

Newsletter of the Mycological Society of America

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— Important Dates —

August 15 Deadline:
Inoculum 56(5)

July 23-28, 2005:
International Union of
Microbiology Societies
(Bacteriology and
Applied Microbiology,
Mycology, and Virology)

July 30-August 5, 2005:
MSA-MSJ, Hilo, HI

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

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Fungal Cell Biology: Centerpiece for a New Department of Microbiology in Mexico

By Meritxell Riquelme

With a strong emphasis on Fungal Cell Biology, a new Department of Microbiology was created at the Center for Scientific Research and Higher Education of Ensenada (CICESE) located in Ensenada, a small city in the northwest of Baja California, Mexico, 60 miles south of the Mexico-US border.

Founded in 1973, CICESE is one of the most prestigious research centers in the country conducting basic and applied research and training both national and international graduate students in the areas of Earth Science, Applied Physics and Oceanology. Just 2 years ago a new Experimental and Applied Biology Division was created under the direction of Salomon Bartnicki-Garcia, who retired after 38 years as faculty member of the Department of Plant Pathology at the University of California, Riverside and decided to move south to his country of origin to create a Division in an area that was not developed at CICESE. The Experimental and Applied Biology Division is

Continued on following page



Current members of the Department of Microbiology with the Ensenada bay in the background as seen from CICESE. Back row, left to right: Miriam Hernández (secretary of the DBEA) and researchers Ernestina Castro-Longoria, Rosa Mouriño-Pérez, Salomon Bartnicki-Garcia, and Meritxell Riquelme. Front row seated, left to right, students: Eddy Sánchez León-Hing, Raul C. Baptista, Cynthia Araujo Palomares, Ivan Galván and Alejandro Beltrán Aguilar.



Fungal foray in the Chichihuas forest (road from Ensenada to Tijuana) with UABC Mycology students during raining season (It does rain from time to time in Baja!).

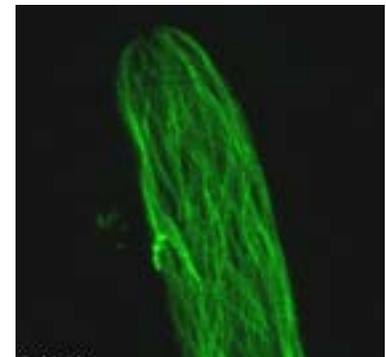
composed of 3 Departments (Microbiology, Marine Biotechnology and Conservation Biology).

The Department of Microbiology gives an opportunity to young investigators to develop independent research projects under the unifying theme of Fungal Cell Biology. Although government funding for research in Mexico is less generous than in other countries, the Department is equipped to conduct both molecular studies and cell biology projects (video-microscopy, confocal microscopy and transmission electron microscopy) and is scheduled to move into a new building this year. An initial core of 4 researchers composes the Department: Salomon Bartnicki-Garcia (Mathematical and computer-assisted modeling of fungal growth), Rosa Mouriño-Perez (The fungal microtubular cytoskeleton), Ernestina Castro-Longoria (Cellular basis of the circadian

rhythm in *Neurospora*) and Meritxell Riquelme (The secretory pathway in filamentous fungi).

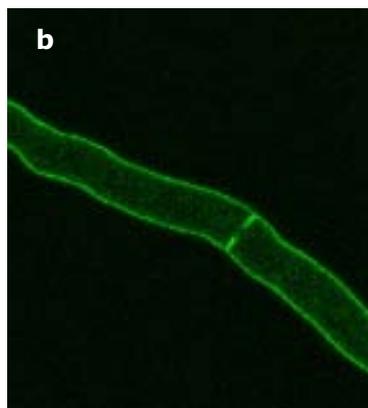
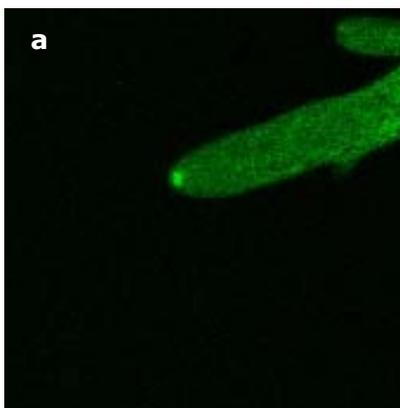
A major aim of the Department is to promote International Research Cooperation. The proximity to the US makes it practical to establish close links with US researchers. We already have ongoing projects with colleagues of the University of California, Arizona State University, the University of Oregon and Massachusetts Institute of Technology. The Department has also established strong links with local institutions, such as the Autonomous University of Baja California (UABC) and the National Institute for Forest and Agricultural Research (INIFAP). We participate in undergraduate Mycology courses at the UABC.

For further information and current openings please visit the websites www.cicese.mx and microbio.cicese.mx/.



Immunolocalization of microtubules in a chemically fixed cell of *Sclerotium rolfsii*. (R. Mouriño-Pérez)

Questions or comments should be sent to Meritxell Riquelme Pérez, Departamento de Microbiología, DBEA, CICESE, Km. 107 Carretera Tijuana-Ensenada, 22860 Ensenada, Baja Califo. Email: riquelme@cicese.mx



Molecular tagging of proteins involved in hyphal growth and morphology with GFP. Laser scanning confocal micrographs of growing hyphae of *N. crassa* with a) a fluorescent Spk; c) fluorescent plasma membrane. (M. Riquelme)

Cordyceps Diversity in Korea

By Jae-Mo Sung, Bhushan Shrestha, Sang-Kuk Han, Su-Young Kim, Young-Jin Park, Won-Ho Lee, Kwang-Yeol Jeong, Sung-Keun Choi

Cordyceps is traditionally known as a highly medicinal mushroom in oriental society of Asia. It is quite diverse in its morphological characters, host range, natural habitat, etc. Due to contrast climatic variation and its unique geographical position, *Cordyceps* diversity is rich in Korea. Research on *Cordyceps* of Korea during last 20 years has shown that some species are widely distributed, while others grow in specific locations. Maturation periods of stromata range from late spring to summer till early autumn every year. Most species show their host specificity, but few species grow in diverse hosts. Microscopically, *Cordyceps* species differ in their spore shape, size, and their conidiation nature.

There are about 300-400 *Cordyceps* species all over the world and are distributed universally (Kobayasi, 1982; Kobayasi and Shimizu, 1983; Sung, 1996). Species of *Cordyceps* (Clavicipitaceae, Hypocreales, Ascomycota) grow inside insect host bodies as endosclerotium during winter and produce stromata in summer. Hosts of *Cordyceps* species include different stages of insect life cycle ranging from larva to adult of different insect orders, bee, wasp, cicadae, beetle, etc., except few which grow on hypogeous *Elaphomyces* species. Their scientific study and cultivation have been done in Korea for a long time. Every year, entomopathogenic fungal specimens including *Cordyceps* species are collected from different parts of Korea and are air-dried and preserved along with their isolates in Entomopathogenic Fungal Culture Collection (EFCC), Kangwon National University, Korea (Sung, 2004). The specimens are identified on the basis of their morphological characters.



Fig. 1. *C. militaris*



Fig. 2. *C. bifusispora*

Continued on following page



Fig. 3. *C. gracilis*



Fig. 4. *C. longissima*

Cordyceps species are collected from different parts of Korea every year from early May to late October. *Cordyceps* species, such as *C. militaris* (Fig. 1), *C. pruinosa* and *C. sphecocephala* are frequently collected, while *C. bifusispora* (Fig. 2), *C. gracilis* (Fig. 3), *C. heteropoda*, *C. longissima* (Fig. 4), *C. nakazawai*, *C. ochraceostromata*, *C. pentatomi*, *C. ramosopulvinata* (Fig. 5), *C. rosea*, *C. scarabaeicola*, *C. staphylinidaecola* and *C. yakushimensis* are moderate or rare in distribution. Ascospores are discharged from fresh specimens and observed for their morphology and germination by staining with cotton blue in Lactophenol. Ascospores are inoculated in nutrient agar media in test-tubes and incubated till profuse mycelium growth occurs. Original isolates and their sub-cultures are preserved at 4C in Entomopathogenic Fungal Culture Collection (EFCC), Kangwon National University, South Korea. Specimens are air-dried and preserved in herbarium boxes.

It is very interesting to observe ascospore morphology and their germination behavior of different *Cordyceps* species. Among the observed species, only few such as *C. bifusispora* and *C. pruinosa* produced filamentous ascospores with threads in the center, while the remaining produced filamentous ascospores with continuous part-spores throughout the length. The germination rate of *C. bifusispora*, *C. militaris*, *C. pentatomi*, *C. pruinosa*, *C. scarabaeicola*, *C. staphylinidaecola* were found faster, while those of *C. gracilis*, *C. heteropoda*, *C. longissima*, *C. nakazawai*, *C. ochraceostromata*, *C. ramosopulvinata*, *C. rosea*, *C. sphecocephala*, *C. yakushimensis* were found slower. Microscopic figures of ascospores are shown in sides of each figure of different *Cordyceps* species. *C. militaris* and *C. pruinosa* developed conidia on germinating hyphae soon, showing microcyclic conidiation character. *Cordyceps* isolates vary in their growth speed and cultural characteristics. Stromata of different *Cordyceps* species, such as *C. militaris*, *C. scarabaeicola*, *C. pruinosa* have been successfully produced in brown rice medium.

References: Kobayasi, Y. 1941., Sci. Rept. Tokyo. Bunrika, Daigaku Sect. B. 5:53-260; Kobayasi, Y. 1982. Trans. Mycol. Soc. Japan. 23:329-364; Kobayasi, Y. and D. Shimizu. 1983. Hoikusha Publishing Company Ltd. Osaka. 280 pp.; Sung, J.M. 1996. Kyo-Hak Publishing Co. Ltd., Seoul. 299 pp.; Sung, J.M. 2004. Inoculum 55(4):1-3.

Questions or comments should be sent to Jae-Moe Sung, Entomopathogenic Fungal Culture Collection (EFCC), Department of Applied Biology, Kangwon National University, Chuncheon 200-701, South Korea. Email: cordyceps@nate.com.



Fig. 5. *C. ramosopulvinata*

MSA ABSTRACTS

From the President's Corner ...

Dear Friends and Colleagues,

The success of the Mycological Society of America depends heavily on the volunteer contributions of its members. We are always looking for volunteers who would like to be involved in the various functions of the society, and there are many of them from annual meeting preparations to specialized committees on subdisciplines within mycology. The list of committees is on the MSA website. We need to hear from you if you would like to participate in some

way. Whether there is a topic in which you would especially like to be involved or whether you would just like to contribute in some way, please consider volunteering. Send and email or talk to me or Vice President **James Anderson** or Secretary **Faye Murrin** and let us know your interest. Participating on a Society committee is a great way to get to know the society and even a small contribution of your time and energy will be very helpful to the Society.



David J. McLaughlin,
MSA President

MSA Secretary Email Express

Council completed five email polls since my May report and approved the following:

- Poll 2005-3. Editor-in-Chief Donald Natvig nominated **Dr. Robby Roberson to serve as Mycologia Associate Editor** for the term 2005-2007. *Approved.*
- Poll 2005-5. It was moved by President McLaughlin and seconded by Secretary Murrin that Executive Council approve a **further increase of \$4000 for the MSA Student Mentor Travel Awards for Hilo**, to be awarded from income from the Uncommitted Endowment Fund. *Approved.* **Background:** The MSA had previously allotted an increased amount for Student Mentor Travel Awards this year, from approximately \$4000 to \$10,000, based on the anticipated increased costs of travel for the Hilo meeting. The Mentor Travel Awards Committee received 38 applications this year, which appears to be a record number. The increase approved here allowed for an additional 5 students to be funded for a total of 18 students. MSA coordinated efforts with **Deep Hypha**, the NSF-funded Research Coordination Network (RCN), which also awarded travel funding for Hilo.
- Polls 2005 6-8: *Approved.* These motions concerned the approval of the Honorary Member and MSA Fellows for 2005 following recommendations by **George Carroll**, Chair of the Honorary Awards Committee, and one other special award. Due to the confidential nature of these decisions until they are announced at the Annual Business Meeting in Hilo, August 3rd, they will not be reported on fully until the next issue of *Inoculum*.

New Members: The MSA extends a warm welcome to all new (and returning) members. New memberships will be formally approved by the Society at the Annual Business Meeting in Hilo, Hawaii (Aug 3rd, 2005).

- Australia: Susanna Ann **Driessen**, Kelli Maria **Gowland**

- Canada: Melissa **Day**
- Ghana: Hubert D **Nyarko**
- Hong Kong: Justin **Bahl**, Wing Yan **Chum**
- Japan: Yuko **Ota**
- Mexico: Cristina **Medina**
- United States: Anabelle **Aranda**, Kelly D **Craven**, Jennifer M. **Davidson**, Joyce **Eberhart**, Javesh **Garan**, Michele Therese **Hoffman**, Bradley Warren **Miller**, Anil Kumar H **Raghavendra**, Kim **Ryall**, Marian N **Viveros**, Sandra W **Woolfolk**

Emeritus membership: There has been one new application for emeritus membership: **L J Wickerham** of Tucson, Arizona. Emeritus memberships will be formally approved by the Society at the Annual Business Meeting in Hilo, Hawaii (Aug 3rd, 2005).

