species of *Candida*. The second group included predominantly saprophytic yeasts. The third lineage was recognized as a monophyletic group of Saccharomycetaceae. The phylogenetic tree was then used to study the evolution of life history traits including pathogenicity, sexuality and alternative codon usage.

*DITULLIO, DENNIS, ROBINSON, ONONG S., MAGNUSSON, SHARON M., BONNER, PATRICK E., HENDRICK, JAMES R., SANGLIER, J-J., AND KNIGNT-CONNONI, VICTORIA K. Cetek Corporation, 260 Cedar Hill Street, Marlborough, MA 01752. **Lichen associated micro flora as a source of secondary metabolites.**

The lichen thallus is a rich source of secondary metabolites and represents a competitive environment for various microorganisms. Lichen specimens were collected from different ecosystems in the New England area and their associated fungi and actinomycetes isolated. Two isolation methods were utilized: One for organisms of the exterior and a second for the interior of the lichen thallus. All isolates within a lichen specimen were dereplicated by morphology. Dereplicated isolates were analyzed by restriction fragment length polymorphism (RFLP) to determine the range of diversity of these microbial populations. Isolates were incubated at 22 ^{0}C or 28 ^{0}C under 5 to 6 shake flask or stationary solid media conditions. Secondary metabolites were extracted and analyzed by thin layer chromatography (TLC) for nitrogen-containing secondary metabolites. The extracts were also screened against a range of targets using capillary electrophoresis (CE). Morphological diversity, RFLP diversity, presence of nitrogen containing compounds and hit rates were analyzed to determine if microorganisms isolated from lichen are useful as a source of secondary metabolites in the pharma/agri/ and cosmetic industries.

*DOUHAN, GREG W.[1], PETERSON, CAROLYN[2], BLEDSOE, CAROLINE S.[3], RIZZO, DAVID M.[1] Depts. of [1]Plant Pathology and [2]Land, Air, and Water Resources, University of California at Davis, Davis, CA 95616 and [3]Dept. of Biological Sciences, Southern Oregon University, Ashland, OR 97520. **Contrasting root associated fungi of three common oak-woodland plant species based on molecular identification; host specificity or non-specific amplification?**

Molecular methods to identify arbuscular mycorrhizal (AM) fungi *in planta* have contradicted the notion of low species diversity and lack of host specificity among AM fungi. An increasingly popular approach is to amplify a portion of the small subunit of AM fungal ribosomal DNA from whole root DNA extractions using the primer pair AM1-NS31 followed by cloning and sequencing. We used this approach in an attempt to study the AM community composition of three common oak-woodland plant species; a grass, *Cynosurus echinatus,* blue oak, *Quercus douglasii*, and a forb, *Torilis arvensis*. We found significant diversity of AM fungi in the roots of *C. echinatus*, which is consistent with previous studies demonstrating the high degree of AM fungal diversity from the roots of various hosts. However, clones from *Q. douglasii* and *T. arvensis* were primarily non-AM fungi of diverse origins within the Ascomycota and Basidiomycota. This work demonstrates the potential nonspecificity of this primer pair. Thus, caution must be taken when using this molecular approach to determine *in planta* AM fungal diversity if non-sequence based methods are used such as terminal restriction fragment length polymorphisms.

*DREHMEL, DENNIS, JAMES, TIM Y., MONCALVO, JEAN-MARC AND VILGALYS, RYTAS. Duke University, Durham, NC 27708. **Biodiversity of the Boletes.**

Boletes from diverse forest habitats were collected and extracted for DNA. Sequences of both nuclear and mitochondrial DNA were studied for their relatedness and the implied biodiversity. Analysis of molecular phylogenic trees showed that the genera *Suillus* and *Leccinum* were well supported. Other major genera were not supported and monophyly is contraindicated. By summing branch lengths within phylogenic trees, the biodiversity of the boletes was studied with respect to included groups and in comparison with the genus *Amanita*. It was found that the boletes have greater diversity than *Amanita*, and that the genus *Gyroporus* has greater diversity per taxon than other groups within the boletes.

*EBBOLE, DANIEL J.[1], FILIPPI, CRISTINA[1], CORTES, CARLOS[1], BECKERMAN, JANNA[1], SWEIGARD, JIM[2], AND VALENT, BARBARA[3]. [1]Dept. of Plant Pathology and Microbiology, Texas A&M University, College Station TX 77843, [2]DuPont Experimental Station, Wilmington DE 19880, [3]Dept. of Plant Pathology, Kansas State University, Manhattan KS 66506. **The F-box leucine rich repeat protein, *PTH1*, is required for appressorium maturation in *Magnaporthe grisea*.**

F-box proteins are components of modular E3 ubiquitin protein ligases called SCF's, which direct protein ubiquitination. In *Saccharomyces cerevisiae*, the F-box protein Grr1 plays a key role in cell cycle progression and response to glucose availability. Mutants of the Grr1 ortholog of *M. grisea*, *pth1*, produce defective appressoria that are sensitive to hyperosmotic stress. We observed a delay in germination and a corresponding delay in lipid and glycogen movement into the appressorium that is likely to be a key factor in the inability to generate the appressorial turgor pressure needed for penetration. In addition, nutritional regulation of *MPG1*, a hydrophobin involved in host recognition, is altered in *pth1* mutants, and further suggests a role for *pth1* in regulation of gene expression that may affect lipid and glycogen metabolism during germination and appressorium development. Thus, disruption of *pth1* appears to prevent the turnover of proteins necessary to allow appressorium maturation. The role of

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pth1 in appressorium maturation has not evolved as a specific trait for pathogenesis since the *N. crassa* ortholog complements the *pth1* defect.

EELLS, REBECCA L., HENK, DANIEL A., ARNOLD*, A. ELIZABETH, LUTZONI, FRANÇOIS, AND VILGALYS, RYTAS. Department of Biology, Duke University, Durham, NC 27708. **Assessing diversity of foliar fungal endophytes in a mature loblolly pine (*Pinus taeda*) plantation.**

We surveyed endophytic fungi associated with healthy foliage of the valued conifer species, loblolly pine (*Pinus taeda*), with dual goals of (1) assessing endophyte abundance, richness, phylogenetic diversity, and species composition; and (2) developing a framework for rapidly assessing endophyte community structure. Culture-based surveys in three sites in Duke Forest (Orange County, NC) generated 441 isolates from 450 needle segments (N = 5 segments/leaf, 10 leaves/tree, 3 trees/site), representing 24 morphotaxa. Subsequent analysis of nrDNA data (ITS) for 140 representative isolates indicated 24, 35, and 59 unique genotypes delimited by 90%, 95%, and 99% sequence similarity. Phylogenetic analyses (5.8s gene + 600bp of nucLSU) indicated several major lineages of Ascomycota (Rhytismatales, Helotiales, Chaetothyriales, Ophiostomatales, Sordariales, Xylariales, Phyllachorales, Myriangiales, Dothideales, Pleosporales), as well as a small number of Basidiomycota. Similarity indices indicated homogenous distribution of endophytes among study plots and trees, which were consistent in terms of richness and diversity (Shannon index) but differed markedly in phylogenetic diversity. Bootstrap analyses indicated that although we captured >90% of estimated richness as inferred from morphotypes, many additional, unique endophyte genotypes await recovery in this simplified forest ecosystem.

*FAY, LAUREN M., VANCE, STANLEY R., HILL, TERRY W., AND LOPRETE, DARLENE M. Departments of Chemistry and Biology, Rhodes College, Memphis, TN 38112. **A gene showing sequence similarity to mannose transporters complements a branching/septation defect in *Aspergillus nidulans*.**

In order to identify novel genes affecting cell wall integrity, we have generated mutant strains of the filamentous fungus *Aspergillus nidulans*, which show hypersensitivity to the chitin synthase inhibitor Calcofluor White (CFW). The phenotype of one of these strains (R205) is hyperbranched and hyperseptate, with irregular hyphal diameter and irregular wall thickness in swollen spores. Using a plasmid genomic DNA library ("AMA *Not*I", Osherov and May, 2000, Genetics 155: 647-656), we have cloned three genomic fragments that complement this mutant's phenotype. Strains transformed with any one of these rescuing plasmids show increased resistance to CFW and a more normal microscopic phenotype. End-sequence analysis of each plasmid was compared to the Whitehead Institute database in order to determine the base sequence of the respective genomic inserts. A translated BLAST search revealed homology between the sole ORF in the smallest of the rescuing inserts and known mannose transporters. A similar but distinct ORF in a second rescuing plasmid shows the same homology. Work is underway to PCR-amplify each putative mannose transporter, in order to identify which, if either, represents the mutated gene in R205, as well as to identify the rescuing sequence in the third complementing plasmid.

*FERRER, ASTRID, SHEARER, CAROL A. University of Illinois at Urbana-Champaign, Urbana, IL 61801. ***Berkleasmium*, *Canalisporium*, and *Dictyosporium* species from aquatic habitats in Panama.**

This study is part of an extensive survey of species of freshwater fungi in the tropical rain forests of Panama. We report collections from three different forest sites for species in the genera *Berkleasmium, Canalisporium*, and *Dictyosporium*. Four species of *Berkleasmium*, five species of *Canalisporium* and five species of *Dictyosporium* were collected. Most of these species have been reported previously from submerged wood in the Asian/Austral tropics. Results of this study provide new insights into the diversity and distribution of aquatic fungi since all these species are first records for Panama, and Central America. These reports suggest that many species of these genera may be more widespread and common than previously recognized. New species of *Berkleasmium* and *Canalisporium* are described and illustrated.

*FRIEDERS, ELIZABETH M.[1], MCLAUGHLIN, DAVID J.[2], SZABO, LES J.[3] AND SWANN, ERIC C.[2] [1]Department of Biology, University of Wisconsin-Platteville, Platteville, WI 53818, [2]Department of Plant Biology, University of Minnesota, St. Paul, MN 55108, [3]USDA-ARS, Cereal Disease Laboratory and the Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108. **Urediniomycetidae: rusts and their close relatives.**

The simple-septate auricularioid phytoparasites have figured prominently in historical concepts of the evolution of basidiomycetes in general and Uredinales (rust fungi) in particular. However, the relationship of these phytoparasites to the rust fungi and to other non-phytoparasitic simple-septate heterobasidiomycetes remains unclear. In this study, we apply cladistic methods to phylogenetic reconstruction and provide a natural taxonomic treatment for this group of fungi. Molecular cladograms were constructed using nuclear large and small subunit rRNA genes. Ultrastructural analyses of the septal pore apparatus and spindle pole bodies of select phytoparasitic taxa were performed; ultrastructural characters supported the molecular phylogenies. A natural group within the Urediniomycetes (Basidiomycota) has emerged consisting of the phytoparasitic Uredinales, *Helicobasidium*, *Jola*, *Eocronartiumi, Platygloea, Herpobasidium* and *Insolibasidium*, as well as the insect-associated Septobasidiales and the wood saprobe *Pachnocybe*. We propose the subclass Urediniomycetidae to house rusts and their close relatives. Based on this new cladistic phylogeny, taxonomic revisions will be required for some genera, families and orders within this subclass.

GARCÍA-SANDOVAL, R.[1], *CIFUENTES, JOAQÍN[1], DELUNA, E.[2], ESTRADA-TORRES, A.[3], VILLEGAS, M.[1] [1]FCME Herbaria, UNAM. PO Box 70-399, CP 04510, Coyoacán, DF, México, [2]Dpto. Sistemática Vegetal, Instituto de Ecología AC, PoBox 63, CP 91000, Xalapa, Veracruz, México, [3]Laboratorio de Sistemática, Centro de Investigaciones en Ciencias Biológicas, UAT, Km 10.5 Cart. San Martín Texmelucan-Tlaxcala, CP 90120, San Felipe Ixtacuixla, Tlaxcala, México. **A phylogeny of *Ramariopsis* and allied taxa.**

Ramariopsis (Donk) Corner was first described as a genus of species with branched basidiomes and ornamented spores. Later Petersen emended the genus to include species with simple basidiomes and smooth spores. The putative monophyly of *Ramariopsis sensu* Petersen was tested with a cladistic analysis of 36 morphological characters coded for 24 representatives of six genera and two families. Representatives of six genera and one family were used as taxonomic outgroups, sampled with reference to previous phylogenies, one phylogenetic prospection, and traditional classifications, to maximize the severity of the test. The results suggest that *Ramariopsis sensu* Petersen is a polyphyletic group. Representatives of *Ramariopsis* (Donk) Corner form a monophyletic group supported by the presence of basidiospores with strongly cyanophilous ornamentation derived from the tunica. A discussion of relevant characters with reference to character mapping is included.

GRAND, LARRY F. Department of Plant Pathology, North Carolina State University, Campus Box 7616, Raleigh, NC, 27695-7616. **Diversity and distribution of poroid wood decay fungi in the Southern Appalachian Mountains.**

Intensive collecting of poroid wood decay fungi in North Carolina from 1999 to present has provided a valuable database and insight into this ecologically and economically important group of fungi. Primary objectives of this study include determining host species associations and distribution of fungal species within North Carolina. Over this five-year period 1657 collections and observations were made. Collections and observations in the three major physiographic regions of North Carolina were Mountains: 674; Piedmont: 628; Coastal Plain: 351. For the entire state 205 species (or species complexes) were recorded with 143 species occurring in the Mountains, 155 species in the Piedmont and 79 species in the Coastal Plain. Seventy-nine species of fungi were recorded as new in North Carolina. More than 800 new host species-fungus species associations were recorded. This study, which is still in progress, suggests that North Carolina is an important transition region as the northern limit of the range of typically southern poroid wood decay species and the southern limit of the range of typically northern species. The distributional data of poroid wood decay fungi, or any group of fungi, in a relatively small geographical area can provide valuable information on the location of species and serve as a valuable base line of information for future biodiversity studies.

*GEISER, DAVID M.[1], LEWIS IVEY, MELANIE L.[2], HAKIZA, G.[3], JUBA, J.H.[1] AND MILLER, S.A.[2] [1]Dept. of Plant Pathology, Penn State Univ., University Park, PA 16802, [2]Dept. of Plant Pathology, Ohio State Univ. OARDC, Wooster, OH 44691, [3]Coffee Research Institute (CORI), P.O. Box 185, Mukono-Kituza, Uganda. ***Fusarium xylarioides*, a causative agent of coffee wilt disease in Africa, is a previously unrecognized member of the *Gibberella fujikuroI* species complex.**

Tracheomycosis or coffee wilt has emerged as a major disease of robusta coffee in Uganda in the last ten years. Coffee wilt historically has been associated with *Fusarium xylarioides* Steyaert (teleomorph *Gibberella xylarioides*

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Heim and Sacc.), a species that has been classified as a member of *Fusarium* section *Lateritium*. We investigated the molecular phylogenetics of fusarial coffee wilt isolates by generating partial DNA sequences from two protein coding regions, translation elongation factor 1-alpha (tef) and beta tubulin (benA), in 36 isolates previously identified as *F. xylarioides* and related fusaria from coffee and other woody hosts, as well as from thirteen isolates into two morphologically and phylogenetically distinct groups. The first group was found to represent previously unidentified members of the *Gibberella fujikuro* species complex (GFC), a clade that replaces the artificial *Fusarium* section *Liseola*. This group of isolates fit the original description of *F. xylarioides*, thus connecting it to the GFC. The second group, which was diverse in its morphology and DNA sequences, comprised four distinct lineages related to *F. lateritium*. One of *F. xylarioides*' close relatives, *F. udum*, also causes vascular wilt diseases of woody hosts.

*GEML, JOZSEF, DAVIS, DONALD D. AND GEISER, DAVID M. Dept. of Plant Pathology, Penn. State University, University Park PA 16802. ***A posteriori* morphological analyses of phylogenetic species in the genus *Sphaerobolus*.**

Despite mycologists' interest in its unique spore dispersal mechanism, systematic studies of the genus *Sphaerobolus* have received little attention. In our previous work, multiple gene genealogies indicated the existence of three deeply divergent lineages in the genus *Sphaerobolus*, each representing a phylogenetic species. Macro- and micro-morphological analyses of colony and fruit body characters indicated that these three phylogenetic species correspond to two known species: *S. iowensis* and *S. stellatus*, and a newly discovered species. Species can be distinguished based colony morphology and growth rate on agar media, and the composition and morphology of cells within the gleba. The new species, named *Sphaerobolus ingoldi* Geml, Davis et Geiser, is described based on both molecular and morphological data. In addition, while *S. iowensis* had previously been reported in only two localities, we foud that it is as common or more common than *S. stellatus* in North America.

*GONZÁLEZ, MARÍA AND CHAVARRIA, ALLAN. Departamento de Botánica, Instituto de Biología, Universidad Nacional Autonoma de México, A. P. 70-233, Ciudad de México, DF, 04510, México. **Some freshwater Ascomycetes from Xochimilco, México.**

The diversity of Mexican freshwater mycobiota is little known, with only two species of Chytridiomycota registered (Cespedes & Castillo 1982); unfortunately, those records cannot be verified because specimens were not preserved and the published records did not include illustrations. Xochimilco is located in the metropolitan region of Mexico City. This area includes 200 square kilometers of navigable canals and waterways that surround raised areas called chinampas, on which flowers and vegetables have been grown since Aztec times. The Xochimilco region is an endangered ecosystem with a significant percentage of the Mexico City diversity, including endemic, rare or endangered species. The Xochimilco freshwater microscopic fungi are undescribed although these fungi comprise basic components of that aquatic ecosystem. Therefore, in this work, some freshwater Ascomycetes from Xochimilco were recorded. Submerged wood panels were incubated in moist chambers at room temperature and examined for fungi periodically. The identified Ascomycetes were preserved ex situ in permanent slides and dehydrated. The recorded freshwater genera were *Ascolacicola, Halosarpheia, Jahnula, Ophioceras,* and *Savoryella*. In addition, several Ascomycetes considered of terrestrial origin were founded in this ecosystem.

GORTON, CAROLINE[1], *KIM, SEONG HWAN[2], HENRICOT, BEATRICE[1], WEBBER, JOAN[3] AND BREUIL, COLETTE[4]. [1]Plant Pathology Department, The Royal Horticultural Society, Wisley, Woking, Surrey, GU23 6QB, UK, [2]Department of Microbiology, Dankook University, Cheonan, Chungnam, 330-714, Korea, [3]Forestry Commission Research Agency, Alice Holt Lodge, Farnham, Surrey, GU10 4LH, UK, [4]Department of Wood Science, Dept. of Wood Science, University of British Columbia, 2424 Main Mall, Vancouver, BC, Canada. **Phylogenetic relationship between the sapstain fungus *Ophiostoma minus* and its related species.**

Ophiostoma minus has long been recognized as a serious agent of sapstain, as well as a pathogen of pine. *Ophiostoma pseudotsugae* and *Ophiostoma minus* var. *barrasii* have been previously classified as *O. minus*. To clarify the phylogenetic relatedness of these species, the 5.8S and internal transcribed spacer (ITS)2 rDNA and b-tubulin gene were amplified by PCR and their nucleotide sequences determined. Sequencing analysis showed that the b-tubulin gene was more informative than the ITS2 rDNA. Phylogenetic analyses based on the b-tubulin gene sequences supported the sub-division of *O. minus* into two groups (European and North American groups) based on geographic origin. However, sequencing analysis did not reveal any polymorphisms between isolates with homothallic as compared to heterothallic mating systems. This was supported by genetic crosses using methylbenzamidazole-2-yl carbamate nuclear markers which showed that hybridization between the homothallic and heterothallic isolates of *O. minus* was possible. Isolates previously classified as *O. pseudotsugae* were confirmed as being clearly distinct from *O. minus*. *Ophiostoma minus* var. *barrasii* was closely related with *O. minus*. Our work proposes that different mating systems may still signal a divergence of isolates of *O. minus*.

*GREIF, MATTHEW D. AND CURRAH, RANDOLPH S. Dept. of Biological Sciences, University of Alberta, Edmonton Alberta T6G 2E9, Canada. **A survey of arthroconidial fungi isolated from insects**.

Arthroconidial fungi in the Onygenales are commonly found in cryptic habitats, such as dung and decaying wood, where air or water dispersal would be unlikely. These substrates are also common habitats for insects, but there are no reports of arthroconidial fungi isolated from living insects in the literature. A field survey in a mixed wood southern boreal forest found evidence of dispersal of these fungi by insects. 77 arthroconidial isolates from the Myxotrichaceae (*Myxotrichum deflexum, Oidiodendron maius, O. griseum, O. periconioides*, the *Oidiodendron* state of *Myxotrichum arcticum*, the *Oidiodendron* state of *Myxotrichum cancellatum*, and *Geomyces pannorus*), Onygenaceae (*Auxarthron conjugatum, A. compactum*, and *Chrysosporium merdarium*), and the Arthrodermataceae (*Arthroderma curreyi*, and *Arthroderma* sp.) were isolated from the exoskeletons of insects representing over 30 families across eight orders. Structural features found in some Onygenalean fungi suggest a reliance on insects for dispersal and this hypothesis has recently been supported with in vitro tests. Our isolates from insects provide additional circumstantial evidence that arthropod-mediated dispersal is occurring in nature.

*GREIF, MATTHEW D. AND CURRAH, RANDOLPH S. Dept. of Biological Sciences, University of Alberta, Edmonton Alberta T6G 2E9, Canada. **The development and function of the cephalothecoid peridium in *Cryptendoxyla hypophloia*.**

Cryptendoxyla hypophloia is a cephalothecoid ascomycete, first reported from under the bark of dead trees, that has a peridium constructed of 6-8 large hinged plates of radiating cells. On drying, the plates separate along well-defined suture lines and evert to expose the ascospores. Once rewetted, the plates assume their concave shape and the ascospores are once again enclosed. Using isolates collected from the exoskeletons of insects we investigated the structural and anatomical characteristics of the peridial plates using LM, SEM and TEM, to understand the mechanistic basis of this unusual dehiscence mechanism. Each peridial plate is formed from a discrete center of growth that arises early in ascocarp ontogeny. Hyphae extend radially from these centers by branching and tip growth. The hyphae at the expanding edges of each primordial plate interdigitate and those of the outer peridial layer develop scalariform thickenings along the inner surface of the cell wall. Suture lines develop across files of cells that lack thickenings. The scalariform cells allow the outer layer to contract so that the plates change shape from concave to convex. Some suture lines rupture between plates, but others persist and function as hinges. The cryptic habitat of *C. hypophloia* suggests that this elaborate and unique dehiscence mechanism is related to encouraging arthropod-mediated dispersal.

*GRUBISHA, LISA C.[1], KRETZER, ANNETTE M.[2], AND BRUNS, THOMAS D.[1] [1]Dept of Plant and Microbial Biology, 111 Koshland, University of California, Berkeley, CA 94720-3102. [2]SUNY College of Environmental Science and Forestry, Faculty of Environmental and Forest Biology, One Forestry Drive, Syracuse NY 13210-2788. **Examination of genetic and geographic structure in *Rhizopogon* using microsatelite loci**.

We are investigating the relationship between genetic and geographic structure in two sympatric species of *Rhizopogon*. *Rhizopogon vulgaris* and *R. occidentalis* are hypogeous, ectomycorrhizal fungi associated with pines. Spore dispersal is by animals that consume fruiting bodies, thus dispersal should be restricted by geographic barriers and distance between populations. *Rhizopogon vulgaris* and *R. occidentalis* were sampled from native pine populations on two islands and coastal mainland sites in California. We have constructed (CAC)n-enriched microsatelite libraries for *R. vulgaris*, and are currently constructing libraries for *R. occidentalis*. We have isolated and tested five loci from an initial screen of the libraries. Analysis of three loci and 99 individuals from northern

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California and Santa Cruz Island shows limited gene flow between Northern and Southern regions. On Santa Cruz Island three bishop pine populations are separated by short distances however the western population is separated from the others by mountain ridges and a large valley. Based on analysis of four loci these barriers appear to restrict gene flow between the western *R. vulgaris* population and eastern and northern populations. This fine-scale restriction in gene flow means that the small isolated populations of pine that are typical of the California coast may provide isolated islands for evolving *Rhizopogon* species.

GRUFF, SUSAN C., LOEFFLER, KENT E., *HODGE, KATHIE T. Dept. of Plant Pathology, Cornell University, Ithaca, NY 14853. **The Cornell Plant Pathology Herbarium, past, present, and future.**

The CUP Herbarium is a collection of dried specimens and photographs of fungi and plant pathogens collected by local and international mycologists and plant pathologists. We hold about 400,000 specimens, making us the fourth or fifth largest fungal herbarium in North America. We will celebrate our centenary in 2007, although many of our specimens precede our official founding, dating back to the 1860s. We are currently digitizing our specimen records; to date over 20,000 of our 400,000 specimens have been entered into a Biota database and are accessible for searching on the internet. We are compiling an inventory of our type specimens and have so far located almost 6,000 types. We have also created digital high resolution images based on highlights of our collection of over 60,000 photographs. The collection features G. F. Atkinson's vouchered mushroom shots dating from the 1880s onward, and the general herbarium's collection of agricultural field equipment and field- and studio-shots of fungi and plant pathogens. The digitized photographs can be searched online and will be of interest to teachers and researchers alike. After several years of storage under adverse conditions, CUP is now housed in rented but adequate space off-campus. Cornell's College of Agriculture and Life Sciences has agreed to renovate a building for us in the near future to become our permanent quarters.

*GULIS, VLADISLAV AND SUBERKROPP, KELLER. Dept. of Biological Sciences, University of Alabama, Tuscaloosa, AL 35487. **Effects of nutrient enrichment on fungal activity and community structure of aquatic hyphomycetes in a southern Appalachian stream**.

Aquatic hyphomycetes (AH) are important decomposers of plant litter in streams and intermediaries in energy flow to higher trophic levels. We studied the effect of long-term N and P fertilization of a small headwater stream on fungal biomass associated with plant litter, sporulation rate of AH, conidia concentration in water and community structure. Comparisons between nutrient-enriched and unenriched reaches of the same stream and between a reference and the enriched stream were made. Nutrient addition resulted in threefold increase in fungal biomass and 112-406 times higher sporulation rate associated with leaf litter in experimental bags. Fungal biomass associated with randomly collected naturally deposited leaves and introduced wood veneers was higher after nutrient addition in comparison to pre-enrichment and to the reference stream. Conidia concentration in water was on average 4-7 times higher after enrichment. Species richness of AH was generally higher from the enriched stream on each sampling date. Although diversity, evenness and total number of species from the reference and enriched stream over a 4-year period were similar, considerable shifts in relative abundances of dominant species occurred. These data suggest that even moderate increases in nutrient levels in water may alter activity and dominance pattern of AH and cause changes in ecosystem functioning.

*GUSSE, ADAM[1], MILLER, PAUL[2], AND VOLK, THOMAS J.[1] [1]Department of Biology and [2]Department of Chemistry, University of Wisconsin-La Crosse. **Biodegradation of phenolic resin plastics using white-rot fungi.**

Historically, plastics have been recalcitrant to degradation by fungi. Phenolic resins, some of the oldest commercially used plastics, are phenol-formaldehyde polymers used at an annual rate of 4.3 billion pounds in several industrial applications, most notably in construction materials as a wood adhesive. The chemical structure of these resins is remarkably similar to that of lignin and even sometimes partially substituted with lignin, making their degradability by white-rot fungi a probability. Our objectives were to determine whether six species of white-rot fungi can degrade these polymers, and to determine some factors affecting their rates of degradation. To date, *Phanerochaete chrysosporium* and *Ceriporiopsis subvermispora* strains have shown the best preliminary evidence of degradative activity, evident in a pink hue forming only three days after introduction of lab-manufactured resin. 13C-labeled resin was utilized to determine the rate of degradation by these two species using Gas Chromatography-Mass Spectroscopy. The breakdown product, 13C-labeled phenol, was found in extracts made as early as three days after introduction. Data on rates of degradation, whether peroxidase enzymes are involved, if wood content of the phenolic resin affects degradation rates, and potential for industrial applications in recycling will be presented.

*HALLEN, HEATHER E.[1], BOUGHER, NEALE[2], LEBEL, TERESA.[3] [1]DOE Plant Research Lab, 106 Plant Biology Laboratories, Michigan State University, East Lansing, MI 48824-1312,[2]CSIRO Forestry and Forest Products, PO Box 5 Wembley, WA 6913, Australia, [3]Royal Botanic Gardens Melbourne, Birdwood Ave., South Yarra, VIC 3141, Australia. **Phylogenetic placement of *Amarrendia* and *Torrendia*: sequestrate *Amanita* - or a mixed bag?**

Several sequestrate affiliates of the genus *Amanita* have been described. These are placed in the genus *Torrendia* (secotioid habit) and the recently described *Amarrendia* from *Amanita* + *Torrendia*; hypogeous habit). While *Torrendia* is known from Australia and Europe, *Amarrendia* is endemic to Australia. We have used molecular phylogenetic analysis of nuclear ribosomal RNA genes to determine the affinities of *Amarrendia* and several *Torrendia* species. The type of the genus *Amarrendia*, *A. oleosa*, forms a well-supported clade within *Amanita*, with *Amarrendia grandispora, Torrendia grandis* and *T. inculta*. This clade is distinct from all described sections of *Amanita*, and likely merits its own section. *Torrendia arenaria* is distinct from the principle *Amarrendia-Torrendia* clade, and is placed, with weak support, in *Amanita* section *Validae*. The placement of the remaining species of *Amarrendia* appears to be well outside *Amanita*. *Amarrendia peridiocrystalis* is affiliated with *Cortinarius* and *Dermocybe*, while *A. nemoribis* shows affinity to the Russulales. Placement of *Amarrendia lignicolor* is problematic as the ITS sequences are not particularly close to any existing sequences, *Amanita* or otherwise, in the databases.

*HALLEN, HEATHER E. AND WALTON, JONATHAN D. MSU DOE Plant Research Laboratory, 106 Plant Biology Labs, Michigan State University, East Lansing, MI 48824-1312**. Examining amatoxins: RNA polymerase II in an amatoxin-producing fungus.**

Amatoxins, the bicyclic peptide toxins responsible for ninety percent of lethal mushroom poisonings in humans, act as specific inhibitors of RNA polymerase II. RNA polymerase II (RNAP II) is responsible for messenger RNA synthesis, and, thus, indirectly, for protein synthesis. Through the existence of amatoxin-resistant mutant lines of *Drosophila, Caenorhabditis* and mouse, and the recent x-ray crystallographic determination of the RNAP II-amatoxin complex in yeast, the amatoxin binding sites are known. My current and ongoing research is examining the nature of RNA polymerase II in *Amanita* species, in order to determine the mechanism of resistance to amatoxins in amatoxin-producing fungi. I have sequenced the entire known amatoxin binding region of RNAP II in several species, both toxin-producers and nonproducers. Initial sequencing results show no differences at the amino acid level between toxin producers and non-producers. Current work focuses on purifying RNAP II from *Amanita* species and testing their sensitivity to amatoxin.

*HALLEN, HEATHER E. AND WALTON, JONATHAN D. MSU DOE Plant Research Laboratory, 106 Plant Biology Labs, Michigan State University, East Lansing, MI 48824-1312. **Examining amatoxins: the *Amanita* Genome Project**.

As part of ongoing investigations into the ecology, biochemistry and evolutionary biology of *Amanita* section Phalloideae, we have initiated the *Amanita* genome project. This project originated as part of our investigations into amatoxin biosynthesis. Amatoxins are presumed to be synthesized via a non-ribosomal peptide synthetase (NRPS), predicted to be encoded by a 30-kb gene. Assuming random sampling across the genome and an average read size of 600 bp, the odds of hitting a 30 kb target in a 40 Mb genome are high: 95% chance in 4,000 random, independent sequences. Consequently, we are generating several thousand genomic sequence reads from *Amanita bisporigera* (7,200 as of March 31, 2004). Sequencing an EST library was impractical, as amatoxin biosynthesis appears to take place in a narrow window at or near the time of button initiation, and transcription of amatoxin biosynthetic genes is therefore not observable in the macroscopic organism. We have generated a public *Amanita* sequence database. Each sequence has been compared to GenBank's non-redundant database (using BLASTX) and the *Coprinus* and *Phanerochaete* genomes (using TBLASTX). Additionally, we maintain all sequences in BLAST-searchable format. This resource is available at http://www.prl.msu.edu/walton/amanita.htm. We envision it being of particular interest to the ectomycorrhizal research community.

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*HALLING, ROY E.[1] AND MUELLER, GREGORY M.[2] [1]New York Botanical Garden, Bronx, NY 10458. [2]Field Museum of Natural History, Chicago, IL 60605. **Mushrooms of the Talamancas, Costa Rica.**

For more than 10 years, we have focused on studying the mushrooms of the Cordillera de Talamanca in Costa Rica to better understand neotropical fungi and to obtain some of the data required for macrofungi to be included in conservation and land management activities. As a result, we have been able to document over 220 species of macrofungi distributed in a small area of 0.1 hectare and, we have produced a field guide with color illustrations describing 111 mushroom species. The Talamancas stretch south down the middle of Costa Rica for 300 km from the Central Volcanic range (south of San Jose) to the border with Panama. The mountain range includes the highest peaks in southern Central America with ten separate peaks reaching 2950 m or higher; Cerro Chirripo reaches 3819 m. The subalpine vegetation on several peaks above 3300 m is characteristic of the wetter northern Andes (Ecuador to Venezuela) and this community reaches its northern latitudinal limit in the Cordillera de Talamanca. *Quercus* species are the dominant canopy trees of the tropical wet montane forests of Costa Rica's Cordillera de Talamanca. They are characterized by being cool and humid, and have a prolonged dry season from December through mid May. Most biological inventories have been made along the Pacific slopes (including all our work on macrofungi) due to difficulties of access from the Caribbean side.

HARRIS, STEVEN. Plant Science Initiative and Department of Plant Pathology, University of Nebraska, Lincoln NE. **Morphogenetic functions of microtubules in *Aspergillus nidulans*.**

The establishment and maintenance of polarized growth are key features underlying hyphal morphogenesis in filamentous fungi. Extensive functional characterization of microtubules in *A. nidulans* has shown that they are generally dispensable for polarized growth. By contrast, actin filaments are strictly required for the establishment of hyphal polarity. Here, we report that when actin filament formation is compromised by mutations in the formin SepA or the GTPase ModA (Cdc42), microtubules become essential for polarity establishment. These observations suggest a previously uncharacterized role for microtubules in hyphal morphogenesis. Based on our results, we propose that one possible role may be to mediate the delivery of SepA, and other polarisome components, to polarization sites.

HAWKINS, LAURAINE. Penn State University - Mont Alto, Mont Alto, PA 17237. **Fungal interactions with animals: a primer for teachers.**

Fungi interact in a wide variety of ways with animals. Animals are affected negatively by fungi behaving as: agents of infection or disease (athlete's foot, yeast infections), allergens (often affecting air quality), and decomposers of our foods and other organic materials. Neutral interactions are most numerous; although fungi surround animals in the environment, in most cases, they do not directly affect us and we do not affect them. Humans benefit from positive interactions that include fungi as: foodstuffs consumed directly (edible mushrooms), components in making foods (yeasts in baking and brewing), and in chemical or pharmaceutical applications (Beano, antibiotics). A variety of nonhuman animals have similar beneficial interactions with fungi. As part of a workshop for high school teachers, this talk will review the range of interactions fungi have with humans and other animals. It will provide background information and protocols for teachers to use in planning class activities.

*HEMMES, DON E.[1], DESJARDIN, DENNIS E.[3] [1]Biology Dept., University of Hawaii at Hilo, 200 W. Kawili St., Hilo, HI 96720, [2]Dept. of Biology, San Francisco State University, 1600 Holloway Ave., San Francisco, CA 94132. **Large mushrooms on lawns and agricultural areas in Hawai'i: *Macrocybe, Amanita, Rhodocybe,* and *Lepista*.**

Macrocybe spectabilis, Amanita aff. *foetidissima, Rhodocybe piperita* and two species of *Lepista* have frequented lawns and agricultural areas on a number of the Hawaiian Islands over the past few years. *Macrocybe spectabilis* has been collected on lawns on Kaua'i and in banana patches on O'ahu. *Amanita* aff. *foetidissima* also appears in lawn grass and has been collected on Kaua'i, O'ahu, and Hawai'i Island. *Lepista tarda* is widely distributed on lawns, in bamboo thickets, and in pastures and other agricultural areas and has been known in the Islands for a number of years. A second species, *Lepista subisabellina* appeared in great numbers recently on lawns and in composted leaf mulch on Hawai'i Island and had not been recorded previously. *Rhodocybe piperita* has become locally abundant in recent years. This species can be found in duff under coastal *Casuarina* and *Cupressus* and on lawns under *Melaleuca* used in landscaping. Until recently, this species was known only from a botanic garden in Wellington, New Zealand. The distribution and recent appearance of thse taxa in Hawai'i will be discussed.