Faye Murrin
MSA Secretary
fmurrin@mun.ca



Canine Foray — Faye Murrin's dog, Rosie, protects the catch from mushroom bandits.

MSA ABSTRACTS

Aaltonen, Ronald E.*, Barrow, Jerry R., Lucero, Mary L., Osuna-Avila, Pedro and Reyes-Vera, Isaac. USDA-ARS Jornada Experimental Range, Las Cruces, NM 88003, USA. jbarrow@nmsu.edu. **The microscopic identification of vertically transferred symbiotic fungi intrinsically integrated with cells, tissues and organs of host plants.**

Dual staining methodology and analysis with light microscopy and scanning electron microscopy were used to determine the nature and extent of symbiotic fungi with native desert grasses shrubs. Trypan Blue that targets fungal chitin and sudan IV that targets lipid bodies attached to fungal structures were used to stain cleared roots and leaves. Trypan blue revealed a densely stained fungal network, bound to the plasmalemma of meristematic cells, that were transferred to cells in culture, tissues and all plant organs. Fungal structures were atypical and were substantially different than commonly observed fungal structures such as hyphae, spores, etc. Fungal associations with meristem cells facilitate their distribution and vertical transfer to all parts of the plant, seed and to succeeding generations. Significant are fungal associations with vascular tissue, photosynthetic cells and with the stomatal complex and suggests significant plant-fungus interactions within these critical plant cells. poster

Abdelzaher, Hani M. A. Faculty of Science, El-Minia University 61519, Egypt. abdelzaher@link.net. **Biological control of damping-off and root rot diseases of soybean caused by *Pythium spinosum* Sawada var. *spinosum* using three rhizosphere species of soil fungi.**

Pythium spinosum was isolated from rhizosphere soil and rhizoplane of healthy and infected soybean roots cultivated in an agricultural field located in Shaheen district, El-Minia city, Egypt in June 2003. Rhizosphere and rhizoplane mycoflora isolated from the same sites were tested for their antagonism toward *Pythium spinosum* in agar plates. Among the isolated fungi, *Aspergillus sulphureus*, *Penicillium islandicum* and *Paecilomyces variotii* were chosen according to their antagonism on agar plates for experimentation to test their effectiveness for biological control in either autoclaved or nonsterilized soil. Coating soybean seeds and roots with spores and mycelia of these three antagonists gave germinating seeds and seedlings a very good protection from root-rot, pre- and post-emergence damping-off caused by *P. spinosum*. Applying these biocontrol agents to autoclaved and nonsterilized soil infested with *P. spinosum* provided an excellent way of protection. contributed presentation

Abe, Jun-ichi P. University of Tsukuba, Graduate School of Life and Environmental Science, 1-1, Tennoudai 1 chome, Tsukuba, Ibaraki 305-8572, Japan. jave@sakura.cc.tsukuba.ac.jp. **An arbuscular mycorrhizal genus in the Ericaceae.**

Enkianthus is an ericaceous genus with about 17 spp. of shrubs and small trees, commonly distributed in Japan and southern China. Four Japanese native species of the genus *Enkianthus* (*E. campanulatus*, *E. cernuus* f. *rubens*, *E. perulatus*, *E. subsessilis*) were examined to determine the mycorrhizal status by comparing with typical ericoid mycorrhizal roots of *Rhododendron kaempferi*. The roots of all species were collected from trees of natural stands or public gardens and from seedlings of *E. cernuus* f. *rubens* grown in controlled conditions. These roots were observed with a compound light microscope and SEM. All examined roots of *Enkianthus* spp. formed only arbuscular mycorrhiza of the *Paris*-type. The fine roots of these species were usually thicker (approx. 150 μ m) than the hair roots of *R. kaempferi* (approx. 80 μ m). Short root hair-like structures with thick walls (approx. 5 μ m) were observed occasionally on the fine roots of all *Enkianthus* spp. and root hairs were observed in *E. subsessilis*. Consequently, the mycorrhizal and root morphology of these four species are completely different from *R. kaempferi*. This result reveals that at least these four species of *Enkianthus* seem to be arbuscular mycorrhizal and lack ericoid mycorrhiza. These findings and the mycorrhizal status of the ancient ericaceous species are discussed. contributed presentation

Aime, M. Catherine. USDA-Agricultural Research Service, Systematic Botany & Mycology Lab, Beltsville, MD 20705, USA. cathie@nt.ars-grin.gov. **Molecular systematics of Uredinales.**

Rust fungi (Basidiomycota, Uredinales) consist of > 7000 species of obligate plant pathogens that possess some of the most complex life cycles in the Eumycota. Traditionally, phylogenetic inference within the Uredinales has been hampered by a lack of morphological characters and incomplete life cycle and host-specificity data. The application of modern molecular characters to rust systematics has been limited by several factors, including, to name a few, the inability to pure culture most rusts or unequivocally separate rust from host cells and other associated fungi in a specimen. Previous molecular systematic studies of rusts have focused on analyses of 28S or 18S ribosomal DNA, but current contradictions in rust systematics, especially in the deeper nodes, have not yet been resolved. In this study, several genes (including 18S, 28S, and EF1 α) were examined across the breadth of the Uredinales to resolve systematic conflicts and provide a framework for the group. It is concluded that morphology alone is a poor predictor of rust relationships at most levels and strict morphology-based classifications and species-delimitations appear obsolete. Host selection, on the other hand, has played a significant role in rust evolution. The difficulties and utility of analyzing protein-coding genes vs. rDNA in rust systematics are also discussed. symposium presentation

Aime, M. Catherine^{1*} and Henkel, Terry W.² ¹USDA-Agricultural Research Service, Systematic Botany & Mycology Lab, Beltsville, MD 20705, USA, ²Hum-boldt State University, Dept. of Biological Sciences, Arcata, CA 95521, USA. cathie@nt.ars-grin.gov. **Strategies for bioinventory: lessons from Guyana.**

Bioinventory, the identification and enumeration of taxa within a given area, provides the foundation for numerous biological and ecological studies. Yet fungal inventories are vastly underrepresented in the literature, and the conduction of such inventories presents a host of unique difficulties and problems. Special problems faced in conducting fungal inventories include deciding at which level to record units (e.g., fruiting bodies, cultures, and/or environmental sequences); how to construct significant sampling strategies (e.g. plot studies, transects, and/or sweeps); and, especially, how to conduct the alpha-taxonomy. We have completed five years of comparative plot studies for fungi in a remote, rain-forested region of west-central Guyana. To date we have documented nearly 1,000 species or morphospecies of macromycetes, both ectomycorrhizal and saprotrophic, and counted >20,000 fruiting bodies. Yet the most time-consuming aspect of this study is the taxonomy. To date, we have been able to identify and publish less than 10% of the Guyanese taxa; > 40% of these have been species or genera new to science. Some ideas for recording, analyzing, and identifying fungal taxa from previously under-sampled areas will be discussed. symposium presentation

Akamatsu, Y. and Saikawa, Masatoshi*. Department of Environmental Science, Tokyo Gakugei University, Koganei-shi, Tokyo 184-8501, Japan. saikawa@ugakugei.ac.jp. **Giant mycelium by *Sommerstorffia spinosa*.**

Since 1984, *Sommerstorffia spinosa* was obtained several times from samples of debris floating on the water of a fire reservoir located in the campus of Tokyo Gakugei University. The species has been known as a rotifer-parasite, to have the ability to capture the animals with a peg, a distal narrow protuberance of hypha, or to parasitize them with a bowling-pin shaped sporeling developed from an encysted, secondary zoospore. In all the strains reported up to now, each of the isolates finished capturing animals after 3 to 7 times of capture by the peg and became solely to produce zoospores. Thus the mycelium was quite limited in size in all cases. However, in spring, 2004, we obtained a strain of the species, the mycelium of which did not finish capturing rotifers (*Lepadella oblonga*) and grew unlimitedly to establish a giant mycelium. At 30 days of cultivation under water, it could be seen with a naked eye, because the size being 0.5-3.0 mm in diameter. The hyphae (7-9 μ m wide) constituting the giant mycelium were empty except only their distal portion terminated with a peg (6-8 μ m long, 3-5 μ m wide). After capturing a rotifer, the peg grew into an endozoic thallus that developed one or two hyphae externally and transformed itself into a zoosporangium with an evacuation tube (50-80 μ m long, 8-10 μ m wide). The primary zoospores encysted at the mouth of the evacuation tube to form a mass of cysts (7-9 μ m). In normal strains, each of the primary cysts soon produces a secondary zoospore, though the cyst of our strain did not produce it, but lost its content, or, in rare occasion, developed a sporeling (ca. 17 μ m long, 8 μ m wide). The giant mycelium of our strain also captured two testaceous rhizopods of *Cryptodiffugia* and *Euglypha*. contributed presentation

Almeida-Leñero, Lucia¹, Ludlow-Wiechers, Beatriz¹, Geel, Bas van², González, María C.^{3*} and Aptroot, André.⁴ ¹Dept. Ecología y Rec. Nat. Fac. Ciencias, UNAM, Mexico DF 04510, ²IBED, Paleocology and Landscape Ecology, Univ. Amsterdam Kruislaan 318, 1098 SM Amsterdam The Netherlands, ³Inst. Biología, UNAM, Mexico, ⁴Centraalbureau voor Schimmelcultures (CBS), Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands. mcgv@ibiologia.unam.mx. **Records of mid-Holocene fungi from Lake Zempoala, Central Mexico.**

The aim of the present study is to describe and illustrate fungal spores recorded on Zempoala lake at 2800 m altitude. The studied interval is of mid-Holocene age. The lake with submerged aqual and hydrosal shore vegetation, lie today in the *Abies religiosa* dominated forest belt. The samples were prepared using standard techniques for palynological studies. A number of selected fungal spores have been identified, described and illustrated. Ecological environmental preferences of present fungi are also given. Among the fungi type spores analysed are 2 basidiospores: *Entorrhiza* (type 527), and *Urocystis*, 3 ascospores: *Astrosphaeriella*, *Ustulina*, *Valsaria*, and 10 mitospores: *Acrodictys*, *Antennatula*, *Brachydesmiella*, *Endophragiella*, *Monodictys*, *Trichocladium* type 1 and 2, *Papulospora*, and *Virgatospora*. These fungus occur together with pollen elements that define a landscape of forest and a water body. *Antennatula* confirm an *Abies* sp. forest, *Acrodictys* suggests species of *Populus* sp., *Virgatospora* of broad leaved tree forest, and *Ustulina* the presence of deciduous trees. *Entorrhiza*, and *Trichocladium* are evidence of freshwater. Environment conditions may be presumed of high air humidity considering the presence of decaying plant debris and soil forming fungi such as *Monodictys* and *Papulospora*. The fungi were recorded for first time in paleoecological studies in Mexico. poster

An, Zhiqiang. Merck Research Laboratories, West Point, PA, USA. **Polyketide synthase genes in the pneumocandin-producing fungus *Glarea lozoyensis*.**

Glarea lozoyensis is the producer of pneumocandin B0, a potent inhibitor

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MSA ABSTRACTS

of fungal glucan synthesis. This industrially important filamentous fungus is slow-growing, is very darkly pigmented, and has not been easy to manipulate genetically. Using a PCR strategy to survey the *G. lozoyensis* genome for secondary metabolic encoding pathways, we have identified three polyketide synthase genes: pks1, pks2, and pks3. pks1 encodes a 2,124 amino-acid protein with five catalytic modules: ketosynthase, acyltransferase, two acyl carrier sites, and thioesterase/Claisen cyclase. Pks2 encodes a 1,791 amino-acid protein with five catalytic modules: α -ketosynthase (KS), acyltransferase (AT), dehydratase (DH), α -ketoacyl reductase (KR), and acyl carrier protein (ACP). The pks3 gene acts as an operon and encodes two enzymes, PKS3-NRPS1 and NRPS2. Cluster analysis of 37 fungal ketosynthase modules grouped the pks1p with PKSs involved in 1,8-dihydroxynaphthalene melanin biosynthesis; the pks2p with PKSs involved in 6-methylsalicylic acid biosynthesis; and the pks3p was grouped with PKSs that synthesize structurally and bioactively complex polyketides. An *Agrobacterium*-mediated transformation system was developed for the disruption of these three pks genes. Disruption of pks1 yielded knockout mutants that displayed an albino phenotype, suggesting that pks1 encodes a tetrahydroxynaphthalene synthase. Heterologous expression of pks2 in *Aspergillus nidulans* showed that pks2 encodes for 6-methylsalicylic acid synthase. Disruption of pks3 showed no difference in chemical profiles under the fermentation conditions used. Other genes reside in the three pks loci will also be discussed. symposium presentation

Anagnost, Susan E.^{1*}, Catranis, Catharine M.², Fernando, Analie A.¹, Morey, Shannon R.¹, Zhou, Shuang¹, Zhang, Lianjun³ and Wang, C.J.K.⁴ ¹Wood Products Engineering, SUNY College of Environmental Science and Forestry, Syracuse, NY 13210, ²American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110 USA, ³Forest and Natural Resources, SUNY-ESF, Syracuse, NY, ⁴Faculty of Environmental and Forest Biology, SUNY-ESF, Syracuse NY 13210, USA. seanagno@esf.edu. **Aeromycology of homes in Syracuse, New York.**

Airborne fungi were recovered at 103 homes in Syracuse, New York as part of an environmental survey of homes of infants predisposed to asthma (EPA project No. R-82860501-0). Total colony-forming units per cubic meter of air (CFU/m³) and isolate identifications were obtained from samples collected with the Andersen N6 sampler. Samples collected on two consecutive days, indoors and outdoors, during 147 visits to these homes yielded 14565 isolates that were classified into 170 fungal taxa. Among the most frequent were Hyaline unknowns, *Cladosporium cladosporioides*, *Penicillium* spp., *Aspergillus* spp., basidiomycetes, *Cladosporium herbarum*, and *Alternaria* spp. *Aspergillus* spp were more frequent indoors (547 isolations) compared to outdoors (59 isolations), as were *Penicillium* spp (771 indoor, 137 outdoor). The total CFU/m³ was greater during the summer and fall seasons; certain species only appeared during summer and fall. Three new records for the USA were: *Acrodontium myxomyceticola*, 173 isolates from 41 homes; *Acremonium roseolum*, 36 isolates from 18 homes; and *Tetracosporium paxianum*, once. A new sub-culturing method (Random-50) allowed the recovery of slow-growing, sometimes rare, fungi. These same Random-50 plates can estimate with high confidence the total fungal concentration in these homes. poster

Aoki, Takayuki^{1*}, Tomomi, Tsunematsu² and Sato, Toyozo³. ¹Genetic Diversity Department, National Institute of Agrobiological Sciences, Kannondai, Tsukuba, Japan, ²University of Tsukuba, Tennodai, Tsukuba, Japan, ³Genebank, National Institute of Agrobiological Sciences, Kannondai, Tsukuba, Japan. taoki@nias.affrc.go.jp. **Re-identification of *Fusarium moniliforme* isolates deposited at the MAFF Genebank, NIAS, Japan based on analysis of DNA sequences of the Histone H3 gene region.**

On a long used fungal name, *Fusarium moniliforme*, a recommendation to refrain its usage was issued by the ISPP/ICTF Subcommittee on *Fusarium* Systematics. This is because of the facts that: (1) the name, *F. moniliforme* represents an unacceptably broad species concept; and (2) *F. verticillioides* as mating population (MP) A of the *Gibberella fujikuroi* (GF) species complex is the older name for the species in strict sense. Microorganisms Section of the MAFF Genebank, NIAS, Japan has been preserving rather many number of strains identified previously as *F. moniliforme* for a distribution purpose. To respond to the recommendation, 70 strains of *F. moniliforme* deposited at MAFF were re-identified based on the DNA sequences of the Histone H3 gene region. By using a PCR primer-set, H3-1a and H3-1b, gene fragments of this region, ca. 520 bps, were amplified and sequenced. DNA sequences were aligned with Clustal X ver. 1.8 and phylogenetic analyses were made with PAUP ver. 4.0b10 by generating NJ and MP trees. Sequence data for the same gene region of related species of *Fusarium* were downloaded from the GenBank site, NCBI, and analyzed together. Out of 70 strains examined, 56, 7 and 4 strains were identified as *F. fujikuroi* (corresponding to the MP-C of the GF-complex.), *F. proliferatum* (MP-D), *F. subglutinans* (MP-E), respectively. Identity of 3 strains was still under consideration. poster

Aranda, Anabelle*, Viveros, Marian N. and Elley, Joanne T. Biological Sciences, The University of Texas at El Paso, El Paso, TX 79968-0519, USA. jellzey@utep.edu. **Localization of G-Protein in *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*.**

It has been suggested that components of the cytoskeleton contribute to the

signal transduction process in association with one or more members of the G protein family. Relatively high-affinity binding between dimeric tubulin and the alpha subunits of Gs and Gi1 has also been reported (Wang N. and Rasenick, 1991). Tubulin has binding domains for microtubule-associated proteins. Tubulin modifies G-protein signaling. Heterotrimeric G-proteins regulate microtubule assembly in mammalian cells. G alpha inhibits microtubule assembly and increases microtubule disassembly by activating the intrinsic GTPase of tubulin. G beta gamma promotes microtubule assembly (Roychowdhury *et al.*, 1999). In the present study, we have analyzed the interaction between alpha and beta gamma subunits of G proteins and tubulin in *Saccharomyces cerevisiae* and the *Schizosaccharomyces pombe* by immunofluorescence (Hagan and Hyams, 1988). Results from the immunofluorescence experiments were confirmed by electrophoresis and immunoblotting. We have obtained protein analyses and immunoblotting for *S. cerevisiae* and *S. pombe*. The visualization of the gamma and alpha tubulin is most evident in *S. cerevisiae*. There is evidence of a G-protein role in microtubule assembly/disassembly. poster

Arenz, Brett E.*, Held, Ben W., Jurgens, Joel A. and Blanchette, Robert A. Department of Plant Pathology, University of Minnesota, 495 Borlaug Hall, 1991 Upper Buford Circle, Saint Paul, MN 55108, USA. aren0058@umn.edu. **Fungal diversity in wood and soils at the historic expedition huts of Ross Island, Antarctica, as revealed by denaturing gradient gel electrophoresis (DGGE).**

Culture-dependent methods have long been the primary tool to determine the biodiversity of microorganisms in soils and other substrates. New molecular methods to study fungal profiles in samples from the environment have shown that these previous methods usually give an incomplete picture of all the organisms present. This study utilized denaturing gradient gel electrophoresis (DGGE) to analyze the fungal diversity in wood and other materials brought to Ross Island, Antarctica by explorers Robert Scott and Ernest Shackleton. Fungal diversity in soils near the historic structures was also analyzed. Fungal specific primers were used to target the ITS 2 region which shows significant variability between species. The DNA was separated by DGGE, and bands extracted and sequenced. Although previously reported Antarctic fungi such as *Geomyces*, *Cladosporium*, *Cadophora*, and *Phoma*, were frequently identified, DNA of many species show very little similarity to sequences available in databases based on BLASTn searching. Species of *Cadophora* and *Cladosporium* were found associated with deteriorating historic woods and other artifacts. These fungi were also found in Antarctic soil samples. This work is providing a more comprehensive understanding of the microbes found in Antarctica and provides new insights on the fungi attacking wood in the historic huts. contributed presentation

Arnold, A. Elizabeth^{1*}, Miadlikowska, Jolanta², Higgins, K. Lindsay², Dalling, James W.³, Gallery, Rachel E.³, Henk, Daniel A.², Eells, Rebecca L.², Vilgalys, Rytas J.² and Lutzoni, François². ¹Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA, ²Department of Biology, Duke University, Durham, NC 27708, USA, ³Department of Plant Biology, University of Illinois, Urbana, IL 61801, USA. arnold@ag.arizona.edu. **What can environmental PCR tell us about foliar fungal endophyte communities?**

While it is clear that a tremendous diversity of endophytic fungi can be isolated from leaves using standard culturing techniques, the potential occurrence of unculturable endophytes limits our understanding of the ecology, evolution, and diversity of endophytic symbioses. In particular, environmental sampling may be key to uncovering endophytes with obligate host associations and/or vertical transmission, slowly growing species that do not occur readily in standard media, and species that lose in competitive interactions within cultured leaf pieces. Results of paired environmental sampling (direct PCR) + culturing approaches to assessing endophyte diversity and community structure in boreal, temperate, and tropical foliage, and tropical seeds, will be compared. In each case, environmental sampling was complementary to culturing: direct PCR recovered numerous lineages that were not represented in cultures from the same hosts, recovered sequences that have few close matches in GenBank, provided evidence for infections in apparently uninfected tissues, and fundamentally changed our view of the taxonomic distribution of endophytes present in each host species. In discussing these case studies, special attention will be given to (1) the importance of multi-locus datasets for phylogenetic analyses of environmental samples; (2) methods of phylogenetic analysis that can result in reliable topologies given limited data from clones; (3) the utility of BLAST results based on ITS data for identifying clones; and (4) the utility of ITS genotype groups as functional taxonomic units for ecological analyses of environmental samples. symposium presentation

Avis, Peter G.*, Leacock, Pat R. and Mueller, Greg M. Department of Botany, The Field Museum of Natural History, 1400 S. Lake Shore Drive, Chicago, IL 60605, USA. pavis@fieldmuseum.org. **Potential changes in ectomycorrhizal fungal communities caused by nitrogen deposition in oak forests of the Chicago region.**

Ectomycorrhizal (ECM) fungi may mediate the impact nitrogen (N) deposition has on temperate deciduous forests. To test this hypothesis, we are documenting the above- and belowground components of ECM communities in con-

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tol and experimentally N-fertilized treatments at three forest sites found along a N deposition gradient in the Chicago region. Field surveys of sporocarps in treatment plots have identified over 90 ECM fungal species across the three sites since 2003. Over 200 of these collections were used to develop a reference database of terminal restriction fragment length polymorphisms (T-RFLP) for the identification of ECM collected belowground. In 2004, we conducted morphological and T-RFLP analyses of ECM collected from soil cores from each treatment plot. Early results indicate that the ECM communities in these sites are rich and potentially vulnerable to N increase. Over 130 likely species of ECM fungi have been identified from over 5000 oak root tips examined. Species richness estimates indicate that significantly fewer numbers of ECM species are found on oak roots in N fertilization treatments at two of three sites. We will continue to monitor ECM community responses to N fertilization over the next two years and also examine how the composition of these communities relates to their function within the context of N deposition. contributed presentation

Badalyan, Suzanna M.*; Garibyan, Narine G. and Sakeyan, Carmen Z. Dept. of Botany, Yerevan State University, Aeg Manoogian St., 375025, Yerevan, Armenia. badalyan_s@yahoo.com. **Culture collection of Basidiomycetes fungi at the Yerevan State University (Armenia).**

Establishment and maintenance of Culture Collection of macroscopic fungi (Basidiomycetes) at the Yerevan State University are the way of preserving biodiversity of mushrooms and extending fungal genetic and biotechnological research in Armenia. Study of mushroom cultures can also be valuable in obtaining novel bio-pharmaceuticals and functional food additives with health-enhancing effect. Presently, the Collection comprises around 210 living strains of 60 mushroom species. They were mostly isolated in Armenia and obtained from other institutions. Among them, 35 species and 197 strains possess known medicinal properties. The *Flammulina velutipes*, *Pleurotus ostreatus* and *Coprinus* spp. collections are represented by a wide eco-geographical diversity of strains. ITS-rDNA nucleotide sequence analyses of collected 25 species and 105 strains were carried out together with international collaborators. The project of genetic identification of Armenian medicinal mushrooms is currently realizing. Further extension of taxonomic, ecological and geographical diversity of species/strains and their genetic identification, as well as digitalization and creation of information DataBase are in progress. The catalogue of Culture Collection will be available soon. This research is supported by NATO (#FEL.RIG.980764) and DAAD (#548.104401.174) grants. poster

Badalyan, Suzanna M.^{1*} and Kües, Ursula.² ¹Dept. of Botany, Yerevan State University, Aeg Manoogian St., 375025, Yerevan, Armenia, ²Section Molecular Wood Biotechnology, Institute of Forest Botany, Georg-August University, Büsingenweg 2, D-37077 Göttingen, Germany. badalyan_s@yahoo.com. **Mycelial morphology and growth characteristics of wood-related coprinoid mushrooms.**

Around 80 species of the traditional genus *Coprinus* (Coprinoid mushrooms) have been observed on wooden material. Mycelial micro-, macromorphology and growth characteristics of xylotrophic species *Coprinus comatus*, *Coprinellus angulatus*, *C. bisporus*, *C. curtus*, *C. disseminatus*, *C. domesticus*, *C. ellisii*, *C. micaceus*, *C. xanthothrix*, *Coprinopsis atramentaria*, *C. cinerea*, *C. cothurnata*, *C. gonophylla*, *C. radians*, *C. romagnesiana*, *C. scobicola*, *C. strossmayeri* and *Parasola plicatilis* have been studied. Cultures were grown on Malt-Extract Agar (MEA), Potato-Dextrose Agar (PDA) and Glucose-Peptide Agar (GPA) at 25 °C and pH 6. Growth rates and growth coefficients were highest on MEA (up to 85 mm and above 20, respectively), then PDA and GPA. Macro-morphological characteristics were described after 10 days of growth. Oval and round shape clamps occur in most of the Coprini. Clamps were not found in some *Coprinellus* species. Material for micromorphological investigations was obtained by slide cultures. Hyphal loops were particularly formed in *Coprinellus* species. Arthroconidia were often observed, whereas blastic sporulation was rare. Chlamydo-spore formation is also typical for Coprini. Mycelial cysts, microfilaments and crystals were detected in some species. Thanks DAAD, NATO and Deutsche Bundesstiftung Umwelt for financial support. poster

Bahl, Justin, Jeewon, Rajesh* and Hyde, Kevin. Dept. Ecology & Biodiversity, The University of Hong Kong, Hong Kong, SAR, China. jbahl@hkusua.hku.hk. **Intergeneric relationships of *Linocarpon* and *Neolinocarpon*: does phylogenetic analysis support the generic delineation?**