*HENKEL, TERRY W., MAYOR, J., WOOLEY, L. Department of Biological Sciences, Humboldt State University, Arcata, CA 95521. **Mast fruiting of the ectomycorrhizal *Dicymbe corymbosa* (Caesalpiniaceae) in Guyana: the 2003 event and implications for monodominance.**

A mast fruiting event was recorded in 2003 for the ectomycorrhizal, monodominant canopy tree species *Dicymbe corymbosa* (Caesalpiniaceae) in the Pakaraima Mountains of western Guyana. In five 0.25 ha study plots in primary *D. corymbosa* - dominated forest, output of large, explosively-dehisced seeds ranged from 66,056 - 161,056 ha and was locally synchronous over a five week sampling period. From 88.9-96.6 % of seeds fell within the mean crown radii of parent trees, indicating poor dispersability. Investment in masting was high for *D. corymbosa*; combined dry mass of seeds, pod valves, and flowering parts ranged from 2225-4082 kg ha^{-1}, nitrogen from 21.2-39.3 kg ha^{-1}, and phosphorus from 0.9-2 kg ha^{-1}. Regional masting synchrony of *D. corymbosa* in the Pakaraima Mountains was confirmed along a 37 km transect, where high, uniform seed output was measured in three disjunct 0.25 ha plots. High densities of *D. corymbosa* seedlings and saplings in all plots indicated successful recruitment following previous supra-annual masting events. Climatic data suggest that masting in *D. corymbosa*was triggered by El Nino-precipitated drought preceeding the flowering season. Ectomycorrhiza-mediated mechanisms allowing high investment of *D. corymbosa* in supra-annual masting are discussed, as well as the consequences of mast seeding for persistent monodominance in the species.

HIBBETT, DAVID S., *NILSSON, HENRIK, SNYDER, MARC AND SHONFELD, MORAN. Biology Department, Clark University, Worcester Massachusetts 01610. **Toward an automated phylogenetic taxonomy of homobasidiomycetes**.

Evolutionary mycologists are making rapid progress toward resolving fungal phylogeny. Changes in taxonomy are not keeping pace with the growth of phylogenetic knowledge, however. A model for automated phylogenetic taxonomy of fungi will be presented, using the homobasidiomycetes as an example. The system involves two components: 1) automated phylogenetic analysis, and 2) automated tree-based classification. The first component has been implemented in a computer program called "mor" that retrieves, aligns, and analyzes nuc-lsu rDNA sequences. The nuc-lsu rDNA was chosen because it is the most widely sampled gene for homobasidiomycete phylogenetics and can be aligned (albeit with ambiguities) across the group. The nuc-lsu rDNA alone does a poor job of resolving many nodes, however, so analyses in mor are performed with a backbone monophyly constraint based on multi-locus analyses. As of this writing, mor has generated trees with over 2000 terminals. The second component of the system, automated tree-based classification, is in development. Phylogenetic taxon definitions will play a central role in this aspect of the system, because they are stable in the face of topological rearrangements. They are also amenable to algorithmic interpretation (unlike Linnaean definitions), which opens the door to automated taxonomy and other phyloinformatics applications.

HOCH, H, C. Department of Plant Pathology, NYSAES, Barton Labs, Cornell University, Geneva, NY 14456. **Contact sensing: A tactilely important phenomenon for phytopathogenic fungi.**

Events preceding appressorium formation, including spore germination and germ tube growth orientation, are triggered by chemical and physical signals in the surrounding environment. For many fungi, sensing of the substratum apart from any chemical signal is all that is required to initiate these events. While many contact sensing phenomena are recognized, the mechanisms of perception are poorly understood; however, for some fungal systems the triggering signal is well documented, such as the abrupt change in substratum topography that initiates appressoria in many rust urediospore germlings. Other fungi, e.g., *Colletotrichum*, that apparently do not rely on discrete topographical features to trigger initiation of appressoria, do require specific measures of contact. Micro- and nanofabrication of substrata with precise features have been used to assess some of these requirements.

HODGE, KATHIE T. Dept. of Plant Pathology, Cornell University, Ithaca, NY 14853. **The teleomorph of the mycoparasitic fungus *Calcarisporium arbuscula*.**

Recent years have seen a dramatic improvement in our understanding of

Continued on following page

fungi in the family Clavicipitaceae, which includes parasites of insects, plants, and fungi. Some of the rare, astromatic members of the family have so far been little studied. In this presentation, an astromatic clavicipitaceous teleomorph is connected for the first time to the widespread mycoparasitic mold *Calcarisporium arbuscula*. Cultural techniques are used to prove the connection, and further support is provided by a molecular phylogenetic analysis of large subunit ribosomal DNA. The placement of the holomorph, its ecology, and the multiple evolutionary origins of mycoparasitism in the Clavicipitaceae are discussed. A new name is provided for the holomorph.

*HOLLOWELL, J.E., MA, JIANXIA, GUTIERREZ, W.A., AND SHEW, B.B. Dept. Plant Pathology, NC State University, Raleigh, NC 27695. **Mycelial compatibility grouping of *Sclerotinia minor* from peanut fields.**

Sclerotinia minor causes serious damage on peanut (*Arachis hypogaea*) in North Carolina. *Sclerotinia minor* has a wide host range and has been isolated from many weed species commonly found during winter fallow in fields used for peanut production. Population variability of isolates collected from peanut and weed hosts was determined by mycelial compatibility grouping (MCG). In addition, MCGs were determined from isolates collected from apothecia and single ascospores during the spring. Mycelial interactions were assessed using a side by side mycelial plug pairing technique on Diana Sermons Medium (DSM). Interactions were scored as compatible or incompatible. Forty isolates obtained from winter-weed species were initially grouped by pairings of all possible combinations. More than 80 additional isolates were grouped using representative testers from each MCG identified in the initial pairings. The 11 MCGs identified included isolates from winter-weed species, peanut, field apothecia and single ascospores of field apothecia. Isolates from a particular field or host were heterogenous according to MCG. Variability in the population of *S. minor* is an important consideration in disease severity assessment and in management with respect to pathogen overwintering and survival on multiple hosts.

HORN, BRUCE W. National Peanut Research Laboratory, USDA-ARS, Dawson, GA 39842. **Infection of wounded peanut seeds by soil fungi: selectivity for species from *Aspergillus* section *Flavi*.**

Insect-damaged peanut seeds are highly susceptible to contamination by carcinogenic aflatoxins produced by *A. flavus* and *A. parasiticus*, fungi belonging to *Aspergillus* section *Flavi*. A laboratory procedure was developed in which viable peanut seeds were wounded and inoculated with field soil containing natural populations of fungi, then incubated under different conditions of seed water activity and temperature. Wounding was required for high incidences of fungal invasion; seed viability had little effect on the colonization patterns by *Aspergillus* species. Section *Flavi* comprised < 1% of total filamentous fungi in soil, but wounded peanut seeds were preferentially colonized by section *Flavi* species as well as *A. niger* over broad ranges of water activity (0.82 - 0.98) and temperature (15 - 37 C). Optimal seed infection occurred at water activities of 0.92 - 0.96 at 30 - 37 C. *Aspergillus parasiticus* invaded peanut seeds at lower temperatures than *A. flavus*. Other fungal genera (*Penicillium, Fusarium* and *Gliocladium*) colonized seeds primarily at water activities and temperatures suboptimal for section *Flavi* species and *A. niger*. The inoculation of wounded viable peanut seeds with soil provides a model system for studying the infection process, the interactions between fungi, and those factors important in aflatoxin formation.

*HUGHES, KAREN W. AND PETERSEN, RONALD H. Department of Botany, University of Tennessee, Knoxville, TN 37996. **Origins of fungal biodiversity in the Southern Appalachians.**

Plants and associated fungi of the Southern Appalachian Mountains have been greatly impacted by a series of glaciation events in the Northern Hemisphere which may have acted as a species pump, creating alternating periods of isolation in refugia and expansion into new habitats. The most recent glacial period ended about 20,000 years ago. Data from our fungal studies suggest that during the glacial maximum, refugia existed in Mexico and Costa Rica but other refugia in the southern US probably existed as well. Many of the Southern Appalachian fungal flora are genetically unique, and genetically variable as might be expected if the current mycota is a mix of fungi derived from different refugia.

*HUGHES, KAREN W. AND PETERSEN, RONALD H. Dept. of Botany, University of Tennessee, Knoxville TN 37996. **Evolution by tandem repeat – an example from *Gymnopus*.**

A short ca. 34 base repeat is present in the ITS2 region of several related *Gymnopus* species. Depending on the species, there may be as few as two and as many as five copies. The copies have diverged from each other with copy 4 being the most widely distributed across *Gymnopus* taxa. For *Gymnopus confluens*, copies 3 and 4 are basal and present as paralogs in all isolates surveyed. The effect of these repeats on phylogenetic analyses and the evolutionary history of the repeats are discussed.

*HUHNDORF, SABINE M.[1], NYBERG, ASA[2], WEDIN, MATS[2], LUNDQVIST, NILS[3], AND *MILLER, ANDREW N.[4] [1]Botany Department, The Field Museum, Chicago, IL 60605, [2]Department of Ecology and Environmental Science, Umeå University, SE-90187 Umeå, Sweden, [3]Mardvagen 8, SE-74340 Storvreta, Sweden, [4]Center for Biodiversity, Illinois Natural History Survey, Champaign, IL 61820. **A reassessment of *Schizothecium* (Sordariales, Ascomycota) based on 28S large subunit nrDNA.**

The genus *Schizothecium* has been used to accommodate species of *Podospora* with outer ascomatal wall layers that form prominent swollen cells or agglutinated hairs around their ascomatal necks. To determine the phylogenetic potential of this ascomatal wall character, maximum parsimony, maximum likelihood, and Bayesian analyses were conducted using partial sequences from the 28S large subunit nrDNA. Sequences were generated from several species of *Schizothecium* and *Podospora* along with numerous additional species in the Sordariales, which possess a wide range of ascomatal wall morphologies. Except for *S. simile*, all sampled species of *Schizothecium* occur as a well-supported monophyletic group, whereas all sampled species of *Podospora* segregate into several clades throughout the Sordariales suggesting ascomatal wall morphology may be a good predictor of phylogenetic relationships and useful for delimiting *Schizothecium*.

*HULVEY, JONATHAN P. AND PADGETT, DAVID E. Dept. of Biological Sciences, Univ. of North Carolina at Wilmington, Wilmington, NC 28403. **An approach to revising the systematics of the watermold genus *Saprolegnia*.**

Systematic organization of the protistan order Saprolegniales (watermolds) is in need of revision because current descriptions of species overlap significantly. This problem is compounded by the fact that no published descriptions of taxa indicate how many measurements were used to determine ranges and mean values for particular diagnostic features. Ideally, morphological criteria used in identification should be unique to each taxon such that overlaps between closely related taxa are resolved. To date, however, no large-scale attempts have been made to reevaluate the taxonomic significance of morphological features and thereby eliminate overlaps. Our approach to resolving species overlaps in the genus *Saprolegnia* is based on the assumption that isolates of this genus that are closely related, as evidenced by ITS gene sequence profiles, represent the same species. Employing this assumption we are reculturing as many *Saprolegnia* isolates as can be acquired and determining which morphological parameters (sporangial, oogonial and/or antheridial) are unique to each ITS grouping alone. This approach will be used to redefine the morphological parameters that circumscribe each taxon of the genus. New taxonomic keys will be developed for the genus.

*HYDE, KEVIN D., JEEWON, RAJESH, BAHL, J., BHILABUT, B, BUSSABAN. CAI, L., DAMODOR, S.B., KODSEUB, R., LAM, C.W.H., LAM, D.M., POTITA, W., PROMPUTTHA, I., TANG, A.M.C., THONGKANTHA, S., VIJAYKRISHNA D. AND YEUNG, S.Y. Centre for Research in Fungal Diversity, The University of Hong Kong, Pokfulam Road, Hong Kong. **Fungal studies at the University of Hong Kong.**

At the University of Hong Kong we are studying in association with other institutes, several groups of ascomycetes and their anamorphs using classical and modern molecular tools. Within the Sordariomycetes modes and rates of molecular evolution of several genes are being investigated to determine the phylogenetic utility of single and multiple genes datasets at different taxonomic ranks. To solve other fungal taxonomic issues, we are also investigating phylogenetic relationships among other unitunicate (e.g, Sordariaceae, Hyponectriaceae, Magnaporthaceae and related families) and bitunicate (Melanommataceae, Lophiostomataceae, Pleosporaceae and Tubeufiaceae) families. Research is also focused on the pathogenic genus *Colletotrichum* (in particular *C. truncatum* and *C. gloeosporioides* complex), where its systematics based on protein and mitochondrial genes will be elucidated. Fungal identification of endophytes, changes in their lifestyle and their genetic relationships with saprobes are also being assessed. By using DGGE, graminicolous and *Pinus* fungal communities are being characterized. Other morphological and molecular studies on taxonomically confused genera such as *Chalara*, *Dactylaria*, *Pyricularia* and *Sporidesmium* complexes, and species in the genera *Apiospo-*

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ra, *Linocarpon, Neolinocarpon* and *Tubeufia* are also being addressed. Results coming out from this work will be included in this paper.

*INDERBITZIN, P.[1], LIM, S.R.[1], VOLKMANN-KOHLMEYER, B.[2], KOHLMEYER, J.[2], BERBEE, M.L.[1]. [1]Department of Botany, 6270 University Boulevard, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4, [2]Institute of Marine Sciences, University of North Carolina at Chapel Hill, Morehead City, North Carolina 28557. ***Spathulospora*: Missing fungal link to red algae, or close relative to insect fungi in the Laboulbeniomycetes?**

Spathulospora is a small genus of ascomycetes, parasitic on marine red algae restricted to the southern hemisphere. Considering its low importance to mankind, *Spathulospora* has been well studied. This is due to its intriguing, highly specialized morphology and to a theory placing *Spathulospora* as the evolutionary link between red algae and ascomycetes. *Spathulospora* was considered to combine morphological features of the insect-parasitic ascomycetes in the Laboulbeniomycetes judged primitive, with the habit of red algae. We investigated the phylogenetic position of *Spathulospora adelpha* and *S. antarctica* using up to 29 year old herbarium specimens. Partial 18S and 28S DNA sequences were obtained, and phylogenetic analyses using Bayesian, parsimony, and neighbor-joining algorithms all agreed with the placement of *Spathulospora*. It was no surprise that the two *Spathulospora* species were each other's closest relatives, given their similar morphology. But the phylogenetic placement was rather unexpected: *Spathulospora* grouped with high bootstrap support within the morphologically dissimilar marine fungi of the Lulworthiales. However, reevaluation of morphology led to the identification of an important shared morphological character for this newly recognized group.

*ITURRIAGA, TERESA[1], URBINA, HECTOR[1] AND LEE, SEONJU[2]. [1]Depto. Biología de Organismos, Universidad Simon Bolivar, Caracas. Venezuela. [2]Dept. of Plant Pathology, University of Stellenbosch, South Africa. **A new species of *Strossmayeria* from South Africa**.

There are 16 species of *Strossmayeria* described to date; most of them wood saprophytes, frequently associated with their *Pseudospiropes* anamorphs. Species are characterized by their superficial apothecia, up to 1 mm diam, with a short point of attachment to the substrate, and excreting yellow exudates when treated with KOH. The ectal excipulum is of textura oblita, medullary excipulum and subhymenium are almost indistinguishable, asci are generally 8-spored, arising from crosiers and usually dextrinoid in Melzer's Reagent. Ascospores are hyaline in all known species except *Strossmayeria ochrospora* in which the ascospores are pale brown. They are usually cylindric-clavate, with the broad end toward the apex of the ascus, 3-7-septate, surrounded by a gel layer that is usually smooth for temperate species, but thicker and usually verrucose in tropical species. The cells in the ascospore are usually uniform, but in some of the tropical species with or without refractocells or disintegrating cells. Ascospores and ectal excipulum are amyloid. This new species was collected by Senjou Lee in South Africa on a fallen branch of *Protea nitida* (Proteaceae), and is characterized by the dark-brown color of its apothecia, by the size of its hyaline amyloid ascospores which are much longer than any other known species, and by having 13-17-septa.

*IVEY, CRYSTAL., ISIKHUEMHEN, OMOANGHE S. North Carolina Agricultural & Technical State Univ., 1601 E. Market St., Greensboro, NC 27411. **Studies on substrate combinations and heat pretreatment suitable for the vegetative growth of *Agaricus brasiliensis* and *subrufescens*.**

Local and abundant agricultural waste products in North Carolina were studied for their ability to support vegetative growth in *Agaricus brasiliensis* and *A. subrufescens*. Different sets of substrate combinations containing cotton waste, sawdust, and aged poultry litter were sterilized at 122 °C for 1, 2, or 3 hours. Similar sets of substrate combinations were separately pasteurized at 90 °C for 24 or 48 hours. Inoculated substrates were allowed to incubate at room temperature. The rate of substrate colonization, abundance of contaminants and the time to primordial initiation were determined. Sterilization was ineffective at eliminating contaminant problems in the substrate combinations tested. Although there were few contaminants in the pasteurized substrates, both species of *Agaricus* were able to overcome them, usually by forming rhizomorphic mycelia strands. A 1:1 ratio combination of hardwood sawdust and 6-year poultry litter appeared to be the substrate combination that supported best mycelia colonization in *A. brasiliensis*. Similarly, a 1:1 ratio combination of hardwood sawdust and 8-year poultry litter supported the best growth and colonization in *A. subrufescens*. Supplementation with organic sources of nitrogen and essential elements reduced substrate colonization time from months to less than two weeks.

*IVORS, K.L.[1], VERSTAPPEN, E.[2], BONANTS, P.[2], WIEJACHA, K.[3], AND GARBELOTTO, M.[1] [1]Dept. of ESPM-ES, University of California, Berkeley, CA. [2]Plant Research International, Wageningen, The Netherlands; [3]Research Institute of Pomology and Floriculture, Skierniewice, Poland. **Investigating the global population structure of *Phytophthora ramorum*.**

Investigating the population genetics of *Phytophthora ramorum*, causal agent of Sudden Oak Death (SOD), is critical to understanding the biology and epidemiology of this newly described pathogen. Raw sequence data (445,000 reads) of *P. ramorum* were provided by the Joint Genome Institute. Our objective was to develop and utilize Simple Sequence Repeat (SSR) techniques for fingerprinting large numbers of *P. ramorum* isolates originating from different host species within Europe and the United States. Primers were selected from over 100 flanking regions of SSRs using a computer program developed within Plant Research International, and tested in PCR reactions to amplify repeats. Thirty-five polymorphic loci were identified and tested both in vitro and in planta to directly genotype the pathogen. This information provided insight regarding the amounts of genetic variation within populations, and separated isolates into two distinct lineages correlated with continental provenance.

JACKSON, JASON[1], VILGALYS, RYTAS[1] AND RICHTER, DANIEL.[2] D. [1]Department of Biology and [2]Nicholas School of the Environment and Earth Sciences, Duke University, Durham, NC 27708. **Recovery of fungal communities after extended land use in the Piedmont of South Carolina.**

Little is known about effects of long-term land use on microbial communities. This study examined changes in microbial communities in forest soils from the Piedmont region of South Carolina. Soils from this region were subjected to over 100 years of intensive cotton production that resulted in massive degradation of soil resources, followed by varying trajectories of ecosystem recovery. As part of a larger study examining the influence of different land use histories on biological complexity within soils, we used molecular-based approaches to assess the microbial community structure from replicated recovered communities that include cultivated fields, pastures, loblolly pine stands, and remnant hardwood stands. Total community DNA was extracted from freshly collected composite soil samples (combined organic and A horizon), and general eukaryote-specific primers were used to amplify and clone libraries for 18S, and intragenic spacer (ITS) regions of the nuclear ribosomal DNA region. Identification of DNA sequences using standard bioinformatics tools (BLAST) and phylogenetic analyses reveal a highly diverse community of eukaryotic microorganisms that is dominated by fungi, but which also includes protistan, chlorophyte and even metazoan lineages. Significant changes in fungal community assemblages can be observed across different habitats, with hardwood and pine forests showing a much greater preponderance of ectomycorrhizal species than cultivated fields and pastured grasslands.

*JEWELL, KELSEA AND VOLK, THOMAS. University of Wisconsin-La Cross, 1725 State St., La Cross, WI 54601. **Preliminary investigations into the use of a killer *Candida* strain to control candidiasis.**

The rising importance of the opportunistic yeast *Candida albicans* and other fungal human pathogens have prompted several investigations into alternative antifungal therapies. One such area is the exploitation of killer yeasts; these fungi are known to produce efficacious fungicidal and fungistatic proteins even against members of their own species. It is hoped that an application of live killer yeasts to already-infected patients would remove the danger of pathogenic *Candida* overgrowth without opening a favorable niche that results from intensive chemical therapy. The purpose of these experiments was to conduct a series of competition assays between pathogenic and nonpathogenic killer strains of *Candida*. Data from assays conducted on solid and liquid media with parameters designed to mimic human conditions will be presented. The second phase of this series will be to design and implement an appropriate genetic control into the killer strain of *Candida* so as to circumvent its own opportunistic nature.

*JIN, WENTAO[1], PENG, JIANGNAN[1], VILGALYS, RYTAS[2] and *ZJAWIONY, JORDAN K.[1] [1]Department of Pharmacognosy and National Center for Natural Products Research, Research Institute of Pharmaceutical Sciences, University of Mississippi, University, MS 38677-1848, and [2]Department of Biology, Duke University, Durham, NC 27708. **Antimicrobial secondary metabolites isolated from a polypore mushroom, *Merulius incarnatus*.**

Merulius incarnatus Schweinitz 1822, known also as *Phlebia incarnata*, Nakesone & Bursdall 1994, or commonly as coral woodcrust, is a saprophytic polypore mushroom growing on a variety of angiosperms particularly fallen

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oaks, beeches, birches and maples. For these studies we collected *M. incarnatus* in fall of 2002 and 2003 at Duke Forest in Durham, North Carolina. A crude extract of this mushroom exhibited significant activity against several microorganisms, particularly *Staphylococcus aureus* and methacillin resistant *S. aureus* (MRSA). The most active fraction showed IC_{50}=3.5 μg/mL against MRSA. The activity-guided chromatographic separation led to an active fraction, mainly composed of 4,6-dihydroxybenzoic acid derivatives bearing long aliphatic side chains with a different degree of unsaturation (merulinic acids). The separation of these compounds proved to be rather difficult due to their close structural similarity. The methylation reaction and further chromatographic separation led to the isolation of a series of merulinic acid esters. The structures of these compounds were established by spectroscopic methods.

*JOHANNESSON, HANNA AND TAYLOR, JOHN W. Dept. Plant Biology, 111 Koshland Hall, UC Berkeley, CA 94720. **Evolution of surface antigens of the human pathogenic fungi *Coccidioides immitis* and *C. posadasii*.**

We have investigated the evolution of two antigens (Proline-rich antigen, PRA, and Spherule outer wall glycoprotein, SOWgp) in the human pathogens *Coccidioides immitis* and *C. posadasii*. By using likelihood-based methods to compare models of selective pressure we verified that PRA evolves under positive selection. No evidence of diversifying selection acting on PRA was found, thus the increased rate of evolution is not a result of avoidance of the host's immune system. The analyses suggest that selection was not stronger on the branch separating pathogenic and non-pathogenic species in the phylogeny of *Coccidioides* spp. and their sister taxa, and we suggest that positive selection acts on PRA as a consequence of spore cell-wall morphogenesis unique to each species. We found that SOWgp consists of repetitive units of 41-47 aa, evolving under concerted evolution by unequal crossing over. The species share repeat number polymorphism, indicating that repeat number of SOWgp is under balancing selection.

*JONES, SEAN. C. AND METHVEN, ANDREW S. Dept. of Biological Sciences, Eastern Illinois University. 600 Lincoln Ave. Charleston IL, 61920. **Morphological variability in interspecific hybrids of *Flamulina*.**

Flammulina (Basidiomycetes, Agaricales, Tricholomatacea) is a saprobe found in the wild, cultivated commercially, and marketed worldwide under the name "Enokitake." Until the early 1960's, the species epithet *velutipes* was uniformly applied to all collections in the genus. Since then, several species have been described from a variety of ecosystems on several different continents based on morphology, mating studies, and molecular data. Interspecific hybrids "fruited" in the laboratory on synthetic logs composed of tulip poplar saw dust and rice bran produced more or less normal basidiomata with viable basidiospores. Macroscopic and microscopic features were subsequently used to describe the morphology of these hybrids. Results of these analyses revealed that a suite of characteristics representing the parental taxa was exhibited by the hybrids.

*JU, YU-MING[1], ROGERS, JACK D.[2], HSIEH, HUEI-MEI[1]. [1]Institute of Botany, Academia Sinica, Nankang, Taipei 115, Taiwan, [2]Department of Plant Pathology, Washington State University, Pullman, WA 99164-6430. ***Amphirosellinia* — a new xylariaceous genus.**

Five fungi—including *Rosellinia evansii* Læssøe & Spooner, *R. americana* (Petr.) F. Rappaz, and three hitherto undescribed fungi—grow inside the bark of dicot trees where their solitary or confluent, perithecate stromata are largely buried or become erumpent through the epidermal layer. These fungi appear to form a coherent group and combination of their characteristics sets them apart from other known xylariaceous genera. A new genus *Amphirosellinia* is thus erected for these fungi. The accepted *Amphirosellinia* species are characterized by the following characteristics: 1. stromata typically developed beneath the epidermal layer of their hosts; 2. a thick, carbonized crust enclosing each individual perithecium; 3. ascal apical rings being higher than broad; 4. inequilateral ascospores with a long, sigmoid germ slit on the less convex side; and 5. a synnematous anamorph with conidiogenous regions that become geniculate and produce lacrymoid conidia.

KANNAN, K.P[1], MUTHUMARY, J.[1] AND UDAYA PRAKASH, N.K.[2] [1]CAS in Botany, University of Madras, Guindy Campus, Chennai, INDIA, [2]Omni Environmental, Inc. 13740, Research Blvd, Suite H-5, Austin, TX 78750. **Endophytic mycobiota of gymnosperms from Austin, Texas, USA.**

Endophytic mycobiota of some of the Gymnosperms viz., *Cycas revoluta, Juniperus asheii, Pinus sylvestris* and *Thuja occidentalis* collected from Austin, Texas, were screened. Altogether 2400 segments (600 each) were screened and a total of 954 endophytic fungal isolates were recovered. Among them, 403 were sterile and 26 were xylarious forms. The remaining were classified into 19 species of fungi belonging to 16 genera. Among them, maximum number of species were recorded from *Pinus sylvestris* and *Thuja occidentalis* (12 each) followed by *Cycas revoluta* (11) and *Juniperus asheii* (10). The fungi, *Nigrospora sphaerica* and *Bartalinia robillardoides* were unique to *Cycas revoluta*; *Alternaria alternata* and *Phomopsis obscurens* to *Juniperus asheii*; *Aspergillus fumigatus, Cladosporium cladosporioides, Trichoderma longibrachiatum* and *Pestalotiopsis breviseta* to *Pinus sylvestris*; *Colletotrichum gloeosporioides, C. dematium, Phoma betae, P. putaminum* and *Phyllosticta* sp. to *Thuja occidentalis*. The Endophytic Infection Rates (EIR %) revealed that 47.3 % of the tissues were colonized by the endophytic fungi in *Juniperus asheii*, 42.3% in *Pinus sylvestris*, 34.7 % in *Thuja occidentalis* and 33 % in *Cycas revoluta*. The following fungi, *Lasiodiplodia theobromae*, *Phomopsis obscurens, Pestalotiopsis breviseta* and *Phyllosticta* sp., were the dominant endophytes recorded.

KELLER, HAROLD W. Dept. of Biology, Central Missouri State University, Warrensburg MO 64093. **Tree canopy biodiversity in Great Smoky Mountains National Park.**

This study represents the first inventory of treetop biota in the Great Smoky Mountains National Park. The All Taxa Biodiversity Inventory aims to survey all life forms in the Park. Student climbers used the double rope climbing technique to obtain tree canopy bark samples from up to 40 meters. Climbers sampled a total of 240 trees representing 35 different tree species during the summers of 2000 and 2001. Students discovered a new myxomycete species in the genus *Diachea* restricted to upper tree canopy heights, collected the fern *Polypodium appalachianum* growing as an epiphyte at 35 to 40 meters, and observed mollusc slugs feeding on the immature sporangial stages of the myxomycete *Stemonitis axifera*. Of the targeted tree canopy biota, including myxomycetes, macrofungi, mosses, liverworts, lichens, and ferns, certain myxomycete species were known only from live trees. There were 95 myxomycete species, including 52 new park records, harvested from moist chamber cultures derived from canopy bark samples. Factors such as bark pH and tree height were analyzed to determine correlation with myxomycete species assemblages. Occurrence and abundance of certain myxomycete species corresponded to differences in bark pH. Funded by the National Science Foundation, Biotic Surveys and Inventories Program, Award #DEB-0079058 and Discover Life in America Awards #2001-26 and 2002-17.

*KERRIGAN, RICHARD W.[1], CALLAC, PHILIPPE[2], GUINBERTEAU, JACQUES[2], AND CHALLEN, MIKE[3] [1]Sylvan Research, Kittanning, PA, [2]INRA CR Bodeaux, France, [3]HRI, Warwick University, UK. **Phylogenetic perspective on diversity within *Agaricus* Section *Xanthodermatei* Singer from the temperate northern hemisphere**.

Samples of members of *Agaricus* Section *Xanthodermatei* Singer from Europe, North America, and Hawaii were evaluated. DNA sequences from the ITS1+2 region of the nuclear rDNA region were obtained and evaluated under maximum parsimony. Eighteen species-level taxa, including two undescribed species, were associated with distinctive ITS1+2 sequences. One traditional taxon requires further study. Relationships within the genus and the section, which were sometimes surprising, will be discussed.

*KIM, CHANGMU AND JUNG, HACK SUNG. School of Biological Sciences, Seoul National University, Seoul 151-747, Korea. **Structural and functional fungal diversities in ginseng cultivated land soils.**

Structural and functional fungal diversities were studied from ginseng (*Panax ginseng*) cultivated lands. To understand soil fungal diversities, culturable species were isolated on media, DNAs of non-culturable species were sequenced, and potential C source utilization patterns were analyzed using Biolog microtiter plates. Total 25 zygomycetes and 36 ascomycetes were cultured on PDA and H media but no basidiomycetes were isolated. Total genomic DNAs were amplified, 389 isolates were ARDRA-tested, and sequences of 292 isolates were used in phylogenetic analysis. Each sampling site represented various species populations. The C source utilization analysis indicated that two sample soils (Kanghwa and Geumsan) had similar carbon utilization patterns but the other sample soil Poongki) had lower utilization ability. In structural diversity study, ginseng cultivated soils proved to hold various fungal species and other soil microorganisms. In functional fungal diversity study, it was indicated

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that fungal species diversity and organic materials in soil might affect C source utilization.

*KIM, J.-J.[1], DE GIULI VALLVERDU, F.[1], ALAMOUTI, S. [1], LEE, S.[1], UZUNOVIC, A.[2] AND BREUIL, C.[1] [1]Dept. of Wood Science, University of British Columbia, Vancouver, B.C. V6T 1Z4, Canada, [2]Forintek Canada Corp., Western Laboratory, Vancouver, B. C. V6T 1W5 Canada. **Database of Ophiostomatoid fungi that cause stain in lumber, logs and trees.**

Sapstain fungi discolour lumber, logs and tree sapwood and are often mistaken for moulds, which cause a superficial discoloration. Stained wood has a lower market value and can be refused by importing customers as such products can potentially carry pathogenic fungi. Addressing these issues involves developing ways for accurately identifying staining fungi, documenting how they are geographically distributed, and developing ways of monitoring fungal transfer in wood products. To respond to some of these needs, we are constructing an Ophiostomatoid fungi database that will be accessible via the Internet. The objective is to provide universities, industry, and government agencies with a resource that offers key information pertinent to environmental and trade issues. The database currently includes information on the genera *Ceratocystis, Ceratocystiopsis*, *Leptographium*, and *Ophiostoma*. To support identifying isolates, it has a flexible taxonomy / morphology search tool that gives access to detailed descriptions of fungal characteristics, micrographs and diagrams. We seek national and international partners who will actively contribute to improving and expanding this resource.

*KIM, J.-J.[1], LEE, S.[1], BREUIL, C.[1], HUMBLE, L.M.[2] AND ALLEN, E.A.[2] [1]Department of Wood Science, University of British Columbia, Vancouver, B.C. V6T 1Z4, Canada. [2]Natural Resources Canada, Pacific Forestry Centre, Victoria, B.C. V8Z 1M5 Canada. **Diversity of fungi isolated from lodgepole pine attacked by the Mountain Pine Beetle.**

The mountain pine beetle (*Dendroctonus ponderosae*, MPB) and its fungal associates are causing extensive losses in lodgepole pine forests in North America. Although the MPB is a normal component of lodgepole pine ecosystems, in an epidemic it threatens wood and fiber supplies. In time, trees killed by MPB and its associated fungi become hosts to a variety of organisms including insects, fungi and nematodes. We are determining the diversity of fungi present in attacked trees in order to assess potential phytosanitary risks associated with exporting products made from such wood. In this work, we report the fungi isolated from MPB infested trees at the green phase from four British Columbia sites: Manning Park, Williams Lake, Radium, and Cranbrook. Fungal identification was based on morphological characteristics and sequences of rDNA and/or beta tubulin genes. Among the Ophiostomatoid fungi seven species were identified: *Ophiostoma clavigerum, O. montium*, and *O. nigrocarpum*, as well as four unknown species that need further identification (*Ambrosiella* sp., *Ceratocystiopsis* sp., *Graphium* sp., and *Leptographium* sp.). Some of the species had not been reported previously. We also isolated basidiomycetes: *Fomitopsis pinicola*, *Heterobasidion annosum*, and *Phlebia radiata*, as well as *Entomocorticium.*

*KIM, KYUNG MO, RYOO, KYUNG HWAN, AND JUNG, HACK SUNG. School of Biological Science, Seoul National University, Seoul 151-747, Korea. **Polymorphism of the nuclear ITS region in *Trametes versicolor* and another method for determining evolutionary speed of fungal species.**

Trametes versicolor is one of the cosmopolitan wood-rotting fungi on dead hardwoods and has extremely variable pileal surfaces with sharply contrasted concentric zones of diverse colors. It produces enzymes such as laccase, lignin peroxidase, carboxymethyl cellulase and avicelase, and causes active decay of ligno-cellulose wood complex. In addition to such morphological variations, there exist polymorphic site variations in nuclear ribosomal ITS region at intraspecies and intra-individual levels of *T. versicolor*. In ITS sequences of 72 clones from eight strains in different habitats, 26 substitutions (eleven in ITS1, one in 5.8S, fourteen in ITS2) and one insertion (in ITS2) were found. Using MODELTEST software, K80+G was determined as the best model of evolutionary substitution for 72 sequences of *T. versicolo*r, and phylogenetic trees were reconstructed with prior information of K80+G under Bayesian criterion. Evolutionary speed of *T. versicolor* was calculated from the Bayesian phylogenetic tree through time calibration. This study may be used as another ideal method for explaining fungal evolution and determining evolutionary speed of fungal species.

KIM, YONG H., CHEONG SU J. AND *CHOI, HYOUNG T. Microbial Physiology Lab, Div. Life Sci., Kangwon National University, Korea. **Cloning and regulation of genes of the lignin degrading enzymes in *Trametes versicolor*.**

Laccase and lignin- and manganese peroxidases are implicated in the lignin degradation. We have cloned cDNA genes of laccase (lac) and manganese peroxidase (mnp) in *Trametes versicolor* isolated in Korea by RT-PCR and RACE. lac showed 65-95% homologies, and mnp showed 61-83% homologies when compared with other white-rot fungal genes. When trinitrotoluene (TNT) was added to the fungal culture, it was degraded quite fast. We have also analyzed the gene expressions under the TNT degrading conditions by RT-PCR.

*KOLJALG, URMAS[1], LARSSON, KARL-HENRIK[2], ABARENKOV, KESSY[1] AND NILSSON, HENRIK R.[2]. [1]Institute of Botany and Ecology, University of Tartu, Tartu, Estonia, [2]Systematic Botany, Göteborg University, Göteborg, Sweden. **UNITE - the first step toward microarray based identification.**

Identification of ectomycorrhizal fungi is often achieved through comparisons of ribosomal DNA internal transcribed spacer (ITS) sequences with accessioned sequences deposited in public databases. A major problem encountered is that annotation of the sequences in these databases is not always complete or trustworthy. In order to overcome this deficiency, we report on UNITE, an open access database comprising well annotated fungal ITS sequences from well-defined herbarium specimens that include full herbarium reference identification data, collector/source, ecological data, etc. UNITE can be searched either by species name or via a sequence similarity search by using program blastn. Database incorporates also phylogenetic species recognition. For this purpose galaxie, a package for sequence identification through automated phylogenetic analysis, is implemented into UNITE.