Species from the genera *Linocarpon* and *Neolinocarpon* are common saprobic fungi found in subtropical to tropical regions and mainly occurs on monocotyledonous hosts. Both genera are often found on the same host. Based on morphology these genera share many similarities and have resulted in difficulties in assigning taxa. The most significant delineating characters are ascomata position and morphology. Based on parsimony and likelihood analyses of multi-locus partial sequences derived from nuclear encoded ribosomal DNA, beta-tubulin and RNA polymerase regions from fresh and dried herbarium material, an attempt has been made to assess which morphological characters are phylogenetically significant for generic delineation or whether the genera should be circumscribed under the priority name, *Linocarpon*. Analysis confirmed that the two genera are not monophyletic and indicates parallel evolution of morphological and ecological

characters. Results are discussed in relation to the significance of morphological characters currently used in the taxonomy of *Linocarpon* and *Neolinocarpon*. contributed presentation

Barnes, Irene*, Wingfield, Michael J. and Wingfield, Brenda D. Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa. irene.barnes@fabi.up.ac.za. **Development of microsatellite markers for the red band needle blight pathogen *Dothistroma septosporum* using two different isolation methods.**

Very little is known regarding the population biology of *Dothistroma septosporum*, one of the most important pathogens of plantation grown pines in the southern hemisphere. Thus, twelve sets of microsatellite markers have been developed to study the population dynamics of this pathogen. Two techniques, ISSR-PCR and FIASCO enrichment were used to screen for microsatellite rich regions. ISSR-PCR was effective in locating many microsatellite sites. However, after the necessary genome walking, many of the microsatellites were found to be redundant artifacts of the initial primers used. With FIASCO, variable success was observed depending primarily on the primer combination used in the enrichment. In one screen, 57 % of the clones contained microsatellites, in others, none were found. From a total of 22 primer pairs, 11 were found to be polymorphic amongst isolates of *D. septosporum*. An additional primer was polymorphic between *D. pini* and *D. septosporum* and can be used for further diagnostic purposes within populations. Cross-species amplification was successful in *D. pini*, *D. rhabdoclinis* and *Mycosphaerella dearnessii*. Future studies using these primers will focus on gaining an improved understanding of the population structure, genetic diversity, gene flow and the genetic relatedness between different populations of these important tree pathogens. poster

Barnes, Irene^{1*}, Crous, Pedro W.², Wingfield, Michael J.¹ and Wingfield, Brenda D.¹ ¹Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa, 0002, ²Centraalbureau voor Schimmelcultures (CBS), Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands. irene.barnes@fabi.up.ac.za. **Multigene phylogenetic analyses reveal that *Dothistroma septosporum* and *D. pini* represent two distinct taxa and a serious threat to pine forestry.**

The sudden increase in severity of the red band needle blight disease in the U.K., Canada and parts of Europe where *Dothistroma* has been present for decades is a matter of great concern. Although the etiology of the disease is well known, phylogenetic and population level relationships amongst isolates of the fungus are poorly understood. We have thus constructed multigene phylogenies for isolates of *Dothistroma* from 13 different countries. These have illustrated that the isolates are separated into two distinct lineages representing two discrete species and supported by morphological differences. The one species, referred to as *D. septosporum* occurs worldwide and infects over 30 species of pines. It is the major cause of the serious blight disease plaguing *Pinus radiata* plantations in New Zealand, Chile and other Southern Hemisphere countries. The second species, *D. pini*, is restricted in its distribution to the North Central United States where it causes a serious disease on exotic *P. nigra*. A simple ITS-PCR-RFLP is also presented that allows accurate and rapid distinction between the two species. contributed presentation

Baroni, Timothy J.^{1*}, Lindner Czederpiltz, Daniel L.², Lodge, D. Jean³, Hofstetter, Valérie⁴ and Franco-Molano, Ana Esperanza⁵. ¹ Department of Biological Sciences, State University of New York, College at Cortland, Cortland, NY 13045, USA, Center for Forest Mycology Research, USDA Forest Service, Forest Products Laboratory, One Gifford Pinchot Dr., Madison, WI 53726-2398, USA, Center for Forest Mycology Research, USDA Forest Service, P.O. Box 1377, Luquillo, PR 00773-1377, USA, ⁴Botany Department, Duke University, Durham, NC 27708-0338, USA, ⁵Laboratorio de Taxonomía de Hongos, Instituto de Biología, Universidad de Antioquia, A.A.1226, Medellín, Colombia. baronitj@cortland.edu. ***Arthrosporella*, a recently rediscovered neotropical genus, is phylogenetically related to *Termitomyces* in the Lyophylleae.**

In 1996, Sharon Cantrell and TJB collected an odd nail-shaped agaric covered with dark brown conidia in Puerto Rico; that collection could not be named at that time. Over the next 9 years of intense collecting, this odd arthrospore-producing species was collected only three more times in Puerto Rico, but also twice in the Dominican Republic. TJB realized this was a new species of *Arthrosporella*, originally described by Rolf Singer as a monotypic genus from Argentina. A second, distinctly different and new conidia producing agaricoid species was found just recently in Colombia by AEFM, and we now know of two other collections of this taxon from the Dominican Republic by Egon Horak and TJB. Very recently (August 2004) a third new, and completely different arthrospore-producing agaricoid species was found by TJB, DJL and CDL, fruiting abundantly in the cloud forest on the highest peak in Belize (Doyle's Delight). All of these new taxa possess siderophilous granules in the basidia. Phylogenetic analysis of nLSU indicates, with significant support, the monophyly of *Arthrosporella* with *Termitomyces* (Lyophylleae) and suggests a sister relationship between these two genera. All collections of *Arthrosporella* appear to be saprotrophic and not termitophilous, thus perhaps indicating a closer relationship with *Podabrella*, which is also in this branch of the Lyophylleae clade. poster

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Barrett, Luke G., Thrall, Peter H., Burdon, Jeremy J. and van der Merwe, Marlien M.* Centre for Plant Biodiversity Research, CSIRO – Plant Industry, GPO Box 1600, Canberra ACT 2601, Australia. marlien.vandermerwe@csiro.au **Pancontinental patterns of genetic variation in the rust fungus *Melampsora lini*.**

The *Linum marginale-Melampsora lini* plant-pathogen interaction is endemic to Australia and has been a focus of epidemiological and coevolutionary studies for more than a decade. Considerable variation for both host resistance and pathogen virulence has been shown at a range of spatial scales from the local to the continental. Here we report on a study using AFLP and SSR markers to examine pancontinental patterns of genetic variation in 102 clonal lines of *M. lini* representing 35 populations. Molecular marker genotypes partition all of the isolates into two major lineages, and in combination with subsequent sequencing of beta-tubulin and elongation factor genes suggest a possible hybrid origin for one of the lineages. Subsequent comparison with data on phenotypic variation for virulence in a subset of these isolates also demonstrates striking differences between the two lineages in terms of pathogenicity on the host *L. marginale*. Molecular genetic variation within the lineages was very limited, and within populations both AFLP and SSR markers regularly failed to distinguish among several lines with different pathotypes. These results are important for developing an understanding of how pathogen virulence might evolve within natural populations. poster

Barrow, Jerry R.*, Lucero, Mary L., Osuna-Avila, Pedro, Reyes-Vera, Isaac and Aaltonen, Ronald E. USDA-ARS Jornada Experimental Range, Las Cruces, NM 88003, USA. jbarrow@nmsu.edu. **Hybrid vigor, structural modification and enhanced plant performance induced by symbiotic fungi-plant interactions.**

Hybrid vigor, structural modification and enhanced plant performance induced by symbiotic fungi-plant interactions. Communities of symbiotic fungi are intrinsically integrated with single cells, tissues and organs of desert plants. They are obligately associated with living tissues and generally cannot be isolated and cultured separately. Symbiotic fungi indigenous to native desert plants were transferred, using cell culture methods, to non-host plants and reciprocally transferred between native grasses. Crop and native plants, with recipient fungi have astounding and increased levels of vigor. Up to five-fold increases in root and shoot biomass and substantial morphological changes and reproductive potential were obtained. Enhanced chlorophyll and phosphorous content were common responses. Once integrated, fungi were intimately interfaced with the plasmalemma of the new host plant and were ecto-cytoplasmically inherited. This technology accesses a previously unexplored source of genetic variability within native ecosystems with the potential of immediate transfer to improve tolerance of native and crop plants to stress, disease and pests. Symbiotic fungal transfers provides a powerful alternative for genetic improvement of plants. contributed presentation

Bartnicki-García, Salomón. Microbiology Dept., CICESE, Ensenada, Baja California, 22860, México. bartnick@cicese.mx. **Introductory remarks: Current perspectives in hyphal morphogenesis.**

Hyphal morphogenesis is clearly the most basic developmental process in mycology. The origin of the fungal kingdom could be traced to the "invention" of hyphal morphogenesis, i.e. the ability of a cell to form long tubular walls by tip growth. Not surprisingly, over the years, fungal biologists have become increasingly interested in elucidating the cellular and molecular basis of hyphal morphogenesis. The problem revolves basically about understanding the mechanism(s) responsible for polarized growth of the cell wall. A number of structural and molecular players have been identified but the mechanism cannot be attributed to a single gene or protein. Polarized secretion probably requires a specific concerted action between cytoskeleton and secretory vesicles to produce a pattern of vesicle discharge that would generate cells with a profile described by the hyphoid equation: $y = x \cot(xV/N)$. This symposium on Advances in Fungal Morphogenesis will cover developments in different fronts: a new way of probing the surface properties of the hyphal wall (S. Kaminskyj), assessing the importance of protein glycosylation in the maintenance of hyphal growth (B. Shaw), and analyzing the role of the Spitzenkörper in apical growth (M. Riquelme). symposium presentation

Baucom, Deana L.*, Bruhn, Johann N. and Mihail, Jeanne D. Division of Plant Sciences, University of Missouri, Columbia MO 65211, USA. dlba3c@mizzou.edu. ***Armillaria* species involved in Missouri Ozark forest decline.**

In the Missouri Ozark Mountains, *Armillaria* spp. contribute to oak decline. To investigate the distributions and roles of *Armillaria* spp., 142 isolates collected in 2002 from 40 plots were identified. Amplification of IGS1 followed by restriction with *AluI* identified 121 isolates as *A. mellea* (52 %), *A. gallica* (38 %), and *A. tabescens* (10 %). Two new RFLP patterns were found to represent 41 % of *A. mellea* and 17 % of *A. gallica* isolates. Isolates yielding these patterns are currently being characterized by sequence analysis of IGS1. Major hosts were dogwood (44 %), red oaks (18 %), and white oaks (7 %). *Armillaria mellea* predominated on both white and red oaks; *A. mellea* and *A. gallica* occurred equally on dogwood. Recently killed trees provided 28 % of study isolates. *Armillaria* was almost universally present on recently killed trees. Red oaks, dogwood, and white oaks provided 38 %, 32 %, and 10 % of recent mortality isolates, respectively. Nearly all recent oak mortality yielded *A. mellea*. Recent dogwood mor-

tality yielded *A. gallica* (54 %) more frequently than *A. mellea* (38 %). Ozark oak decline affects red oaks and dogwoods most heavily. The *Armillaria* sp. which most commonly contributed to oak mortality on our plots in 2002 was *A. mellea*, though *A. gallica* was more commonly recovered from recent dogwood mortality. We found little evidence of mortality caused by *A. tabescens*. poster

Beeson, Esther¹, Beltz, Shannon², Klich, Maren² and Bennett, Joan W.^{1*} ¹Tulane University, New Orleans, LA, USA, ² Southern Regional Resource Center, New Orleans, LA, USA. ebeeson1@cox.net. **Sclerotial production in *Aspergillus flavus* varies with temperature and nitrogen source.**

Twenty strains of *Aspergillus flavus* from the culture collection of the Southern Regional Research Laboratory, New Orleans, LA, were grown on defined and complex media at 25 °C and 37 °C for one week. Colonies were screened for sclerotial production as well as other colony characters including production of conidia, floccose hyphae, and mycelial pigment. When grown on complex media with yeast extract as the nitrogen source, 9 of the strains produced sclerotia at 25 °C and 11 produced sclerotia at 37 °C. When grown on a defined medium with nitrate as nitrogen source, 8 of the strains produced sclerotia at 37 °C and 5 produced sclerotia at 25 °C. When ammonium was used as the nitrogen source, only one strain produced sclerotia at 37 °C and there was no sclerotial production at 25 °C. Sporulation was sparse or absent for all strains grown on ammonium at 37 °C. When microarrays of the *A. flavus* genome become available, these data will be useful in designing conditions for RNA isolation in order to probe the genes involved in sclerotial formation. poster

Bennett, Chandalin^{1*}, Newcombe, George¹ and Aime, M. Catherine². ¹Department of Forest Resources, University of Idaho, Moscow, Idaho 83844, USA, ²USDA ARS Systematic Botany and Mycology Lab, Beltsville, Maryland 20705, USA. benn4449@uidaho.edu. **Regional studies of *Melampsora* on *Salix* in the Pacific Northwest.**

Melampsora epitea Thum. is a species complex that represents all willow rusts in N. America. To better understand how much host-specialization and genetic diversity exists in the Pacific Northwest (PNW), a large-scale host-range inoculation study was performed along with ITS sequencing, morphological analysis, and a two-year field survey. Distinct host-specificity was shown for three different *Melampsora* isolates inoculated on nearly equal sets of 440 willows. Less than 20 percent of the plants in each experiment were susceptible to the inoculum and greater than 15 percent of those showed some signs of resistance. The genetic sequencing resulted in four distinct clades, the largest of which likely represents a complex in this region. The other three clades were strongly divergent from the complex. There was up to three genetically distinct rusts present in a given geographic location and four or more genetically distinct rusts on a given *Salix* sp. There was found at most two distinct rusts on the same species from the same population. It's evident that willow rusts are incredibly diverse in the PNW. Every experimental inoculum was specialized in its host range and the genetic diversity was spread across four unique and highly divergent clades. symposium presentation

Bennett, Joan W. Tulane University, New Orleans, LA 70118, USA. jrbennett@tulane.edu. **Industrial mycology: from Takamine's diastase to TIGR's database.**

Industrial mycology has its roots in numerous food fermentations that were developed early in human history. Of these, the Japanese koji process, utilizing *Aspergillus oryzae*, is of particular interest because the first microbial enzyme ever patented was a secreted diastase (amylase) isolated from *A. oryzae* by Dr. Jokichi Takamine, a Japanese chemist working in the U.S.A during the late nineteenth century. In the first half of the twentieth century, several filamentous fungi were harnessed for the production of additional commercial enzymes and for organic acids. Although the discovery of penicillin and the subsequent golden age of antibiotics transformed fermentation technology, the molecular biology of industrial molds lagged behind that of model species. Now, in the twenty-first century, genomic research has ushered in a new era of understanding. Genome projects for several *Aspergillus* species are completed or underway, revealing new insights into secondary metabolism, carbon and nitrogen regulation, and other genetic control mechanisms. symposium presentation

Berbee, Mary L.^{1*}, James, Tim Y.², Longcore, Joyce E.³, Stajich, Jason⁴ and Vilgalys, Rytas J.² ¹Dept. of Botany, University of British Columbia, V6T 1Z4 Canada, ²Dept. of Biology, Duke University, Durham, NC 27708 USA, ³Biological Sciences, University of Maine, Orono, ME 04469-5722 USA, ⁴Dept. of Molecular Genetics and Microbiology, Duke University, Durham, NC 27708, USA. berbee@interchange.ubc.ca. **What makes a fungus? Fungal-specific genes from EST libraries of the basal fungi *Batrachochytrium dendrobatidis* and *Mortierella verticillata*.**

The Chytridiomycota and Zygomycota include ancient fungal lineages that may have originated hundreds of millions of years before plants invaded land. We looked for shared genes that distinguish the fungi from other kingdoms through comparison of expressed sequence tag (EST) libraries, from a chytrid, *Batrachochytrium dendrobatidis* (1588 ESTs, average length, 572 nucleotides) and

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from *Mortierella verticillata*, a readily cultured terrestrial mold in the Zygomycota (1278 ESTs, average length, 556 nucleotides). Of 1247 non-redundant ESTs from *B. dendrobatidis*, 100 were 'fungal-specific' in that sequence similarity within fungi is high but drops off sharply beyond the kingdom level. From *M. verticillata*, 64 ESTs were fungal-specific. Fungal-specific genes included six sub-families of chitin synthases that arose through ancient gene duplications. Suggesting that early fungi had to scavenge for iron, *B. dendrobatidis* and higher fungi share a high affinity iron permease. Septins are also present in animals, but they help control the form of fungi during development. We found four septin paralogues among ESTs from *Batrachochytrium dendrobatidis* and two from *Mortierella verticillata*. The septins from the spheroidal chytrid appeared to be basal to genes from other fungi. contributed presentation

Bérube, Jean A.^{1*}, Stefani, Frank O.P.¹ and Sokolski, S.¹ Canadian Forest Service, 1055 du PEPS, P.O. Box 3800, Ste-Foy, QC, G1V 4C7 Canada. jberube@cfl.forestry.ca. **Comparison of foliar endophyte biodiversity from three boreal conifers.**

We compared the foliar endophyte biodiversity of white spruce (*Picea glauca*), black spruce (*P. mariana*) and eastern white pine (*Pinus strobus*). Asymptomatic healthy needles were collected from 67 conifer populations in eastern Canada, surface sterilized and then plated on nutrient agar. The ribosomal ITS region were amplified, sequenced and analyzed using maximum parsimony and Bayesian inference. Results from morphological and molecular studies indicate white spruce is hosting as many as 49 fungal endophyte species, black spruce is hosting 42 species and white pine is hosting 30 species. Only four endophyte species were common among these three hosts, among them *Hormonema dematioides* and *Phaeocryptopus gaeumannii*. Some fourteen species were common to the two spruces and only one species was common between black spruce and white pine. Five other species were also found on other conifers not examined in this study. The remaining 85 species were unique to one conifer host only. They represent a source of new species needed to fill the gap between known number of species, 76000 and the 1.5 million estimated number by Hawksworth. contributed presentation

Bérube, Jean A.^{1*}, Stefani, Frank O.P.¹, Piercey-Normore, Michele D.², Guillaumin, Jean-Jacques³ and Hamelin, Richard C.¹. ¹Canadian Forest Service, 1055 du PEPS, P.O. Box 3800, Ste-Foy, QC, G1V 4C7 Canada, ²Department of Botany, University of Manitoba, Winnipeg, MB, R3T2N2, Canada, ³INRA Centre de Clermont-Ferrand, UMR 234 Brestet, 63039, Clermont-Ferrand, France. jberube@cfl.forestry.ca. **Evidence of ancient recombination in genus *Armillaria*.**

The genus *Armillaria* has been studied extensively to determine its evolutionary history in relation to virulence, hosts and distribution. Four coding genes (actin, beta-tubulin, G3PD and MLL) from 21 species of *Armillaria* from North America, Europe, Africa, Asia, Australia and South America were sequenced and analyzed. Phylogeny of combined genes showed important differences with published ITS phylogenies. The basal position of *A. ostoyae*, *A. gemina*, *A. borealis* in the phylogenetic trees inferred from the actin and G3PD genes is evidence of ancient recombination events in the northern hemisphere that took place after the Gondwanian disjunction (100 Myr BP) but before the Laurasian disjunction (60 Myr BP). Once recombinant sites removed from phylogenetic analysis, corrected trees indicate that *Armillaria* seems to be an ancient genus that originated in the Jurassic, with some species that have radiated throughout the southern hemisphere before the Gondwana disjunction. The evolutionary history of many *Armillaria* species in relation to continental drift will be presented. contributed presentation

Beyer, David M.*; Paley, Kimerley and Wilkinson, Vija. Dept. of Plant Pathology, The Pennsylvania State University, University Park, PA 16802 USA. dmb8@psu.edu. **Influence of organic acids on the growth and development of *Trichoderma harzianum*, a pathogen of *Agaricus bisporus*.**

Previous research has shown that Phase I substrate for *Agaricus bisporus* prepared under low oxygen conditions resulted in earlier and more severe development of *Trichoderma harzianum* green mold disease. Organic acids are known to be produced under anaerobic conditions, and their residual compounds may be involved in the development of the pathogen in mushroom substrate. This research looked at the influence of several organic acids at different concentrations on the growth of *Trichoderma harzianum* *in vitro* and *in vivo*. Results suggested that *in vitro* higher concentrations of most organic acids had a negative influence on the growth of the pathogen while lower concentrations of Fumaric, Succinic and Lactic acid did not. *In vivo* assays suggested that when Fumaric acid was added to the substrate it predisposed the substrate to disease development. poster

Binder, Manfred^{1*}, Bodensteiner, Philomena², Wang, Zheng¹ and Hibbett, David S.¹. ¹Clark University, Biology Department, Lasry Bioscience Center, 950 Main Street, Worcester, Massachusetts 01610-1477, USA, ²Fakultät für Biologie der Ludwig-Maximilians Universität München, Department I: Biodiversitätsforschung, Systematische Mykol., Munich, Germany. mbinder@clarku.edu. **Phylogenetic relationships of cyphelloid and aquatic homobasidiomycetes.**

Cyphelloid fungi include minute terrestrial, cupulate or tubular-shaped forms in the euagarics clade. Our previous studies showed that some aquatic fungi like the marine gasteromycete *Nia vibrissa* have been derived from cyphelloid

forms, while others (e. g., *Mycaureola dilseae*) are derived from agaricoid forms and represent separate lineages of aquatic fungi in the euagarics. In a broad phylogenetic survey of cyphelloid and aquatic homobasidiomycetes, we used a two-pronged approach generating nuc-lsu and ITS data for 140 collections of cyphelloid fungi consisting of multiple samples of 57 well described species. Data from multiple rDNA regions (nuc-ssu, nuc-lsu, mt-ssu, mt-lsu, ITS) that were additionally sequenced for a subset of 25 cyphelloid species served as a backbone in weighted parsimony and Bayesian analyses to identify the major lineages of cyphelloids within the euagarics and their closest relatives. It has long been suspected that cyphelloid fungi form a polyphyletic group and our study suggests there may be at least 18 independent origins, which will be presented in detail. Thus, morphological reduction via cyphellization is a major theme in the evolution of euagarics. One of the most remarkable examples of evolutionary transitions from the terrestrial cyphelloid habit to fungi living in aquatic habitats can be observed in the *Nia* clade, which contains the largest proportion of cyphelloid fungi studied so far. Our preliminary results indicate that the marine fungi in this clade are a monophyletic group including *N. vibrissa*, *Halocyphina villosa*, *Calathella mangrovei*, and as a new result *Digitatispora marina*, a resupinate species that has lost the ability of active spore discharge. poster

Bischoff, Joseph F.^{1*}, Rehner, Stephen A.² and Humber, Richard A.³. ¹GenBank, NCBI-NIH, Bethesda, Maryland 20892, USA, ²Insect Biocontrol Laboratory, USDA-ARS, Beltsville, Maryland 20705, USA, ³Plant Protection Research Unit, USDA-ARS-ARSEF, Ithaca, New York 14853, USA. bischoff@ncbi.nlm.nih.gov. **A multilocus phylogenetic analysis of the entomopathogen *Metarhizium*.**

Species of the cosmopolitan entomopathogenic form genus *Metarhizium* play important ecological roles by regulating arthropod populations and recycling insect biomass. The ubiquity of *Metarhizium* species and their broad host range have made them an attractive alternative to chemical pesticides. Despite commercial interest in the genus and its widespread occurrence, species delimitation, intragenetic relationships, and placement within the Clavicipitaceae remain undefined. Historically, two species and a single variety were accepted in the genus. However, in a recent molecular phylogenetic study 10 lineages (i.e., species and varieties) were proposed. The purpose of this study is to, 1) determine if *Metarhizium* is monophyletic, 2) identify its sister lineage within Clavicipitaceae, 3) resolve phylogenetic species and infer intragenetic relationships. A multilocus dataset (EF1-alpha, RPB1, beta-tubulin and RPB2) supports the monophyly of *Metarhizium* and its close association with the largely plant associated members of Clavicipitaceae (subfamily Clavicipitoideae). In addition, a minimum of 12 distinct lineages has been resolved, exceeding prior estimates of diversity in the genus. contributed presentation

Branco, Sara. The Committee on Evolutionary Biology, University of Chicago, Chicago, IL 60637 USA. sbranco@uchicago.edu. **Macrofungal communities of northeastern Portugal.**

Quercus pyrenaica woodlands and serpentine *Quercus rotundifolia* woodlands are two important plant communities of northeastern Portugal. These forests are significant natural habitats in the region and are considered priorities in terms of nature conservation. *Quercus pyrenaica* is a native and widespread oak species. Serpentine woodlands are communities with an impoverished flora characterized by *Quercus rotundifolia* and several endemic herbaceous species. They are confined to serpentine soils, characterized by high heavy metal content and low nutrient levels. In each woodland one 1000 sqm permanent plot was established and macrofungi were surveyed biweekly during 2001, 2002 and 2003. In both woodlands the sporocarp fruiting occurred throughout autumn, between October and December. The *Quercus pyrenaica* plot had much higher species diversity (146 species) than the serpentine plot (73 species) and only 17% of the recorded species occurred in both plots. Mycorrhizal species composed more than 60% of all the species found in either habitat. Twenty three of the identified taxa were new records for the country and 47 were new records for the region. These results indicate that these forests are diverse and distinct in macrofungal species and require proper management and conservation. poster

Bruhn, Johann N.¹, Kromroy, Kathryn², Baucum, Deana¹ and Mihail, Jeanne D.^{1*}. ¹Division of Plant Sciences, University of Missouri, Columbia MO 65211, USA, ²USDA Forest Service, North Central Research Station, St. Paul, MN 55108, USA. bruhnj@missouri.edu. ***Armillaria* species associated with oak stump sprout regeneration in upland Missouri Ozark forests.**

Stump sprouts are favored in North American oak regeneration. Many trees selected for cutting in upland Missouri Ozark forests are infected with one or more *Armillaria* spp., especially in oak stands experiencing forest decline. After harvest, *Armillaria* infections in these trees spread to the root crown, reducing stump sprout production and causing sprout mortality. We examined the implications of these infections for survival and growth of remaining sprouts. During 2003 and 2004, we characterized sprouting and presence of *Armillaria* on oak stumps created in 1996 on 35 study plots. Single *Armillaria* isolates were collected from 145 stumps; dual isolates were collected from widely-spaced roots of 29 additional stumps. Dual isolates from 14 stumps represent different genets. We have found

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one new IGS1 RFLP banding pattern for each of *A. mellea* and *A. gallica*. *Armillaria mellea* is widely represented in the stump populations in our plots, raising concern that models of stump sprout regeneration may be optimistic, especially in stands experiencing oak decline. Stump sprout regeneration can result in the establishment of crop trees on previously infected root systems. Our study also focuses attention on the disparity between stem age and the age of their root systems including existing *Armillaria* infections, in stands managed using stump sprout regeneration. poster