*KRETZER, ANNETTE M.[1], DUNHAM, SUSIE M.[2], MOLINA, RANDY[3] AND SPATAFORA, JOSEPH W. [4] [1]SUNY-ESF, 1 Forestry Drive, Syracuse, NY 13210, [2]Albertson College of Idaho, Biology Dept., 2112 Cleveland Blvd., Caldwell, ID 83605, [3]USDA Forest Service, 2300 SW Jefferson Way, Corvallis, OR 97331, [4]Oregon State University, Dept. of Botany and Plant Pathology, Corvallis, OR 97331. **Molecular ecology of tuberculate ectomycorrhizae: a tripartite symbiosis?**

In tuberculate ectomycorrhizae, ectomycorrhizal fine roots are formed in tight clusters, which are surrounded by wefts of hyphae. The tuberculate morphology has evolved multiple times, especially within the genera R*hizopogon* and *Suillus* (Boletales, Basidiomycota), but is particularly pronounced in *Rhizopogon vinicolor* and *R. vesiculosus* where individual tubercles can get up to several centimeters in diameter. Because they allow for easy sampling of vegetative structures, these taxa offer nearly ideal systems to study the population structure of ectomycorrhizal fungi in general and of hypogeous fungi in particular. Detailed comparative studies on the small-scale population structure of *Rhizopogon vinicolor* and *R. vesiculosus* will be presented. Tuberculate ectomycorrhizae also raise questions with respect to their adaptive role. We hypothesize that it lies in their symbiotic relationship with bacteria. Evidence from the literature as well as preliminary data from own investigations into bacterial communities associated with tuberculate ectomycorrhizae will be presented.

*KULDAU, GRETCHEN A., GOLITZ, MARA C. AND MANSFIELD, MICHELE A. Dept. of Plant Pathology, Penn. State University, University Park, PA 16802. **Isolation and characterization of penicillin-producing Penicillia from silages.**

Federal authorities regulate antibiotics in milk and milk products and as a result fluid milk from tankers is routinely tested. Anecdotal reports from producers and agriculture professionals in Pennsylvania indicate that at low frequency unexplained antibiotics in milk are detected. We hypothesized that the source of these antibiotics may be from antibiotic-producing Penicillia resident in cattle silage feeds. To investigate this we surveyed corn and grass silages for the presence of *Penicillium chrysogenum* a known penicillin producer. Our survey resulted in a collection of *P. chrysogenum* isolates primarily from the grass silage samples. The initial morphological identification is being confirmed by DNA sequencing and the antibiotic production potential of the isolates is being characterized using a bacterial inhibition assay.

LACEY, LANCE C.[1], *BARONI, TIMOTHY J.[1] AND LODGE, D. JEAN[2]. [1]Dept. Biological Sciences, State Univ. New York – College at Cortland, Cortland, NY 13045; [2]Cntr. for Forest Mycology Research, USDA-FS, Forest Products Lab, Luquillo PR 00773-1377. ***Lactarius*** **from Belize and the Dominican Republic, new taxa and biogeographic patterns.**

Continued on following page

Members of the genus *Lactarius* are commonly found in subtropical and tropical forests in ectomycorrhizal associations with pine (*Pinus* spp.) and oak (*Quercus* spp.). A few taxa are found in apparent associations with *Coccoloba* spp. and *Pisonia* spp. Recent studies of Neotropical species of *Lactarius* have documented 25 new taxa in the genus from the Lesser and Greater Antilles, Mexico, Costa Rica and areas in and around the Amazonian forests in publications by Pegler (1983 – no new taxa), Pegler and Fiard (1979 – 6 new taxa), Singer et al. (1983 – 11 new taxa), Montoya et al. (1996; 1998 – 2 new taxa), Montoya and Bandala (2003; 2004 – 3 new taxa), Miller et al. (2002 – 2 new taxa) and Miller et al. (2000 – 1 new taxon). Ongoing studies of macrofungi of Belize and the Dominican Republic by Baroni, Lodge, Miller, Cifuentes, Lacey and collaborators have discovered to date four new species and one new variety of *Lactarius* from Belize, and one new sequestrate taxon from the Dominican Republic. Thus currently, five of the seven taxa of *Lactarius* encountered in Belize are new (71%) and one sequestrate lactarioid species of the 10 known taxa from the Dominican Republic are new. Interestingly, the *Lactarius* species found in Belize have a distinct association with southeastern North American species, while the taxa from the Dominican Republic show a mixture of eastern and western North American components. A list of species and a discussion of biogeographic patterns will be presented. Selected taxa will also be illustrated with color photographs of the basidiomata and diagnostic microscopic features.

LAMPMAN, AARON M. Dept. of Anthropology, University of Georgia, 250 Baldwin Hall, Athens, GA 30602. **Tzeltal Ethnomycology: Mushroom Folk Classification and Use in Highland Chiapas, Mexico.**

The Tzeltal Maya of Highland Chiapas have sophisticated and extensive knowledge of the macrofungi that are distributed throughout the local environment. This knowledge developed through a long history of interaction and experimentation, and is orally transmitted from generation to generation. Although 60% of the "average" folk ethnobiological system is made up of culturally "useless" species, the Tzeltal ethnomycological system appears to be limited to those species that are considered useful. This highly unusual feature leads to a "lopsided" folk classification in which the majority of macrofungi in the region are simply ignored, or lumped into a large residual category that might be glossed into English as "toadstools." Culturally useful species are given consistent linguistic designations that are widely recognized throughout the highlands, and are classified according to gross morphology rather than utility. Knowledge of culturally useful species is highly detailed, and includes an understanding of seasonality, substrate preference, life cycles, and association with tree species. Tzeltal use of macrofungi as non-cultivated resources is extremely important during the "hunger months" when supplies of staple foods are running low. A number of species are thought to provide nourishment, and a number are used as medicine.

LANDOLT, JOHN C.[1], CAVENDER, JAMES C.[2], AND *STEPHENSON, STEVEN L.[3] [1]Dept. of Biology, Shepherd College, Shepherdstown, WV 25443, [2]Dept. of Environmental and Plant Biology, Ohio University, Athens, OH 45701, [3]Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701. **Dictyostelid cellular slime molds of Australia.**

The continent of Australia, with a total extent of approximately 7,682,300 km^2, covers about 5% of the earth's land area. Most of the continent is low, flat and dry; deserts and dry grasslands are the predominant vegetation types. During the past three field seasons, samples for isolation of dictyostelid cellular slime molds have been collected from a number of localities in Queensland, the Northern Territory, Western Australia, New South Wales, and Victoria. The majority of these samples were collected from the soil/litter layer on the ground, but some additional samples were obtained from the layer of organic matter ("canopy soil") associated with the bases of vascular epiphytes on the trunks and branches of trees in the tropical forests of northern Queensland. Some of these samples were collected at heights of more than 20 meters above the forest floor. Many of the forms that have been recovered from these samples could be assigned to described taxa, including such cosmopolitan species as *Dictyostelium mucoroides, Polysphondylium pallidum, P. violaceum,* and *D. giganteum*. However, a significant number of others (possibly as many as a dozen different examples) appear to represent species new to science. The number of apparently undescribed forms suggests that the dictyostelid biota of Australia is relatively distinct when compared to that of any other continent.

LANGDON, KEITH R. Inventory & Monitoring Coordinator, Great Smoky Mountains National Park, 1314 Cherokee Orchard Rd, Gatlinburg, TN 37738. **Trees and tree canopies in Great Smoky Mountains National Park.**

Great Smoky Mountains National Park is a 2,200 square kilometer reserve that straddles the North Carolina – Tennessee boundary, in the higher mountains of the Southern Appalachian mountains. The mountains have a complex geo-chemical foundation and relief that ranges from 300 to 2,000 meters above sea level. These and other factors influence the natural species richness of the Park. There are over 100 species of native trees, including taxa associated with the boreal, northeastern US and southern coastal plain regions. The Park also has been reported to have many height records for individual species of trees, nearly 20 national champion and co-champion trees, and some of the highest canopied forests in the eastern US. The remote, rugged topography make the Smokies an area of active discovery, and the Park is interested in accelerating its inventories, monitoring and research, especially in the 20-30% of its area that was never cut. Over 400 species new to science, and over 3,000 new geographic records of species have been documented in the park in the last several years.

*LARSSON, KARL-HENRIK[1], LARSSON, ELLEN[1], TAYLOR, ANDY[2], ROSLING, ANNA[2], KJØLLER, RASMUS[3] AND ERLAND, SUSANNE[4]. [1]Dept. Botany, Göteborg Univ., Box 461, SE 405 30 Göteborg, Sweden, [2]Forest Mycology and Pathology, SLU, Box 7026, SE 750 07 Uppsala, Sweden, [3]Dept. Mycology, Univ. Copenhagen, Ø. Farimagsgade 2D, DK 1353 Copenhagen K, Denmark, [4]Microbial Ecology, Lund Univ., SE 223 62 Lund, Sweden**. Taxonomy and belowground diversity of the ectomycorrhizal genus *Piloderma*.**

The basidiomycete genus *Piloderma* includes the well-known ectomycorrhizal species *P. fallax* and *P. byssinum*. When introduced in 1972 the genus counted five species but three of them, *P. lapillicolum, P. reticulatum*, and *P. sphaerosporum* have never been widely accepted as distinct species. We extracted DNA from recently collected fruiting bodies of *Piloderma* specimens from Norway and Sweden and sequenced the nuclear ribosomal ITS region. Sequences were manually aligned and phylogenetically analysed using the maximum parsimony method. Statistical support for nodes was evaluated by bootstrapping. We recovered six clades corresponding to *P. fallax, P. byssinum, P. lanatum, P. reticulatum*, and two undescribed species. Sequence variation within the *P. fallax* clade is comparatively large which indicates that the name covers a complex of closely related taxa. Not all of these varieties have the typical bright yellow colour on the rhizomorphs. Sequences generated from EM from Nordic forest soils confirm that all described *Piloderma* species are mycorrhizal. The molecular diversity belowground exceeds that found among sequences generated from fruiting bodies. Implications for taxonomy and for future studies are discussed.

*LEACOCK, PATRICK R. AND MUELLER, GREGORY M. Dept. of Botany, The Field Museum, Chicago IL 60605. **Fungi of the Chicago region: a century of progress.**

We have over 100 years of data on Chicago area fungi. Early and prolific collectors were Edward T. and Susan A. Harper who focused on the western Great Lakes region, preserving 4150 specimens of macrofungi during 1885 to 1920. Many of the 650 Chicago area collections include their excellent black and white photos. Will Sayer Moffatt was active here from 1891 to 1924. Sporadic collecting in the region occurred between 1924 and 1994. Our ongoing intensive sampling of macrofungi began in 1994. These data are now being compiled for dissemination via a multi-institutional collection digitization project, vPlants, with funding by IMLS. The vPlants.org website is an online herbarium for the vascular plant collections (more than 90,000 specimens, 2500 species) of the 24 county Chicago region. The current project's expansion is adding the estimated 1,000 species of fungi for the region plus descriptive pages and images for each plant and fungus taxon. This effort will pull together the knowledge of fungal diversity for a region located on the prairie edge of the eastern deciduous forest biome.

LEBAUER, DAVID S. Department of Natural Resources, NC A&T State University, Greensboro, NC 27411. **Nutritional and medicinal properties of commercially available Shiitake (*Lentinula edodes*).**

Shiitake (*Lentinula edodes*) are consumed for culinary, medicinal, and nutritional properties. Shiitake available to American consumers primarily come from three sources: dried Asian, fresh indoor sawdust, and fresh local log grown. Contents of nutritional and medicinal compounds in Shiitake from these sources were compared. Sawdust-grown Shiitake had more protein, glucose, sodium and selenium compared to log-grown and Asian-imported. Imported Asian Shiitake had more sulfate and glucose than NC log grown. Results indicate that there are large differences in nutritional values of Shiitake from vari-

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ous sources. Investigations of the medicinally active compounds, -glucans and lentinan, are ongoing.

*LEBEL, TERESA[1] AND TONKIN, JENNIFER. E.[2] [1]Royal Botanic Gardens Melbourne, Birdwood Avenue, South Yarra, Vic.3141 Australia, [2]ILFR, University of Melbourne, Burnley, Vic.3140 Australia. **Sequestrate Russulaceae from "down-under".**

Australasia is a hot spot of sequestrate Russulaceae diversity, with some 75 species currently known. In the present study we investigate the phylogeny and evolution of the sequestrate fungi in relation to their gilled relatives. Analyses of ITS and nLSU sequences from gilled and sequestrate taxa from Australia, New Zealand, Spain and North America were performed. Results support the monophyly of Australasian species of *Lactarius* and sequestrate *Zelleromyces*, and *Russula* and sequestrate *Cystangium*, *Macowanites* and *Gymnomyces*. Additionally, within the *Russula* and *Lactarius* clades, the sequestrate forms have multiple origins. However, the sequestrate genus *Cystangium*, containing gastroid and intermediate forms, appears to form a monophyletic clade within *Russula*.

LEE, HYANG BURM[1], *KIM, KYUNG MO[1], YU, SEUNG HUN[2], AND JUNG, HACK SUNG[1]. [1]School of Biological Sciences, Seoul National University, Seoul 151-747, Korea. [2]Divison of Applied Biology, Chemistry & Food Science, Chungnam National University, Daejeon 305-764, Korea. **Black fruit rot of strawberry caused by *Alternaria tenuissima* and its ability to produce mycotoxins.**

Black fruit rot disease of strawberry (*Fragaria* x *ananasa* Duch.) has been observed in vinyl house fields at Nonsan, Puyeo and Daejeon, Chungnam Province area, Korea, especially following moist and cool conditions in spring and in September. Based on morphological characteristics and molecular data, the fungus isolated from infected fruit tissues was identified as *Alternaria tenuissima* (Fries) Wiltshire. *Alternaria* cultures were extracted with methanol and purified using solvent partition, thin-layer chromatography, and high performance liquid chromatography. Out of ten isolates of *A. tenuissima*, eight isolates produced five known mycotoxins such as alternariol (AOH), alternariol monomethyl ether (AME), altenuene (ALT), altertoxin-I (ATX-I) and tenuazonic acid (TeA). The quantities and kinds of mycotoxins varied according to tested isolates. However, most of them produced a large amount of AOH, AME and TeA up to 1 ug/g fruit, but nil or trace to small amount of ALT and ATX-1 depending on isolates.

LEE, HYANG BURM[1], *PARK, JAE YOUNG[1], SUMMERBELL, RICHARD C.[2], AND JUNG, HACK SUNG1[1]. [1]School of Biological Sciences, Seoul National University, Seoul 151-747, Korea, [2]Centraalbureau voor Schimmelcultures, P.O. Box 85167, 3508 AD Utrecht, The Netherlands. **A new genus and two new species of epiphytic fungi isolated from pine tree leaves.**

During investigation of epiphytic fungal occurrence on Korean pine tree (*Pinus densiflora* S. & Z.) leaves, a new genus and two new species have been isolated. These isolates have been compared with related taxa of genera such as *Phaeomoniella*, *Phialemonium*, *Moristroma* and *Cadophora*. Based on morphological characters as well as molecular data of ITS and 28S rDNA sequences, three isolates were completely distinguished from *Phaeomoniella* and represented a new species within a new genus. Another isolate was clustered with *Phaeomoniella chlamydospora* but differed in morphology and had <90% sequence identity. Isolates of the new genus made extensive patches of greenish black mycelium as well as some whitish patches, and they appeared yeasty (slimy) on oatmeal and potato dextrose agar media. No other species examined matched this appearance. Elongated phialides were seen but were hyaline or nearly so, unlike those of *Phaeomoniella*. These observations suggest that our three isolates belong to a new species within a new genus relatively closely related to *Phaeomoniella*, while the fourth isolate corresponds to a new species of *Phaeomoniella*.

*LEE, MARIA[1], VOLK, THOMAS J.[2], AND COOPER, CHESTER R.[3] [1]Department of Microbiology, [2]Department of Biology, University of Wisconsin-La Crosse, [3]Department of Biological Sciences, Youngstown State University, Ohio. **Preliminary proteomic profiling of dimorphism in *Penicillium marneffei*, an opportunistic fungal pathogen of humans.**

Penicillium marneffei is a thermal dimorphic fungus in which reversible interconversion between mold and yeast phase is easily achieved by controlling incubation temperature. The mold phase resembles other *Penicillium* species with their classic "paintbrush" structure. The alternate growth morphology is a yeast phase that multiples by fission. The fungus causes disease among immunocompromised patients and is endemic in southeast Asia, especially Thailand, Malaysia and Hong Kong. Inhalation of conidia is thought to initiate pulmonary infection, with the conversion to yeast allowing evasion of the immune system. The yeasts can disseminate to other organs and cause fatalities if not properly diagnosed and treated. The long-term goal of this project is to develop a comprehensive molecular-based understanding of dimorphism in *P. marneffei*. The main objective of this proteomics research is to characterize the proteins produced by *P. marneffei* that effect dimorphism. To date, there have not been global protein profiles established for any phase of growth in *P. marneffei*. From the data presented here, we hope to correlate specific proteins with genes known to be associated with dimorphism. From these profiles, genomics will be integrated with proteomics, and one or more selected proteins will be studied as possible diagnostic marker(s) or antifungal target(s) for the disease.

*LEE, SANGWON[1], HAMELIN, R.C.[2] AND BREUIL, COLETTE[1] [1]Department of Wood Science, University of British Columbia, 2424 Main Mall, Vancouver, BC, V6T 1Z4, Canada, [2]Canadian Forest Service, Laurentian Forestry Centre, 1055 rue du PEPS, Sainte-Foy, Québec, G1V 4C7, Canada. **Genetic variability of *Ophiostoma clavigerum* associated with *Dendroctonus ponderosae* Hopkins in North America.**

In this study, the genetic diversity of the *O. clavigerum* (Robinson-Jeffrey & Davidson) Harrington was assessed. This pathogenic, sapstaining fungus is associated with the mountain pine beetle (*D. ponderosae* Hopkins), which is a native insect in North America and causes an extensive damage in the forest. As of 2003, in British Columbia only, fourteen million hectares of lodgepole pine (*Pinus contorta Dougl.* var. *latifolia* Engelm.) has been infested. To collect the fungi from a broad geographic range, a total of eight locations in Canada (British Columbia) and USA (Montana, and Idaho) were selected. The fungi were isolated from the lodgepole pine sapwood attacked by MPB, galleries or mycangia of the MPB. A total of 200 single-spore isolates, recovered from the field sampling were analyzed for their genetic variability by the amplified fragment length polymorphism generated with four primer combinations. In this work, we described the genetic variation and differentiation within/among the *O. clavigerum* populations. We also examined the possible correlation of genetic distances with geographic distances among sampling locations. Overall, it appeared that the genetic polymorphism in *O. clavigerum* is low, which might be related to relatively rare sexual reproduction.

*LETCHER, PETER M. AND POWELL, MARTHA J. Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487. ***Kappamyces*, a new genus in the Chytridiales**.

A new genus for a chytrid member of the *Rhizophydium* clade is described. Many *Rhizophydium* clade members exhibit simple and variable thallus morphology, and thus some species may be identical, while others may be members of species complexes and represent distinct genera. A minute chytrid that colonized pollen grains was found that had zoospore ultrastructure and large subunit secondary ribosomal rRNA molecular constitution different from the core *Rhizophydium* clade with 24 isolates. Unlike typical *Rhizophydium* zoospores, the *Kappamyces laurelensis* gen. et sp. nov. zoospore lacked a rumposome, kinetosome-associated electron-opaque spur, and kinetosome-associated microtubular root. Distinct from the typical *Rhizophydium* zoospore, the kinetosome abutted a single mitochondrion, both the kinetosome and non-flagellated centriole had an electron-opaque core, and several vesicles surrounded the kinetosome. In a parsimony analysis of large subunit rRNA sequences, a grouping of *K. laurelensis* and two other isolates were sister to the core *Rhizophydium* clade, and both the *K. laurelensis* group and the core *Rhizophydium* clade had 100% bootstrap support. The zoospore of *K. laurelensis* may be the simplest type of zoospore in the Chytridiales.

*LIM, YOUNG WOON[1], KIM, JAE-JIN[1], CHEDGY, RUSSELL[1], MORRIS, PAUL I.[2] AND BREUIL, COLETTE[1]. [1]Department of Wood Science, University of British Columbia, Vancouver, B.C. V6T 1Z4, Canada, [2]Forintek Canada Corp., Vancouver, B.C. V6T 1W5 Canada. **Fungal diversity from western red cedar fence and their resistance to beta-thujaplicin**.

We investigated the fungal community inhabiting western red cedar fence material with a focus on species colonizing wood below the surface of which little is known. From seven pieces of fence materials, we isolated and characterized twenty three different species using traditional morphological and molecular methods; The species identified included thirteen ascomycetes and ten basidiomycetes fungi. Isolates were tested for their resistance to beta-thujaplicin – one of the prin-

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ciple fungicidal agents of WRC heartwood extractives. Most of ascomyceteous fungi exhibited greater resistance than basidiomyceteous fungi. Interestingly, 3 ascomycetes and 2 basidiomycetes species isolated with high frequencies exhibited resistance to this compound - tolerance may be analogous with an ability to detoxify it. These species could be candidate 'pioneer' species that colonize and detoxify WRC extractives allowing the colonization by decay fungi.

*LIM, YOUNG WOON[1], YEUNG, YU CHING ALAN[1], CHEDGY, RUSSELL[1], STURROCK, RONA[2], LEAL, ISABEL[2] AND BREUIL, COLETTE[1]. [1]Department of Wood Science, University of British Columbia, Vancouver, B.C. V6T 1Z4 Canada, [2]Canadian Forest Service, Pacific Forestry Centre, Victoria, B.C. V8Z 1M5 Canada. **Differentiating and evaluating the phylogenic position of two forms of *Phellinus weirii: P. weirii* and *P. sulphurascens*.**

P. weirii causes butt rot on western red cedar (*Thuja plicata* Donn), and laminated root rot on Douglas fir [*Pseudotsuga menziesii* (Mirb.) Franco.] and on other conifers. Accurate and efficient methods were developed to separate two forms of *Phellinus werii: P. weirii* (cedar form) and *P. sulphurascens* (Douglas fir form). New primers were designed from the internal transcribed spacer (ITS) region of *P. weirii*. They amplified and differentiated *P. weirii* (cedar form), *P. sulphurascens* and other decay fungi that are frequently found in coniferous trees. RFLP patterns that differentiated the two fungal forms were also obtained by cutting the ITS region with the restriction enzyme Rsa I, and the large subunit region with Age I and Nci I. Phylogenetic analysis of both regions suggests that these two species may have diverged recently and may be closely related to *P. ferreus, P. ferrugineofuscus, P. fragrans* and *P. viticola*.

LINCOFF, GARY The New York Botanical Garden, Bronx, NY 10458. **Pattern Recognition in the Mycoflora of the Southern Appalachians.**

Ectomycorrhizal fungi would seem to be more restricted in their distribution than fungal decomposers. Nevertheless, ectomycorrhizal fungi in such disparate and floristically distinct locations as Madagascar, New Zealand, and Thailand can be used to predict patterns in the mycoflora of the southern Appalachians. Ectomycorrhizal fungi represent a conspicuous component of the fungal biodiversity of the southern Appalachians. At 3 major NAMA fall forays in North Carolina, in 1974, 1980, and 1994, just ectomycorrhizal fungi in the genus *Amanita*, in the boletes, and the Russulaceae comprised about 25% of all the fungi collected at these forays (checklists record totals of about 500 in '74, 400 in '80, and more than 500 in '94).The ectomycorrhizal fungi in the southern Appalachians occur primarily with trees in the Pinaceae, Betulaceae, Fagaceae, Juglandaceae, and Salicaceae. These families are absent as native flora in Madagascar, and all but Fagaceae are absent in New Zealand. Even in Thailand, where pines and oaks occur, the dominant ectomycorrhizal tree family is the Dipterocarpaceae, which is absent in North America. Nevertheless, Amanitas, boletes, Lactarii and Russulas occur in all these places. While the species composition is different, recognizing the taxa above the species level allows one to predict the presence of these groups of fungi in the southern Appalachians.

*LIU, M., CHAVERRI, P., HODGE, K.T. Dept. of Plant Pathology, Cornell University, Ithaca NY 14853. **Where are we? *Hypocrella/Aschersonia* in the family Clavicipitaceae.**

Members of Clavicipitaceae are associated with plants, arthropods, or fungi. The genus *Hypocrella* (anamorph: *Aschersonia*) includes obligate pathogens of whiteflies or scale insects. Some *Hypocrella* species with large stromata (i.e. 10 times larger than their scale insect hosts) may also assimilate nutriment from plants indirectly. We therefore hypothesize that *Hypocrella* might represent an evolutionary bridge between plant-associated and arthropod-associated clavicipitacean fungi. *Hypocrella* species have not yet been extensively included in phylogenetic study in the family. In this study, we have included multiple species of *Hypocrella* along with other genera in the Clavicipitaceae in a molecular phylogenetic analysis based on nuclear LSU ribosomal DNA sequence data. We sought to address the origin of *Hypocrella* within the Clavicipitaceae in light of Diehl's ideas about clavicipitacean subfamilies. We also intend to answer the question of whether or not *Hypocrella* is monophyletic.

*LIU, MIAO[1], ROMBACH, MICHIEL C.[2], HUMBER, RICHARD A.[3], HODGE, KATHIE T.[1] [1]Department of Plant Pathology, Cornell University, Ithaca, New York 14853, [2]Overaseweg 9, 4836 BA Breda, The Netherlands, [3]USDA-ARS Plant Protection Research Unit, US Plant, Soil, and Nutrition Laboratory, Tower Road, Ithaca, New York 14853. **What's in a name? *Aschersonia insperata*: a new pleoanamorphic fungus with characteristics of *Aschersonia* and *Hirsutella*.**

We discuss a new pleoanamorphic species from a Philippine tropical forest that occurs as orange to reddish-orange, tuberculate stromata on unidentified homopteran larvae, and produces both *Aschersonia* and *Hirsutella*-like synanamorphs. To determine the most appropriate generic placement for this fungus, we conducted a molecular phylogenetic analysis using nuclear LSU ribosomal DNA. Based on its phylogenetic relationships, a comparison of the complexity and persistence of each anamorph, and the speculated relevance of each synanamorph to survival, we consider the new fungus should be included in genus *Aschersonia* thus intend to describe it as *Aschersonia insperata* anam. nov.

LÓPEZ LASTRA, CLAUDIA C.[1], *SIRI, AUGUSTO, SCORSETTI, ANA C., MARTI, GERARDO A., COSCARON, SIXTO, LICHTWARDT, ROBERT W.[3] [1]Centro de Estudios Parasitologicos y de Vectores, Calle 2 N# 584, La Plata, Argentina, [2]Museo de Ciencias Naturales, paseo del bosque s/n, (1900) La Plata, Argentina, [3]Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, Kansas 66045. **Trichomycete fungi associated with insect larvae from aquatic environments in Misiones and Tierra del Fuego, provinces of Argentina.**

Trichomycete fungi live obligately associated with arthropod guts from all over the world. Fifteen species of Trichomycetes living in the guts of aquatic insects are reported from two provinces of Argentina at the two territorial extremes: Misiones in the Northeast, and Tierra del Fuego, the southernmost extreme of the country and of the world. Species recorded belong mostly to the Harpellales, and they were identified from guts (hindguts and midguts) of immature stages of Culicidae, Chironomidae, Ceratopogonidae, Simuliidae, (Insecta: Diptera), Ephemeroptera and Plecoptera. Five species of Harpellales were obtained from Misiones and eight species from Tierra del Fuego. In Tierra del Fuego, two of the species belong to the Order Amoebidiales. Most of the species of Trichomycetes reported here were also reported before for other hosts and regions of Argentina, however most are new records for the country and for South America. The lower diversity of Trichomycetes found in Misiones aquatic environments could possibly be due to warmer temperatures of the streams and ponds (15-24º C), compared to Tierra del Fuego with temperatures ranging from 9-15º C.

*LOPRETE, DARLENE M. AND HILL, TERRY W. Departments of Chemistry and Biology, Rhodes College, Memphis, TN 38112. **Complementation of Calcofluor hypersensitivity in an *Aspergillus nidulans* mutant by a gene coding for a putative O-glycosylated transmembrane protein.**

In a search for cell wall-defective mutants in *Aspergillus nidulans*, we have screened the Harris temperature sensitive mutant collection for elevated sensitivity to the wall-compromising agent Calcofluor White (CFW). We have designated one strain from the Harris collection (ts 1-161) as *calC*, and we have complemented the hypersensitive phenotype with a plasmid from the Osherov and May "AMA *Not* I" genomic DNA library. Random transposon insertions localized the complementing sequence to a region containing a single predicted gene, designated AN4897.1. Site-directed mutagenesis of the start codon eliminates rescuing ability. The hypothetical translated product is an ST-rich protein (42% S/T) of 27.4 kDa mass (unprocessed), with a cleavable N-terminal ER-targeting domain and a probable internal membrane anchor. No known homologies have been identified in the databases. Sequencing of the corresponding region in the mutant has revealed no mutations in the ORF or within 300 base pairs upstream, leading to the conclusion that the gene is a high copy extragenic suppressor of the *calC* mutation. Work is underway to formally eliminate from consideration two smaller ORFs in the complementing region (using site-directed mutagenesis of start codons) and to construct a GFP-fusion protein of the AN4897.1 protein in order to confirm its predicted membrane localization.

LUMBSCH, H. THORSTEN. Department of Botany, The Field Museum, 1400 S. Lake Shore Drive, Chicago, IL 60605. **Lichen-forming fungi in the tree canopies in the Great Smoky Mountains National Park**.

Lichens, fungi that form stable symbiotic associations with photosynthetic partners, are common epiphytes in temperate regions. The species composition often differs between taxa growing on twigs and those on stems of trees. In most lichenological studies species occurring in canopies are underrepresented. The current project by H. Keller concentrates on these largely neglected epiphytes. This talk will give an overview of the lichen flora and vegetation of the Great Smokey National Park and addresses questions of differences in the species composition of stem and twig species in that area. Since lichens often have a

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very wide and disjunct distribution, the importance of the National Park as a glacial refugium for widely disjunct species is demonstrated by lichen species that occur in eastern North America and the Pontis region and those occurring in eastern North America and eastern Asia, showing the classical Asa Gray distribution. The lichen flora of the National Park has been studied by many lichenologists since the monograph by Degelius in 1941. However, many new additions, including new species (such as *Vainionora americana* described in 2004) are constantly being made.

*LUTZONI, FRANÇOIS[1], KAUFF, F.[1], COX, C.J.[1], MCLAUGHLIN, D.[2], CELIO G.[2], DENTINGER, B.[2], PADAMSEE, M.[2], HIBBETT, D.[3], JAMES, T.Y.[1], BALOCH, E.[4], GRUBE, M.[4], REEB, V.[1], HOFSTETTER, V.[1], SCHOCH, C.[5], ARNOLD, A.E.[1], MIADLIKOWSKA, J.[1,6], SPATAFORA, J.[5], JOHNSON, D.[5], HAMBLETON, S.[7], CROCKETT, M.[5], SHOEMAKER, R.[7], SUNG, G.-H.[5], LÜCKING, R.[8], LUMBSCH, T.[8], O'DONNELL, K.[9], BINDER, M.[3], DIEDERICH, P.[10], ERTZ, D.[11], GUEIDAN, C.[1], HALL, B.[12], HANSEN, K.[13], HARRIS, R. C.[14], HOSAKA, K.[5], LIM, Y.-W.[3,15], LIU, Y.[12], MATHENY, B.[3], NISHIDA, H.[16], PFISTER, D.[13], ROGERS, J.[17], ROSSMAN, A.[18], SCHMITT, I.[8], SIPMAN, H.[19], STONE, J.[5], SUGIYAMA, J.[20], YAHR, R.[1] AND VILGALYS, R.[1] [1]Duke University, USA. [2]University of Minnesota, USA, [3]Clark University, USA, [4]Karl-Franzens-University, Austria, [5]Oregon State University, USA, [6]Gdansk University, Poland, [7]Agriculture and Agri-Food Canada, [8]The Field Museum, USA, [9]U.S. Dept. of Agriculture, IL, USA, [10]National Natural History Museum, Luxembourg, [11]National Botanic Garden of Belgium, [12]University of Washington, USA, [13]Harvard University Herbaria, USA, [14]New York Botanical Garden, USA, [15]Curr. addr.: University of British Columbia, Canada, [16]The Institute of Physical and Chemical Research, Japan, [17]Washington State University, Pullman, USA, [18]U.S. Dept. of Agriculture, MD, USA, [19]Botanischer Garten und Botanisches Museum Berlin-Dahlem, Germany, [20]The University of Tokyo, Japan, **Where are we in assembling the fungal tree of life, classifying the fungi, and understanding the evolution of their subcellular traits?** (poster presentation)

We present an overview of progress in molecular systematics of fungi since 1990, and demonstrate that overlap among data matrices has been very low. As a result, many of the currently available data cannot be used in multi-locus analyses to infer fungal relationships on a large scale. We report here the results of four Bayesian analyses with complementary bootstrap assessment of phylogenetic confidence using neighbor joining, maximum parsimony, and Bayesian methods on: 1) combined two-locus data set (nucSSU and nucLSU rDNA) with 558 species representing all traditionally recognized fungal phyla (Ascomycota, Basidiomycota, Chytridiomycota, Zygomycota) and the Glomeromycota; 2) combined three-locus data set (nucSSU, nucLSU and mitSSU rDNA) with 236 species; 3) combined three-locus data set (nucSSU, nucLSU rDNA and *RPB2*) with 157 species; and 4) combined four-locus data set (nucSSU, nucLSU, mitSSU rDNA, and *RPB2*) with 103 species. The latter three analyses included only members of the Ascomycota and Basidiomycota. The four-locus analysis resolved multiple deep relationships within the Ascomycota and Basidiomycota that were not revealed previously, or that received only weak support values in prior studies. Based on these results and reanalysis of subcellular data, we also synthesize current knowledge regarding the evolution of septal features of fungal hyphae and present a preliminary reassessment of ascomal evolution. The main goal of the poster version of this study is to display the resulting phylogenetic trees for a closer examination of the inferred relationships.

*LUTZONI, F.[1], KAUFF, F.[1], COX, C. J.[1], MCLAUGHLIN, D.[2], CELIO, G.[2], DENTINGER, B.[2], PADAMSEE, M.[2], HIBBETT, D.[3], JAMES, T. Y.[1], BALOCH, E.[4], GRUBE, M.[4], REEB, V.[1], HOFSTETTER, V.[1], SCHOCH, C.[5], ARNOLD, A. E.[1], MIADLIKOWSKA, J.[1,6], SPATAFORA, J.[5], JOHNSON, D.[5], HAMBLETON, S.[7], CROCKETT, M.[5], SHOEMAKER, R.[7], SUNG, G.-H.[5], LÜCKING, R.[8], LUMBSCH, T.[8], O'DONNELL, K.[9], BINDER, M.[3], DIEDERICH, P.[10], ERTZ, D.[11], GUEIDAN, C.[1], HALL, B.[12], HANSEN, K.[13], HARRIS, R. C.[14], HOSAKA, K.[5], LIM, Y.-W.[3,15], LIU, Y.[12], MATHENY, B.[3], NISHIDA, H.[16], PFISTER, D.[13], ROGERS, J.[17], ROSSMAN, A.[18], SCHMITT, I.[8], SIPMAN, H.[19], STONE, J.[5], SUGIYAMA, J.[20], YAHR, R.[1], and VILGALYS, R.[1]. [1]Duke University, USA. [2]University of Minnesota, USA. [3]Clark University, USA. [4]Karl-Franzens-University, Austria. [5]Oregon State University, USA. [6]Gdansk University, Poland. [7]Agriculture and Agri-Food Canada. [8]The Field Museum, USA. [9]U.S. Dept. of Agriculture, IL. [10]National Natural History Museum, Luxembourg. [11]National Botanic Garden of Belgium. [12]University of Washington, USA. [13]Harvard University Herbaria, USA. [14]New York Botanical Garden, USA. [15]Curr. addr.: University of British Columbia, Canada. [16]The Institute of Physical and Chemical Research, Japan. [17]Washington State University, Pullman, USA. [18]U.S. Dept. of Agriculture, MD. [19]Botanischer Garten und Botanisches Museum Berlin-Dahlem, Germany. [20]The University of Tokyo, Japan. **Where are we in assembling the fungal tree of life, classifying the fungi, and understanding the evolution of their subcellular traits?** (oral presentation)

We present an overview of progress in molecular systematics of Fungi since 1990, and demonstrate that overlap among data matrices has been very low. As a result, many of the currently available data cannot be used in multi-locus analyses to infer fungal relationships on a large scale. We report here the results of four Bayesian analyses with complementary bootstrap assessment of phylogenetic confidence using neighbor joining, maximum parsimony, and Bayesian methods on: 1) combined two-locus data set (nucSSU and nucLSU rDNA) with 558 species representing all traditionally recognized fungal phyla (Ascomycota, Basidiomycota, Chytridiomycota, Zygomycota) and the Glomeromycota; 2) combined three-locus data set (nucSSU, nucLSU and mitSSU rDNA) with 236 species; 3) combined three-locus data set (nucSSU, nucLSU rDNA and *RPB2*) with 157 species; and 4) combined four-locus data set (nucSSU, nucLSU, mitSSU rDNA, and *RPB2*) with 103 species. The latter three analyses included only members of the Ascomycota and Basidiomycota. The four-locus analysis resolved multiple deep relationships within the Ascomycota and Basidiomycota that were not revealed previously, or that received only weak support values in prior studies. Based on these results and reanalysis of subcellular data, we also synthesize current knowledge regarding the evolution of septal features of fungal hyphae and present a preliminary reassessment of ascomal evolution. Together, these findings provide an overview of our present understanding of the structure of, and approaches to, inferring the fungal tree of life.