Bruns, Thomas D.*, Boynton, Primrose, Shamiéh, Karimeh, Szaro, Timothy M. and Kennedy, Peter G. Department of Plant & Microbial Biology, University of California, Berkeley 94720-3102, USA. pogon@berkeley.edu. **Spatial and temporal structure of *Rhizopogon* sporebanks.**

Rhizopogon species are ectomycorrhizal associates of the Pinaceae. In young, disturbed pine forests they are often among the dominant fungi colonizing seedlings and saplings. This dominance is due to abundant sporebanks that are produced by deposition of spores in place and by dispersal through mammal mycophagy. We have used rodent baiting, bioassays, spore burial, and PCR-based analyses to examine the distance and frequency of dispersal from forest to non-forested borders and the longevity of spores. We then compared these parameters to the spatial distribution of sporebanks. We found *Rhizopogon* is efficiently dispersed at distances of 40 meters from a border in a single year, and that the distances and quantity of spores dispersed are greatest from young post-fire forests. Current dispersal appears to be sufficient to account for the spatial pattern of the sporebank for the four most common species. However our results suggest that longevity of the spores may be substantial, and we think that longevity is likely to be important at greater spatial and temporal scales. symposium presentation

Burdsall, Harold H. Jr. USDA - FPL - Cntr. Forest Mycol. Res., Madison, WI and Fungal & Decay Diagnostics, LLC, Black Earth, WI, USA. burdsall@fungaldcay.com. **Cyphellaceae in the Arctic and subantarctic islands.**

Members of the family "Cyphellaceae" in the traditional sense are now known to be distributed among several families of the homobasidiomycetes. However, they are recognizable in the field as a "morphological group", unnatural as it may be. Collecting in the subantarctic islands of New Zealand and near and above the Arctic Circle in Alaska has provided a number of specimens for comparing the occurrence of these fungi from opposite ends of the globe. Species of *Lachnella*, *Henningsomyces* and *Cyphellopsis* were collected. Species of *Lachnella* were common on the subantarctic islands while *Henningsomyces* and *Cyphellopsis* were lacking. The reverse was true in the Arctic collecting sites. Differences in types of substrate may explain this difference, there being more wood in the Arctic collecting sites than on the subantarctic islands. However, the lack of *Lachnella* specimens from the Arctic may be a result of collecting bias and collecting for forbs and ferns on the Arctic sites may provide more specimens of *Lachnella* species. These comparisons are continuing. symposium presentation

Burgess, Joshua W.¹, Schwan, William² and Volk, Thomas J.^{2*}. Departments of ¹Microbiology and ²Biology, University of Wisconsin-La Crosse, La Crosse WI 54601, USA. volk.thom@uwlax.edu. **Detection of *Blastomyces dermatitidis* DNA from natural samples using rapid PCR-based methods.**

Blastomyces dermatitidis is the dimorphic fungal agent of blastomycosis, a disease that primarily affects humans and dogs. The clinical appearance of this mycosis is well characterized, but there is still little known about its environmental niche, having been isolated from nature only 21 times. We have developed a PCR-based assay to detect *B. dermatitidis* from soil samples using primers specific to a portion of the promoter region of the virulence gene BAD1. An internal standard control, pTJV2-2, was designed to ensure that negative results from soil samples were not the result of PCR failure due to soil inhibitors. The lower detection limit of the plasmid, using *Blastomyces* specific primers (BSP), was 0.1 femtograms. With chromosomal DNA, the lower detection limit is 500 fg. To test the assay for cross reactivity, the BSP were tested successfully against many fungi, bacteria, and actinomycetes, especially those genetically related or found in the same geographic areas. This method is sensitive to 304 copies when detecting pTJV2-2 DNA spiked directly into the soil extraction. When extracting live *Blastomyces* yeast, this newly developed method can detect as few as 8,450 live cells. We plan on using this method to screen soils to better determine the environmental niche of *Blastomyces*. contributed presentation

Buyck, Bart^{1*}, Parrent, Jeri Lynn² and Vilgalys, Rytas J.². ¹Dépt. Systématique et Evolution, Muséum National d'Histoire Naturelle, 75005 Paris, France, ²Dept. of Biology, Duke University, Durham, NC 27708-0338, USA. buyck@mnhn.fr. **The *Russula virescens-crustosa* species complex (Russulales, Basidiomycotina) from eastern North America.**

The type species of the subsection *Virescentinae*, *R. virescens* Fr. was originally described from Europe, but is common throughout most of the northern hemisphere, including the eastern US. *R. crustosa* Peck and *R. heterosporoides* Murrill are currently the only other North American species placed in this subsection. Since their original description, revisions of these taxa did not reveal major identification problems, although microscopic observation was needed to separate green forms of *R. crustosa* and *R. virescens*. Recent field work by the senior au-

thor and several American amateur mycologists suggests additional taxa are likely to belong in *Virescentinae*. In this study we have combined morphological and molecular data generated from over 100 north American, as well as some selected Asian, African and Australian collections to examine the *virescens-crustosa* complex. This work is part of a complete revision of the genus *Russula* in the eastern US by the senior author. Detailed morphological study revealed that commonly used characters for identifying *Russula* species, spore ornamentation and form of hyphal extremities, are too variable within the *virescens-crustosa* complex to discriminate among taxa, except for *R. parvovirescens* sp.nov. Results from the multilocus molecular analysis confirm the placement of several undescribed north American taxa in the *virescens-crustosa* complex, highlight the speciose nature of this subsection, and allow for a firm placement of these species in a more worldwide phylogenetic dataset. Poster

Cafaro, Matias J.¹ and Lichtwardt, Robert W.^{2*}. ¹Department of Bacteriology, University of Wisconsin, Madison, WI 53706, USA, ²Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66045, USA. cafarom@wisc.edu. **Unveiling cryptic relationships of the Eccrinales.**

The order Eccrinales includes a diverse group of arthropod-associated organisms, most of which present relatively simple morphology. Unbranched, non-septate, multinucleate thalli and sporangiospores that are formed basipetally from the thallus apex have been used as characters to relate the group to the class Trichomycetes. No member of the Eccrinales has been cultured. In order to address the phylogenetic relationships of the group, DNA was extracted from material collected from different arthropods and ribosomal genes were amplified using specific primers. Twelve sequences for the 18S gene and five for the 28S gene were generated. Maximum parsimony, maximum likelihood and Bayesian analyses confirmed the monophyly of the Eccrinales as well as their close relationship to the Amoebozoales in the protist class Mesomycetozoa rather than the fungal class Trichomycetes. The classification of the Eccrinales in three families is not supported and needs revision. There is some phylogenetic structure that indicates that Eccrinales associated with crustaceans are a monophyletic group different from those species associated with millipedes. At a more refined scale, three species associated with isopod hosts (*Palavascia patagonica*, *Alacrinella limoriae* and *Astreptonema* sp.) form a well supported clade. Future addition of taxa and other genes may improve patterns presented in these analyses. symposium presentation

Cai, Lei*, Jeewon, Rajesh and Hyde, Kevin D. Centre for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Hong Kong, SAR, China. leicai@hkust.hk.hk. **Phylogenetic relationships of *Podospora* and allied genera based on multi-gene sequences and morphology.**

Podospora and allied genera were investigated for phylogenetic relationships. Multiple gene sequences (partial nuclear 28S ribosomal DNA, nuclear ITS/5.8S ribosomal DNA and partial nuclear beta-tubulin) were analyzed using maximum parsimony and Bayesian analysis with Markov Chain Monte Carlo algorithms. Analyses of different gene datasets were performed individually and then combined to generate phylogenies. In all analyses, *Podospora* was found to be a highly polyphyletic genus, consisting of a group of morphologically heterogeneous and phylogenetically distant species. *Podospora* species possessing ascospores adorned with swollen agglutinated hairs or prominent protruding peridial cells formed a strongly supported monophyletic clade in all analyses. The generic name *Schizothectum* is reintroduced to accommodate species possessing above morphological characters. *Zopfella* is restricted to species having ascospores with septum in the dark cell. Other species lacking spore septum in the dark cell (so-called *Tripterospora* species) should be transferred to other genera. The redefined *Zopfella* becomes a natural group. *Cercophora* is also found to be a polyphyletic genus and should be restricted to a few species bearing morphological similarity to the type species. The family Lasiosphaeriaceae was found to be polyphyletic based on morphological and molecular data. poster

Cantrell, Sharon A. Science & Technology, Universidad del Turabo, P. O. Box 3030, Gurabo, PR 00778, USA. scantrel@suagm.edu. **Fungal inventory of the discomycetes of the Greater Antilles.**

The Greater Antilles (Cuba, Hispaniola, Puerto Rico & Jamaica) are considered a diversity hotspot of the world. Discomycetes, particularly inoperculate, have been poorly studied in the GA. A total of 117 Pezizales, 171 Helotiales, 28 Rhytismatales and 451 Ostropales have been reported from 11,268 fungal species. For Dominican Republic and Puerto Rico, 75 % of the species are characteristic of the tropics and 25 % are temperate. A study in the Dominican Republic revealed the lack of information on this group where 17 % of the taxa recorded were new species and 38 % were new reports. Many species of discomycetes are very small and tend to be habitat and substrate specific. This helps to explain the lack of information on the inoperculate discomycetes. The fungal inventories that have been conducted in the region have not incorporated systematic and standardized methods. Because of this, a study was conducted to develop an optimal sampling method for discomycetes. In summary, the sampling method should select study areas based on diversity and distribution of plant species, be conducted along transects with a minimum of 10 plots of 1 m² at 5-10 m intervals and be conducted for

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at least a year. While the works in Dominican Republic and Puerto Rico have provided good information on the discomycetes of the region, more studies should be conducted on other islands, habitats and substrates. symposium presentation

Carpenter, Margaret A.*, Stringer, Alison, Stewart, Alison and Ridgway, Hayley. National Centre for Advanced Bio-Protection Technologies, Lincoln University, Canterbury, New Zealand. carpentm@lincoln.ac.nz. **Mycoparasitism by *Trichoderma hamatum* involves expression of a novel FAD-dependent monoxygenase.**

Biological control of fungal plant diseases by the mycoparasite *Trichoderma hamatum* is facilitated by the actions of a range of cell wall degrading enzymes. As mycoparasitism is a complex process, it is likely that *T. hamatum* uses additional mechanisms to attack its hosts. Any unknown genes involved in mycoparasitism may show changes in expression when *T. hamatum* makes contact with a host fungus. Subtractive hybridization was used to target *T. hamatum* genes up-regulated during mycoparasitism of the plant pathogen *Sclerotinia sclerotiorum*. One of the genes identified encoded an FAD-dependent monoxygenase. The gene product was 66 % identical to an *Aspergillus flavus* monoxygenase which is encoded by a gene that lies adjacent to, and may be part of, a gene cluster involved in synthesis of a mycotoxin. The *T. hamatum* monoxygenase gene was not expressed when *T. hamatum* was growing alone, nor in dual culture with itself. However when *T. hamatum* was grown in dual culture with *S. sclerotiorum*, expression of the gene was detected when the two colonies overlapped, but not prior to contact. Analysis of the promoter region of the gene revealed motifs suggesting that expression of the gene may be affected by carbon and nitrogen repression, and by pH. Gene expression in response to these factors has been investigated by northern blotting. poster

Carris, Lori M.^{1*} and Castlebury, Lisa A.². ¹Dept. of Plant Pathology, Washington State University, Pullman WA 99164, USA. ²USDA ARS Systematic Botany and Mycology Lab, 10300 Baltimore Ave., Beltsville, MD 20705, USA. carris@wsu.edu. **Identification of species of *Tilletia* in U.S. wheat and grass seed exports.**

Tilletia controversa (dwarf bunt of wheat) is a quarantine pest with major impact on the worldwide movement of wheat and grass seed. Commonly used identification methods rely on morphological features of teliospores found in seed washes. However, teliospores of closely related species are difficult to identify based only on morphological features, and the source of spores in wheat and grass seed may be contaminating weeds. For example, in 2004 teliospores of *T. bromi* from *Bromus tectorum* (downy brome, cheatgrass), misidentified as *T. controversa*, were present in sufficiently high levels in some fields in the Pacific Northwest to prevent the export of that wheat to China. Similarly, shipments of Kentucky bluegrass seed (*Poa pratensis*) have been refused for import to China because they are contaminated with spores of *T. bromi*. In contrast, two putative new species of *Tilletia* have recently been intercepted by Chinese quarantine officials, one in seed of *Puccinellia distans* (alkali grass) from the U.S., and a second in *Festuca rubra* (fine fescue) from the U.S. and *Lolium perenne* (perennial ryegrass) from Australia. Species of *Tilletia* commonly encountered in wheat or grass seed shipments, including the new species from *Puccinellia* and *Festuca/Lolium*, are morphologically characterized and relationships among the weedy grass-infecting bunts and wheat bunt species are presented. poster

Castlebury, Lisa A. USDA ARS SBML, 10300 Baltimore Ave, Beltsville, MD 20705, USA. castlebury@nt.ars-grin.gov. **The *Diaporthe vaccinii* complex of fruit pathogens.**