MIADLIKOWSKA, JOLANTA, O'BRIEN, HEATH, AND LUTZONI, FRANÇOIS. Dept. Biology, Duke Univ., Durham, NC 27708. **Molecular phylogenetic analysis of mycobiont-photobiont population structure in *Peltigera* communities.**

Many *Peltigera* species co-occur within a single lichen community. Their mycobionts form bi-membered symbiotic associations with the cyanobacterium *Nostoc* as the exclusive photobiont, or tri-membered symbiotic associations with *Nostoc* and the green alga *Coccomyxa*. Most of the taxa are part of two highly polymorphic species complexes, *P. canina* and *P. aphthosa*, which incorporate many individuals with phenotypically intermediary and atypical characteristics. It is unknown if these unusual morphotypes represent undescribed species, intraspecific polymorphism within recognized *Peltigera* species, hybrids between existing taxa or reflect differences in the photobiont incorporated. Here, we present the results of a study we have undertaken to use multiple molecular markers to permit fine-scale discrimination of mycobiont and photobiont genotypes of all *Peltigera* specimens located within 1m diameter plots in British Columbia, Canada. We also identified the photobionts of other cyanolichens in the plots and used direct PCR to amplify *Nostoc* DNA from substrate samples to identify other potential photobionts that are available at the site. Inferences from these data will allow us to better understand the population dynamics, and interspecific interactions that underlie the structure of lichen communities, which will in turn illuminate our understanding of *Peltigera* systematics.

MANDYAM, KEERTHI AND *JUMPPONEN, ARI. Division of Biology, Kansas State University, Manhattan, KS66506. ***Periconia* spp. are common root-colonizing fungi in the tallgrass prairie.**

Seasonal data over two years at the Konza Prairie LTER site suggest that dark septate endophytes (DSE) may be more abundant than the arbuscular mycorrhizae. To identify the common DSE fungi, we isolated root-colonizing fungi at Konza Prairie. The anamorphic genus *Periconia* accounted for nearly half of the isolates and represented three conspecific groups identified by restriction fragment length polymorphism (RFLP) of the internal transcribed spacer within the ribosomal RNA gene. Multiple representatives from each group were tested for their ability to colonize *Allium porrum* L. (leek) in an in vitro resynthesis system. *Periconia* spp. colonized the leek seedlings and formed DSE structures observed in the field-collected samples. Colonization of native tallgrass prairie plants by *Periconia* spp. ranged from significant growth inhibition to neutral asymptomatic symbiosis and significant growth increase. We conclude that *Periconia* spp. are common DSE fungi causing the abundant colonization observed in the tallgrass prairie. Based on their great abundance and resynthesis studies with native plants, we hypothesize that the *Periconia*

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spp. provide nutritional and non-nutritional benefits to some hosts and may drive community dynamics in mixed tallgrass prairie plant communities.

*MANSFIELD, MICHELE A. AND KULDAU, GRETCHEN A. The Pennsylvania State University, Department of Plant Pathology, 417 Buckhout Laboratory, University Park, PA 16802. **Survey of fungi in maize silage using microbiological and molecular techniques.**

Fungal infestation of maize-based feeds can result in contamination with mycotoxins. Toxigenic fungal genera reported in maize and silage include *Fusarium, Alternaria, Aspergillus* and *Penicillium*. The objective of this research is to investigate fungal species in maize silage. Silage was collected at 30-40 dairies in 2001 and 2002 during harvest and after storage. Fungi isolated by plating were identified by morphology and sequencing the internal transcribed spacer (ITS), or the translation elongation factor 1-alpha locus. For molecular analysis, total DNA was extracted from silage, the ITS region amplified by PCR, and the products used to create a plasmid ITS library. Initial data revealed that several yeast species made up a large percent of the library. To avoid repetitively analyzing these species, screening was performed using Southern hybridization with probes generated from ITS sequences of these fungi. Microbiological techniques isolated several species of *Fusarium, Penicillium*, yeast and other filamentous fungi. The DNA-based method detected all of these species and additionally revealed the presence of the toxigenic *Alternaria alternata* and other filamentous and yeast species. These data suggests that a molecular approach will provide a more comprehensive assessment of fungi in maize silage than traditional microbiological techniques.

MACHADO, CAROLINE [1], WANG, JINGHONG[1], PANACCIONE, DANIEL G[2] AND SCHARDL, CHRISTOPHER L.[1] [1]Department of Plant Pathology, University of Kentucky, Lexington, KY 40546-0091, [2]Division of Plant and Soil Sciences, West Virginia University, Morgantown, WV 26506-6058. **Elimination of anti-mammalian toxin genes in Epichloë endophytes of forage grasses.**

Epichloë endophytes (*Epichloë* and *Neotyphodium* spp.) seedborne fungal symbionts of cool-season grasses, enhance host fitness and stress tolerance, but also produce biologically active alkaloids including ergot alkaloids associated with fescue toxicosis in grazing animals. One approach to reduce fescue toxicosis is to manipulate genes in the ergot alkaloid pathway. The gene, *dmaW*, encoding the first pathway-specific step, was cloned from *Claviceps* spp. and its biochemical function was demonstrated by expression in yeast. Homologs were cloned from *Neotyphodium coenophialum* (from tall fescue) and *Neotyphodium* sp. Lp1 (from perennial ryegrass). In order to confirm its function in ergot alkaloid production, *dmaW* in *Neotyphodium* sp. Lp1 was knocked out by gene replacement. The *dmaW* knockout mutant produced no detectable ergovaline or simpler ergot alkaloids, and complementation with *C. fusiformis dmaW* restored ergovaline production. These results confirmed that the cloned endophyte gene was *dmaW*, and that *dmaW* is required for ergot alkaloid biosynthesis. *Neotyphodium coenophialum,* a common endophyte of tall fescue, has two homologs of *dmaW*. A Cre/lox site-specific system recombination system has been chosen to obtain marker-free mutants of *N. coenophialum*. One *dmaW* homolog (*dmaW-2*) was knocked out in *N. coenophialum* and the marker gene was eliminated when a *cre* gene construct was introduced into the mutant. The *dmaW-2* knockout transformant produced ergovaline, suggesting that the *dmaW-1* was active in *N. coenophialum*. The next step will be to knockout *dmaW-1* in *N. coenophialum* to test its role, and for possible use in tall fescue cultivars.

MARCHESE, RON, *MCLAUGHLIN, JOSEPH, VOISEY, LAUREN, GORGOL, LAURA, MCCANN, MICHAEL, AND SNETSELAAR, KAREN. Saint Josephs University, Philadelphia PA 19131. **Isolation of *Ustilago maydis* from soil**.

Infection by *Ustilago maydis*, the corn smut fungus, is characterized by the formation of galls filled with diploid thick-walled teliospores. Upon germination teliospores undergo meiosis to produce haploid yeast-like cells that survive on many substrates. For infection to occur, the haploid cells first fuse and the resulting dikaryon must infect a plant. Infection only occurs when haploid cells are fully compatible, i.e. they have unlike alleles at two genetic loci, termed a and b. There are two alleles at a and many b alleles. The identity of a and b alleles can be determined using rich medium containing charcoal. We isolated *U. maydis* from soil and used the charcoal test to show that the isolates came from haploid as well as diploid propagules. Diploid isolates predominated in winter months, but the presence of haploid isolates year-round indicated that *U. maydis* grows vegetatively in soil. These studies used soil from an outdoor research plot where only two b alleles were used. To our surprise, we found that many isolates had some b allele other than those used. We are characterizing the b alleles of these isolates using the charcoal test as well as a method that distinguishes alleles based on patterns generated by restriction enzymes. So far, at least three alleles other than those we used have been found. We speculate that they came into the corn plot on seeds.

*MATA, JUAN L., HUGHES, KAREN W. AND PETERSEN, RONALD H. The University of Tennessee, Dept. of Botany, 437 Hesler Biology Bldg., Knoxville, TN 37996-1100. **A phylogenetic study of *Megacollybia platyphylla*.**

Megacollybia platyphylla (Pers.: Fr.) Kotl. & Pouz. is a commonly collected mushroom in the Northern Hemisphere and putatively recognized as one single morphological species. However, a preliminary nrITS sequence analysis revealed a biogeographic signal. In this cladogram, sequences of collections from northwestern United States are more closely aligned with those from of European origin, while eastern United States representatives form a clade with those from Mexico and Costa Rica. While some differences in field characteristics are observable, micro-morphological examination of all voucher specimens from different geographic locations did not offer substantial differences between them. Examination of the type specimen of *Tricholompsios fallax* A.H. Smith indicates it may be an available name for the western United States collections.

*MATHENY, P. BRANDON[1], AMMIRATI, J.F.[2], AOKI, T.[3], BARONI, T.J.[4], BINDER, M.[1], CELIO, G.[5], CRANE, P.E.[6], DE NITIS, M.[1], DENTINGER, B.[5], FRØSLEV, T.[7], GE, Z.W.[8], HALLING, R.[9], HOSAKA, K.[10], HUGHES, K.W.[11], KERRIGAN, R.W.[12], KROPP, B.R.[13], LANGER, E.[14], MATSUURA, K.[15], MCLAUGHLIN. D.J.[5], NILSSON, R.H.[16], NISHIDA, H.[17], PADAMSEE, M.[5], PETERSEN. R.H.[11], PIEPENBRING, M.[18], SLOT, J.[1], VAURAS, J.[19], VELLINGA, E.C.[20], WANG, Z.[1], WILSON, A.[1], YANG, Z.L[8], AND HIBBETT, D.S.[1] [1]Biology Dept., Clark Univ., 950 Main St., Worcester, MA 01610 USA; [2]Biology Dept., Univ. of Washington, Seattle, WA; [3]National Inst. Agrobiological Sciences, Ibaraki, Japan; [4]Dept. Biological Sciences, State Univ. New York Cortland, NY; [5]Dept. Plant Biology, Univ. of Minnesota, St. Paul, MN; [6]Northern Forestry Centre, Canadian Forest Service, Edmonton, Canada; [7]Botanical Inst., Univ. of Copenhagen, Denmark; [8]Kunming Inst. Botany, Chinese Academy of Sciences, P. R. China; [9]Inst. Systematic Botany, New York Botanical Garden, Bronx, NY; [10]Dept. Botany & Plant Pathology, Oregon State Univ., Corvallis, OR; [11]Botany Dept., Univ. of Tennessee, Knoxville, TN; [12]Sylvan Research, Kittanning, PA; [13]Dept. Biology, Utah St. Univ., Logan, UT; [14]Univ. Kassel, Germany; [15]Dept. Organismic & Evol. Biology, Harvard Univ., Cambridge, MA; [16]Göeteborg Univ., Botaniska Inst., Göeteborg, Sweden; [17]Inst. Molecular & Cellular Biosciences, Univ. Tokyo, Japan; [18]Botanisches Inst., J. W. Göethe-Univ., Frankfurt, Germany; [19]Herbarium, Biology Dept., Univ. of Turku, Finland; [20]Plant & Microbial Biol. Dept., Univ. of California, Berkely, CA. **Progress towards assembling the tree of life for the Basidiomycota.**

A phylogeny of the Basidiomycota is presented drawing upon nucleotide and amino acid sequences of nuclear ribosomal RNA loci (18S and 25S) and protein-coding genes that include RPB1 and RPB2 (which encode the largest and second largest subunits of RNA polymerase II, respectively), elongation factor 1-alpha, and mitochondrial ATP6. Taxon sampling, gene structure, primer design, and data sets of different gene combinations will be presented in an effort to resolve relationships among the Urediniomycetes, Ustilaginomycetes, and Hymenomycetes; the heterobasidiomycetes and Homobasidiomycetes; and along the backbone of the homobasidiomycete tree.

MATHENY, P. BRANDON. Biology Dept., Box 351330, University of Washington, Seattle, WA 98195-5325 USA. **Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (*Inocybe*; Agaricales).**

Approximately 3000 bp across 84 taxa have been sequenced for variable regions of RPB1, RPB2, and nLSU-rDNA to infer phylogenetic relationships in the large ectomycorrhizal mushroom genus *Inocybe* (Agaricales; Basidiomycota). This study represents the first effort to combine variable regions of RPB1 and RPB2 with nLSU-rDNA for low-level phylogenetic studies in mushroom-forming fungi. Combination of the three loci increases non-parametric bootstrap support, Bayesian likelihood posterior probabilities, and resolution for numerous clades compared to separate gene analyses. These data suggest the evolution of at least five major lineages in *Inocybe*—the *Inocybe* clade, the *Mallocybe* clade, the *Auritella* clade, the *Inosperma* clade, and the *Pseudosperma*

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clade. Additionally, many monophyletic groups nested within each major lineage are strongly supported. These results also suggest the family Crepidotaceae *sensu stricto* is sister to *Inocybe*. Recognition of *Inocybe* at the family level, the Inocybaceae, is recommended.

*MAYOR, JORDAN R. AND HENKEL, TERRY W. Dept. of Biological Sciences, Humboldt State University, Arcata CA 95518. **Ectomycorrhizal influence on leaf litter decomposition within a monodominant *Dicymbe corymbosa* (Caesalpiniaceae) forest in Guyana.**

The influence of ectomycorrhizal (EM) fungi on leaf litter decomposition within a monodominant neotropical forest in Guyana was examined. The forest, comprised of ~80% basal area of the EM leguminous canopy species *Dicymbe corymbosa*, harbors >150 putatively-EM fungal species which are absent from the surrounding AM-dominated mixed rain forest. EM-excluding trench plots and controls in *D. corymbosa* forest, as well as reciprocal leaf litter transplants to mixed forest were established in the summer of 2003. Two harvests of leaf litter bags (at 1 & 6 months respectively) have revealed interesting and unexpected results. At 1 month the dry mass loss of trenched vs. control litter was not significantly different. At 6 months the dry mass loss of the trench vs. control was equivalent despite the control plot litter bags, unlike the trench plot, being thoroughly explored by putatively-EM hyphae and EM rootlets. In reciprocal litter transplants, at 6 months the *D. corymbosa* leaf litter was shown to decompose faster in EM presence ($p \leq .02$). The potential role of foliar endophytes as latent saprotrophs involved with initial leaf litter decomposition is discussed, as well as hypothesized nutrient cycling mechanisms and litter-binding by EM fungi within this monodominant forest.

*MCCLENON, TERRY M.[1] AND MONCALVO, JEAN-MARC[2]. [1]University of Toronto, 125 Willcocks St., Toronto, ON M5S 3B2, and [2]Royal Ontario Museum, 2100 Queen's Park, Toronto, ON M5S 2C6, Canada. **Molecular phylogenetic methods detect unique fungal lineages in forest soil.**

While describing the phylogenetic diversity of fungi in a Hemlock forest in southern Ontario, several groups of "unknown" fungal sequences were found. These fungi were identified by cloning the first 900bp of the nLSU-rDNA region from DNA extracted from soil. 215 LSU sequences cloned from soil were assigned an identification based on BLAST similarity and phylogenetic analyses. A total of 89 ascomycete sequences were recovered, from which 30 have very poor similarity to known fungal LSU sequences in GenBank. Many of these 30 sequences cluster with, but are distinct from Group III fungal sequences in Schadt et al. (2003) that were recovered from tundra soil. We recovered 75 basidiomycete sequences, including sequences from many ectomycorrhizal taxa. 27 zygomycete sequences were also recovered, as well as 8 alveolate sequences. The remainder of the cloned sequences may be chimeric sequences generated during the PCR amplification of mixed DNA samples extracted from soil, or may represent still unknown organisms. The 75 cloned LSU basidiomycete sequences are also directly compared to sequences obtained from fruiting bodies collected from the same plot.

*MENDGEN, KURT, STRUCK, CHRISTINE, HAHN, MATTHIAS, KEMEN, ERIC, HAERTER, ARIANE AND VOEGELE, RALF. Dept. of Phytopathology, University of Konstanz, 78464 Konstanz, Germany. **Slurp, slurp: Nutrient uptake by haustoria**.

Haustorium differentiation of *Uromyces fabae* is the result of a series of recognition events with the host. We have compared gene expression in infection hyphae and haustoria. Some 20% of the genes were highly expressed in haustoria, but only at low levels or not at all in spores and the other early infection stages. Our experiments suggest haustorial function as follows: The plasma membrane H+-ATPase pumps protons into the fungus-plant interface and provides the driving force for metabolite uptake. A fungal invertase hydrolyzes sucrose that is derived from the host plant. The resulting metabolites, glucose and fructose, are taken up by a haustorial hexose transporter. Within the haustorium, hexoses are metabolized, but are also converted to mannitol and arabitol. These compounds likely serve as storage metabolites, in osmoprotection and / or protection from free radicals. In addition, several amino acid transporters are present in rust haustoria. Currently, we elucidate their specificity, transport properties and localization. Other proteins with potential signal sequences are secreted by haustoria and may contribute to the communication between host and parasite. One of these rust transferred proteins, RTP1p, can be detected in the host nucleus of infected host cells. Currently, we study the mechanism of transfer through the host-parasite interface.

*MICALES-GLAESER, J.A.[1], BANIK, M.T.[1], HAIGHT, J.[1], TRUMMER, L.[2] [1]USDA-Forest Service, Forest Products Laboratory, Madison, WI. [2]USDA Forest Service, Forest Health Protection, Anchorage, AK. **Wood decay fungi of Lutz spruce from the Kenai Peninsula, AK.**

Large numbers of beetle-killed trees present a serious fire hazard in south central Alaska's Kenai Peninsula. Determining the rate of decomposition of this material will provide managers with information for critical stand management decisions. A key component of understanding decomposition patterns is to know which wood decay fungi are associated with each decay class and mortality agent. In this study, wood decay fungi were identified from 64 dead Lutz spruce in 5 beetle-killed stands and 4 stands with other mortality agents. Identification was based on the presence of fruiting bodies and by DNA sequencing of cultures obtained from selected samples. Trees were selected from each of four different decay classes. Fruiting bodies of *Fomitopsis pinicola, Stereum sanguinulentum*, and *Trichaptum abietinum* were prevalent in beetle-killed stands (Decay class 1 & 2). Decay class 3 and 4 logs displayed a much wider variety of decay fungi. Species of the genera *Trametes, Antrodia*, and *Phellinus* were particularly frequent in the more highly decayed material. Cultures of fungi from selected class 1 and 2 logs from a beetle-killed site included species of *Amylostereum, Fomitopsis, Antrodia, Phellinus*, and *Trichaptum*. DNA sequencing will be used to identify fungi directly from sapwood without culturing. These results will be contrasted with fruiting body and culture data.

*MILLER, ANDREW N.[1], FOURNIER, JACQUES[2], HUHNDORF, SABINE M.[3], AND ADIE, ANDREA[3]. [1]Center for Biodiversity, Illinois Natural History Survey, Champaign, IL 61820, [2]Las Muros, F-09420 Rimont, France, [3]Botany Department, The Field Museum, Chicago, IL 60605. **Problems and perils of gene sequencing for estimating phylogenetic relationships of three species of *Lasiosphaeria*.**

In an ongoing effort to monograph the genus *Lasiosphaeria,* it was desirable to obtain estimates of the phylogenetic relationships of three species, *L. coacta, L. punctata*, and *L. stuppea*. These species are believed to have relations elsewhere based on various ambiguous morphological characters so an independent dataset from one or more genes was needed to resolve their phylogenetic affinities. Attempts were made to sequence portions of several mitochondrial and nuclear genes including mtSSU, mtLSU, nuLSU, and beta-tubulin. Primers were redesigned for both mtSSU and mtLSU. However, PCR amplification failed for all three taxa. Although PCR products of nuLSU were obtained for *L. punctata* and *L. stuppea*, sequencing failed due to the presence of multiple paralogous copies. Finally, a 650bp region of beta-tubulin was successfully amplified and sequenced. Subsequent phylogenetic analyses indicate these taxa belong in the Helminthosphaeriaceae and therefore, should be transferred out of *Lasiosphaeria*.

*MILLER, JESSICA L.[1], *VARGAS, ALAN-MICHAEL[2], TUININGA, AMY R.[2], DANIELS, THOMAS J.[2], STAFFORD, KIRBY C.[3], FALCO, RICHARD C.[2] [1]Dept. of Biology, Yale University, New Haven, CT 06520, [2]Louis Calder Center, Fordham University, Armonk, NY 10504, [3]Connecticut Agricultural Experiment Station, New Haven, CT 06504. **Entomopathogenic fungal infections of *Ixodes scapularis* (Acari: Ixodidae)**.

Entomopathogenic fungi such as *Metarhizium anisopliae, Beauveria bassiana, Paecilomyces* spp., and *Lecanicillium lecanii* may act as biocontrol agents of *Ixodes sca*pularis, the Black-legged tick that transmits *Borrelia burgdorferi*, the causative agent of Lyme disease. However, the role that such fungi play in controlling tick populations in nature is unknown. Isolates of these fungi were identified from soils at the Calder Center (Westchester Co., NY) and rate of infection in *I. scapularis* was determined. Entomopathogenic fungi were isolated directly from 5.5% (4 of 73) and 1% (4 of 400) of field-collected adult ticks in summer and fall, respectively. Laboratory experiments compared the virulence of the Calder strains to ATCC strains and determined effects of the fungi on three life stages of *I. scapularis*. Spores from ATCC cultures and Calder isolates were applied to unfed *I. scapularis* ticks. *M. anisopliae* (ATCC #16085) was found to be the most virulent. Experiments are ongoing to investigate the virulence of entomopathogenic fungi in nature, associated edaphic conditions, and mechanisms of infection. Though entomopathogenic fungi were not prevalent on field-sampled ticks, they appear to play a role in the natural mortality of this vector. Preliminary data suggest that virulence may also be influenced by source of the fungus, life stage, and sex of the tick.

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MSA ABSTRACTS

MILLER, STEVEN L. Botany Dept. 3165, University of Wyoming, 1000 E University Ave., Laramie WY 82071. **Interesting dilemmas in Russulaceae taxonomy and systematics.**

Recent molecular studies in the Russulaceae have elucidated relationships among genera and species that may dramatically impact classical taxonomic treatments. Generic limits between *Russula* and *Lactarius*, and between these genera and closely related gasteroid taxa are in question. With increased sampling in the tropics the distinction between *Russula* and *Lactarius* has become obscure. Molecular analyses indicate that *Lactarius* is phylogenetically positioned inside *Russula*. Two possibilities exist to rectify this taxonomic dilemma: accommodate species assigned to *Lactarius* in *Russula*, or reassign species in clades of *Russula* sister to *Lactarius* to *Lactarius*. Characters that delimit infrageneric taxa in *Russula* and *Lactarius* are used to circumscribe genera of gasteroid taxa. Molecular analyses indicate that gasteroid genera are polyphyletic and fall out within infrageneric groups in *Russula* and *Lactarius*. This suggests that gasteroid genera should be synonymized. However, certain clades appear to be composed exclusively of gasteroid forms, opening the possibility for a more innovative taxonomic treatment. Finally, identification of broadly distributed species has necessitated a close examination of morphological and molecular characters that serve to delimit species. Discussion of these interesting systematic dilemmas will introduce the Russulaceae symposium.

MIMS, CHARLES W. Dept. of Plant Pathology, University of Georgia, Athens GA 30602-7274. **Ultrastructure of haustoria produced by plant pathogenic fungi and oomycetes.**

Electron microscopy has contributed tremendously to our understanding of the haustoria of plant pathogenic fungi and Oomycetes and their interactions with host cells. Haustoria are specialized hyphal branches that form intimate relationships with living host cells. Although haustoria breach host cell walls, they do not penetrate the plasma membrane of an invaded host cell. Instead, the plasma membrane is invaginated by a developing haustorium and forms the so-called extrahaustorial membrane that separates the haustorium from the host cell cytoplasm. Between the haustorium and the extrahaustorial membrane is a layer of material known as the extrahaustorial matrix. Although haustoria long have been suspected of playing a role in nutrient absorption from host cells, this function has been difficult to document. Recently, however, there is growing evidence that haustoria function not only in nutrient absorption, but also in the suppression of host defense responses, the redirection or reprogramming of the host's metabolic flow and in biosynthesis. This presentation provides an overview of morphological features of various types of fungal haustoria as well as detailed information on the interfaces between haustoria and host cells. Results from TEM studies utilizing both conventional fixation as well as high-pressure freezing/freeze substitution will be discussed.

*MINNIS, ANDREW M.[1], SUNDBERG, WALTER J.[1], NICKRENT, DANIEL L.[1] AND METHVEN, ANDREW S.[2]. [1]Dept. of Plant Biology, Southern Illinois University, Carbondale, IL 62901, [2] Dept. of Biological Sciences, Eastern Illinois University, Charleston, IL 61920. ***Chamaeota* placed on a fungal tree**.

Chamaeota (W.G.Sm.) Earle is a rare genus traditionally classified in the agaric family Pluteaceae. *Chamaeota* shares pink spores and free lamellae with *Pluteus* Fr. and *Volvariella* Speg., the other members of the family, but differs from the other genera by the possession of an annulus. Contrary to the traditional concept of Pluteaceae, recent molecular evidence based on nuclear LSU ribosomal RNA sequences suggests that *Pluteus* and *Volvariella* are phylogenetically unrelated. A collection from Mingo National Wildlife Refuge, near Puxico, Missouri, U.S.A. tentatively identified as *Chamaeota sphaerospora* (Peck) Kauffman was selected for phylogenetic analysis to determine its relationship to the traditional genera of Pluteaceae and its potential use as an outgroup for *Pluteus*. A partial nuclear LSU rDNA sequence was obtained and subsequently aligned with those of 877 taxa reported by Moncalvo et. al. (2002). A brief analysis was performed to roughly place *Chamaeota* in the global agaric phylogeny. Another analysis was then performed with a reduced data set containing 127 representative taxa. In the latter, *Pluteus* was monophyletic (82% BS) with *Chamaeota* embedded within it. This result indicates that *Chamaeota* should continue to be classified in Pluteaceae.

*MISHRA, PRASHANT K.[1], CASTRILLO, LOUELA A.[2], ANNIS, SEANNA L.[1], GRODEN, ELEANOR[1], AND VANDENBERG JOHN D.[3] [1]Dept. of Biological Sciences, University of Maine, Orono ME 04469, [2] Dept. of Entomology, Cornell University, Ithaca NY 14853, [3] Plant, Soil and Nutrition Lab, USDA-ARS, Ithaca NY 14853. **Assessment of the genetic diversity and gene flow in populations of the entomopathogenic fungus *Beauveria bassiana*.**

The entomopathogenic fungus *Beauveria bassiana* has been used extensively for the biological control of various agricultural insect pests. The impact of commercial formulations on indigenous populations of the fungus is unknown. In this study, we have analysed the genetic diversity in indigenous populations of *B. bassiana* and the changes that have occurred after the application of a commercial formulation of the Mycotrol isolate, GHA (Emerald BioAgriculture Corp., Lansing, MI). Isolates of *B. bassiana* were collected from three unsprayed and three sprayed fields (2 ME and 1 NY each) and amplified fragment length polymorphisms (AFLP) markers were generated. The analysis of AFLP data indicated substantial genetic diversity and restricted gene flow within indigenous populations. The application of GHA resulted in displacement of indigenous genotypes, however, there was recovery of indigenous genotypes five years after treatment. This study can serve as a model for assessing the risk associated with the release of genetically modified fungi on their conspecifics.

*MOLINA, RANDY, SMITH, JANE AND CASTELLANO, MICHAEL. Forestry Sciences Laboratory, 3200 Jefferson Way, Corvallis OR 97331. **Conservation of forest fungi in the Pacific Northwest: issues of rare species detection and management**.

The international scientific community has increasingly called for conservation of biological diversity, with a strong emphasis on protecting rare and threatened species. Most attention focuses, however, on charismatic fauna and flora. Fungi are rarely considered, even though their critical ecosystem functions are well known. Several fungus diversity studies have reported declines in species based on temporal changes in sporocarp presence and RED lists have also been published for some countries. Although mycologists have clearly demonstrated the ecological importance of fungus diversity, we have not systematically addressed the need and methods for conserving this vast diversity, nor how to deal with rare species at landscape scales. This presentation synthesizes eight years of results and lessons learned from fungal conservation efforts in forests of the Pacific Northwest. Over 230 rare forest fungi were listed for protection as part of a regional ecosystem management plan. Our results from regionwide fungal surveys, species habitat modeling, and population studies illustrate the scientific and managerial challenges in providing protection at landscape scales for forest fungi. This presentation focuses on concepts of species rarity and detection, and asks the provocative question of whether we should be concerned about rare fungal species.

MOLK, JEFF AND *BLOOM, KERRY. University of North Carolina, Chapel Hill, NC. **Microtubule function during mating in the yeast *Saccharomyces cerevisiae*.**

Microtubules are polarized, heterodimeric polymers of the cytoskeleton that function to translocate objects such as chromosomes and the nucleus within the cell volume. The budding yeast *Saccharomyces cerevisiae* is a model genetic system used to study the function of microtubules at the molecular level. *S. cerevisiae* haploid cells can reproduce by mitosis or when mixed with cells of the opposite mating type will form a mating projection ("shmoo") to facilitate cell fusion, followed by nuclear congression and fusion (karyogamy). This process results in a diploid cell that reproduces by mitosis. Microtubules attach to the shmoo tip and drive nuclear congression (Maddox et al., 1999; 2003). Kar3p, a member of the C-terminal family of microtubule-based motors (kinesin), is proposed to crosslink microtubules during mating to allow nuclear congression to occur. Kar9p, the putative APC (Adenoma Polyposis Coli) homolog in budding yeast is proposed to tether microtubules to the shmoo tip, promoting efficient nuclear congression. By analyzing spindle dynamics using GFP-Tubulin we have been able to monitor nuclear congression, mitotic spindle formation and deposition into the zygotic bud to determine the role of these proteins in mating.

*MORGENSTERN, INGO, MATHENY, BRANDON P., HIBBETT, DAVID S. Department of Biology, 950 Main Street, Worcester, MA 01610. **Evolutionary diversity of manganese dependent peroxidase genes in ligninolytic homobasidiomycetes belonging to the phlebioid clade.**

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*, a member of the phlebioid clade, three different MnP isoforms

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(MnP1-MnP3) have been described and their genes have been characterized. We have developed specific primers for PCR amplification of MnP genes and are studying their evolutionary diversity in saprotrophic phlebioid/polyporoid homobasidiomycetes. Molecular cloning and sequence analysis of the amplified products allows the identification of various forms, including paralogs or alternative allele MnP isoforms. Preliminary results suggest that gene duplication in the MnP gene family has occurred repeatedly within the phlebioid clade, as has been described for other fungal lineages. Continuing research addresses whether the pattern of occurrence of ligninolytic enzymes may reflect also the phylogenetic relationships of ligninolytic fungal lineages.

*MOTHEY, DEEPA, SNETSELAAR, KAREN, AND MCCANN, MICHAEL. Saint Josephs University, Philadelphia PA. **Functional complementation of an mRNA processing gene from *Ustilago*.**

TS2844, a temperature sensitive strain of *Ustilago maydis*, was constructed by UV mutagenesis of the wild-type strain FB2. It grows at the permissive temperature of 24C but is unable to grow at the non-permissive temperature of 34C. While morphology of TS2844 cells is similar to that of wild-type cells at 24C, the morphology of the mutant cells changes at 34C. The cells become lumpy, bud abnormally and their nuclei enlarge and seem to fragment. Cultures of TS2844 increase in biomass for five hours when shifted to 34C, after which time the optical density remains constant and viability studies show that most cells are dead. The mutant was complemented using a wild type genomic DNA library. The complementing insert contained an open reading frame that would produce a polypeptide with sequence similarity to proteins involved in RNA processing. This hypothetical *U. maydis* polypeptide has 27% identity and 50% similarity to Prp24 (a pre-RNA protein) from *Saccharomyces cerevisiae*. Complementation assays using prp24 showed that it partially restores wild-type growth in the *U. maydis* mutant. Based on the above studies we conclude that the mutation may be in the *U. maydis* version of the prp24 gene.

*MOZLEY-STANDRIDGE, SHARON E. AND PORTER, DAVID. Department of Plant Biology, University of Georgia, Athens, GA, 30602. **Systematics of Chytrid fungi: genus level assessment of 18S and 28S nuclear ribosomal gene sequences using multiple methods of phylogenetic inference.**

Chytrid fungi represent a comparatively small group of organisms in the Kingdom Fungi with only 1000 species and 100 genera. Lacking large numbers of species that cause serious human or agricultural problems, chytrid fungi are relatively understudied. The lack of research is reflected in the problematic state of chytrid systematics. All levels of chytrid classification are considered artificial and there is a great need for a re-evaluation of families, genera and species. The "*Nowakowskiella* clade" outlined by James et al. 2000 provided a focus for determining the usefullness of nuclear ribosomal genes (18S and 28S) in delineating genera and in identifying phylogenetically informative morphological characters. Maximum parsimony, maximum likelihood, and the Bayesian method of phylogenetic analysis were used to analyze separate and combined ribosomal datasets. All three methods showed improvement in tree resolution using 28S alone and the combined dataset. The 28S gene proved to be more phylogenetically informative than the 18S gene. The genera *Cladochytrium* and *Nowakowskiella* were supported by trees from all three methods but *Nephrochytrium* and *Catenochytridium* were shown to be polyphyletic. The analyses supported the continued use of certain thallus characters but also highlighted the need for further study of thallus development.

*NELDER, MARK P.[1], COSCARON, C.[2], BROCKHOUSE, CHARLES, L.[3], AND MCREADIE, JOHN W.[3] [1]Department of Entomology, Soils, and Plant Sciences, Clemson University, Clemson, SC 29634, [2]Charles Darwin Foundation for the Galapagos Islands, Post Box 17-01-3891, Quito, Ecuador, [3]Department of Biological Sciences, University of south Alabama, Mobile, AL 36688. **First report of a Trichomycete from the Galapagos Islands, Ecuador.**

We present the first record of a trichomycete (Zygomycota) from the Galapagos Islands and a preliminary report regarding its ecology with respect to larval black flies (Diptera: Simuliidae). Filter feeding larvae of *Simulium ochraceum* (Walker) complex were collected from six lotic habitats on San Cristobal Island, Galapagos Islands, Ecuador and their hindgut cuticle and peritrophic matrix inspected for the presence of fungal symbionts. A possible new species of *Smittium* (Harpellales), provisionally designated as *Smittium* near *brasiliense*, was found in the hindguts of larvae at three of the sites examined. Trichospores of *Smittium* nr. *brasiliense* (3 μm) were wider than those reported for *Smittium brasiliense* Alencar, Lichtwardt, Rios-Velasquez & Hamada (1.6 μm), however, the width, branching pattern, and holdfast are similar. *Simulium ochraceum s.l.* is considered a recent (ca. 1989) introduction to the Galapagos Archipelago, thereby raising questions regarding trichomycete dispersal and biogeography. Were the gut fungi present before the black flies arrived or are they a contemporary introduction as well? What are the possible mechanisms for trichomycete dispersal to the Galapagos Islands and other islands?