Diaporthe vaccinii (anamorph *Phomopsis vaccinii*) causes twig blight and upright dieback of *Vaccinium corymbosum* (blueberry) and *V. macrocarpon* (cranberry). However, other species of *Diaporthe/Phomopsis* have also been reported on *Vaccinium* spp. In addition, isolates from a variety of hosts are reported to be closely related to *D. vaccinii*. Relationships among this complex of fungi were characterized with the ITS regions of the nuclear rDNA and intron regions in the actin and translation elongation factor-1 alpha genes. Four species were resolved: *D. vaccinii*, *P. fukushii*, *D. allegheniensis* and an as-yet unidentified species with a broad host range. In this analysis, only *D. vaccinii* was host specific and limited to species of *Vaccinium*. Authentic isolates of *P. fukushii*, a pathogen of *Pyrus*, grouped with isolates from *Vaccinium*, *Chamaecyparis* and *Ulmus*. *Diaporthe allegheniensis* from *Betula* was most closely related to *D. vaccinii*. A large group of isolates from a variety of hosts including *Vaccinium*, *Acer*, *Rubus*, *Malus*, *Corylus*, *Glycine*, *Viburnum* and *Vitis* form a separate and well-supported species in this complex. Several isolates in this group are from specimens identified as *D. eres*, the type species of the genus, which has been reported to have a broad host range and variable morphology. Results of this study suggest that although certain pathogenic species in *Diaporthe/Phomopsis* may be host specific, many taxa in this genus will have a broad host range. poster

Celio, Gail J.^{1*}, Padamsee, Mahajabeen¹, Detinger, Bryn C.¹, McLaughlin, David J.¹, Hibbett, David S.², Lutzoni, François³, Spatafora, Joseph W.⁴, and Vilgalys, Rytas J.³. ¹Dept. of Plant Biology, Univ. of Minnesota, St. Paul, MN 55018, USA, ²Biology Department, Clark University, Worcester, MA 01610, USA, ³Dept. of Biology, Duke University, Durham, NC 27708, USA, ⁴Dept. of Botany and Plant

Pathology, Oregon State University, Corvallis, OR 97331, USA. celio001@umn.edu. **The Nucleus in the AFTOL Non-Molecular Database.**

Subcellular characters relating to polar structures and nuclear division have been useful for inferring evolutionary relationships since the 1960s. Nuclear division features are shared by all eukaryotes. The long evolutionary history of the Fungi has permitted diversification of nuclear division and related processes. In motile fungal cells polar structures include centrioles, while in other fungi they appear as electron-opaque spindle pole bodies (SPBs). SPBs vary among taxa in shape, position relative to the nuclear envelope, and timing of replication, migration, and spindle initiation. The nuclear envelope may remain intact, become disrupted, or disperse completely and reappear at various times during nuclear division. Several patterns of nucleolus behavior are observed during the cell cycle. Perinuclear endoplasmic reticulum and/or spindle pole body caps may be associated with dividing nuclei. The database currently contains 17 characters and 67 character states from 81 species of the estimated 85,000 species of fungi. Compilation of data from published nuclear division studies reveals the need for comprehensive examination of representative species. poster

Charlton, Nikki D.¹, Carbone, Ignazio¹, Tavantzis, Stellos M.² and Cubeta, Marc A.^{1*}. ¹Dept. of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7616, USA, ²Dept. of Biological Sciences, University of Maine, Orono, ME 04469-5722, USA. marc_cubeta@ncsu.edu. **Genetic diversity and genealogical history of the M2 dsRNA mycovirus in a field population of *Rhizoctonia solani* anastomosis group 3.**

Populations of the soil fungus *Rhizoctonia solani* anastomosis group 3 (AG-3) (teleomorph = *Thanatephorus cucumeris*) are genetically diverse and can harbor double stranded RNA (dsRNA) mycoviruses. Recently, Tavantzis and colleagues have demonstrated that isogenic strains of *R. solani* AG-3 that possess the 3.6 kb dsRNA (M2) exhibited reduced virulence on potato stems. In this study, a sample of 115 isolates from a field population of *R. solani* AG-3 was examined for the M2 dsRNA with reverse transcription PCR (RT-PCR). The M2 dsRNA was detected in approximately 48% of the sample. Three regions consisting of 3248 bp of the M2 dsRNA from a subsample of 11 isolates were sequenced to examine the genetic diversity and to reconstruct the genealogical history of the M2 dsRNA. Ten haplotypes were inferred for each of the three regions and mutation rates were not significantly different between these three regions. A preliminary site compatibility analysis performed using SNAP Workbench for all putative clades in the M2 mycovirus strict consensus tree identified recombination events among the clades. M2 dsRNA haplotypes and clades will be examined further to determine their relationship with phenotypic characteristics of the fungus and to design transmission experiments. contributed presentation

Chatasiri, Sinchai^{1*} and Ono, Yoshitaka². ¹Graduate School of Science and Engineering, Ibaraki University, ²College of Education, Ibaraki University, 2-1-1 Bunkyo, Mito, Ibaraki 310-8512, Japan. herb-iba@mx.ibaraki.ac.jp. **Taxonomy and phylogeny of the *Puccinia hemerocallidis* species complex.**

Puccinia hemerocallidis is a pathogen of daylily rust native of East Asia; and it has recently invaded and established in North America and Australia. The fungus has long been believed to cause plantainlily rust as well. However, *P. hemerocallidis* and a pathogen of plantainlily rust, once named as *P. funkiae*, are found distinct in host specificity in their macrocyclic life cycle and urediniospore morphology; thus, the two fungi are taxonomically separated. *Puccinia patriniae* and *P. melanoplaca* are microcyclic, producing only telia/teliospores on different species of *Patrinia*, a spermogonial- aecial host genus of *P. hemerocallidis* and *P. funkiae*. *Puccinia patriniae* and *P. melanoplaca* are similar to *P. hemerocallidis* and *P. funkiae* in teliospore morphology. These suggest monophyly of the four species and evolutionary derivation of either one of the two or both microcyclic species from either *P. hemerocallidis* or *P. funkiae*. To determine possible phylogenetic relationships of the four species, ITS regions including 5.8S gene of small subunit rDNA were amplified by a PCR method, sequenced and analyzed. During the course of the study, *P. melanoplaca* was deleted from the consideration due to failure of rDNA amplification. The results show that the three species are monophyletic as indicated by their host specificity and teliospore morphology and indicate that *P. hemerocallidis* and *P. funkiae* had derived from a hypothetical common ancestor and *P. patriniae* had branched off from a hypothetical common ancestor shared by *P. hemerocallidis*. symposium presentation

Chavarria, Allan* and González, María C. Departamento de Botánica, Instituto de Biología, UNAM, Mexico. acchs2002@yahoo.com.mx. **Some freshwater mitospore fungi from Xochimilco, Mexico City.**

New records of freshwater mitospore fungi from Xochimilco, Mexico City, are described and illustrated. Sixty wood blocks (*Pinus* sp.) were submerged during 2 months in two canals and one lagoon. All the samples were placed in plastic bags and returned to the laboratory. Collected material was washed in tap water and placed in sterile plastic boxes containing paper towels and the samples were incubated at laboratory conditions. Woody substrates were examined periodically for the presence of fungal structures. The common recorded genera were *Arthrotrichum*, *Phoma*, *Taeniollla*, and *Trichocladium*. The present study is the

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first contribution on the knowledge of the biodiversity of the mitosporic fungi on submerged wood in lentic habitats of Mexico. poster

Chaverri, Priscila and Hodge, Kathie T.*. Dept. of Plant Pathology, Cornell University, Ithaca NY 14853, USA. pc234@cornell.edu. **Systematics of the entomopathogenic genus *Hypocrella*/Aschersonia: Stroma morphology correlates with monophyletic groups.**

Hypocrella (anamorph *Aschersonia*) contains species that are pathogenic on scale insects and white flies. Systematics research on the genus is scarce and outdated and its classification has been primarily based on phenotype (e.g. presence of paraphyses in the conidiomata) and ecology (e.g. insect host). The objectives of the present research are to study the systematics and phylogenetics of the genus *Hypocrella* and reveal morphological characters that correlate with monophyletic groups. To accomplish this, several phenotypic variables were evaluated for species of *Hypocrella*/*Aschersonia*: stroma morphology, presence of paraphyses in the conidiomata, and insect host (white fly vs. scale insect), among others. The morphological characters were then mapped onto a phylogenetic tree. The phylogenetic tree was constructed based on Bayesian Inference and Maximum Parsimony analyses of three gene loci: large subunit nuclear ribosomal DNA (LSU), translation elongation factor 1-alpha (TEF), and RNA polymerase II subunit 1 (RPB1). The results reveal three major monophyletic groups that correlate with stroma morphology: "Globose", "Effuse", and "Pulvinate". The Globose group contains species that have round, compact, hard or coriaceous, large stromata without hypothalli. The Effuse group includes species with effuse, flat stromata composed of loose hyphal tissue, with hypothalli. Species in the Pulvinate group are pulvinate or cushion-like, with or without hypothalli. On the other hand, molecular phylogenetic analyses reveal that presence of paraphyses and type of insect host are polyphyletic characters. The results of this research show that stroma morphology in *Hypocrella*/*Aschersonia* can be used to define natural monophyletic groups at the subgeneric level. poster

Chedgy, Russell¹, Lim, Young Woon^{1*}, Daniels, Robert², Morris, Paul I² and Breuil, Colette¹. ¹Department of Wood Science, University of British Columbia, Vancouver, BC, ²Forintek Canada Corp., 2665 East Mall, Vancouver, BC, V6T 1Z4 Canada. ywlim@interchange.ubc.ca. **Black stain of western red-cedar siding and shingles by *Aureobasidium pullulans* and its relationship with extractive depletion by weathering.**

Western red-cedar (WRC) (*Thuja plicata* (Donn.)) is valued for its natural durability conferred by fungicidal extractive chemicals present in its heartwood. As a result, this softwood is utilized heavily in the manufacture of exterior housing decor products which account for a significant proportion of Canada's value added forest products industry. However, such products are susceptible to black stain at weathered surfaces caused by the fungus *Aureobasidium pullulans* which drastically reduce their aesthetic qualities and in turn their useful service life. The effect of weathering on the extractive content of heartwood was characterized and correlated with the ability of *A. pullulans* to colonize the same weathered surfaces. Water spray and UV plus water spray regimes severely reduced extractive content but did not lead to increased colonization compared to un-weathered wood. Less decrease in extractive content was measured with the UV-only treatment, however, fungal colonization significantly increased. Isolates exhibited high tolerance to the tropolone beta-thujaplicin (considered a major fungicidal constituent of WRC extractives) in vitro; extractive content may not be the sole factor that determines colonization ability, products of lignin photo-degradation by UV could also be an important growth limiting factor; such compounds are likely washed away by water spray, leaving the surface void of accessible carbon sources. poster

Chiu, Siu-Wai*, Cheung, Ka-Wan, Chu, Mabel, Koo, Owen and Chuang, Philip. Dept. of Biology, The Chinese University of Hong Kong, Shatin, N.T., Hong Kong SAR, China. SWChiu@cuhk.edu.hk. **Pathogenesis of *Ganoderma lucidum*.**

Phenotypic plasticity leads to proliferation of names and misidentification in the species complex *Ganoderma lucidum*. The present study integrates field observation and artificial infection to define pathology of *G. lucidum* (W. Curt.: Fr.). Aerial basidiomes of *G. lucidum* were found on live *Acacia confusa*, *Albizia lebbek*, *Lephostemon confertus*, *Litsea cubeba* and *Cerbera manghas*. The latter three hosts are first reported. *A. confusa*, *L. cubeba* and *L. confertus* are popular afforestation species while *A. confusa* and *A. lebbek* are commonly planted in urban areas. This practice may explain the cosmopolitan distribution of *G. lucidum* in Hong Kong with *A. confusa* as the major host. Artificial infection failed with intact susceptible hosts but was established in artificially wounded plants of *A. confusa*, *L. cubeba* and *L. confertus* by *Ganoderma*-colonized grains of *Triticum aestivum*. *L. cubeba* was the most susceptible host with complete infection. This pathogen consumed host reserve materials, degraded host cell wall, spread intracellularly and ramified through wall pits or penetrated wall in host tissues as revealed by scanning electron microscopy. Using basidiospore suspension as inoculum, the infection rate was only 40% with wounded *L. cubeba*. Wounding in host seems to be a prerequisite for establishment of an infection. poster

Chiu, Siu-Wai, Yau, Sze-Nga*, Chan, Kam-Chi and Wang, Pui. Department of Biology, The Chinese University of Hong Kong, Shatin, N.T., Hong Kong SAR, China. SWChiu@cuhk.edu.hk. **Differential gene expression and activities of**

lignolytic enzymes of *Pleurotus pulmonarius* by lignocellulosic substrates and organopollutants.