*NEVES, MARIA ALICE AND HALLING, ROY E. New York Botanical Garden, Bronx, NY 10458. **Phylogenetics of selected *Phylloporus* (Boletales) species based on morphological characters.**

Phylloporus consists of species that produce a lamellate rather than poroid hymenophore; however, the basidiome, spores, chemical and molecular data support placement in the Boletales. *Phylloporus* has been reduced to synonymy with *Xerocomus* based on DNA analysis of two European taxa and has been seen as an unnatural group because of the hymenophore morphology. The majority of *Phylloporus* species have a pantropical distribution, occurring in the New World, Asia and Africa, but few studies on this group have included tropical species; only few North Temperate taxa. In this work, twenty species belonging to the 'gilled bolete' *Phylloporus* were evaluated in a phylogenetic analysis based on morphological characters. Species were selected on the basis of geographical location. One group included neotropical species while the second included African species. Phylogenetic relationships of selected species of *Phylloporus, Leccinum*, and *Boletus* subgenus *Xerocomus* were estimated by maximum parsimony analysis of morphological characters determined from field collections or drawn from literature sources; *Suillus luteus* was used as an outgroup. The analysis revealed distinct clades corresponding to neotropical and African taxa, with the African taxa subdivided into two distinct subclades.

NORVELL, LORELEI L. Pacific Northwest Mycology Service, Portland OR 97229-1309. **Fungi and the Northwest Forest Plan: lessons learned about epigeous basidiomycetes in surveyed & managed west slope forests.**

"There's no need to spend millions and millions of dollars having people crawling around on their hands and knees looking for these species anymore." Thus the logging industry greets what it hopes are the death throes of the US Northwest Forest Plan's (NFP) Survey & Manage (S&M) of old-growth forests. From 1998 onward, the NFP sent federal workers out to scout prospective timber sales for targeted indicator organisms, in the process amassing 20,000 collections of fungi alone. It also contracted this battle-hardened veteran as taxonomic expert to verify 1500 herbarium collections and document historical sites for 41 basidiomycetes, determine 4,000 S&M collections to 141 genera & 539 spp, rank 51 fungi for the Natural Heritage Foundation, conduct two 5-year myco-ecological studies in variably aged/managed Douglas fir stands, and oversee the Oregon Caves National Monument macrofungal inventory. Insights on the NFP mycological legacy promised: Is *Phaeocollybia* an old-growth indicator - and rare? Does *Galerina sphagnicola* occur in the PNW? (Anywhere?) What comes after quaternary mold? Why did Triage think a digital color photo printed with only magenta ink is worth a 1,000 words? Can you ID a "fresh" *Mycena* kept in a tightly-locked vial for 2 years? Is *Marasmius applanatipes* endangered or did I only just now recognize it? What's right and what's wrong with American field mycology?

*NUYTINCK, JORINDE AND VERBEKEN, ANNEMIEKE. Ghent University, Dept. of Biology, Research Group Mycology, K.L. Ledeganckstraat 35, B-9000 Ghent, Belgium. **Species delimitation and phylogenetic relationships in *Lactarius* section *Deliciosi*.**

Representatives of *Lactarius* section *Deliciosi* are easily distinguished from other members of the genus by their bright coloured latex and the remarkable colour changes of the context caused by the presence of guaiane sesquiterpenes. Seventy names for about 35 species and varieties have been published in this section, mainly from the northern hemisphere. There is no consensus on the species concept in this section and eventual intercontinental conspecificity has never been studied. Microscopic features are very similar in most taxa and the taxonomic value of the striking field characters is still under discussion. Carefully observed macro- and micromorphological characters are combined here with molecular data. ITS rDNA and gpd sequences are being provided for over 80 specimens from a wide geographical range. The results of the phylogenetic analysis and the monophyly of the section are discussed. Hypotheses about species relationships and synonymy are proposed.

OAKLEY, BERL R. Department of Molecular Genetics, Ohio State University. **Gamma-tubulin functions in late mitotic events and mitotic exit.**

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Although the role of gamma-tubulin in the nucleation of mitotic spindle microtubules is well established, recent data indicate that gamma-tubulin has other essential, but incompletely defined, functions. To investigate these functions, we examined the phenotype of mipAD159, a cold-sensitive gamma-tubulin allele of *Aspergillus nidulans*. Immunofluorescence microscopy of synchronized material revealed that mipAD159 does not inhibit mitotic spindle formation at a restrictive temperature. In many nuclei anaphase A was inhibited, however, and after a slight delay in mitosis, most nuclei re-entered interphase without dividing. Time-lapse observations of chromosomes revealed that at a restrictive temperature mipAD159 caused failure of the coordination of late mitotic events (anaphase A, anaphase B, chromosomal disjunction and mitotic exit). Time-lapse microscopy with GFP-tubulin revealed that transient mitotic spindle abnormalities, in particular bent spindles, were more prevalent in mipAD159 strains than in controls. In experiments in which microtubules were depolymerized with benomyl, mipAD159 nuclei exited mitosis significantly more quickly (as judged by chromosomal condensation) than control nuclei. These data reveal that gamma-tubulin has an essential role in the coordination of late mitotic events, and a microtubule-independent function in mitotic exit.

*OREILLY, BERNADETTE AND VOLK, THOMAS J. Dept. Biology, University of Wisconsin-La Crosse. **Preliminary isolation and identification of fungi and bacteria associated with morel fruiting.**

Morel mushrooms are notoriously difficult to produce in culture. It may be that, like *Agaricus bisporus*, *Morchella* spp. require the aid of bacteria and/or other fungi to fruit. To test this, morel mushrooms were obtained from various "secret" sites in MN, WI, OR and PA. Samples taken from the inner and outer tissue layers of the cap, stalk and base were inoculated on PDA and Blood Agar plates using flame sterilized tweezers. Water suspensions from soil near the mushroom base were spread on PDA and Blood Agar plates. Pure isolates of all the bacteria and fungi were obtained and are being identified. As noticed in our previous studies, certain isolates were consistently found in association with morel tissue. These isolates were added to morel hyphae to test their ability to induce fruiting. Cultured morel strains are being tested for compatibility on CYM by all possible strain crossings. Compatible strains will then be induced to form sclerotia using a method similar to that described in the patents by Ower *et al*. However, two compatible strains will be inoculated into the same container. After sclerotia formation, the bacterial and fungal isolates will be added to test their ability to aid in fruiting. The sclerotia and isolates will be subjected to "proper" growing conditions and observed for fruiting. Pictures and data on the interactions will be presented at the meeting.

*ORTIZ, ZULMA[1], SILVA, ELSIE[1], SIFUENTES, MELISSA[1], DIAZ, ROSELYN[1], CANTRELL, SHARON A.[1] AND CASILLAS, LILLIAM[2]. [1]Science & Technology, Universidad del Turabo, Gurabo, PR 00778, [2]Department of Biology, University of Puerto Rico, Humacao, PR 00791. **Halotolerant fungi from the Cabo Rojo Solar Salterns in Puerto Rico.**

The study area is located on the southwest coast of Puerto Rico and is characterized by high solar radiation and low precipitation. These conditions favor the development of a hypersaline environment, with salinity up to 600 ppt. The objective was to isolate and characterize the fungi in the water, sediments and air. Water was filtered through a 0.45 μm membrane and placed in MA with water from the same pond and MEA. Fungi from sediments were isolated by the dilution technique using MA with seawater and MEA. Air samples were taken using a MAirT with SDA. A total of 150 isolates have been obtained, most in the genera *Aspergillus, Cladosporium, Penicillium and Fusarium*. From the water a total of 93 isolates were obtained, 43 halotolerant (growing in MA and MEA), and one halophilic (growing only in MA) in the genus *Penicillium*. Eleven isolates are *Aspergillus,* such as *A. candidus*, *A. caespitosus, A. ostianus, A. flavus, A. flavipes* and *A. unguis*. Most of the sediment isolates are *Mycelia Sterilia* but few belong to *Chaetomium globossum*, a cosmopolitan ascomycete isolated from several environments including saline ones. *Hortaea werneckii* was isolated from the sediments as well as from the salt pond water. In the air samples, *Fusarium semitectum* is the predominant isolate. A very interesting blue-green isolate was obtained from the water and probably represents a new species of *Periconia*.

*ORTIZ-SANTANA, BEATRIZ[1], LODGE, D. JEAN[1] AND BARONI, TIMOTHY J.[2] [1]Center for Forest Mycology Research, USDA-FS, FPL, Luquillo PR 00773-1377, [2]Department of Biological Sciences, SUNY, College at Cortland, Cortland, NY 13045. **New records of boletes from Belize.**

Preliminary results are presented from a three-year survey of boletes in Belize, located on the Yucatan Peninsula in northeastern Central America. The main goal of this study is to compare the boletes from Belize with those of Dominican Republic and eastern and western North America to determine the phylogenetic relationships between them. The final results of this research will contribute to the understanding of the dispersal patterns of ectomycorrhizal fungi from North America to the Caribbean region. Out of approximately 60 bolete species that have been collected, 22 species in 11 genera are new records for Belize. Most of the identified species were described from eastern North America, two from Mexico and one from Honduras, while *Boletus aureissimus* and *B. dupainii* are new records for the region. This research is supported by a grant of the Biotic Surveys and Inventories Program of the National Science Foundation and by the USDA, Forest Service, Forest Products Laboratory.

*OSMUNDSON, TODD W.[1,2,3] AND HALLING, ROY E.[1,3]. [1]Institute of Systematic Botany, and [2] The Lewis B. and Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458-5126, [3]Department of Ecology, Evolution and Environmental Biology, Columbia University, New York, NY 10027-6902. **Morphological and molecular evidence supporting an arbutoid mycorrhizal relationship in the Costa Rican páramo.**

Páramo is a fragile habitat occurring above timberline in the Neotropics. Characterized by high plant endemicity and important in regulating hydrological function, yet threatened by land transformation and global climate change, the páramo is of significant conservation concern. *Comarostaphylis arbutoides* (Ericaceae) often forms dense thickets in Central American páramo habitats. It has been suggested, based on phylogenetic classification, that *C. arbutoides* forms arbutoid mycorrhizae with diverse Basidiomycetes and Ascomycetes; however, this assumption has not previously been confirmed. *Leccinum monticola*, recently described from páramo in the Cordillera de Talamanca of Costa Rica, is suspected as a mycorrhizal symbiont of *C. arbutoides*. The present study examines evidence for this association using morphological and molecular data. Root samples collected beneath *L. monticola* basidiomes were examined for mycorrhizal structures, and rDNA ITS sequences were compared between plant or fungal portions of mycorrhizal root tips and leaf or basidiome material of the suspected symbionts. Root cross-sections showed a thin mantle and intracellular hyphal coils typical of arbutoid mycorrhizae. DNA sequence comparisons confirmed the identity of *C. arbutoides* and *L. monticola* as mycorrhizal symbionts. Ecological and biogeographic contexts of this association will be discussed.

*OVREBO, CLARK L.[1] AND LODGE, D. JEAN[2]. [1]Dept. of Biology, Univ. of Central Oklahoma, Edmond, OK 73034, [2]Center for Forest Mycology Research, USDA-Forest Service, Forest Products Lab., Luquillo, PR 00773-1377. **First records of Hygrophoraceae from Panama including two new species.**

The first author collected six species of Hygrophoraceae on Barro Colorado Island, Panama. These collections are the first records for the family from Panama. Three identified species are *Hygrocybe batistae, H. hypohaemacta*, and *H. chloochlora* in section *Firmae*. A fourth species is close to *Hygrocybe earlei* but differs by having a white stipe. Another collection is a new species of *Cuphophyllus*. It resembles *C. ferruginealba* but differs in having much larger spores. The final fungus is a new species of *Hygrocybe*. The spores and basidia are dimorphic indicating that it belongs in the genus *Hygrocybe* section *Firmae*. The fungus is unique to section *Firmae* in having a partial veil and a pale pink pileus and stipe. The outer velar material is made up of hyphae emanating from the pileus margin and the inner veil material is composed of hyphae originating on the lamellar edge.

*PALMER, JONATHAN, KINNEY, DANIEL T. AND VOLK, THOMAS J. Department of Biology, University of Wisconsin-La Crosse. **Survey of fungi associated with a disjunct stand of American chestnuts (*Castanea dentata*) in Wisconsin.**

Circa 1900 a farmer from Pennsylvania planted eleven American chestnut (*Castanea dentata*) seeds on a new farm near West Salem in the "driftless" area of western Wisconsin. In about 100 years, these 11 trees have multiplied to about 6000 trees larger than 15 cm dbh. Since they are well out of the natural range of chestnut, the trees were free from chestnut blight, caused by *Cryphonectria parasitica*, until 1988. This stand of trees affords an excellent opportunity to study mycorrhizal and wood-decay fungi associated with the chestnuts. Fungal fruiting bodies have been collected and identified to species for the past three seasons from the chestnut site, as well as from two local "control"

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sites that are likely similar to what the chestnut site would have been without the chestnuts. The fungi have been catalogued and compared to fungi that have historically been associated with chestnut and to fungi likely naturally occurring in the area prior to chestnut colonization. Our major question to be answered is "Have the local fungi adapted to grow on or with the chestnuts, or have chestnut specific fungi 'found' the disjunct stand?" Although most seem to be local fungi, we have found examples of fungi besides *Cryphonectria* that have found the chestnut stand, including *Ciboria americana*, specific to chestnut burs, and *Fistulina hepatica*, otherwise unknown from western Wisconsin.

PARK, HYUK GU[1], KO, HAN GYU[1], *KIM, SEONG HWAN[2], AND PARK, WON MOK[1]. [1]School of Life Sciences and Biotechnology, Korea University, Seoul, 136-701, Korea, [2]Department of Microbiology, Dankook University, Cheonan, Chungnam, 330-714, Korea. **ITS1 rDNA is useful for the identification of Asian isolates of *Hericium erinaceum*, an edible and medicinal mushroom.**

Hericium erinaceum is known to be the most industrially valuable fungi for its use as food and medicinal sources. To develop a molecular method for the identification of *H. erinaceum*, PCR and sequencing were performed against 6 *Hericium* species including *H. erinaceum, H. abietis, H. alpestre, H. americanum, H. coralloides*, and *H. laciniatum* and 23 isolates of *H. erinaceum* from different geographic origins. Analyses of the PCR-amplified ITS and 5.8S rDNA from those *Hericium* fungi showed that there were variations in nucleotide sequences and size. Nucleotide sequence identity levels among *Hericium* species were 89-99% in ITS1 and 78-99% in ITS2. The length of ITS1 was longer than that of ITS2 in all the isolates. Pairwise comparisons of *Hericium* ITS1 and ITS2 nucleotide sequences showed that ITS1 region is more conserved than ITS2. The ITS1 and ITS2 regions provided different levels of information on the relationship of *H. erinaceum* to other *Hericium* species. Both the parsimony and neighbor joining trees based on the ITS1 sequence clearly distinguished Asian *H. erinaceum* isolates from other *Hericium* species and isolates. The results of RAPD and the beta-tubulin gene analyses would also be discussed.

*PATINO-CONDE, VIOLETA[1], CIFUENTES, JOAQUÍN[1], GONZÁLEZ, DOLORES[2], MAGALLON SUSANA[3], LEON-REGAGNON, VIRGINIA[3]. [1]Herbario FCME UNAM PO. Box 70-399 Ciudad Universitaria, C.P. 04510, Mexico, D.F. México, [2]Lab. de Sistematica Molecular, INECOL Km 2.5 Carretera Antigua a Coatepec C.P. 91070, Xalapa, Veracruz, Mexico, [3]Instituto de Biología, UNAM, Ciudad Universitaria C.P.04510, México, D.F., México **Taxonomic boundaries of *Sarcodon imbricatus sensu lato* from Mexico.**

The taxonomic boundaries of *Sarcodon imbricatus* (L.:Fr.)P. Karst. have been source of several controversies. Johannesson et al (1999) revised this issue for European specimens and concluded that there are macromorphological, molecular and ecological differences that support the existence of two species, *S. imbricatus* and *S. squamosus* (Schaeff.) Quél. Nevertheless, *S. imbricatus sensu lato* has been reported from other regions of the world, including central Mexico (Cifuentes, 1996). The present research tries to clarify the taxonomic status of the Mexican samples of *S. imbricatus sensu lato*, which don't correspond to the ecological associations found in the European groups. We performed a phylogenetic analysis based on ITS sequences of Mexican and European samples of *S. imbricatus sensu lato* and species of *Sarcodon*, *Hydnellum* and *Phellodon*, as outgroups. The results suggest that *S. imbricatus sensu lato* comprises at least three clades, each one corresponding to particular plant associations. These results support those found it by Johannesson et al (1999), and suggest the existence of a third species present in Mexican forests of *Quercus* or *Quercus-Pinus*.

*PERRY, BRIAN A., HANSEN, KAREN, AND PFISTER, DONALD H. Dept. of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138. **Phylogenetic relationships in the Pyronemataceae (Ascomycota, Pezizales).**

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 Sarcosomataceae, Sarcoscyphaceae, Ascodesmidaceae, and Glaziellaceae. 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 to resolve relationships of the family and genera, and infer evolutionary patterns of morphological, cytological and ecological characters. Results based on nuclear large subunit rDNA sequence data will be presented and discussed.

*PETERSEN, RONALD H. AND HUGHES, KAREN, W. Botany Department, University of Tennessee, Knoxville, TN 37996-1100. **The changing faces of mycology in the southern mountains.**

Over the 85 years since L.R. Hesler arrived in Tennessee, mycological investigation has had a strong tradition in the Great Smoky Mountains and nearby Blue Ridge. In 1939, the MSA held its annual foray in Gatlinburg, with several notable mycologists in attendance. Post-World War II, Hesler formed a partnership with Alexander Smith, a collaboration which produced North American monographs of several agaric genera. While inventorying in the Smokies continued, Hesler was also instrumental in establishing Highlands Biological Station in Macon County, North Carolina, along with William C. Coker of the University of North Carolina. That Station is currently supported by over 30 regional educational and governmental institutions. These two efforts have produced extensive lists of agaric (and other) taxa from these mountains. The Hesler Endowment Fund has supported a score of visiting mycologists who have added to the recorded richness of southern Appalachian fungi. Recently, renewed interest has been spurred by the ATBI in the Smokies Park. Projects underway promise to provide not only vouchered specimens with written and photographic documentation, but DNA for sequencing and, if possible, cultures for sexual compatibility experiments and/or bioprospecting. New taxa continue to be discovered, with more sure to be found.

PHILLIPS, ANITA N 10801 University Boulevard, Manassas, VA 20110. **Exciting new special collections at ATCC.**

Exciting New Special Collections at ATCC Microorganisms isolated from National Parks in the United States are now available through the National Park Service Special Collection at ATCC. These organisms offer a fascinating study of microbial ecology, from the hot springs of Yellowstone to the deserts of Big Bend National Park. Fungi, protozoa, extremophile bacteria, methanogenic archaea, and more are currently available in this Special Collection, and the list will continue to grow. Take a tour of U.S. National Parks on a microscopic level. ATCC, in partnership with the University of Arkansas, Fayetteville, will be launching the Eumycetozoa Special Collection in summer of 2004. The new collection is a critical component of the National Science Foundation's Planetary Biodiversity Inventory: Global Biodiversity of Eumycetozoans project organized by Fred Spiegel and Steve Stephenson of UArk, James Cavender of Ohio University, Martin Schnittler of Universitätschor Greifswald, and Carlos Lado of Real Jardín Botánico, CSIC. ATCC, which currently houses hundreds of Eumycetozoa, will serve as a repository, culturing and preserving new strains as they arrive from South America, Russia, Madagascar, Antarctic Peninsula, India, and numerous other collection sites.

*PIEL, WILLIAM H[1] AND PAGE, RODERIC D.M.[2] [1]Dept. Biol. Sci., University at Buffalo, Buffalo NY 14260, [2]Graham Kerr Building, University of Glasgow, Glasgow G12 8QP, UK. **Phyloinformatics of mycological data in TreeBASE.**

TreeBASE is a database of phylogenetic information that serves principally as a digital library, but also as a tool for phyloinformatic research and meta-analysis. In recent years the number of mycological contributions has grown steadily, and this group now represents a substantial portion of the database. The operational taxonomic units (OTU) of trees in TreeBASE are not always in the form of standard binomial names, particularly in trees with subspecific sampling (that require suffix codes or culture numbers to distinguish them), in instances of unidentified anamorphs, and in the event of misspellings. Yet a proper mapping of TreeBASE's OTUs is required for assembling supertrees, analyzing tree connectivity, and building data availability matrices. Here we report an effort to map TreeBASE OTUs with binomial names, and we describe the results of phyloinformatic meta-analyses that we performed as a consequence.

*PRINGLE, ANNE AND BRUNS, THOMAS D. University of California, Dept. of Plant and Microbial Biology, 111 Koshland Hall, Berkeley CA 94720-3102. **Is *Amanita phalloides* an invasive species?**

The European death cap mushroom *Amanita phalloides* is hypothesized to be an invasive species in North America. Because *A. phalloides* is deadly, a rich mycological literature records the distribution of the mushroom on both the East and West Coasts. A comprehensive review of both the available literature and

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herbarium collections is used to establish that *A. phalloides* is an invasive species in California. The complementary historical approaches also provide evidence on when and where *A. phalloides* was first introduced. Data collected for invasive species of fungi are typically collected from plant pathogens, but *A. phalloides* is a plant mutualist. The invasion biology of *A. phalloides* may suggest common mechanisms of invasion by microbial mutualists.

PRUETT, GRECHEN. University of Missouri, 108 Waters Hall, Columbia MO 65211. **Truffles as a Commercial Crop in the South-Central US.**

European truffles including *Tuber melanosporum* (Perigord black truffle) and *T. aestivum* (Burgundy truffle), are valuable food commodities selling for hundreds of dollars per pound and may be profitable crops in the US. These fungi are native to Europe, forming ectomycorrhizae with the roots of host trees, including oaks (*Quercus* spp.) and hazels (*Corylus* spp.). *Tuber melanosporum* and *T. aestivum* have environmental requirements compatible with the south central US and are good candidates for production. Generally, *T. melanosporum* has more stringent growth requirements than *T. aestivum*, but also commands a higher price. Truffles are cultivated artificially by germinating host seeds, inoculating the seedlings with truffle spores, growing the seedlings in greenhouses until the mycorrhizal relationship is established, and then outplanting the seedlings. Questions at each production step must be answered. Candidate hosts adapted to US conditions must be evaluated for their abilities to form mycorrhizal relationships and withstand the high pH soils required by truffles. Truffle strains adapted to US climates must be selected to ensure maximum fruit body production. Identification of fungal competitors in orchards will allow development of management techniques to limit their spread. These questions are being addressed at the University of Missouri - Center for Agroforestry.

*PRYOR, BARRY M.[1], ROMERO, J.[2], AND CREAMER, R.[2] [1]Department of Plant Sciences, University of Arizona, Tucson, AZ, [2]Department of Entomology, Plant Pathology, and Weed Science, New Mexico State University, Las Cruses, NM. **Morphological and molecular characterization of a new species of *Embellisia* isolated from locoweed.**

The isolation of an endophytic fungus was recently reported from several species of locoweed, toxic plants of the legume family endemic to arid and semi-arid desert regions of the western U.S. The endophyte was originally described as a member of the genus *Alternaria*, then *Embellisia*, based upon incomplete morphological and genetic analysis. Additional analyses based upon detailed microscopy and sequence analyses revealed this taxon as a new *Embellisia* species. On agar media, colonies are extremely slow growing, 10-20 mm diameter after 50 days with irregular or torn margins. Conidia are solitary, long ovoid to long ellipsoid, straight to decidedly inequilateral with transverse septa that are often distinctively pigmented. Longitudinal septa are absent. Conidiogeny is primarily poric at a restricted locus, but commonly conidia are broadly holoblastic in origin. Phylogenetic analysis of ITS and glyceraldehydes 3-phosphate dehydrogenase gene sequences revealed that locoweed isolates clustered in a clade distinct from related *Embellisia*, *Nimbya*, *Alternaria*, and *Ulocladium* species. The distinct morphology is characteristic of the genus *Embellisia*, and the genetics, combined with its unique endophytic habit and production of the toxin swainsonine, demonstrate that this is a new species.

*RAJA, HUZEFA A., CAMPBELL, JINX AND SHEARER, CAROL A. Dept. of Plant Biology, University of Illinois at Urbana-Champaign, Urbana IL 61801. **Additional reports of freshwater lignicolous meiosporic and mitosporic euascomycetes from the Great Smoky Mountains National Park.**

A survey of freshwater lignicolous meiosporic and mitosporic euascomycetes from the Great Smoky Mountains National Park (GSMNP) is underway as part of an All Taxa Biotic Inventory. Submerged wood and herbaceous debris were collected in 1999-2003 from various freshwater habitats throughout the GSMNP. Samples were incubated in moist chambers and examined periodically for the presence of meiosporic and mitosporic euascomycetes. Samples from approximately 40 different collection sites throughout the GSMNP have been screened to date. Forty-one meiosporic and thirty-two mitosporic euascomycetes are reported thus far. During the inventory three new genera and one new species of meiosporic euascomycetes were discovered and *Aquaticola longicolla* is reported for the first time from North America. Except for *Casaresia sphagnorum*, all the fungi reported herein are new records for the GSMNP. Eight of the seventy-three taxa have been reported only from the GSMNP and the Austral/Asian tropics and subtropics. Distribution maps are presented for the most commonly occurring species and new and noteworthy species are illustrated.

*RAJGURU, SATYENDRA N.[1], MONCALVO, JEAN-MARC[2] AND STEPHENSON, STEVEN L.[3] [1]Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, [2]Royal Ontario Museum, Centre for Biodiversity & Conservation Biology, 100 Queen's Park, Toronto, ON, Canada M5S 2C6. **Molecular studies of mycetozoans**.

Dictyostelids (cellular slime molds) and myxomycetes (myxogastrids or plasmodial slime molds) are two groups of mycetozoans widely distributed in nature. To assess the extent of the genetic variation that exists for particular species of dictyostelids and myxomycetes collected from diverse geographic locations, a variety of molecular markers are being utilized. Sequence variation in the ITS region and EF1 sequences are being analyzed. Our goals include environmental sampling, and identifying and differentiating these organisms on a molecular level.

REHNER, STEPHEN A. Insect Biocontrol Lab, Beltsville, MD. **Sex and recombination in the entomopathogenic hyphomycete *Beauveria bassiana*: insights from the mating type locus and microsatellite markers.**

The potential for and signature of sexual reproduction in the entomopathogenic hyphomycete *B. bassiana* was investigated via characterization and evolutionary analyses of the locus determining mating type (MAT) and by population genetic analysis of microsatellite markers. Using a positional PCR walking strategy, the structure of the MAT locus was determined to contain homologues to either MAT-1 or MAT-2 ascomycete mating type idiomorphs, which suggests that *B. bassiana* possesses a heterothallic mating system. Further, roughly equal frequencies of each MAT idiomorph were observed in separate *B. bassiana* population samples, which is consistent with their maintenance by frequency dependent selection. The phylogeny of DNA lyase, a gene tightly linked to the MAT locus, is concordant with the nuclear phylogeny. This indicates that the history of the MAT locus, and thus both idiomorphs, mirrors the inferred organismal phylogeny. Random allele associations at 11 polymorphic microsatellite loci assayed within several disjunct populations indicate that *B. bassiana* is consistently recombining. Evidence derived from both the MAT locus and microsatellite markers are consistent with sexual reproduction by *B. bassiana* but do not resolve the conundrum as to why it has so rarely been observed.

REYNOLDS, BARBARA C. University of North Carolina at Asheville. **Canopy inputs to soil ecosystems: what's the connection with fungi?**

Soil microorganisms are vital participants in the decomposition process. Nematodes and soil mircroarthropods also affect decomposition, either directly, through comminution of litter, or indirectly, through feeding on and transporting propagules of, fungi and bacteria. This study examined the effect of inputs from the canopy, such as throughfall and insect frass, on soil processes and soil organisms along an elevation gradient. The response of fungal-feeding nematodes to these inputs varied with season and elevation.

RINKER, H. BRUCE. Marie Selby Botanical Gardens, 811 South Palm Avenue, Sarasota, FL 34236. **Ecology from the treetops: Accessing the 8th continent**.

Until recently, our perspective on forest ecology was ground-based and uncertain about canopy processes. Only during the past 25 years, especially since the 1990s, has our understanding of treetop ecology expanded substantially beyond this bipedal bias – in large part because of the dauntless efforts of a handful of temperate and tropical biologists working from ropes, walkways, airships, cranes, and towers sometime 40 or 50 meters above the forest floor. This keynote address will illustrate many of these access systems, discuss their advantages and disadvantages, and provide anecdotal perspectives on our discoveries in the eighth continent. The presentation will close with a speculative "Future Directions" for forest canopy ecology in both temperate and tropical systems.

ROBERSON, ROBERT W. School of Life Sciences, Arizona State University, Tempe, AZ 85287-4501. **Microtubules and their role in hyphal tip growth**.

Polarized growth of fungal hyphae requires the strict regulation of numerous cellular events and conditions, such as polarized vesicle transport and exocytosis, localized cell wall synthesis, turgor pressure generation, organelle motility, and cytoplasmic migration. Molecular genetic studies are providing invaluable insights into how many of these events are involved in regulating hyphal growth. Also essential for understanding hyphal growth are data elucidating cytoplasmic organization and behavior. We are using light and transmission electron microscopy to document the 3-D organization and behavior of the hy-

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phal cytoplasm with particular attention being placed on secretory vesicles and their associations with cytoskeletal elements, especially microtubules. It is thought that microtubules play a fundamental role in tip growth by providing the "tracks" along which secretory vesicle are transported from Golgi-equivalents to the Spitzenkörper, at which point vesicles are targeted to and fuse with the apical plasma membrane. Recent data from our lab will be integrated with published work to present the current state of knowledge of microtubule behavior, organization, and associations with cytoplasmic components relative to hyphal tip growth.

ROKAS, ANTONIS. Howard Hughes Medical Institute and Laboratory of Molecular Biology, R. M. Bock Laboratories, University of Wisconsin, 1525 Linden Drive, Madison, WI 53706, USA. **Genome-scale approaches to addressing important phylogenetic questions: incongruence and the effect of taxon sampling.**

The presence of incongruence between phylogenies obtained using different datasets and the relative contribution of taxon sampling and sequence dataset size to confidence in phylogenetic inference represent two major issues in phylogenetic research. Recent advances in genome sequencing of multiple fungal species offers a unique opportunity to address these questions on a genomic scale. The presence of incongruence generates uncertainty as to what are the true phylogenetic associations of the organisms in question. We systematically investigated the extent of incongruence, and potential ways of overcoming it, by analyzing the recently published genome data from eight yeast species. Our results show that there is a widespread incongruence between phylogenies obtained from individual genes. Perhaps surprisingly, none of the factors known to mislead phylogenetic reconstruction (such as base composition bias, gene length, etc.) could systematically account for the observed incongruence. In sharp contrast, analyses of the entire data set (a concatenation of 106 genes) yielded a single, fully resolved species tree with absolute support. Similar results were obtained with concatenation of a minimum of twenty genes. Therefore, reliance on single or a small number of genes has a significant probability of supporting incorrect relationships. The relative contribution of taxon sampling and sequence data set size to confidence in phylogenetic inference also has important implications for phylogenetic inference. The strategy favored by most phylogeneticists is increasing the number of taxa. This approach has gained support by simulation studies which have demonstrated that this is crucial in phylogenies containing long branches. To examine the trade-offs involved in increasing the number of taxa while keeping the amount of sequence data stable and vice versa, we have taken advantage of published genomic data available from 17 closely related yeast species. We have devised multiple tests to evaluate the relative merits of each approach under a variety of conditions using biological sequence data on a genomic scale. Our data argue for a very significant effect of data set size on the confidence of the inferred phylogeny. In summary, our results suggest that resolution of contentious branches of the Tree of Life may be accomplished by the tremendous power offered by genome-wide datasets.

*ROSSMAN, AMY Y., AIME, M. CATHERINE, CASTLEBURY, LISA A. AND FARR, DAVID F. Systematic Botany & Mycology Laboratory, USDA-ARS, Beltsville, Maryland 20705. **Revealing undiscovered lineages in the Ascomycetes**.

With the increased use of molecular tools to study biological diversity, ecologists are demonstrating the ubiquitous presence of diverse fungi in terrestrial habitats. Assuming that most described fungi are already in GenBank, these lineages are interpreted as new to science. Recent systematic studies have revealed a number of "new" lineages for fungal species that are well known, named and described. Examples of newly discovered lineages of Ascomycetes will be presented. The well-known coelomycetous fungi *Chaetomella raphigera* and *Pilidium concavum* with related species represent a new lineage allied with the Leotioales. *Stachybotrys chartarum*, the notorious indoor air fungus known as black mold, and other species of *Stachybotrys* were determined to be closely related to *Myrothecium* and the obscure tropical fungus *Didymostilbe echinostriata*. These fungi represent a new lineage in the well-studied Hypocreales. The common reed grass, *Phragmites australis*, harbors a new genus in the Schizothyriaceae that is rather widespread in North America and represent a previously unsequenced lineage. Given the number of fungi yet to be studied using both molecular and morphological approaches, it is premature to assume that sequences of fungi that do not have a match in GenBank represent undescribed lineages.

RUIZ, ROSALVA AND *LITTLE, CHRISTOPHER R. University of Texas - Pan American, Department of Biology, 1201 West University Drive, Edinburg, TX 78541-2999. **The effect of ferulic acid on growth and development of *Aspergillus niger*, *A. fumigatus*, *A. flavus*, and *A. parasiticus*.**

Ferulic acid (FA) is a phenolic compound commonly found in seed endosperm cell walls that may possess antifungal properties. The objective of this investigation was to determine the effective concentration of FA at which growth and development of four aspergilli (*Aspergillus niger*, *A. fumigatus*, *A. flavus*, and *A. parasiticus*) were inhibited to 50% of their normal rate (as in the absence of FA). For each *Aspergillus* species, the effect of FA on fungal growth was examined using a radial growth assay consisting of plates containing minimal media (MM) or MM+FA and a mycelial weight assay consisting of culture flasks containing the above media in liquid form. To determine the effect of FA on fungal development for each *Aspergillus* species, four experiments were performed using MM and MM+FA: (1) mature conidiophores were examined and quantified from agar plugs extracted from plates, (2) conidia production was assessed using a hemacytometer, (3) conidial germination was examined by using a colony forming unit assay *and* direct visual examination using light microscopy, and (4) germ-tube elongation was assessed using an ocular micrometer. To determine the effects of FA on mycotoxin production for each *Aspergillus* species, mycotoxin pigment in liquid coconut medium (CM) and CM+FA will be assessed by spectrophotometry.

*RYDHOLM,CARLA[1], PAOLETTI, MATHIEU[2], DYER, PAUL[2] AND LUTZONI, FRANÇOIS[1]. [1]Dept. Biology, Duke Univ., Durham, NC 27708, [2]School of Life Sciences, Univ. Notthingham, Nottingham NG72RD, UK. **Recombination and mating loci in the "asexual" *Aspergillus fumigatus* and sexual *Neosartorya fischeri* species pair.**

One hypothesis for the origins of strictly or predominantly asexual species is that they emerge from sexual lineages that have adapted to selective forces in a given environment; this has been suggested for some species pairs of fungi. The population biology parameters and mating system of the predominantly asexual fungal species, *Aspergillus fumigatus*, with those of its most closely related sister taxon, *Neosartorya fischeri*, that does reproduce sexually will be compared. A focus on the population demographics of these closely related asexual and sexual species presents a unique opportunity to test, using natural populations, long-held theoretical hypotheses regarding reproductive mode and its effects on population structure, adaptive potential, and evolution of mating systems. Using DNA sequence data from intergenic and coding loci, including mating type genes, recombination levels before and after speciation of *A. fumigatus* and effective population sizes are estimated. Of the two species, gene and genotype diversity is greater within *N. fischeri*. No spatial structure was found either within or among populations of *A. fumigatus* worldwide.

*RYVARDEN, LEIF[1] AND ITURRIAGA, TERESA.[2] [1]Department of Biology, University of Oslo, Oslo, Norway, [2]Depto. Biologia de Organismos, Univ. Simon Bolivar, Caracas, Venezuela. **Two new species in the Ganodermataceae from Venezuela**.

Two new species, belonging to the genera *Amauroderma* and *Ganoderma* (Ganodermataceae) are reported from the Venezuelan states of Bolivar and Amazonas respectively. The new species of *Amauroderma* has basidiocarps, that are annual, centrally to laterally stipitate, found on dead deciduous wood from Gran Sabana Venezuela, Roraima in Brazil and Mt. Wokomung in Guyana, which indicate that it may be widespread in the highland of the Guyana granite shield. This is a very distinct species, firstly by its elegant thin and small basidiocarps on conspicuously thin stipes, the oblong pale yellow spores, but above all by its hyphal construction. The short setae-like skeletal hyphae of the trama are also seen in *A. schomburgkii*, which however has smaller globose basidiospores and where the basidiocarps are much larger and sturdier than for this new species. The new species of *Ganoderma* is distinct in having basidiocarps, which are perennial, laterally stipitate with one or two pilei on the same stipe, occurring on an unknown hardwood log, known only from the type locality. This is a striking species because of its irregular large stipe; the citric yellow pore surface and the oblong relatively narrow spores, all characters distinct from *G. australe* to which it is apparently related.

SARMIENTO, ELIA[1] AND *CARRANZA, JULIETA.[2] [1]Universidad Nacional Autonoma de Honduras, [2]Universidad de Costa Rica. **Variations on physical, chemical, mechanical and anatomical properties of teak (*Tectona grandis*) caused by *Rigidoporus* sp. in Costa Rica.**

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Variations in the physical, chemical, mechanical and anatomical properties of teak caused by the white rot fungus *Rigidoporus* sp. were studied on wood samples taken from 6 and 10 year old plantations. Sapwood samples from 6 year old trees showed the greatest variation in all the properties studied compared with heartwood samples from 10 year old trees.

*SAUNDERS, MEGAN AND KOHN, LINDA. Dept. of Botany, University of Toronto, Mississauga ON L5L1C6, Canada. **Assessing the effects of benzoxazolinones on competition between species of *Fusarium in vitro*.**

The community structure of fungi in planta can play an important role in host plant health, and is influenced by numerous biotic and abiotic factors, including fungal competition. We are evaluating the effect of the benzoxazolinones, anti-microbial compounds produced by many members of Poaceae, on the interaction between several species of *Fusarium* collected from maize. One of the defense strategies of maize is the production of two benzoxazinoids that spontaneously degrade to the benzoxazolinones 6-methoxy-2-benzoxazolinone (MBOA) and 2-benzoxazolinone-one (BOA) upon plant cell disruption. These compounds are highly toxic to a wide variety of microbes. The precursors to MBOA and BOA are synthesized upon germination and accumulated within the tissues of the growing seedling, thereby providing a constitutive defense. While several Fusaria are able to catabolize these compounds, *F. verticillioides* has thus far demonstrated the highest degree of tolerance to MBOA and BOA, an ability suggested to increase its ecological fitness in maize fields. We are beginning to investigate the role of MBOA and BOA in shaping maize endophyte community structure by conducting in vitro competition assays to assess the possible effects of i) benzoxazolinone concentration, ii) the byproducts of metabolized MBOA and BOA, and iii) various co-inoculation parameters on fungal fitness.

SCHADT, CHRISTOPHER W.[1]*, MONCALVO, JEAN-MARC[2], MCLENON, TERRI[2], SCOTT-DENTON, LAURA[3], MEYER, ALLEN[3], MARTIN, ANDREW P.[3] AND SCHMIDT, STEVEN K.[3] [1]Oak Ridge National Lab, [2]University of Toronto, [3]University of Colorado **Digging Deeper: Novel fungal lineages are widespread and common within soils of diverse origins.**

Recent research in microbial ecology has seen dramatic developments in our understanding of microbial diversity in natural habitats via the application of direct PCR-based methods to study environmental DNA. We recently adapted and applied direct rDNA based methods to the study tundra soil fungi in Colorado (Schadt et al., Science, 2003) and revealed a high number of rDNA types that while clearly phylogeneticly associated with the phylum Ascomycota, were highly divergent from any recognized classes or even subphyla within this group. Building on this study, we used the same methods to survey three additional boreal forest soils from Colorado and Canada, and a tropical forest soil from Costa Rica. These studies revealed that the previously identified subphylum-level Group 1 sequences are widespread and common in all four of these additional soils. These types contributed 9-35% of the recovered clones from these additional libraries. Within the Group 1 lineage most subgroups were found only in one sample, suggesting significant by site variation. In contrast, only one additional clone each was revealed to be associated with the class-level Groups 2 and 3, suggesting their distributions may be limited. That further diversity in Group 1 types continues to be revealed with additional studies, suggests that this group may be very broadly distributed and diverse.

*SCHMIT, JOHN PAUL AND SHEARER, CAROL A. Dept. of Plant Biology, 265 Morrill Hall, 505 S Goodwin, University of Illinois at Urbana, Champaign, Urbana, IL 61801 **Diversity and structure of mangrove fungal communities in response to fertilization**.

We present the current results of a multi-year investigation of the response of fungi inhabiting a mangrove swamp to nutrient addition. The fungal community was studied across a gradient from large nitrogen-limited trees to small, phosphorus-limited trees. Nitrogen and phosphorus were added to separate transects along this gradient. Fungal species richness, fungal community composition and fungal biomass were measured across the gradient. Fungi on different substrates (peat, wood, leaves) responded differently to nutrient addition and tree height. Fungi on wood responded most strongly to P (triple super phosphate) fertilization, whereas fungi on leaves and in peat responded more strongly to tree height zonation.

*SCHMITT, IMKE, MUELLER, GREGORY M., LUMBSCH, H. THORSTEN. The Field Museum, Department of Botany, 1400 S. Lake Shore Dr., Chicago, IL 60605. **Ascoma morphology is homoplaseous in some pyrenocarpous lichens.**

Among lichen-forming ascomycetes, discocarpous species by far outnumber pyrenocarpous taxa. Hence, most phylogenetic studies concentrate on lichen-forming discomycetes. The classification of pyrenocarpous lichen-forming fungi, especially at higher taxonomic levels, is still largely unsettled. While the majority of pyrenocarpous lichens seem to belong to the Verrucariales, an order with gelatinising paraphyses, which is closely related to the non-lichenized Chaetothyriales, many other groups containing lichenized pyrenocarpous ascomycetes are considered "of uncertain position" in the most recent outline of the Ascomycota (e.g. Pyrenulales, Trichotheliales, Protothelenellaceae, Thelenellaceae, or Thrombiaceae). In the current study we use nuLSU and mtSSU rDNA sequence data of members of seven families of pyrenocarpous lichens to infer their phylogenetic position within groups of lichenized and non-lichenized ascomycetes. Members of the perithecioid Protothelenellaceae, Thelenellaceae, and Thrombiaceae surprisingly cluster within the mainly discocarpous Lecanoromycetes, while Strigulaceae, Verrucariaceae, and Pyrenulaceae are related to the ascolocular Chaetothyriomycetes. Micromorphological studies of the ascomata show that the two main groups of pyrenocarpous lichen-forming fungi have different ascus types.

*SHADWICK, JOHN D., STEPHENSON, STEVEN L. AND SPIEGEL, FREDERICK W. Dept. of Biological Sciences, University of Arkansas, Fayetteville AR 72701. **Report on the protostelids of the Great Smoky Mountains National Park**.

As part of the Slime Mold Twig of the All Taxa Biodiversity Inventory (ATBI) in the Great Smoky Mountains National Park we have sampled a broad range of communities for protostelids. We report at least 24 species from the park. This level of species richness is comparable to that reported for Hawai'i and Puerto Rico, and higher than what is known from other studies carried out in temperate North America. The relative abundance of species is different from tropical habitats, and, at least for the common species, more similar to what has been found in temperate North America. Within the park, protostelid abundance appears to decrease with increasing elevation. The richest habitats appear to be old fields. The ground litter microhabitat is distinct from the aerial dead plant microhabitat, with microhabitat preferences among species similar to those reported in other areas of temperate North America. These preliminary results suggest that Great Smoky Mountain National Park may be one of the richest sites for protostelids in the North Temperate region.

*SIMPSON, NICHOLAS B., WALKER, JOHN F., TROWBRIDGE, JUSTIN AND JUMPPONEN, ARI. Division of Biology, 421 Ackert Hall, Kansas State University, Manhattan, Kansas 66506. **How important are interspecific and intraspecific variation in arctic ericoid mycorrhizal communities?**

Ericoid mycorrhizal fungi utilize a broad range of organic and inorganic nitrogen sources ranging from nitrates to complex amino acids and polypeptides. Although capable of using diverse nitrogen sources, mycorrhizal fungi within these communities show preference for the use of different nitrogen sources. It has remained unclear, however, whether this variability in nitrogen uptake occurs mainly within a species or among species. To address this question, we isolated 540 fungal pure cultures from the surface-sterilized hair roots from twelve individuals of five ericaceous plant species from Toolik Lake LTER in northern Alaska. The cultures were segregated into RFLP phenotypes and the dominant fungi identified by sequencing. Five pure cultures representing each of the eight most frequent taxa – approximately ten percent of the cultures – were randomly sampled and grown for three weeks in liquid cultures with a single inorganic or organic nitrogen source. Using biomass as proxy for successful uptake of a particular nitrogen source, we will be able to partition the variance within and among taxa and determine the relative proportions of the intra- and interspecific variation. Importance of diversity within and among species along with the importance of bio-redundancy and its conservation will be discussed.

*SIRI, AUGUSTO, LÓPEZ LASTRA, CLAUDIA C., DIKGOLZ, VANESA E., MICIELI, MARÍA V. AND GIAMBELLUCA, LUÍS. Centro de Estudios Parasitológicos y de Vectores, Calle 2 N# 584, La Plata 1900, Argentina. **Prevalence and seasonality of two Harpellales (Zygomycotina: Trichomycetes) species living in the guts of aquatic insects in phytotelmata environments at Punta Lara, Buenos Aires province, Argentina.**

Two species of Harpellales, *Smittium* sp. and *Stachylina* sp., have been identified from hindguts and midguts of Chironomidae larvae (Insecta: Diptera) liv-

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ing in leaf axils (phytotelmata) at Punta Lara, Buenos Aires province. Samples were obtained every two weeks by sucking up water from the axils of individual *Eryngium cabrerae* and *Cortaderia* sp. plants from January 2003 to March 2004. Ten plants selected randomly were sampled. The volume, pH and temperature of the rainwater in the leaf axils were measured. The larvae were dissected in the laboratory under stereo and phase-contrast microscopes, and the guts were observed for the presence of trichomycete fungi. Thalli of *Smittium* sp. were found in the hindgut and *Stachylina* sp. in the midgut of Chironomidae larvae. Prevalence of fungi was determined throughout the year. *Smittium* sp. was constant during most of the year, but was not recorded in January, February, April, June and July 2003 nor in January 2004. *Stachylina* sp. was recorded most of the time except from February to July 2003, and January, February and March 2004. Prevalence and seasonality are reported for both fungal species as well as the relation of fungal presence to environmental factors.

*SMITH, DAMON L. AND SHEW, BARBARA B. Department of Plant Pathology, NC State University, Raleigh, NC, 27695. **Predicting Sclerotinia Blight epidemics on peanut in North Carolina.**

Sclerotinia blight caused by *Sclerotinia minor* is a serious disease of peanut (*Arachis hypogaea*). Sclerotinia blight advisories are based on rainfall, relative humidity (RH), leaf wetness (LW), and air or soil temperature (ST). Recently, modeled site-specific weather data have been used in disease forecasters for several pathosystems. These forecasters do not require the use of on-site sensors and can be accessed over the Internet. The purpose of this project was to improve a site-specific Sclerotinia blight advisory by better defining the conditions favorable for germination, growth, and parasitism of peanut by the fungus. In the laboratory, maximum sclerotial germination occurred at -7.2 kPa and 30 C. Rates of mycelial expansion and lesion development on detached leaflets were maximal at 18-22 C. Lesions failed to develop on detached leaflets and oxalic acid production was negligible at temperatures > 29 C. Incremental Disease Incidence (IDI) was measured weekly at three field sites and 5-da moving averages of 17 weather parameters were calculated. Six parameters selected based on a principal components analysis were input in a stepwise regression with IDI as the dependent variable. Finally, nonlinear and interaction effects of the variables were tested. The result was the model: IDI = -79.52 + 3.04 RH - 0.020 RH2 -0.47ST- 5.30LW, which will be evaluated further in 2004.

*SMITH, MATHEW E., DOUHAN, GREG W. AND RIZZO, DAVE M. Department of Plant Pathology, University of California at Davis, Davis CA 95616 **A snapshot of ectomycorrhizal fungal diversity in a mature stand of Blue Oak (*Quercus douglasii*).**

Blue oak (*Q. douglasii*) dominated woodlands are the most extensive hardwood type in California. These forests cover nearly 3 million acres and are under intense ecological pressures due to grazing, felling of trees for firewood, and land conversion. Despite their ecological importance, knowledge of the biodiversity of fungi in blue oak woodlands is limited. In March 2003, as part of a larger study on ectomycorrhizal (EM) fungi associated with blue oak, we extracted 48 large soil cores from a 32x32m hierarchical grid. Here we present preliminary data based on 1,200 colonized EM root tips. DNA was extracted from 100 bulked EM roots per core. The ITS region and part of the ribosomal large subunit were amplified and then cloned. Forty-eight clones were screened by RFLP with Hinf1 and Alu1 and several clones per RFLP type were sequenced using ITS-1F. The dominant EM species all formed either resupinate or sequestrate fruiting bodies and fell mostly within the Thelephoraceae, Sebacinaceae, and the Tuberaceae. The Thelephoraceae were particularly diverse and dominant with at least five taxa represented. Notably, none of the dominant species were fleshy, epigeous basidiomycetes. Contrary to the results of most other EM studies, we found that many of the EM species dominant on roots did produce fruiting bodies beneath *Q. douglasii*.

*SNETSELAAR, KAREN M.[1], GOPINATHAN, AARTHI[2] AND MCCANN, MICHAEL P.[1] [1]Saint Josephs University, [2]University of Pennsylvania, Philadelphia PA. **Multiple roles of cAMP in filamentous growth of *Ustilago maydis*.**

Adding exogenous cAMP to vegetative *Ustilago maydis* cells induces a multiple-budding phenotype, while mutants unable to make cAMP are filamentous. Thus, cAMP has been considered a negative influence on filament formation. However, we have found that exogenous cAMP promotes formation of *U. maydis* mating filaments. Closer examination of the filaments produced by mutants unable to make cAMP showed that the filaments differed from mating and infection filaments in that their growth was bipolar and their nuclei did not arrest in G2. The pattern of new cell formation in these mutant filaments was very similar to that seen in budding cells, but differed in that cells were not separated by constrictions, and new cells failed to separate from the parent cells. Although the presence of exogenous cAMP promoted growth of mating filaments in both mutant and wild-type cells, in both cases cell fusion was impaired but not completely prevented. Addition of exogenous cAMP to mutant cells inoculated onto plants resulted in production of appressoria and infection of epidermal cells, but the infection filaments rarely grew past a few plant cells. These observations suggest that cAMP may influence filamentous growth in *U. maydis* indirectly through effects on cell polarity, control of cytokinesis, and nutrient sensing.

*SOGONOV, M.V.[1], CASTLEBURY, L.A.[2], FARR, D.F.[2] AND WHITE, J.F.[1] [1]Dept. of Plant Biology, Rutgers Univ., New Brunswick, NJ 08901, [2]USDA ARS SBML Beltsville MD 20705. **The taxonomy of the genus *Gnomonia*: distinction between *G. gnomon* and *G. setacea*.**

Species of the diaporthalean genus *Gnomonia* are common though poorly known microfungi occurring mostly on overwintered leaves of trees and shrubs in the temperate zone of Northern hemisphere. There has been some confusion in a literature concerning the type species of *Gnomonia*, since a type was not designated by the authors of the genus. Three specific names have been mentioned in literature as the type species: *G. gnomon, G. vulgaris* and *G. setacea*. Von Höehnel designated *G. gnomon* as the lectotype species; however some authors have considered all to be synonyms. Our nomenclatural investigation based on literature and herbarium material has determined that *G. vulgaris* is a synonym of *G. gnomon*. The epithet "*gnomon*" has priority over "*vulgaris*" since the former is older. On the basis of descriptions previously published by other authors as well as our own observations of type specimens and fresh material of *G. gnomon* and *G. setacea*, we conclude that these two are distinct. These two species can be distinguished by position of the perithecium in the leaf tissue and ascospore morphology. These observations are also supported by LSU sequence analysis.

*SPIEGEL, F.W.[1], SHADWICK, J.D.[1], HEMMES, D.E.[2] [1]Department of Biological Sciences, University of Arkansas, Fayetteville AR 72701, [2]Biology Discipline, University of Hawaii, Hilo HI 96720. **Inside and out; patterns of protostelid diversity in Hawaiian kipuka and their surrounding lava flows.**

The Island of Hawaii has two very active volcanoes, Mauna Loa and Kilauea. Lava flows from these mountains create islands of untouched vegetation, kipuka, when they split and flow around patches of uneven terrain. Kipuka vegetation can be of several types, including rainforest, mesic forest, dry woodland, and grassland. Over the last six years we have sampled for protostelids both inside kipuka and from the vegetation that is beginning to invade the surrounding lava flows. Detrended Correspondence Analysis of our data suggests that the open areas of the lava flows are more similar to each other than to the particular kipuka that they surround, especially in areas where the kipuka vegetation has a closed canopy. This may suggest that the dynamics by which protostelids invade lava flows have little to do with the nearest kipuka being the source for colonizing species.

*SPIEGEL, F.W. AND STEPHENSON, S.L. Department of Biological Sciences, University of Arkansas, Fayetteville AR 72701. **A report on the status of eumycetozoan systematics and biogeography.**

The taxon Eumycetozoa contains the monophyletic groups, the myxomycetes and dictyostelid cellular slime molds, and the paraphyletic protostelids. The most recent monographic treatment of the whole taxon was published 30 years ago, and the most recent monograph of one of the subgroups, the dictyostelids, was published 20 years ago. Although collections of eumycetozoans have been made in various parts of the world over the last 150 years, little synthesis has occurred. We are in the process of carrying out two major, complementary projects to revise the systematics of the eumycetozoans and to inventory and document their global diversity. We report here on the state of our knowledge of the diversity of all three subgroups, the areas where our knowledge of the relationship among and within the groups is weak, and the first new steps we are taking to document their characters and diversity.

STEPHENSON, STEVEN L. Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701. **Mycetozoan biodiversity in the Great Smoky Mountains National Park.**

The Great Smoky Mountains National Park encompasses an area of 2080

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square km^2 in eastern Tennessee and western North Carolina between 35º28' and 35º47' N latitude. Elevations range from approximately 270 to 2000 m above sea level, and the topography and vegetation are as diverse as any region of the southern Appalachians. During the period of 1998 to 2003, surveys for mycetozoans were carried out at numerous study sites throughout the Park as one component of the All Taxa Biodiversity Inventory (ATBI) project. These study sites included examples of all major forest types along with the more common types of non-forest vegetation. Primary emphasis was placed on the myxomycetes (plasmodial slime molds), but samples for isolation for dictyostelids (cellular slime molds) and protostelids (protostelid slime molds) in the laboratory also were collected. Since the surveys began, the number of species of myxomycetes known from the Park has increased from 88 to more than 220, and the number of dictyostelids from 12 to more than 30. There were no reports of protostelids from the Park prior to the ATBI, but more than 25 species have been recorded since 1998.

*STEPHENSON, STEVEN L.[1], LANDOLT, JOHN C.[2], POWERS, DONNA M.[3], DILLON, LINDSAY A.[3], AND PEARCE, CERIDWEN A.[4] [1]Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, [2]Dept. of Biology, Shepherd College, Shepherdstown, WV 25443, [3]Biology and Chemistry Division, Corning Community College, Corning, NY 14830, and [4]Australian Tropical Mycology Research Centre, Queensland, Australia. **Eumycetozoans associated with tropical forests in northern Queensland, Australia**.

Biotic surveys for eumycetozoans were carried out in northern Queensland during the 2003 field season to document more completely the species associated with tropical forests in this region of the world. Primary emphasis was on myxomycetes (plasmodial slime molds); more limited data were obtained for dictyostelids (cellular slime molds) and protostelids (protostelid slime molds), two other groups of eumycetozoans that share some of the same microhabitats as myxomycetes. Microhabitats examined for myxomycetes included coarse woody debris, forest floor leaf litter, aerial litter (dead but still attached plant parts), dead lianas, and inflorescences of large tropical herbs. Dictyostelids were isolated from samples of the soil/humus layer on the forest floor and aerial soil (the mass of "soil-like" organic matter often found in association with bases of vascular epiphytes in the forest canopy), whereas samples of soil and aerial litter (both natural substrates and sterile straws, introduced into selected study field sites to assess colonization rates of these organisms) were examined for protostelids. Data obtained thus far suggest that all three groups of organisms exhibit levels of biodiversity and patterns of occurrence not unlike those already known from studies carried out in the Neotropics of Central America.

*SUBERKROPP, K. AND GULIS, VLADISLAV. Dept. of Biological Sciences, University of Alabama, Tuscaloosa, AL 35487. **Effects of leaf litter manipulations on communities of aquatic hyphomycetes in a southern Appalachian stream.**

We are examining the effects of manipulating leaf litter inputs on the aquatic hyphomycete community in a headwater Appalachian stream. Leaf litter had been excluded from the treatment stream for eight years at the beginning of the study. In the autumn of two years, rapidly decomposing leaves of three tree species (dogwood, yellow poplar, sweet gum) were added to the stream at the rate that leaf litter naturally fell into a reference stream nearby. Fungal biomass associated with submerged leaf litter estimated from ergosterol concentrations increased after leaf input and was similar in the reference and treatment streams when leaf litter was present in both streams. However, conidia in transport in the treatment stream peaked at higher concentrations (3 to 15 times) than observed in the reference stream during April-May in the first year and February in the second following leaf addition in the previous November. Species richness of aquatic hyphomycetes was not affected by leaf litter addition (on average 16-17 species on each sampling date in both streams); however, relative abundances and ranking of dominant species changed. Currently, the treatment stream has received input of three leaf species that decompose slowly (rhododendron, red oak, white pine) and spore concentrations in the water have not exhibited the sharp increases observed in the previous two years.

*SUPER, PAUL E.[1] AND NICHOLS, BECKY.[2] [1]Appalachian Highlands Science Learning Center, Great Smoky Mountains National Park, P.O. Box 357, Lake Junaluska, NC 28745, [2]Great Smoky Mountains National Park, Gattlinburg, TN 37738. **Calling All Life Forms: An All Taxa Biodiversity Inventory of Great Smoky Mountains National Park.**

In 1998, Great Smoky Mountains National Park joined with taxonomists from across the world to launch what will be the first comprehensive inventory of life forms within a protected area in North America. The National Park Service, charged with protecting the cultural and natural resources and natural processes within the park from an ever increasing list of threats, seeks a better understanding of what it is trying to protect. The expected products include not just a checklist of species, but distributional maps and habitat associations for as many species as possible, educational products such as species web pages and interactive keys, a public with a better understanding and appreciation of biodiversity, and the sort of baseline information that facilitates proactive management and attracts more detailed scientific study. In addition to drawing on the skills of taxonomists, this project also draws upon the help of parataxonomists, students, and volunteers from the general public to assist the taxonomists and collect data under their direction that extends what the taxonomists can do. An example is the Smokies FungiMap project, launched in the fall of 2002 with the Asheville Mushroom Club and under the direction of Dr. Dennis Drehmel, based on a similar project in Australia.

*SWANSON, ANDREW R.[1], HEMMES, DON E.[2], SPIEGEL, FREDERICK W.[1] [1]Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas 72701, [2]Department of Biology, University of Hawaii, Hilo, Hawaii 96720. **Investigations into the biogeography, distribution, and ecology of dictyostelid slime molds on the island of Hawaii.**

The Hawaiian Archipelago is the most isolated island chain in the world. According to classical island biogeography theory, this isolation should preclude colonization by organisms with low dispersal potential. Dictyostelid slime molds have low dispersal potential, their spores dispersed by fresh water and animal vectors rather than by wind. Although previous data have suggested a depauperate collection of dictyostelids on Hawaii (the largest and youngest of the Hawaiian Islands), our work over the past 5 years has revealed a fairly diverse (17 described and 4 undescribed species), albeit sparse dictyostelid biota. Common species in Hawaii include the typically cosmopolitan species, along with those common to North America and Japan, rather than those characteristic of other pantropical regions. The number of undescribed species is not altogether different from other similarly-sampled continental localities. Distribution patterns of dictyostelids on Hawaii are related to altitude and moisture; dictyostelids are most abundant and diverse at montane mesic sites. Within montane mesic sites however, dictyostelid distributions seem to be governed by a geographic component. These observations support the notion that dictyostelids may have been introduced to Hawaii relatively recently.

*SWANSON, ANDREW R.[1], HEMMES, DON E.[2], SPIEGEL, FREDERICK W.[1]. [1]Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas 72701, [2]Department of Biology, University of Hawaii, Hilo, Hawaii 96720. **The primary habitat of dictyostelid slime molds on Hawaii.**

Increased diversity of vegetation has long been thought to affect the variety and quality of soil litter inputs, thereby influencing the soil bacterial community, and subsequent bactivorous predators as well. One such group of bacterivores, the dictyostelid slime molds, are easily recovered, cultured, and enumerated from surface soils and litter. In an attempt to ascertain the distribution of dictyostelids from variously-aged substrates on the island of Hawaii, soil litter samples were collected from older "islands" of mature vegetation (locally known as "kipukas") as well as from sparse pockets of litter found on the hardened surfaces of more recent surrounding lava flows. The results were counterintuitive: dictyostelid density and diversity were highest in litter collected from seemingly barren sites with open canopies rather than in litter collected from mature, richly-vegetated sites with closed canopies. To confirm and further elucidate these results, a second more intensive study was initiated wherein litter samples were collected every 10m along four 120m transects, each of which terminated within a mature kipuka. Again, the highest density and diversity of dictyostelids was found outside, rather than within the kipuka. These results call into question the long-standing view that the primary habitat for dictyostelid slime molds is mature forest soils.

*TODA, TAKESHI[1], MGHALU, JOSEPH M.[1], HAYAKAWA, TOSHIHIRO[2] AND HYAKUMACHI, MITSURO[1]. [1]Faculty of Applied Biological Science, Gifu University, 1-1 Yanagido, 501-1193 Gifu, Japan, [2]Riken Green Co. Ltd., 859-1 Minamida-iheishinden, Fukuda, Iwata, Shizuoka, Japan. **Development of specific primers for each variety of *Rhizoctonia circinata*.**

Four varieties of *Rhizoctonia circinata*; var. *agrostis*, var. *circinata*, var. *oryzae* and var. *zeae*, are the causal agents of turfgrass diseases during warm seasons. As their symptoms are quite similar, it is difficult to distinguish among

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these four varieties. Conventional identification technique based on the cultural morphology of the isolated pathogen is laborious and time-consuming. For rapid detection of each variety of *R. circinata*, specific primers were designed from the sequence data of internal transcribed spacers of ribosomal DNA (rDNA-ITS region). The primers were Agro-1F for *R. c.* var. *agrostis*, Cir-2F for *R. c.* var. *circinata*, Ory-1F for *R. c.* var. *oryzae* and Zea-2F for *R. c.* var. *zeae*. Each primer pair of Agro-1F/ITS 4, Cir-1F/ITS 4, Ory-1F/ITS 4 and Zea-2F/ITS 4 could respectively produce a single PCR product from pure fungal DNA for each variety of *R. circinata*. When the primers were tested on other fungal pathogens of turfgrass, they showed no PCR products. The primer pairs of Agro-1F/ITS 4, Cir-2F/ITS 4, Ory-1F/ITS 4 and Zea-2F/ITS 4 are specific and useful for the rapid detection of respective *R. circinata* varieties.

*TOOLEY, PAUL W.[1], MARTIN, FRANK N.[2], CARRAS, MARIE M.[1] AND FREDERICK, REID D.[1]. [1]USDA-ARS Foreign Disease-Weed Science Research Unit, Ft. Detrick, MD 21702, [2]USDA-ARS, 1636 E. Alisal St., Salinas, CA 93905. **Real-time fluorescent PCR detection of the sudden oak death pathogen *Phytophthora ramorum*.**

Phytophthora ramorum causes sudden oak death, a disease that has killed many oaks in California and which also threatens the nursery industry due to its ability to cause foliar infection on rhododendrons and many other ornamentals. A real-time PCR detection method for *P. ramorum* was developed based on mitochondrial DNA sequence and using an ABI Prism 7700 Sequence Detection System (Taqman). Primers and probes were also developed for detecting *P. pseudosyringae*, a newly described species which causes symptoms similar to those of *P. ramorum* on certain hosts. The *Phytophthora*-specific primer-probe system was used in a multiplex assay with a plant primer-probe system utilizing the dyes FAM and CAL Orange to allow plant DNA to serve as a positive control in each reaction. With the FAM dye system, detection of genomic *P. ramorum* DNA was achieved down to 1 fg of DNA. *Phytophthora ramorum* could be detected from inoculated *Rhododendron* cv.'Cunningham's White'(12 mg fresh weight tissue) down to a 1:100,000 dilution. In a blind test, the method also successfully detected *P. ramorum* in California field samples previously found to be positive based on conventional PCR and isolation of the pathogen in pure culture. This system should prove useful in allowing rapid, sensitive and specific detection of the sudden oak death pathogen on ornamentals and other host species.

*TOURNAS, VALERIE H.[1], HEERES, J.[2] AND BURGESS, L.[2] [1]FDA/CFSAN, College Park, MD, [2]JFSAN/University of Maryland, College Park, MD. **Moulds and yeasts in fruit salads and fruit juices.**

Forty fruit salad samples including apple, cantaloupe, citrus fruits, honeydew, pineapple, cut strawberries and mixed fruit salads, and 80 pasteurized fruit juice samples (apple cider, apple, carrot, coconut, grapefruit, grape and orange juice, raspberry cider, various smoothies and fruit juice nectars, and soy milk) were purchased from local supermarkets in the Washington, D.C. area and tested for fungal contamination. Results indicated that 97.5 % of the fruit salads were contaminated with moulds and yeasts. Yeasts were the predominant organisms found in 95.5% of tested samples and ranging from <100-5.2 x 10^9 cfu/g. Frequently encounter yeasts were *Pichia* spp., *Candida pulcherrima, C. lambica, C. sake, Rhodotorula* spp., and *Debaryomyces polymorphus*. Low numbers of *Penicillium* were found in apple and pineapple salads, whereas *Cladosporium* spp. were present in mixed fruit, cut strawberries and pineapple salads. All other products showed no mould contamination. Twenty per cent of the fruit juice samples tested showed fungal contamination. Yeasts were the predominant contaminants ranging from <10-1.1 x 10^8 cfu/mL. Yeasts commonly found in fruit juices were *Candida lambica, C. sake Rhodotorula* and *Sporobolomyces* spp. *Geotrichum* spp. and low numbers of *Penicillium* and *Fusarium* spp.(50 and 40 cfu/mL, respectively) were present in grapefruit juice.

*TRAIL, FRANCES, VELASQUEZ, LUIS, AND LETOURNEAU, YVONNE. Dept. of Plant Biology, Michigan State University, East Lansing MI 48824. **Forcible ascospore discharge in *Gibberella zeae*: Generation of turgor pressure**.

The ascus evolved as a tubular gun used to shoot ascospores into the air. It is likely that this mechanism is conserved over the Ascomycota. The physiological and genetic basis for ascospore discharge in *Gibberella zeae*, the causal agent of head blight of wheat and barley, is being explored through a variety of molecular, histological and physiological techniques. The recent availability of a genomic sequence for *G. zeae* has also greatly facilitated these studies. Among the findings presented will be evidence that accumulation of osmolytes is important to generation of the turgor pressure for discharge of these spores.

TSUI, CLEMENT K.M. Department of Botany, The University of British Columbia, #3529-6270 University Blvd., Vancouver V6T 1Z4, Canada. **Molecular phylogeny of helicosporous hyphomycetes.**

The phylogenetic relationships among helicosporous fungi in the anamorph genera *Helicoma, Helicomyces, Helicosporium*, *Helicodendron* and *Helicoon* and the telemorph genus *Tubeufia* (Tubeufiaceae) have been using nucleotide sequence of the SSU, ITS and partial LSU ribosomal DNA sequences. An initial set of 30 taxa and related sequences from GenBank, analysed using maximum parsimony and neighbour joining showed that the origins of helicosporous hyphomycetes were polyphyletic. The majority of *Tubeufia* spp. and their anamorphs, however, appeared as a monophyletic lineage with high support. A second, more detailed analysis of the major monophyletic lineage used more representatives and sequence to suggest that none of the three anamorph genera *Helicoma, Helicomyces* and *Helicosporium* is monophyletic. Within the major, monophyletic lineage, two well-supported groups could be distinguished. The first group including *Tubeufia cerea* and *Helicosporium vegetum* and other representatives of *Helicosporium* produced erect conidiophores. The other group consisted of *T. helicoma* and its anamorph *Helicoma muelleri*, and other *Helicoma* spp. having a triangular basal cell, that may be a significant character in phylogeny.

*TUININGA, AMY R.[1], HUSKINS, R.E.[1], DIGHTON, JOHN[2], GRAY, D.M.[2], BELTON, T.[3] [1]Louis Calder Center, Fordham University, Armonk, NY 10504, [2]Rutgers University Pinelands Field Station, New Lisbon, NJ 08064, [3]NJDEP, Trenton, NJ 08625. **Nitrogen deposition effects on pine ectomycorrhizal fungal communities in New Jersey: identifying potential indicator species.**

An eastern to western transect through forests in northern New Jersey was identified to study nitrogen deposition effects. Nitrogen content in bulk precipitation and in soils, along with their relation to ectomycorrhizal fungal (EMF) community structure, was examined at three sites in northern NJ (Palisades, Ringwood, High Point) and a reference site in southern NJ (Lebanon). Bulk precipitation showed highest levels of NH_4^+ (mg m^{-2}) at Ringwood and lowest levels at Lebanon. Soil NH_4^+ and NO_3^- (μg g^{-1}), however, did not vary among northern NJ sites, but all of the northern NJ sites were higher in N content than Lebanon. A total of 34 ectomycorrhizal morphotypes were identified in the northern sites, four potentially nitrophobic and one potentially nitrophilic. Richness of mycorrhizal fungi at these sites was only decreased at Palisades, which exhibited intermediate levels of N deposition. Overall, however, EMF richness was positively related to concentration of NH_4^+ (mg l^{-1}) deposited in precipitation ($r^2 = 0.3504$, $p = 0.0426$). This contradicts our prediction that EMF richness would be decreased at sites with highest N deposition as indicated by our studies the previous year on a transect of sandy soils in southern NJ pine barrens. This may be the result of incomplete N saturation in loamy soils and more N sensitive species present in the oligotrophic pine barrens soils.

*UCHIDA, MAHO AND ROBERSON, ROBERT W. School of Life Sciences, Arizona State University, Tempe, AZ 85287-4501. **Towards predicting cytoplasmic function from order and dynamics: 4-D cytoplasmic analysis of polarized hyphal tip growth**.

Fungi produce tubular-like hyphae through polarized growth. Mechanisms of this mode of growth are believed to be the result of directed and constitutive exocytosis controlled by cytoskeletal function. Previous observations lead us to speculate that microtubules (MTs) are involved in long-distance transport of vesicles from Golgi-equivalents to the Spitzenkörper (Spk), followed by a switch at the Spk from MTs to actin microfilament-based motility. We employed both advanced light and electron microscopy methods to evaluate Spk dynamics and its organization, and to map the distributions of MTs and other cytoplasmic components in fungal hyphae to better understand the mechanisms of polarized growth. The images obtained by digital phase contrast light microscopy revealed a unique organization of the Spk and novel details of internal dynamics in *Neurospora crassa*. The Spk consisted of three discrete phase-dark layers subtended by a phase-bright core. Unidentified materials, at or below the level of resolution of LM, traveled through the core towards the hyphal apex. Serial cross-section reconstructions and quantitative analysis of TEM data of apical and sub-apical hyphal regions have been analyzed. Furthermore, the 3-D ultrastructural organization of the apical cytoplasmic components has been analyzed using dual-axis electron tomography and modeling in *Aspergillus nidulans.*

Continued on following page

UDAYA PRAKASH, N.K. Omni Environmental, Inc. 13740, Research Blvd, Suite H-5, Austin, TX 78750. **Thermophilic fungi: are they allergens?**

Awareness on airborne mesophilic fungi indoors in inducing sick building syndrome and other respiratory disease are going on well in different parts of the world. However, is that the same in case of thermophilic fungi? Although, thermophilic actinomycetes are reported in inducing hayfever, to say the same about thermophilic fungi that they possess allergenic property is a question before us. To reveal that they are potential allergens, they must possess (i) airborne ability so as to reach the respiratory system when the subjects are inhaling the atmospheric air, (ii) their number in the atmosphere must be significant enough to induce allergic reaction, and finally (iii) they must possess the potency to induce allergic reaction in susceptible individuals. However, the presence of thermophilic fungi in the environment is interdependent on the substrate availability and the temperature. These are readily available in the occupational environments and the workforce present in these environments is exposed to thermophilic fungi. The study conducted in Madras, India on this aspect reveals that the thermophilic fungi are airborne, and are in significant numbers and are potential allergens in inducing atopicity on the subjects reporting respiratory allergy. Hence, it is recommended to diagnose the subjects for their exposure to thermophilic fungi too.

UPADHYAY, SRIJANA AND *SHAW, BRIAN D. Program For the Biology of Filamentous Fungi, Department of Plant Pathology and Microbiology, Texas A&M University, College Station, TX, 77843. ***Aspergillus nidulans* developmental mutants, *swoK* and *swoM*, reveal genes important for cellular polarity.**

Polarized cellular morphogenesis is common to all eukaryotic systems, but is taken to an extreme in filamentous fungi where polarized growth dominates the life cycle. The *A. nidulans* swollen cell (*swo*) mutants exhibit abnormal polarized development when incubated at restrictive temperature 42 C. Upon germination, the *swoK*mutant extends a primary germ tube that quickly swells to an enlarged, non-uniform cell with pronounced wall thickenings. The *swoK* mutant is fully restored to wild type growth when transformed with a 9.2 kb fragment of genomic DNA. The fragment contains five predicted genes (designated 5799, 5800, 5801, 5802, 5803 in The Broad Institute genomic database). Transposon insertion within 5802 disrupts the ability of this clone to complement the *swoK* mutant. The 5802 predicted protein contains an N-terminal RNA binding domain while the C-terminal half has low homology to any known proteins. The *swoM* mutant also extends a primary germ tube but this germ tube quickly swells to a uniform 20+μm diameter cell. The *swoM* mutant is complemented by a 9.7 kb fragment of genomic DNA containing ORFs 6035, 6036 and 6037. The *swoM* mutant is partially complemented by a different 8 kb genomic fragment containing ORFs 7738, 7739, 7740 and 7741. Current work establishing which of the ORFs is the complementing gene will be discussed.

*VAUGHANS-WARD, KASEY, ISIKHUEMHEN, OMOANGHE S. North Carolina Agricultural & Technical State University, 1601 E. Market St., Greensboro, NC 27411. **Effect of temperature on spore germination in *Grifola frondosa*.**

Grifola frondosa (Dicks: Fr.) S. F. Gray (Maitake) is a fungus of high economic importance that grows on hardwood trees in the northern temperate forests of the eastern Unites States, Canada, Europe, and Asia. The difficulty we encountered trying to germinate spores of *G. frondosa in vitro* led us to testing the effect of temperature shock on spore germination. Spore solutions were incubated in water baths at 4, 30 and 40 ºC for 6 hours. Spore solution incubated at room temperature (25 ºC) served as the control for this experiment. Treated spores were plated on 2% potato dextrose agar plates (9.0 cm diameter) and incubated at 25 ºC for 15 days. Plates were inspected for germination every other day. Germination data collected was analyzed using ANOVA. Germination values at all treatments were significantly different among all treatments. The average number of spores germinated in the 30 ºC treatment was 28.6 per agar plate compared to control which was 2.8 per plate. The results indicates that temperature shock treatment is important in stimulating spore germination in *G. frondosa* and we are applying this shock treatment in the germination of spores of other isolates in our further studies on the genetics and breeding *G. frondosa*.

VERBEKEN, ANNEMIEKE. Ghent University, Dept. of Biology, Research Group Mycology, K.L. Ledeganckstraat 35, B-9000 Ghent, Belgium. ***Lactarius* in tropical Africa**.

In tropical Africa, up to 85 endemic *Lactarius* species are currently known. It is estimated that the total number could reach 150, if the area is further explored and unsolved species complexes are unraveled. Some infrageneric groups relatively poorly represented in other continents, such as subgenus *Lactariopsis* and *Lactiflui*, have a distinct centre of diversity in African tropical or subtropical vegetation. In contrast, there are few representatives of the subgenus *Piperites* in tropical Africa. Some species show remarkable characters, unknown in *Lactarius* from other areas. Sequestrate taxa occur but are apparently sparsely represented. In some subgenera, species complexes need more research. The question of how much morphological variation can be accepted within a taxon – and what to use as a criterion to base new species on – is especially difficult in cases where few collections with insufficient field data are available. Molecular data are included, but it is clear that more sampling is needed.

*WALKER, JOHN F.[1] AND MILLER, ORSON K. JR.[2] [1]Division of Biology, Kansas State University, Manhattan KS 66506, [2]Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg VA 24062. **Ectomycorrhizal fungus assemblages appear to be seasonally dynamic on oak seedlings in the southeastern Appalachian Mountains.**

We examined ectomycorrhizal (EM) fungus distributions on root systems of out-planted oak seedlings at two sites in mixed southeastern Appalachian Mountain forests, comparing samples collected in mid-June and early-September. Species level EM fungus matching, and identification in some cases, was enabled by direct sequencing of the mycobionts from the seedling roots. Seventy three EM fungus ITS-types were recorded, most of which occurred only in either the mid- or late-summer samples. Generalistic dominants were found fairly equally at both sites and on both sample dates. Dramatic shifts in mycobiont assemblages were observed in relation to sample date, including increases in *Cortinarius* spp. richness, decreases in Thelephoraceae richness, and the absence of *Amanita* spp. types in the late- compared to mid-summer samples. Spatio-temporal variation and richness of rare species were both high. However, patterns similar to sporophore assessments, systematic affinity of shifting EM types, and the generalistic nature of non-seasonal types all lend support to our assessment of seasonal variability in EM associations in this system. Based on these results we propose a model of seasonal EM dynamics wherein certain groups of fungi occur predominantly on roots in a specific season, while other more ubiquitous fungi form mycorrhizae throughout the growing season. Area of interest: Ecology Pathology

*WANG ZHENG AND HIBBETT, DAVID S. Department of Biolgy, Clark University, 950 Main Street, Worcester, MA 01610. **Life history and phylogeny of *Mitrula* species, aero-aquatic fungi in the Helotiales.**

Mitrula species represent a group of aquatic discomycetes with an uncertain position in the Helotiales and an unknown life history. *Mitrula* species have been thought to be members of the family Geoglossaceae or Sclerotiniaceae based on morphological studies and molecular studies. Recently pure colonies were isolated from a wild *Mitrula* collection and studied. Conidiospores of *Mitrula paludosa* were observed and described. Herbarium materials of *Mitrula* species from Europe, Asia, and North America were studied . Sequences of rDNA, including partial ssu-rDNA, lsu-rDNA and ITS, were generated. Special attention was also given to other stiptate inoperculate discomycetes. Equally weighted parsimony analyses and Bayesian analyses were performed. Our preliminary results suggest that 1) Four species might recognized in *Mitrula* based on molecular and morphological data; 2) Close relationships between *Mitrula* and either Geoglossaceae or Sclerotiniaceae are not supported; 3) A clade can be recognized within the Helotiales that includes aero-aquatic genera *Mitrula, Vibrissea, Ombrophila, Hymenoscyphus*, and *Cudoniella*.

*WESTMORELAND, SEAN E. AND VOLK, THOMAS J. Department of Biology, University of Wisconsin-La Crosse, La Crosse WI 54601. **Comparison of chemosystematics and ITS sequencing in the systematics of *Hydnellum* (Basidiomycota, Thelephoraceae).**

CHUMS, or chemosystematics with high performance liquid chromatography (HPLC) using mass spectroscopy, is a newly created technique that we've developed for delimiting *Hydnellum* species based on chemical differences. The CHUMS method generates data based on the presence or absence of chemical compounds, which are then analyzed to determine relatedness. A total of 54 compounds were scrutinized to construct a chemical "sequence," somewhat akin to a nucleotide sequence, that can be analyzed using phylogenetic programs. This presentation compares the CHUMS data with morphological and molecular (DNA seq) studies of *Hydnellum* species. Although previous mor-

Continued on following page

phological and chemical works have been useful, there are many disagreements between authors as to the correct delimitation and systematic placement of *Hydnellum* species. Ninety-nine collections were examined morphologically, 36 collections were analyzed by comparing ITS sequences, and 15 collections were examined with CHUMS. From these data we are able to construct phylogenies that show relatedness of species. All three lines of evidence were combined (morphological, chemical, and DNA) to determine final systematic and taxonomic placements of 15 *Hydnellum* species. There is some level of congruence of phylogenetic trees between the three techniques, but also some significant differences in relatedness of some species.

*WILSON, ANDREW W.[1], HIBBETT, DAVID S.[1] AND HOBBIE, ERIK A.[2] [1]Department of Biology, Clark University, Worcester, MA, [2]Institute for the Study of Earth, Oceans, and Space, University of New Hampshire, Durham, NH. **Saprotrophic or symbiotic? Establishing the ecological role of *Calostoma cinnabarina*.**

The genus *Calostoma* forms unusual gasteroid fruiting bodies that are characterized by a thick, gelatinized cuticle, rubbery stalk and brightly colored peristome from which the spores are released. In recent molecular studies, *Calostoma* has been established as a member of the Boletales. However, several reports suggest that *Calostoma* is saprotrophic. This contradicts its relationship to the largely mycorrhizal Boletales, along with its putative association with ectomycorrhizal (ECM) flora. Evidence supporting either hypothesis has not been established. This study employs two methods for exploring the ecology of *Calostoma cinnabarina*: 1) Molecular analysis of *C. cinnabarina* fruiting bodies and associated mycorrhizae, using Basidiomycete and *Calostoma*-specific primers: 2) Comparing carbon and nitrogen isotope profiles of *C. cinnabarina* and other mycorrhizal and wood/litter-decomposing fungi found in the same location. Results of molecular analysis of ECM suggest that *C. cinnabarina* is ectomycorrhizal. Sequences from ITS 1 & 2 in several ECM root tips, and gelatinized rhizoids, matched ITS sequences from *C. cinnabarina* fruiting bodies. Ectomycorrhizae associated with *C. cinnabarina* have a gelatinous cuticle similar to that from the fruiting bodies. Results of the isotopic analysis also suggest that *C. cinnabarina* is mycorrhizal.

YAHR, REBECCA[1,2], VILGALYS RYTAS[1], AND DEPRIEST, PAULA T.[2] [1]Dept. of Biology, Duke University, Box 90338, Durham, NC 27708, [2]Smithsonian Institution, National Museum of Natural History, Washington, D.C. 20560. **Geographic variation in photobiont specificity points to ecological, not evolutionary, specialization in *Cladonia*.**

In lichen symbioses, a fungus that is a photobiont specialist may be a better competitor than a generalist in a particular ecological setting. However, few lichen associations have been examined in detail across communities, and the ecological and evolutionary mechanisms dictating associations are generally poorly known. We intensively studied a suite of lichens on two spatial scales. Eight *Cladonia* species were sampled from five Florida scrub sites, for a total of more than 200 samples. One of these, *C. subtenuis*, was sampled in several communities across eastern North America to investigate geographic and ecological variation in photobiont specificity. We used ITS sequences of both *Cladonia* and *Asterochloris* for phylogenetic and population genetic analyses and identified three major photobiont lineages or clades. At the community level, all Florida scrub sites with the same fungal species contained a statistically equivalent set of potential *Cladonia* photobionts, i.e. photobionts from each of the three clades were available in each site. At this same spatial scale, however, most fungal species including *C. subtenuis* were only associated with a single *Asterochloris* clade. On a regional scale, *C. subtenuis* photobiont specificity was lower, including three additional algal clades. At all scales studied, fungi associated in unequal frequencies with compatible genotypes or clades. These associations were independent of fungal phylogeny, indicating strong fungal selectivity. At the larger geographic scale, these frequencies of photobiont association are correlated with latitude and physiographic region. Therefore, lichen associations may be products of ecological specialization of fungi for photobionts, perhaps linked with fitness benefits of preferential partnership across sites.

*ZALAMEA, MARCELA[1] AND GONZÁLEZ, GRIZELLE[2]. [1]University of Puerto Rico, Rio Piedras, [2]USDA Forest Service, International Institute of Tropical Forestry, Rio Piedras, PR. **Basal and substrate induced respiration of soils from a subtropical wet forest in Puerto Rico.**

Soil respiration could be used as a measure of microbial (fungi and bacteria) biomass and metabolic activity. We performed essays of Substrate Induced Respiration (SIR) using glucose as the metabolic stimulant to determine the minimum concentration of glucose required to achieve a maximum respiratory response (MRR), and compared soil respiration rates for the same soil at two different seasons (wet and dry). CO^2 evolved at MRR was used to estimate microbial biomass (MB). The study was done in a sub tropical wet forest in Puerto Rico. Patterns of rainfall are lightly seasonal, with a rainy season between Sep-Dec, and a drier season between Jan-Apr. Soil samples (10 gr dry wt soil per treatment) were sieved and incubated in an ER-10 respirometer; either at basal conditions, after adding 1 mL of glucose solutions (2 to 9 mg C-glu/g dry soil) or water (control). We found no significant differences in CO^2 among the dates. MRR was obtained at 4 mg- glu/g dry soil. The amendment resulted in a respiration rate 6 times higher than the basal values and 4 times higher than the control. The response of soil to amendment was similar in all dates indicating that the capacity of soil to respond to rapid changes in substrate availability did not depend on the seasonality, and supporting the suitability of SIR as a technique to estimate MB, which was calculated as 1072.994 μg MB-C/g dry soil.

*ZHANG, NING[1], NALIM, FATHIMA, A.[1], SUTTON, DEANNA A.[2], EPSTEIN, LYNN[3], O'DONNELL, KERRY[4] AND GEISER, DAVID M.[1]. [1]Dept. of Plant Pathology, Penn State University, University Park, PA 16802, [2]Dept. of Pathology, UTHSC, 7703 Floyd Curl Drive, San Antonio, TX 78229, [3]Dept of Plant Pathology, UC Davis, Davis, CA 95616, [4]Microbial Genomics and Bioprocessing Research Unit, NCAUR, USDA-ARS, Peoria, IL. **Association of clinical, environmental and plant pathogenic isolates within the *Fusarium solani* species complex.**

Members of the *Fusarium solani* species complex are increasingly implicated as the causative agents of human mycoses, particularly in the immunocompromised patient population. Previously members of this complex were shown to comprise at least 26 phylogenetically distinct species, including ubiquitous saprophytes and economically important plant pathogens. To identify phylogenetic species associated with human infections, we generated four partial gene sequences (totaling 2305 bp per isolate) from 471 isolates from clinical human N= 278, hospital environmental N =21) and non-clinical (N = 172) sources chosen to represent the known genetic diversity in the complex. We identified 269 four-locus haplotypes among these isolates, 138 of which included clinical isolates, representing at least 30 distinct phylogenetic species. Nineteen haplotypes included clinical and non-clinical isolates. Monophyly of the clinical isolates was rejected. Clinical isolates shared haplotypes with plant pathogenic, animal-associated, and environmental isolates. Members of the most common environmental species, including those found in hospitals, are responsible for the majority of *Fusarium solani* infections. Incongruence among gene genealogies within the major clinical species lineages suggest the potential for an active sexual cycle.

*ZITOMER, NICHOLAS C.[1], GEISER, DAVID M.[1], ARCHIBALD, DOUG D.[2], JIMENEZ-GASCO, MARIA M.[1], O'DONNELL, KERRY[3] AND KULDAU, GRETCHEN A.[1] [1]Dept. of Plant Pathology and [2]Dept. of Crop & Soil Sciences, Pennsylvania State University, University Park, PA, [3]Microbial Genomics and Bioprocessing Research Unit, NCAUR, USDA-ARS, Peoria, IL. **The phylogenetics of fumonisin production in the *Gibberella fujikuroi* species complex.**

Fusarium species have traditionally been and still are problematic to identify using morphology. This is an issue of concern many Fusaria are toxigenic, producing such toxins as trichothecenes, fumonisins and zearalenone. Fumonisins are sphingolipid analogues associated with the *Gibberella fujikuroi* species complex (GFC) that cause fatal diseases in horses and swine and are associated with cancers. The goal in this study was to make precise connections between phylogenetically well-defined *Fusarium* species and the production of fumonisins. We first generated a database of translation elongation factor 1-alpha sequences from putative isolates in the GFC to accurately identify isolates to known and potentially new species. Members of new and previously uncharacterized species will be analyzed for fumonisin production. To aid in this analysis, we are screening isolates using a PCR assay of the FUM1 gene, which controls a central step in fumonisin biosynthesis. Cultures from isolates that test positive in the PCR assay will be analyzed for fumonisin production using a High Pressure Liquid Chromatography (HPLC) method.

MYCOLOGICAL NEWS

Happy 100th birthday to Dr. George B. Cummins, Purdue University's "LORD OF THE RUSTS"

On 29 August 2004 Prof. George Baker Cummins will celebrate his 100th birthday. Cummins' professional specialty for almost his entire career has been and remains the taxonomy, biology and geographic distribution of the rust fungi (Uredinales), a group of more than 7000 species of obligate plant parasites, which he studied in the internationally renowned **Arthur Herbarium** at Purdue University, West Lafayette, Indiana. He published nearly 120 refereed papers and 10 books, the most recent at the age of 98 (the third edition of The Genera of Rust Fungi (2003) co-authored by his student Y. Hiratsuka). For his authoritative and vast scientific productivity, he is recognized as the world's foremost authority on the rust fungi.

Dr. Cummins in 2001
(Arthur Herbarium archive)

Backed by this scientific reputation, his personal attributes of modesty and gentlemanly behaviour [British spellings? see yellow highlight below], keen sense of humour, motivating character and organizational skills, led him to make not only significant contributions to mycology in general, but also to the School of Agriculture at Purdue University in particular where he ably served as department member and department head. Purdue University honoured this service in 1981 by awarding Cummins an honorary doctoral degree. His achievements also were honoured by Montana State University in 1963 (honorary doctoral degree), the Mycological Society of America, in which he held all the offices of the society (including the presidency in1946, life membership in 1967, and the highest award of the society, the Distinguished Mycologist Award in 1981), and the Banco Nacional of Mexico named him "Mencion honorifica" in 1982. **Dr. Charles Bracker**, upon his own retirement from Purdue University, held a distinguished professorship that he named the George B. Cummins Distinguished Professor Emeritus of Mycology in honour of Cummins.

Cummins grew up in Darby, Nebraska, where he graduated from high school in 1923. He received a B. S. in Botany and Bacteriology at Montana State College (1927) and became a teaching assistant under **Dr. C. H. Kaufman** at Michigan State University. After receiving his M. S. in 1928 he went to Purdue University to continue his graduate studies and assist the famous **Dr. Joseph C. Arthur**. Arthur, the foremost authority on rust fungi of his generation and first head of what is today the Department of Botany and Plant Pathology, needed a mycologist to illustrate his rust flora of North America and to continue rust research after his retirement. In his Ph.D. thesis (1935), Cummins surveyed the variation and distribution of germination pores in rust urediniospores, officially completing his degree under the direction of Dr. Ralph M. Caldwell. He remained at Purdue University for more than three decades until his retirement. He became full professor in 1947 and was head of the department from 1966 to1969. After retirement, he moved with his wife Mildred to Tucson, Arizona and became Visiting Research Professor at the University of Arizona. His student, **Dr. Joe F. Hennen**, replaced him as the third (of four) curators of the Herbaria at Purdue University who mainly worked on rust fungi, indicating the strength of the rust fungus program.

Cummins' path to Dr. Arthur and the rust fungi may have been a fortuitous accident. Nevertheless, as son of a farmer Cummins had become familiar with the economic consequences of rust infestations quite early in his life. He learned about the black stem rust problem while participating in the barberry eradication program as a student and was fascinated by the beauty of rose rust teliospores under the light microscope in a mycology-plant pathology course at Montana State University (then Montana State College). His first publication, however, was not on rust fungi but on the Discomycetes of Flathead National Forest (Papers Mich. Acad. Sc. 11: 105-115, 1930). An annotation on this publication in an unpublished short autobiography of the period before he came to Purdue University, illustrates his fine sense of humour: "This paper apparently made a great impression on the scientific world; I received not one request for a reprint and I cannot recall ever seeing my opus cited in the literature!" We are happy to report that the paper was not done in vain; the information may have been used by many, but firm documentation of one citation by S. P. Abbott and R. S. Currah (Mycotaxon 62: 1-125, 1997) provides proof of its use (ISI Web of Science Database)!

From that time on, however, it was almost all rust fungi for Cummins with his second publication (1931) describing heterothallism in corn rust and subsequent publications covering a diverse array of research on rust fungi. His Ph.D. dissertation, his monographic studies and his books on rusts of grasses, legumes and composites are milestones in the international rust literature. Because of his wealth of experience and his vivid illustrations, he has been able to synthesize and summarize a substantial amount of information on the taxonomy, nomenclature, morphology and biology in his several books, some of which continue to be standard diagnostic references for plant pathologists, mycologists, and other scientists. Cummins has published more than 480 new species, 125 new combinations, four new genera, and seven new families of rusts Cummins' contributions to Purdue University have been enormous. As Curator of the Arthur Herbarium Cummins cooperated with plant pathologists and mycologists from all over the world who sent him large collections of rust specimens for identification. He increased the collections in the herbarium (which today total more than 105,000 specimens) and maintained it as an important modern research facility attracting countless students and scientists. He integrated the herbarium into the courses he taught in botany, plant pathology and mycology and made it one of the few places in the University where archived documents preserve the history of the School of Agriculture and Purdue University. It is also thanks to Cummins' collecting and preservation activities that the specimens are well-organized and used more than ever, in recent years particu-

Continued on following page

larly by molecular biologists. Dr. Cummins donated his massive literature collection to the Purdue University Herbaria in 2000. He was optimistic that long-term support would be provided for the Herbaria. After retiring from Purdue, Cummins and his wife Mildred moved to Tucson and Cummins continued to study rust fungi in the laboratory of **Dr. Robert L. Gilbertson** as an adjunct professor at the University of Arizona. In retirement at Arizona Cummins completed more than 25 publications including 5 books! In Tucson Cummins walked about a mile to and from work to his home in a retirement community about a mile from the fungal herbarium. In addition to his work on rust fungi in Tucson, Cummins continued to charm new generations of students and visiting mycologists with his own brand of humour, sometimes expressed in direct translations into Spanish, such as the translation of navy bean soup as "frioles del mar soup" and referring to the second edition of the Illustrated Genera of Rust Fungi as "Son of Illustrated Genera."

Reaching the century mark, is a notable accomplishment, dependent primarily on good genes and luck. It is the lifetime of the accomplishments of this remarkable man, however, that we celebrate, merely using the anniversary as a reminder of the many debts owed to him by mycology. Cummins also is the last known charter member of the Mycological Society of America. We are not certain that Dr. Cummins is the oldest living mycologist, but he merits the title "Oldest Uredinologist who ever lived" having published for 73 years. The previous "record holder" was the Swiss uredinologist, Eugène Mayor (1877-1976). Unlike some flashy modern papers that are quickly surpassed by a new technique, Cummins' 73 years of publications, even the first, continue to be cited and endure in citation indexes, validating the power of the microscope and logical thought.

We wish Dr. George B. and Mildred Cummins all the best, and we are looking forward to the fourth edition of The Genera of Rust Fungi, that Cummins undoubtedly will dub "Great Grandson of Illustrated Genera."

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MSA Abstracts – The Official Report Card For 2004

For the past two years, I have had the honor of being one of the first to see the abstracts for the annual meeting as they come in through the website. This is often an interesting experience because I get to see who will be coming to the meeting and what they are currently working on. It has also fallen to me and the other committee members to proofread the abstracts and help turn them into something that our Society is proud of in its final published form. I thought that MSA members might like some feedback on how we are doing in this process. I present a short report card of what we are doing well, and what could be improved!

Content (A+) – We, of course, have the most interesting abstracts of all scientific societies.

Use of English (A) – The writing in the abstracts is usually very good. Even non-native speakers seem to get their writing proofread before submission. There were very few cases where we actually change an abstract for spelling or grammar.

Use of HTML for italics, etc. (A) – In general, it seems that most people are pretty careful about using the codes properly - turning them off and on when necessary. Hopefully we will not need to do this in upcoming years as the abstract submission process is upgraded.

Following other formatting directions (C-) – Common formatting errors include: not designating the presenting author with an asterisk, not using the last names of the authors first, not using superscripts to specify the authors' institutions, and not writing the authors names in uppercase. All of these errors require quite a bit of editing. In some cases, it was necessary to track people down by e-mail or check their affiliation in the MSA directory. Much of this could have been avoided by a simple reading of the directions!

Punctuality (C) – Some people get "A's," especially those who submitted their abstracts as soon as the web page was available in late February. Unfortunately, their score was dragged down by the more dilatory of us. Of 227 abstracts submitted for 2004, 78 were submitted on the actual due date of April 15, and 28 were submitted after the deadline. The last abstract was submitted on May 24! We were able to fit all of the abstracts into the program, but some may not be included in *Inoculum.*

These observations are offered in the spirit of fun, especially now that the task of editing the abstracts is done and largely forgotten. There is an important take-home message for next year. Please, please, please - read the directions that accompany the abstract submission page. A little extra care will save your fellow society members countless hours of tedious editing!

Jessie A. Micales-Glaeser
MSA Program Chair, 2004

Akamatsu Wins Young Scientist Award

Dr. Hajime Akamatsu, Research Associate in the Department of Plant Pathology, Washington State University was recently awarded the 2004 Young Scientist Award by the Phytopathological Society of Japan. This annual award recognizes the contributions of three scientists under the age of 35 to the field of plant pathology in Japan. Awards were presented at the Annual Meeting of the Japanese Phytopathological Society in April 2004 and abstracts of awardee research will appear in an upcoming volume of the Journal of General Plant Pathology. Dr. Akamatsu received his B.S., M.S. and Ph.D. degrees in Plant Pathology from Tottori University, Tottori, Japan.

Hajime Akamatsu

MYCOLOGICAL NEWS

Food for Thought

Each semester I teach a junior level lecture only course at the University of Georgia entitled Fungi: friends and foes. The course is jointly listed under Plant Pathology, Plant Biology and Anthropology and routinely has an enrollment of about 140 students per semester. In the course I always spend some time discussing the use of fungi as food and in food production. One of the topics I discuss is Quorn. I always encourage members of the class to buy some and give it a try. During a test review session in the class this past Spring Semester, I asked if anyone had tried Quorn yet and no one had. Without thinking, I pulled out my wallet, removed $5 and handed it to one of the students and asked him to buy some Quorn, sample it and report to the class on his thoughts regarding the product. Much to my amazement he did what I asked! Shown below is his "report" on Quorn. In my opinion, his approach was rather neat and I thought it might be of interest to the readers of *Inoculum*.

Introduction

What if someone told you that one of the healthiest things you could eat are chicken nuggets? I bet most would be pretty amazed by that statement then immediately question the merits of said testimonial. Well, there is some truth to that very proclamation. A company has invented a product called "Quorn" that not only tastes like chicken, but also has similar texture and "meatiness" of chicken. What's the catch? The product is made from the hyphae of a fungus! Many might be grossed out by this statement and immediately refuse to try the product but I implore those with open minds to give Quorn a try. You may reach the same conclusion I did. It's pretty darn tasty!

Materials and Methods

A box of Quorn brand chicken nuggets
A box of Boca brand soybean chicken nuggets
McDonald's chicken nuggets
Chick-Fil-A chicken nuggets
Some eager friends willing to help with the taste tests

Because the nuggets could be identified simply by looking at them, they first were cut up so only I would know their true identity. Each friend was then asked to close his/her eyes before eating the nuggets. Each friend tasted each brand and then provided a response regarding the taste using a ranking system of 1-4 with 1 being the best.

Results

Person 1. 1. Chick-Fil-A; 2. Boca; 3. Quorn; 4. McDonald's.
Person 2. 1. Boca; 2. Quorn; 3. Chick-Fil-A; 4. McDonald's.
Person 3. 1. Chick-Fil-A; 2. Quorn; 3. Boca; 4. McDonald's. (Person 3 commented that ALL of the nuggets were pretty darn tasty!)

Discussion

As one can see, the tasters in this experiment never saw the fungus nuggets coming! While even I preferred some other nuggets over Quorn, all tasters agreed that the Quorn nuggets weren't the crummiest nuggets they'd ever eaten! When fungal nature of Quorn was revealed to the testers, they were really surprised. Their comments included statements like "It wasn't meaty enough." "If they were thicker I would have liked them better." I too agree with these statements but, overall, I'm impressed with Quorn. So, give it a try. It's almost certainly healthier than the fast food brands and probably just as healthy as the Boca brand soybean nuggets!

Charles W. Mims
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From the 2004 MSA Program Committee

By the time you read this, the 2004 MSA annual meeting will be fast upon us! I predict that it will be a great success, and that mycologists will be talking about it for years to come! I would just like to take a few minutes to thank some key people who worked hard this year to make it so.

First and foremost is **D. Jean Lodge**, my coworker in the Center for Forest Mycology Research as well as my co-conspirator on the Program Committee. I must state here that Jean is absolutely amazing! She knows everyone and what they do. The scheduling of our sessions and posters was done entirely by Jean who worked hard to minimize conflicts and make sure that no one had to be in two places at one time. I'm afraid that I created some stress for Jean over the past year - a situation exacerbated by the unlucky coincidence that I am also her long distance supervisor in the U.S. Forest Service! Jean will do a tremendous job next year for the meeting in Hawaii. I'm sure she already has it well under control!

Michelle Momany was also a member of the Program Committee this year and was instrumental in making sure that there were two symposia dedicated to topics in molecular biology. Unfortunately Michelle has resigned from the Program Committee due to an extremely large workload in her job. I wish her the best of luck. By the time this is published, Carol Shearer will have appointed Michelle's replacement. I would like to welcome Dr. Terry Hill from Rhodes College in Memphis, TN, to the committee. He is a long time member of MSA and will do an excellent job in the coming years.

I would also like to thank **Rytas Vilgalys** and the other members of the Local Arrangements Committee with whom we worked closely. Rytas and I went to graduate school together, so it was nice to work with an "old" colleague from Virginia Tech. I learned that if there is anything worse than being Program Committee Chair, it must be Local Arrangements Chair! Rytas's student, Jeri Parrent, is working on the hardcopy program, which you will all receive at the meeting. I thank her profusely for volunteering to do this demanding job. It is really nice to see young people entering our profession who already show a dedication to the MSA.

My thanks also go to the organizers of our 2004 symposia. They have invited speakers who are at the tops of their fields. I am sure they will stimulate many interesting late night discussions and that the flow of scientific knowledge will go in both directions! I wish them safe travel and look forward to meeting all of them.

Jim Worrall, MSA Treasurer, was very helpful to me in

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explaining how things worked and keeping track of the bills. I'm afraid that I probably didn't do things exactly how he would have preferred, but hopefully we'll both muddle through on the financial end of this meeting.

And finally, a sincere note of appreciation for our sponsors and the MSA members who arranged these sponsorships. We generated over $5000 to help defray expenses of the symposium speakers this year, allowing us to invite international experts who normally would not be able to attend our meeting.

And now, after a short prayer to the Mycological Muses, I wish you all safe travel to Asheville. May the foray collecting baskets overflow!

Jessie A. Micales-Glaeser
Program Chair

Obituary: Dr. Miguel Rodriguez

An outstanding Cuban mycologist, **Dr. Miguel Rodriguez** (1949-2003) passed away on 8 November 2003 in La Habana, Cuba, after a rapid and complicated cancer problem. With his death, Latin American mycology lost one of its best mycologist. It is of great surprise the dead of Dr. Rodriguez, because he was recently in Mexico in the IV Latin American Mycological Congress in 2002, where he was invited to present a General Lecture. Dr. Rodriguez was born in La Habana, on 8th October, 1949. He earned his PhD at the University of La Habana in 1984, under the direction of Drs. Hans Kreisel and Gunter Arnold, and until his death, he was the Director of the National Botanical Garden of Cuba, where he was the editor of Revista del Jardín Botanico de Cuba. At the same time, he was the Head of the Mycological Laboratory in that Institution. His speciality was in epiphylous ascomycetes, such as the families Asterinaceae, Capnodiaceae, Meliolaceae and others, on which he published several papers. He was also Professor at the University of La Habana teaching botany and mycology, and there he published textbooks on cryptogams. In 1981, 1986, 1989 and 1992 he was a Visiting Professor in the University of Jena (Germany), and in 1998, 2000 and 2002 he was a Visiting Fellow at CAB Bioscience in Great Britain. Dr. Rodriguez organized the V Latin American Congress of Botany held in La Habana in 1990, where the Latin American Mycological Association was created. He was the first and second President of this association serving consecutive in 1990-1992 and in 1993-1996. He organized the first and second Latin American Congresses of Mycology in 1993 and 1996, respectively, both held in La Habana. Dr. Rodriguez organized the first mycological fair in Cuba, during the second Latin American Congress of Mycology. He coauthored with D.W. Minter and J. Mena the book "An annotated Checklist of Fungi the Caribbean" published in 2001.

Dr. Gaston Guzman

Obituary: Darryl William Grund

Darryl William Grund, 66, of Wolfville, Nova Scotia, Canada, and formerly of Seattle, Washington, passed away on March 18, 2004, after a long battle with multiple myeloma. On Saturday evening, April 10, a celebration of Darryl's life was held in Greenwich, NS, attended by some 300 people. While Darryl's roles as teacher and mycologist are well-known to MSA members, his many other interests may have gone unnoticed. Among them were: mountain climbing, butterfly collecting, Boy Scout leadership, ski patrol, stage manager and set designer for dance studio concerts, woodworking, sailing (included design, engineering and building of his own sailboat in his front yard), and teacher in navigation courses. Unbeknown to most, he also played the accordion and loved to party. Mycologically, he collaborated with Dr. Dan Stuntz on western *Russula* and Nova Scotia *Inocybe*, and had a twenty-year partnership with Dr. Ken Harrison on the boletes and hydnums of Nova Scotia. In 2003, he and Harrison were commemorated on a plaque set at "The Ravine" [see Inoculum 55(1): 4-5]. Never seeking prominence in MSA, he was a cordial host to itinerant mycologists, and will be missed by students and friends.

Ron Petersen

Change of Address

Send all corrections of directory information, including email addresses, directly to Allen Press

Mycological Society of America
Attn: Kay Rose, Association Manager
P.O. Box 1897 [810 E 10th St]
Lawrence, KS 66044-8897

Vox (800) 627-0629 (US and Canada)
or (785) 843-1221
Fax (785) 843-1274
Email krose@allenpress.com

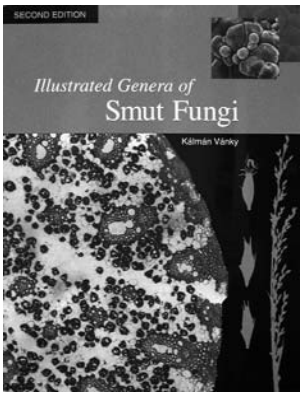
Note: Members may also submit directory corrections via the form included in the MSA directory via the MSA Home Page: www.msafungi.org

MYCOLOGIST'S BOOKSHELF

Five book reviews are presented below along with books received since April and books published in 2003 for which reviews have not yet been published. If you see a book that is of interest to you in either section, please volunteer to review it. I will send you the book to review, then you can keep it! All requests for books to review should be sent to Dr. Amy Rossman at arossman@nt.ars-grin.gov.

Illustrated Genera of Smut Fungi

ILLUSTRATED GENERA OF SMUT FUNGI. 2ND EDITION. 2002. K Vánky. American Phytopathological Society Press, 3340 Pilot Knob Road, St. Paul, MN 55121, www.shopapspress.org/ 238 pp. Price: $69.00.



This is an excellent reference that belongs in every plant disease diagnostic laboratory. The introductory section is clearly written and illustrated. It explains the development of the new classification system for the smuts, using recent molecular studies as well as the classical morphological approach. The Key to the Genera is logical and usable. Inclusion of plant host information as part of the key process is helpful. I appreciated the placement of the Glossary of Terms immediately after the key. Many users of the book will need to refer to the glossary.

As a working diagnostician, I immediately went to the Descriptions and Illustrations of Genera section. I like the use of a mixture of line drawings and photomicrographs to illustrate the symptoms and signs on the plant as well as key fungal structures. Most diagnosticians will have a plant specimen in hand and the ability to examine with a light microscope. The scanning electron micrographs are still useful. The essay for each genus includes information on geographic distribution. Diagnosticians will consult this book most frequently when they encounter unusual specimens that are not listed in other references. It will also be used in making the decision to report a newly detected of smut fungus. It would be helpful to have the known geographic distribution information in a small, clearly identified section so the reader could see if this genus is considered exotic or indigenous.

I found the index less complete than many diagnosticians might want because host plant information was not included. However, most diagnostic labs will be creating their "list of suspects" from other references, especially "*Fungi on Plants and Plant Products in the United States*". It would be useful if future editions of the book included a host list and a summary of geographic distribution information.

— Ethel Dutky
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The European Species of the Genus *Tuber* – A Historical Revision

LE SPECIE EUROPEE DEL GENERE *TUBER* – UNA REVISONE STORICA (THE EUROPEAN SPECIES OF THE GENUS *TUBER* – A HISTORICAL REVISION). 2003. A Ceruti, A Fontana and C Nosenzo. Museo Regionale di Scienze Naturali, via Giolitti, 36, 10123 Torino, Italy. Biblioteca.mrsn@regione.piemonte.it 467 pp. 45 color plates. Price: € 40 (± US $48).

This is an exceptional book. Not since Paoletti covered the genus *Tuber* in Saccardo's *Sylloge Fungorum* has anyone attempted such a comprehensive historical coverage of the taxonomy and nomenclature of the genus. Prof. Ceruti, who did not live to see the volume published, spent most of his long, professional career in study of the hypogeous *Ascomycota.* The Istituto per la Protezione delle Piante (formerly the Istituto ed Orto Botanico), the authors' institution, owns an historically unrivaled herbarium of sequestrate fungi, with collections dating back to the early 19th century, including many of Vittadini, the brothers Tulasne, and later specialists such as Oreste Mattirolo. The library of the Institute is replete with original books and papers from before Linnaeus on. This was the ideal home base for producing this book.

The book's special virtue is its complete quotation and precise literature citation of all the original descriptions of genera, species and varieties of European taxa now ascribed to the genus *Tuber*. This is an invaluable resource to those of us in the academic hinterlands, where mycological libraries contain few pre-20th century works. That resource is particularly important in the genus *Tuber,* which holds primacy in the hypogeous mycological world because of its millenia of cultural traditions. Its nomenclatural history is messy, and the literature sources are scattered in rare, early floras and journals.

The major chapter on the genus *Tuber* from the 18th to the 21st centuries provides everything needed to sort out the nomenclature of the genus, starting with Micheli's pre-Linnaean description followed by the first valid description in terms of the International Code of Botanical Nomenclature by Wiggers in 1780, the indirect sanctioning of Wiggers' description by Fries, then on through to recent molecular studies. The matter of Wiggers' description in 1780 and its presumed sanctioning by Fries

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is unfortunate. In total it reads "Fungus subglobosus succo pulposo repletus" ("Subglobose fungus filled with pulpy sap"), useless for any purpose whatsoever. But, the book does not address that and other problems revolving around the Code's principle of priority and sanctioning of names by Fries. For its purposes, that is just as well: resolution of those problems will be complicated and no doubt controversial.

The species recognized by the authors are presented in alphabetical order. Each begins with its original protolog quoted in total, including the original author's discussion, all in the original language. Then supplementary descriptions as pertinent are quoted, followed by comments of the present authors and a listing of specimens in the Institute's herbarium. After that comes a list of synonyms (more on that later); citation of other descriptions and illustrations of the species; a modern description by Ceruti *et al*. in Italian with reference to plates at the end of the book; notes on molecular analyses, habitat, seasonality, mycorrhizal hosts, and distribution; whether the species has been pure-cultured and, if so, with what tree species it has formed mycorrhizae in synthesis experiments; insects associated with fruiting bodies; history and techniques of commercial cultivation; and general observations. Wait, we are not done yet! Then the original protolog of each species earlier listed as a synonym is quoted, along with comments by Ceruti *et al*. on the reasons for the synonymization. Finally, a comprehensive and, I would think, complete or nearly complete citation of papers in which any aspect of the species is discussed. In the case of the first species, *Tuber aestivum,* that listing takes more than 14 pages, all in fine print. The total coverage of *T. aestivum* occupies 30 pages. Whew! The time and effort the authors saved for the rest of us interested in *Tuber* is huge: we owe Ceruti, Fontana and Nosenzo a profound debt of gratitude!

After the treatments of species comes an array of lists: European species, varieties and forms with their synonyms, species represented in Mattirolo's herbarium at the Institute, species placed earlier in other genera but now recognized as belonging in *Tuber,* species earlier placed in *Tuber* but now assigned to other genera, 13 more pages of general bibliography, authors of the taxa, an index of every page on which each taxon occurs and an "analytical index" of all taxa.

At the back of the book are 45 color plates with splendid reproductions of elegant, previously published paintings of *Tuber* species and photomicrographs of spores and peridial structures. The photomicrographs are generally serviceable but not always attractive, compared to those in other recent European books on hypogeous fungi. A little tweaking with Photoshop could have done wonders.

I have one caution: the synonymies listed for some species are not to be accepted without further critical study. In many cases it does not matter, because *Tuber* is rife with synonyms since the time of Linnaeus, and many of the old names are inadequately described and not represented by types. Most of my disagreements with the authors resulted from their not studying the existing holotypes of species they propose as synonyms. For example, one of the more abundant species on the Northwest Coast of North America is *Tuber gibbosum*. Along with some closely related species, it has a distinctive peridial structure unknown for any hypogeous ascomycete in Europe. Yet the authors propose it as a possible synonym of *T. foetidum* of Europe. I have studied the types of both species; they bear scant resemblance to each other, certainly not in peridial structure. Unfortunately, the photomicrographs of the peridia of the two species are inadequate to show the difference. Or, *T. murinum* is listed as a possible synonym of *T. puberulum,* even though the former has a verrucose peridium whereas the latter does not, and the latter has long, tapered dermatocystidia that are lacking on the former.

Despite those shortcomings, the positive features of this book readily justify its acquisition for any comprehensive mycological library and certainly for anyone interested in the taxonomy and ecology of *Tuber*. It is hardbound and printed on high-quality paper. At €40, it is a rarity among the premium 21st century mycological books: a true bargain.

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Fungal Populations and Species

FUNGAL POPULATIONS AND SPECIES. 2003. J Burnett. Oxford University Press, UK. http://www.oup.co.uk/ 362 pp. Price: Paperback £39.95, Hardback £80.00.

The time is rapidly approaching when a comprehensive textbook on "fungal populations" and "fungal species" will be out of reach for an individual author. Both explicit literature on these subjects and intrinsic information, i.e. work ostensibly dealing with tangential subjects such as pathogenicity, drug resistance, and systematics, but with harvestable information on populations and species, are growing so rapidly that a certain denominationalism must occur, with the general foundation left to be absorbed experientially as necessary. For chronological, scientific, societal and philosophical reasons John Burnett's book may be the last possible attempt at summarization of these complex topics. It ought to be on every mycologist's bookshelf, both for its role as a reference for professor and student alike, and because it is a well-rounded, nearly encyclopedic gathering of pertinent information.

Formalities first: Four grand divisions comprise the text: Basic Mycology (25 pp); Methodology (74 pp); Processes in Populations (134 pp); and Species and Speciation (51 pp). Subdivisions are numerous and usually short, but almost always include a principle or two plus a very few descriptions of data on

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the point. Anything more would be overwhelming.

After 40 years in mycology, I found some difficulty in following lines of evidence dealing with unfamiliar principles of fungi. Although understandably used for brevity, acronyms must be memorized and are numerous enough to require a table of their own (p. 328).

The body of the text is supplemented with a long bibliography (35 pp) which ends at about 1998, a mycological glossary, a classification schema for fungi cited in the text, and a species index. All are useful but not outstanding. It is the text that rightfully carries the volume.

In such works, there is always a "catch-22." For anyone who can understand and appreciate the middle of the text, i.e. "Selection for oligogenically determined traits relevant to agricultural situations," and "Experimental transplantation as a tool to detect selection", the section "Basic Mycology" is largely an unneeded recapitulation. For anyone requiring the primer course in basic mycology, the rest of the book may be out of easy reach. Both texts are mandatory because both audiences exist, but if Burnett's book is to be used for teaching purposes, it will be at the advanced graduate level, after the prerequisite introductory mycology and fungal genetics courses have been completed.

As a milestone synthesis of the field, the book is superior, especially coming at this pivotal juncture. As a capstone to an illustrious mycological career, John Burnett can be rightfully proud of his latest offering.

— Ron Petersen
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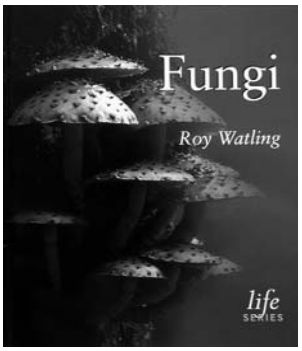
Fungi



FUNGI. 2003. R Watling. Smithsonian Institution Press, Washington, DC. 222.sipress.si.edu/ 96 pp plus numerous color illustrations. Price: $16.95

Mycologists, a rare and possibly endangered species, must welcome every new publication that aims at expanding public awareness of fungi. From the atmospheric, brooding but beautiful cover picture of *Pholiota* to the plethora of fine pictures within, this laconically titled book of just under 100 pages is eye-catching and inviting.

To give some idea of the broad coverage of the book, the chapter titles are: (1) How important are fungi? (Subsections: Fungal helpmates; Invisible providers; Evolution of fungi). (2) What is a fungus? (Subsections: A mixed bag; Types of reproduction; Reproductive organs; The major groups of fungi; How many species?) (3) The larger fungi. (4) When and where? (5) Collecting and studying fungi. (6) Fungi and humans. (7) Conservation.

The author, now retired, has wide experience collecting macrofungi around the globe, so was well-prepared to undertake this project. The book forays into many areas of mycology, and of the world, and will not fail to give the newcomer a feel for the breadth and complexity of the subject. Open-minded readers will find much to intrigue them. The color pictures are well-reproduced, and the text is at its best when dealing with fungal ecology (pp 46-56) and broaching the issues of conservation (pp 81-91). Not surprisingly, since Watling is an agaricologist, the book concentrates on macrofungi, and there is a United Kingdom slant. However, the wide range of habitats and taxa examined, the many stories of fungal relationships with other organisms, and the explanations of the vital importance of fungi in most ecosystems, should bring new converts to mycology. I can certainly recommend it to the layperson who is not too concerned with the finer points of mycology. The chapter on Conservation is particularly important, given the ongoing, worldwide losses of biodiversity resulting from human activities. The list of web sites on p.96 is a useful contemporary touch.

From the point of view of a mycologist, however, my recommendation comes with reservations. While the presentation is good, there is a regrettable lack of attention to detail. One of the most important deficiencies is that the illustrations are not numbered or comprehensively labeled, and few of the pictures are directly referred to in the text. Since introductory mycology is intensely visual, and many of the specialized terms with which the text is liberally laced really need to be illustrated if they are to be properly comprehended; this lack of cross-referencing is a serious loss that is difficult to understand, since potentially appropriate illustrations are often present.

While most of the pictures, as noted, are excellent, a few are disappointing. In addition, there are too many typos and other one-word glitches: stromalites for stromatolites (p.7); forceably for forcibly (p.11); ago for old (p.7); flagellae for flagella (p.15), and others. Since stromatolites are among the oldest traces of life on the planet, and were built by some of the earliest photosynthetic prokaryotes, it seems unlikely that fungi, being much younger eukaryotes, were contemporaneous with them (p.7). There is no mention of the *Oomycetes*, cause of potato blight, sudden oak death, etc. Although these are really members of Kingdom *Chromista* (*Stramenopila*), they are certainly much more fungus-like than the *Myxomycetes*, which are accorded a paragraph. This reviewer is unhappy that the author chose to reintroduce the term Phycomycetes (p.13) many years after it had been abandoned by most mycologists as being archaic and obsolete, since it embraces phylogenetically disparate groups. The use of the term Deuteromycetes (p.17) is also retrograde, since this

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pseudotaxon refers only to anamorphs which can invariably be ascribed to either the Ascomycetes or Basidiomycetes. The chosen definition of necrotrophs (p.26) is unusual. Most mycologists do not think of rust and smut fungi as necrotrophs, but as obligate biotrophs, for example, many smut fungi enter young seedlings, become systemic, and remain symptomless through the development of their host until the stage of the host life cycle that they exploit e.g., anther, bulb, seed. In the text, fungi are often referred to by their common names, which are only sometimes accompanied by the Latin binomials. In my opinion, the scientific names should *always* be given, if only because this reduces possible confusion. The segment on Garden Dwellers (p.54) mentions only one fungus by name, and many other sections are similarly reticent concerning the genera of fungi involved. Short lists of genera would make valuable additions to these sections.

In conclusion, it seems reasonable to suggest that this new introduction to fungi is attractive and almost comprehensive, but not entirely reliable. Perhaps a second printing will correct these minor irritants.

(Reviewer's note: This attractive, inexpensive book is such a superb introduction to the fungi that we have purchased them in bulk to give to our non-mycological student workers. Our hope is that they will at least look at the beautiful illustrations and gain some appreciation for the fungi. These books can be purchased on amazon.com for about $10 each.)

—Bryce Kendrick
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The Rainbox Beneath My Feet: A Mushroom Dyer's Field Guide

THE RAINBOX BENEATH MY FEET: A MUSHROOM DYER'S FIELD GUIDE. 2001. A R Bessette and A E Bessette. Syracuse University Press, Suite 110, Syracuse, New York 13244. syracuseuniversitypress.syr.edu ISBN 0-8156-0680x, 176 pp. Price: $24.95.

A self-described "unique how-to reference" this book gives detailed descriptions of the best methods for dying wool and silk using dyes from fungi. The emphasis is on dyeing wool. There is even a picture of a handsome gray sheep and instructions for "scouring" wool fibers to remove the lanolin before adding the dye. Recipes are provided for fixing the colors, preparing dye baths and after baths, and boiling sporocarps. It's a new kind of mushroom cookbook! Pictures demonstrate how pH affects colors, and methods are given for saddening (darkening) and blooming (brightening) the hues. This exquisitely illustrated book is printed on expensive glossy paper.

It is the fungi that receive pride of place. The book has over 200 color photographs, of which more than 150 depict fungal fruiting bodies. Bessette and Bessette use the term "mushroom" generously to encompass a variety of shelf fungi, coral fungi, earthstars, puffballs, resupinate species and even morels. Each species is identified with a Latin name, a photograph and an accurate morphological description, including habitat, spore prints and possible macrochemical tests.

In addition to all the lovely pictures of fungi, there are also whimsical photographs of crocheted hats, silk scarves, skeins of yarn, knitted vests and toy gnomes dyed with mushroom pigments. Further, there are pictures of happy people preparing the dye baths, checking for color and "swinging the skeins". Mycologists who have prized boletes solely for their delectable flavor will be pleased to discover that they also can be harvested for the tinctures they yield. An appendix gives a list of species organized by the dye color each one yields. Extracts of *Collybia iocephala* mycelia yield blue tints, *Bankera violascens* gives greens and *Chroogomplus vinicolor* gives reds, for example. Appendix C is a list of "dye duds", which are the species that yielded little to no dye when tested. Included in the duds are *Armillaria mellea, Lentinus torulosus, Morchella esculenta* and *Xylaria polymorpha*. Curiously, lichens are ignored in this book, despite their rich history as a source of pigments for textile coloring.

The Rainbow Beneath My Feet is aimed at weavers and dyers, so the excellent glossary is comprised largely of mycological terms that they will need to identify fungi. There are also definitions of terms that were unfamiliar to me. For example, Glauber's salt is sodium sulfate, "a mordant that prevents streaking and ensures even distribution of color;" and a mordant is "a chemical added to fiber that causes a certain color to bind to the fiber." "In the grease" refers to wool before it has been washed to remove the lanolin

Flipping through this field guide is a visual pleasure. It has an emotional appeal that evokes earlier times. Indeed, until the middle of the 19th century, all dyes used in textiles came from plants, animals or fungi. Important plant dyes, such as indigo, woad, saffron and tumeric, were big business and allowed textile manufactures to produce their wares in various shades of blues, reds, yellows and browns. Then came William Perkin (1838-1907). Working in his home laboratory, Perkin unsuccessfully tried to synthesize quinine from coal tar, stumbling instead on the first synthetic dye, an excellent purple that he later named "mauve". Perkin's father financed the construction of a factory devoted to the production of synthetic dyes. It was the beginning of a vast new industry. The human world became far more colorful. Industrial chemists learned how to tweak molecules, turning magenta into aniline yellow, creating a range of dazzling blues. The bright hues that were previously the rare privilege of flowers, corals and bird plumage became commonplace. Yet, after a century of living with synthetic colors, our attitudes have changed. We have learned that rivers, streams and canals near dye manufacturing plants can turn strange colors. Synthetic dyes

Continued on following page

have become serious environmental pollutants. Aesthetically, what once was seen as desirable and fashionable is now just gaudy. The subtle hues of mushroom pigments presented by Bessette and Bessette have serenity and dignity. As such, this book celebrates the revival of vanishing lost folk traditions and preserves a pre-industrial form of natural products chemistry.

My only complaint with this book has to do with the treatment of color names. "Color is so subjective," the Bessettes write at the beginning of Appendix A. "One of the most difficult tasks in writing this book was reaching agreement on the difference between green-blue and blue or green, or deciding what was gold versus brownish yellow…." They proceed to do their best, describing color ranges and using general color names. For example, under *Cortinarius cinnamomeus* the dye notes read: "No mordant, light brown; alum pinkish brown... tin-golden brown; copper-brownish green..." These color names are somewhat informative but the book would have far more value if the authors had done a little more research. They seem unaware of the various standardized color languages that have been developed by Ridgeway, Methuen and others. The National Bureau of Standards and the Inter Society Color Council developed A Universal Color Language during the 1960s, originally intended to describe the colors of drugs and chemicals. The ISCC-NBS system is useful to all who want to make concise color designations widely understandable. It would not have taken much effort to find these resources. For example, when I googled "Methuen color" the second item on the list was "an index to color concordance" from Ron Peterson's mycology home page at the University of Tennessee (fp.bio.utk.edu/mycology/Color/Color-index.htm). If Bessette and Bessette continue their interesting research in myco-dye stuffs, let us hope their future publications take advantage of this and other resources for color standardization.

In summary, if you appreciate the visually dazzling attributes of fungi, you will love this book. It makes a valuable gift for the mycophile who has everything.

— J. W. Bennett
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Books and Publications Received May – June 2004

- **Cytology and Plectology of the Hymenomycetes.** 2004. H Clémençon. Bibliotheca Mycologica vol. 199. J. Cramer. www.schweizerbart.de 488 pp. Price: € 96. Requested from publisher.
- **Cultivation and diseases of Proteaceae: *Leucadendron*, *Leucospermum* and *Protea*.** 2004. PW Crous, S Denman, JE Taylor, L Swart, and ME Palm. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands, www.cbs.knaw.nl/publications/index.htm 227 pp. Price: € 60.00. *Review needed.*
- **Dothideal dictiosporicos/Dictyospóric Dothideales**. 2004. J Checa. Flora Mycological Iberica vol. 6. J. Cramer. www.schweizerbart.de 162 pp. Price: € 58.00. *Requested from publisher*.
- **Laboulbeniales, II. *Acompsomyces-Ilyomyces***. 2003. S Santamaria. Flora Mycologica Iberica vol. 5. J. Cramer. www.schweizerbart.de 344 pp. Price: € 78.00. *Requested from publisher*.
- **Revision of the Genus *Amphisphaeria*.** 2004. YZ Wang, A Aptroot and KD Hyde. Fungal Diversity Press, Centre for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Hong Kong SAR, China. www.hku.hk/ecology/mycology/FDP.html. ISBN 962-86765-5, 168 pp. Price: $60.00. *Review needed.*

Previously Listed Books

- **The Advance of the Fungi**. 2003. EC Large. APS Press, 3340 Pilot Knob Road, St. Paul, MN 55121, aps@scisoc.org, 510 pp. Price: $69.00. *Review in progress*.
- **The Biology of Fungal Pathogens. Vol 2: Fungal Pathogens and Diseases in Cereals**. 2003. J-Alexander Vereet and H Klink (eds), APS Press, 3340 Pilot Knob Road, St. Paul, MN 55121, aps@scisoc.org, Video or DVD. Price: $99.00. *Requested from publisher*.
- **Catalogue and Bioliography of Australian Fungi 2. Basidiomycota p.p.and Myxomycota p.p.: Fungi of Australia Volume 2B.** 2003. TW May, J Milne, S. Shingles and RH Jones. CSIRO Publishing, PO Box 1139, Collingwood VIC 3066. www.publish.csiro.au. 494 pp. Price: $99.00 AU. *Review needed.*
- **Ecology of Soil Decomposition**. 2003. SM Adl. CABI Publishing, CAB International, Wallingford, Oxon, OX10 8DE, UK. www.cabi-publishing.org. 335 pp. Price: $100.00. *Review in progress*.
- **Edible and Poisonous Mushrooms of the World**. 2003. IR Hall, SS Stephenson, PK Buchanan, W Yun, and ALJ Cole. , Timber Press, Inc, www.timberpress.com, 372 pp. Price: $40.00 U.S. *Review in progress*.
- **Forest Fungi Phytogeography of China, North America, and Siberia and International Quarantine of Tree Pathogens**. 2003. M-M Chen. Pacific Mushroom Research and Education Center, P.O. Box 189326, Sacramento, CA 95818. 495 pp. Hardcopy Price: $175.00. *Review needed.*
- **Fungal Biotechnology in Agricultural, Food and Environmental Applications.** 2004. DK Arora (ed). Marcel Dekker, Cimarron Road, P.O. Box 5005, Monticello, NY 12701-5185. www.dekker.com, 509 pp. Price: $195.00. *Review in progress.*
- **Fungal Populations and Species.** 2003. J Burnett. Oxford University Press, Academic Division, Great Clarendon St., Oxford, OX2 6DP, United Kingdom,

Continued on following page

MYCOLOGIST'S BOOKSHELF

email: science.books@oup.co.uk. 348 pp. Price: Softbound £37.50, Hardbound £80.00. *Reviewed in this issue*.

- **Fungi.** 2003. R Watling. Smithsonian Books, Washington, DC. 96 pp. Price: $16.95. *Reviewed in this issue*.
- **The Fungi of New Zealand and Hga Harore o Aotearoa. Volume 3. Myxomycetes of New Zealand**. 2003. SL Stephenson. Fungal Diversity Press, Centre for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Hong Kong SAR, China. www.hku.hk/ecology/mycology/FDP.html. 238 pp. Price: $50.00. *Review needed*.
- **Fungi in Ecosystem Processes**, Mycology Series 17. 2003. J Dighton. Marcel Dekker, Inc., Cimarron Road, PO Box 5005, Monticello, NY 12701, bookorders@dekker.com, 424 pp. Price: $175.00. *Requested from publisher*.
- **Genomics of Plants and Fungi**, Mycology Series 18. 2003. R Prade and HJ Bohnert (eds), Marcel Dekker, Inc., 270 Madison Ave., New York, NY 10016, custserv@dekker.com, 440 pp. Price: $195.00. *Requested from publisher*.
- **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, 329 pp. *Review needed*.
- **Handbook of Fungal Biotechnology 2nd Edition, Revised and Expanded.** 2004. DK Arora (ed). Marcel Dekker, Cimarron Road, P.O. Box 5005, Monticello, NY 12701-5185. www.dekker.com, 592 pp. Price: $225.00. *Review in progress*.
- ***Illustrated Genera of Rust Fungi***. 2003. GB Cummins and Y Hiratsuka. APS Press, 3340 Pilot Knob Road, St. Paul, MN 5521-2097. www.apsnet.org. 240 pp. Price: $65.00. *Review needed*.
- **Invasive Species: Vectors and Management Strategies.** 2003. GM Ruiz and JT Carlton (eds). Island Press 76381 Commercial Street, P.O. Box 7, Covelo, CA 95428, www.islandpress.org, 518 pp. Price: Paperbound $40.00, Handbound $75.00. *Review in progress*.
- **Microfungi of Tropical and Temperate Palms**. 2003. JE Taylor and KD Hyde. Fungal Diversity Press, Centre for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Hong Kong SAR, China. www.hku.hk/ecology/mycology/FDP.html

MYCOLOGICAL CLASSIFIEDS

Free Journals Available

The following mycological journals are available including Mycologia 1966-present, Mycologia Index 1904-1960, TBMS/Mycological Research 1977-present, and Mycotaxon Vol 1-73. Botanical journals are American Journal of Botany 1951-1985 (vols 43-72) and El Aliso (Rancho Santa Ana Botanic Garden) Vol 1-8 (Bound), vol 9-12 (unbound). Please direct all inquiries to Bruce Tucker at tuckerb2@adelphia.net.

Free Books Available

Water-damaged copies of the book titled "*Genera of the Hypocreales*". I have five water-damaged but useable copies of the Genera of the Bionectriaceae, Hypocreaceae and Nectriaceae (Hypocreales, Ascomycetes) by Rossman, et al. 1999 available for free to whomever would find this publication useful. Please send an email to Amy Rossman at Arossman@nt.ars-grin.gov.

APS Meeting Scheduled

The 2004 annual meeting of the American Phytopathological Society will be held July 31 – August 4 in Anaheim, California. In addition to the oral and poster sessions, the annual meeting offers over 30 special sessions. Although plant pathogenic fungi will be the focus of many of these sessions, the APS Mycology Committee is organizing and co-sponsoring the following two symposia: "Co-evolution of Fungi and Plants" and "Fungal Melanins: Biology and Pathogenesis." For more information, visit the APS website at www.apsnet.org/ or contact Carol Stiles at cstiles@ufl.edu.

Mold Testing and Identification

Identification and contamination control for buildings, food technology, spawn technology, plant diseases. ASTM & Mil-Spec testing for fungal resistance of materials. 10% discount for regular and sustaining MSA members. For more information please contact Dr. Steve Carpenter at microbe@pioneer.net or by voice mail at 541.929.5984. Surface mail Abbey Lane Laboratory, LLC, PO Box 1665, Philomath, OR 97370 USA. For additional details go to www.pioneer.net/~microbe/abbeylab.html for more information.

Microbial Diversity Symposium

An International symposium on Microbial Diversity will be held during 19th -21st November 2004 at JABALPUR (M.P.) INDIA. This seminar is organized by the department of Biological Sciences of R.D. University, Jabalpur, INDIA. Research papers on microbes & agriculture/food/medicine/environment/ industry/human and animal health are invited by mycologists and microbiologists. All expanses for traveling within India and lodging and boarding are paid by the organizers. Due date for abstract submission is July 30th 2004. Contact Dr. Tara Dubey at tdubey@forensica.com <mailto:tdubey@forensica.com>, (510-887-8828 x 352) for further details to register.

African Mycological Congress

The 5th Congress of the African Mycological Association, incorporating a one-day symposium on medical mycology in Africa, will be held under the auspices of The Southern African Society For Plant Pathology during their 43rd Congress during 23-26 January 2005. Previous meetings of The African Mycological Association (AMA) were held in Mauritius, Egypt, Zimbabwe and, most recently, in Kenya in 1998. During the previous International Mycological Conference (IMC) held in Oslo, Norway an interim committee was established to revive AMA. You are therefore cordially invited to participate in the coming AMA congress, to be held at the Hartenbos Beach Resort near Mossel Bay in the Western Cape, South Africa. This meeting will also provide delegates with an excellent opportunity to attend the Southern African Society for Plant Pathology Congress (SASPP) on 23-26 January 2005 and the 4th International Workshop on Grapevine Trunk Diseases on 20-21 January.

Apart from providing African mycologists with a unique opportunity to foster collaboration and present their latest research findings, an AMA general meeting will be held to elect a new executive committee and to discuss, amongst other aspects, amendments to the Association's constitution.

REGISTRATION: Further details about the event are provided in a follow-up circular and will also be available at the following web sites: AMA, 194.203.77.69/AfricanMycologicalAssociation/; Southern African Society for Plant Pathology, www.saspp.org/list_circular.php; and Symposium on Medical Mycology in Africa, www.cbs.knaw.nl/Africafund/index.htm.

Please direct all general inquiries about the AMA and SASSP congresses to: SASPP Congress Organising Committee 2005, **Dr. Cheryl Lennox** – Chair at vredcl@plant3.agric.za or by phone at 27 (0)21 8874690-Fax: +27 (0)21 8875096

Other inquiries about the AMA congress scientific programme and General Meeting should be directed to: **Dr. Isabel Rong** at vrehir@plant5.agric.za and isabelrong@yahoo.ca or by phone at +27 (0)02 304 9569 -Fax: +27 (0)12 325 6998.

Medicinal Mushroom Conference

Fungi Perfecti, LLC, will present the **Third International Medicinal Mushroom Conference** in Port Townsend, Washington, on October 12-17, 2005. These continuing conferences bring together experts from throughout the world to promote the understanding of mushrooms in medicine and the environment. Join the leaders in this field at the historic Fort Worden Conference Center to explore the most recent innovations in medicinal mushrooms.

In the past few years, the body of evidence confirming the medicinal properties of mushrooms has expanded significantly. Researchers are discovering the mushroom genome is surprisingly complex in its molecular constituents and the manner with which they interact with human and environmental health. As sources for new antibiotics (both antibacterial and antiviral), immunomodulators, enzymes, enzyme-inhibitors and other medicines, mushrooms play a unique role in complementary therapies.

The tentative list of topics includes active constituents; biotechnological applications and mushroom products; cultivation and processing of medicinal mushrooms; distribution and ecology; ethnomycology of

Continued on following page

medicinal mushrooms; health regulations and proposals on dietary supplements; medicinal mushroom studies; mycorestoration – mycofiltration, mycoforestry and mycoremediation; nutrition; ongoing and planned clinical studies; special sessions on select medicinal species; systematics, genomics, taxonomy and culture collections; and toxicology. The program will be based on the main topics and will include keynote lectures, symposia, poster presentations and a trade exhibition.

The close proximity to the virgin Old Growth forests on the Olympic Peninsula will provide a unique opportunity of foraying into ancient woodlands at a time when mushroom season will be at its peak. Fungi Perfecti will host pre-conference Mushroom Forays on October 10 and 11. These expeditions will be led by professional mycologists with extensive knowledge of the native northwestern mushroom species.

Those intending to make presentations at the conference must submit abstracts to the Publications Committee no later than December 2004. Abstracts should be at least 500 words in length, submitted in Microsoft Word or Rich Text format (RTF) on a 3.5 inch, PC-formatted floppy disk. Abstracts approved by the Publications Committee will be included in the International Journal of Medicinal Mushrooms in 2005. **Send your abstracts to Solomon P. Wasser of the Haifa University Institute of Evolution at spwasser@research.haifa.ac.il.**

Registration fee for the conference is $600 per attendee for check or money order transactions, $610 for credit cards and $630 for bank wires. Fungi Perfecti is offering advance registration pricing of $500, $510 and $530 per attendee until January 3, 2005. This fee does not include food or lodging. A limited number of discounted student registrations will be made available in due course.

For more information or to register, contact Fungi Perfecti: by mail at P.O. Box 7634, Olympia, WA 98507, USA; via the Internet at the IMMC section of our Web site at www.fungi.com; by telephone at 800-780-9126; or by email at mycomedia@aol.com.

Trichoderma and the Environment

The 8th International Workshop on *Trichoderma* and *Gliocladium* will be held in Hangzhou, China on 20-23 September, 2004 and is organized by Zhejiang University, China and Mycological Society of China. This workshop will incorporate the International Subcommittee of Trichoderma and Hypocrea Annual meeting of 2004.

On behalf of the Organizing Committee of the 8th International Workshop on Trichoderma and Gliocladium, we take great pleasure in extending an invitation to you to visit Hangzhou in September 2004. We are honored to organize for the first time the workshop in an Asian country.

We look forward to hosting as many of you as possible for an inspiring exchange of ideas and information with focus of the Workshop topic: TRICHODERMA AND THE ENVIRONMENT. The scientific program will contain several sessions: Diversity and Systematic, Role in Natural Ecosystems, Applications and Biotechnology in Agriculture and Industry, Proteomics and Genomics, and Trichoderma in Developing Countries. In addition, we will offer the opportunity to enjoy site-seeing tours in the beautiful West Lake region and visit many cultural highlights of Hangzhou and Zhejiang Province.

We warmly invite all of you to Hangzhou for an exotic and exciting scientific and cultural experiences. Please contact **Prof. XU, Tong,** Department of Plant Protection and Institute of Biotechnology, College of Agriculture and Biotechnology, Zhejiang University, (www.zju.edu.cn), Hangzhou 310029, CHINA or at xutong@zju.edu.cn. You can call at the number 86-571-86971208-Fax: 86-571-86046615.

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For further information, see www.mycological-progress.com or contact Reinhard Agerer, president of the German Mycologcial Society

Recent Graduate

Ameena Nalim received her Ph.D degree in Plant Pathology from Pennsylvania State University in May 2004 under the direction of David M. Geiser, Associate Professor and Director of the Penn State Fusarium Research Center. Her dissertation is titled "Studies in Molecular Phylogenetics of *Fusarium* species." She received her B.S from Cornell University and M.S in Plant Pathology from Texas A&M University. Ameena will be teaching at The American University of Sharjah, UAE, in the fall and spring before returning to the United States.

Books For Sale

Flora Agaricina Danica – original edition is for sale. The five volumes original edition in a bound edition. Any reasonable offer above 2000 US dollar is considered. Last known time on market was in 1993 at US dollar 2100. Please write to Leif Ryvarden at leif.ryvarden@bio.uio.no.

MYCOLOGY ON-LINE

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

Asociacion Latinoamericana de Micologia (51-5)
www.alm.org.br

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

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

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

Bibliography of Systematic Mycology (51-6)
194.131.255.3/cabipages/BSM/bsm.htm

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

Cordyceps Website
www.mushtech.org

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

European Powdery mildews (52-2)
nt.ars-grin.gov

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

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

Hadrianus Junius Stinkhorns (52-2)
www.collectivesource.com/hadrianus

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

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

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

Interactive Catalogue of Australian Fungi (52-1)
www.rbgmelb.org.au/fungi/

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

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

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

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

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

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

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

Pathogenic Fungi From South Africa (52-4, page 29)
nt.ars-grin.gov/fungaldatabases/southafrica or **www.saspp.co.za/**

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

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

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

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

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

CALENDAR OF EVENTS

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

2004 (August 16-22)
Root and Butt Rots of Forest Trees. 11th International Conference on Root and Butt Rots. IUFRO WP 7.02.01.
Poznan, Bialowieza, POLAND
Pietro Lakomy
plakomy@owl.au.poznan.pl

2004 (September 13-15)
British Mycological Society Annual Scientific Meeting
DETAILS: *Inoculum* 55(3):30
University of Nottingham, UK
John Peberdy
John.peberdy@nottingham.ac.uk
www.britmycolsoc.org.uk/meetings/scientific.asp

2004 (September 26- October 2)
International Fusarium Laboratory Workshop
Pretoria, SOUTH AFRICA
Forestry and Agricultural Biotechnology Institute
Teresa A. Coutinho
University of Pretoria
Department of Microbiology and Plant Pathology
+27-12-420 3934 (phone)
+27-12-420 3960 (fax)
teresa.coutinho@fabi.up.ac.za
fabinet.up.ac.za/fusarium

2004 (October 20-24)
First International Fungal Proteomics Symposium
Hotel Vintage Plaza, Portland, OR
Scott Baker
Matt Sachs
scott.baker@pnl.gov
msachs@ebs.ogi.edu
http://www.fgsc.net/2004proteomicsflyer.jpg

2004 (November 14-19)
IV Asian Mycological Congress and IX International Marine and Freshwater Mycology Symposia
DETAILS: *Inoculum* 55(3):30
Chiang Mai, THAILAND
www.thai.net/amc4imfms9ex/index.htm

2004 (November 19-21)
International Symposium on Microbial Diversity
DETAILS: *Inoculum* 55(4):50
Jabalpur (*M.P.*), *India*
Tara Dubey
tdubey@forensica.com

2005 (March 15-20)
23rd Fungal Genetics Conference at Asilomar
Asilomar Conference Center, Pacific Grove, CA
www.fgsc.net/asil2005/asil2005.htm

2005 (March 19-20)
SouthEastern Regional Yeast Meeting (SERYM)
Georgia Institute of Technology, Atlanta, GA
Yury Chernoff
yury.chernoff@biology.gatech.edu

2005 (June 3-6)
Sixth International Meeting on Genetics and Cellular Biology of Basidiomycetes (GCBB VI)
DETAILS: *Inoculum* 55(3):31
Pamplona, SPAIN
Antionio G. Pisabarro
gpisabarro@ybavarra.es

2005 (June 12-16)
XII International *Sclerotinia* Workshop
Monterey, CALIFORNIA
Steven Koike
831.759.7350
stkoike@ucdavis.edu
entoplp.okstate.edu/iswg/index.html

2005 (June 24-28)
6th International Conference on Cryptococcus and Cryptococcosis
Boston Marriott Long Wharf, *Boston, MA*
Stuart M. Levitz
cme@bu.edu
www.bu.edu/cme/iccc.html

2005 (July 30 - August 5)
2005 MSA Annual Meeting
University of Hawaii in Hilo
Hilo, HAWAII

2005 (August 15-19)
International Congress on the Systematics and Ecology of Myxomycetes V
DETAILS: *Inoculum* 54(6):21
Tlaxcala, MEXICO
Arturo Estrada Torres
arturomixo@hotmail.com

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

inoculum

The Newsletter of the Mycological Society of America

Supplement to Mycologia
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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 Times font), on disk (MS Word 6.0, WordPerfect, *.tif. *.jpg), or hard copy. Line drawings and sharp glossy photos are welcome. The Editor reserves the right to edit copy submitted in accordance with the policies of *Inoculum* and the Council of the Mycological Society of America.

Richard E. Baird, Editor
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