Laccase (lac) and manganese-dependent peroxidase (MnP) can degrade both nutrient lignocellulosic substrates and a variety of organopollutants. This study examines the effect of normal substrates, straw and sawdust, and 7 organopollutants, namely: wood preservative PCP, plasticizer DEHP, DDT dead-end metabolite DDE, azo dye Congo red, and 3 PAHs, on lignolytic enzymes and their gene expression of *Pleurotus pulmonarius*, an edible fungus commercially cultivated in tropical and subtropical regions. PCP and the PAHs were toxic to *P. pulmonarius*. Most organopollutants were efficiently removed in 4 days except PCP. Constitutive low levels of laccase and MnP were detected in all cultures. PCP, straw and sawdust greatly increased specific laccase and MnP activities but only PCP increased laccase and MnP productivities. By RT-PCR, differential expression profiles comprised of 5 MnP genes and 7 laccase genes under the modulation of these substrates revealed differences. Gene PPMnPI was totally repressed by the lignocellulosic substrates. Gene PPlac6 was upregulated by all the organopollutants tested. Even at the first hour of exposure to PCP, up-regulation of expression of gene PPlac6 was significantly detected and peaked at 48 hours by real-time PCR. Thus *P. pulmonarius* is a potential bioremediating agent for environmental cleanup. contributed presentation

Chum, Wing Yan, Ng, Tak-Pan, Bian, Xue-Lin, Shih, Sheung-Mei and Kwan, Hoi-Shan. Dept. of Biology, The Chinese University of Hong Kong, Shatin, Hong Kong SAR, China. winnie_chum@yahoo.com. **Serial analysis of gene expression of dikaryotic mycelium and primordium of Shiitake mushroom, *Lentinula edodes*.**

Lentinula edodes (*L. edodes*) is a popular cultivated mushroom because of its high nutritional value and good taste. We used Serial Analysis of Gene Expression (SAGE) to analyze genes expressed in different developmental stages of *L. edodes*. SAGE is an efficient molecular method to count transcripts and identify novel genes, using 3 steps: 1) 9-13bp sequence tags are extracted from mRNAs by NlaIII anchoring enzyme 2) Concatemers are created from tags for cloning and sequencing 3) SAGE tags are extracted from raw sequences and analyzed by the SAGE™ analysis software mRNAs from the dikaryotic mycelial and the primordial stages of *L. edodes* were extracted to generate SAGE libraries. Over 200 colonies were randomly selected from each SAGE library for sequencing. A total of 6844 tags were collected, 3395 tags from the primordium SAGE library and 3349 tags from the dikaryotic mycelium SAGE library. About 200 unique tags were matched to the ESTs generated from primordial stage of *L. edodes* and were catalogued using the Expressed Gene Anatomy Database (EGAD). In dikaryotic mycelial stage, among the matched unique tags, 1.1 % was involved in cell division, 4.4 % in cell signalling, 3.3 % in cell structure, 9.8 % cell defence, 21.7 % in gene/protein expression, and 16.3 % in metabolism. In the primordial stage, among the matched unique tags, 6.7 % was involved in cell division, 3.4 % in cell signalling, 1.7 % in cell structure, 10.9% in cell defence, 29.4 % in gene/protein expression, and 16.8 % in metabolism. Most interestingly, genes expressed at high levels in one stage were expressed at low levels in the other stage. When comparing SAGE tags of these 2 developmental stages, we have a better understanding of *L. edodes* development. To validate the result obtained from SAGE, cDNA microarray analysis on the ESTs in mycelial and primordial stages was performed. Also, the expression profile of some abundant SAGE tags was confirmed by Northern blotting. Our studies indicate that SAGE is reliable to determine gene expression profiles and to identify differentially expressed novel genes, providing data that are difficult to achieve by conventional methods. poster

Chung, Wen-Hsin*, Chen, Chi-Yu², Huang, Jenn-Wen², Yamaoka, Yuichi¹, Ono, Yoshitaka³ and Kakishima, Makoto¹. ¹Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan, ²Department of Plant Pathology, National Chung Hsing University, Taichung 402, Taiwan, ROC, ³College of Education, Ibaraki University, Mito, Ibaraki, Japan. wenchung@niaes.affrc.go.jp. **Rust fungi newly recorded in Taiwan.**

In Taiwan, 334 species in 41 teleomorphic genera and 109 anamorphic species have been recorded. These figures are far greater in terms of species number per unit area than those calculated for Japan, one of the most intensively studied geographic regions for the rust fungi. This indicates that more intensive explorations than what had been done in the past would find new taxa or new host/distribution records in Taiwan. In the field studies undertaken central and southern Taiwan in the past two years, over 200 rust specimens were collected. Among these specimens, *Puccinia fusispora* on *Urtica thunbergiana* (Urticaceae), *P. paullula* on *Raphidophora* sp. (Araceae) and *Pucciniastrum potentillae* on *Fragaria hayatai* (Rosaceae) were found as new geographic distribution records. A rust fungus on *Alpinia* sp. (Zingiberaceae) was found unique in producing urediniospores in the substomatal cavity of the host tissues as in *Marvalia pseudo-suprastomatilis* that occurs on *Globba* sp. (Zingiberaceae) and considered as a new anamorphic species. A rust fungus on *Dioscorea* sp. collected in Shanping Forest Park, Kaohsiung Co. was identified as *Uredo spinulosa*. This is the second record of this rare rust fungus, which was first recorded in Hengchun, Pingtung Co. poster

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MSA ABSTRACTS

Clark, Malcolm* and Bailey, Chris. Gourmet Mushrooms, Inc., P.O. Box 180, Sebastopol, CA 95473, USA. chris@mycopia.com. **Organic mushroom production.**

There is a clear and growing desire in markets around the world for natural foods, free of pesticides and additives that may be harmful to human health. Additionally, the call for foods free of genetic manipulation (GMO-free) is increasing. There is debate in the scientific community over the health advantages of such mushrooms and mushroom products. However, it is possible to produce organic mushrooms with relatively few cost disadvantages and it therefore behooves growers to consider filling this market niche. We at Gourmet Mushrooms, Inc. take the position that it is our responsibility to present the highest quality product to the consumer. Organic certification is one route we take to do this. poster

Clark, Travis A.* and Anderson, James B. Department of Botany, University of Toronto, Mississauga, Ontario L5L 1C6, Canada. travis.clark@utoronto.ca. **Ploidy determines evolvability in filamentous basidiomycetes.**

The dikaryon represents a novel alternative to diploidy in that both gametic genomes are present, but are maintained in separate nuclei in each cell. The objective of our research was to evaluate the adaptive and evolutionary implications of dikaryosis, relative to those of haploidy and diploidy. Laboratory populations have been maintained over long-term evolution (24 months or ~17,500 generations) to determine if haploid and dikaryotic mycelia of *Schizophyllum commune* adapt to novel environments under natural selection. The fitness of the experimental lines was evaluated in 20 different environments to determine the extent of changes in phenotypic plasticity over time. The results strongly suggest that the dikaryotic phase of the lifecycle has the greater potential for expressing phenotypic change than the haploid stage. Additional experiments have been conducted to compare the adaptive potential of the dikaryon with the isogenic diploid. The dikaryons and diploids differ with respect to their patterns of gene by environment interaction. They had an equivalent response in 24 treatments (48 %), the dikaryons grew better in 15 treatments (30 %) and the diploids grew better in 11 treatments (22 %). The results clearly show that dikaryons and diploids have differences in the expression of their phenotype associated with the spatial distribution of equivalent genomes within a cell. contributed presentation

Coetzee, Martin, P.A.¹, Maphosa, Lance¹, Mwenje, Eddie², Wingfield, Michael J.¹ and Wingfield, Brenda D.^{1*}. ¹Dept. Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa, ²Dept. Applied Biology and Biochemistry, National University of Science and Technology, P.O. Box AC 939, Ascot, Bulawayo, Zimbabwe. martin.coetzee@fabi.up.ac.za. **Biochemical and DNA based characterization of *Armillaria* spp.**

Armillaria spp. are important pathogens that cause Armillaria root rot on a wide variety of plants. Species of *Armillaria* are found worldwide where they can cause major losses to the forestry and agricultural industries. Reliable identification of *Armillaria* spp. is essential for successful disease management. Accurate identification of these fungi has improved greatly subsequent to the application of DNA sequence analyses. This technology is, however, not available in many institutes in developing world countries. Isozyme based identification systems are less expensive than DNA-based techniques and have been successfully used to identify *Armillaria* spp. The aim of this study was to determine congruence in the relationships between different *Armillaria* spp. based on isozyme and DNA sequence data. Isozymes employed were pectin lyase, pectin methylesterase and polygalacturonase. DNA sequence data were obtained from the Elongation Factor (EF) 1-alpha gene. Euclidean distances were calculated from the isozyme patterns and used to generate a dendrogram. Cladograms were obtained from the EF 1-alpha sequences based on parsimony analysis. The trees were then compared with each other as well as with cladograms previously published based on ITS and IGS-1 sequence data. Results showed that isozyme data could be used to separate isolates into groups representing their respective species. Generally, the topologies of trees from this study were similar. They also correlated well with those emerging from previous comparisons using ITS and IGS-1 sequence data. Isozymes, therefore, provide an inexpensive and useful tool for identifying *Armillaria* species. poster

Cohen, Susan D. USDA APHIS, Policy and Program Development, Animal and Plant Health Inspection Service, U.S. Department of Agriculture, Riverdale, MD 20737, USA. susan.d.cohen@aphis.usda.gov. **Potential distribution of *Melampsora larici-populina* in the USA predicted based on physiological responses of spore types to climate variables.**

The labyrinthulids are common marine protists, some of which cause devastating diseases on seagrasses and other marine organisms. On the basis of morphological characteristics that typify the genus, a *Labyrinthula* sp. has recently been reported as the causal agent of an emerging disease of land plants, namely "rapid blight" in cool-season turfgrasses. We previously utilized ssRNA gene sequences to determine the phylogenetic relationships of 11 "rapid blight" pathogens isolated from four species of diseased turfgrass collected across the U.S. All of the isolates grouped very closely to other *Labyrinthula* spp., confirming their genetic identity and supporting previous morphological characterization. Further, our analysis showed that all of the turf pathogens examined form a monophyletic clade and have very little genetic diversity, suggesting they share a recent

common ancestor and that colonization of land plants may have occurred once in the evolution of these unique organisms. We are currently sequencing additional gene fragments from the translation elongation factor (*tefl-a*) and mating type (*mat*) loci to examine whether detectable genetic diversity exists among rapid blight pathogens. We will present results of these investigations to date. poster

Crane, Patricia E. Forest Research, P.O. Box 3020, Rotorua, New Zealand. pat.crane@forestresearch.co.nz. **Taxonomy and species relationships in the genus *Chrysomyxa*.**

Most species in the genus *Chrysomyxa* are part of a closely related group of heteroecious rust fungi that alternate between *Picea* and plants in the Ericaceae, particularly *Rhododendron*. In a systematic study of the genus, scanning electron microscopy was applied to the spore morphology for the first time, and has resulted in a new understanding of the diversity of species in the genus. In particular, several taxa in North America and Asia that have traditionally been named *C. rhododendri* or *C. ledi*, based on European species, have been shown to have unique morphology that correlates with host specificity. Furthermore, taxa that infect the same subgenus of *Rhododendron* often share similar spore and sorus morphology, suggesting coevolution with these hosts. Many questions remain unanswered for the genus, including the relationship of autoecious to heteroecious species and the relationship of species with stalked telia to those with sessile telia. symposium presentation

Craven, Kelly D.^{1*}, Lawrence, Christopher B.² and Mitchell, Thomas K.¹. ¹Dept. of Plant Pathology, North Carolina State University, Raleigh, NC 27606, USA, ²Virginia Bioinformatics Institute, Blacksburg, VA, USA. kdcraven@ncsu.edu. **Acquisition and transmission of pathogenicity factors in the genus *Alternaria* through horizontal gene transfer.**

Many distinct pathotypes and species of *Alternaria* have been shown to produce host-selective toxins required for disease on plants, and further, that the toxin biosynthetic genes are typically located on small, conditionally dispensable (CD) chromosomes. Despite their crucial role in disease development, such chromosomes are not characteristic of all isolates of a given fungal species, and thus are likely to be under-represented in genome sequences of organisms containing them. We chose the tomato pathogen, *A. arborescens*, from which to isolate a known 1.0 Mb CD chromosome for library construction and sequencing. Approximately 500 sequences have been obtained thus far, of which roughly half appear bacterial in nature, with no known fungal homologs in publicly available databases. It has been postulated that the clustering of pathogenicity genes on CD chromosomes may allow for efficient horizontal transfer between fungal strains or species through hyphal fusion (anastomosis). We are investigating the role anastomosis plays in mediating gene flow within and between *Alternaria* species through the construction of nitrate-utilization mutants and strains marked with distinct antibiotic resistance genes. Our evidence shows that hyphal anastomosis occurs readily both within and between *Alternaria* species, suggesting that genes required for pathogenicity may be transferred between *Alternaria* fungi in nature. poster

Craven, Kelly D.^{1*}, Peterson, Paul D.², Martin, Stan B.² and Mitchell, Thomas K.¹. ¹Dept. of Plant Pathology, North Carolina State University, Raleigh, NC 27606, USA, ²Clemson University, Clemson, SC, USA. kdcraven@ncsu.edu. **Genetic diversity among rapid blight pathogens of cool-season turfgrass.**

Melampsora larici-populina (Eurasian Poplar Leaf Rust) is considered a recent exotic introduction to the USA; however, the extent of its potential geographic distribution range in the USA is unknown. A climate modeling approach using Climex version 2.0, was used to estimate this potential distribution. Climex usually contains data from 3,935 meteorological stations in the USA; this study was supplemented with an additional 1,589 stations. Each station contains a 30-year dataset with monthly averages for maximum temperature, minimum temperature, and precipitation from 1979-2000. Germination responses of urediniospores and teliospores to temperature and rainfall were modeled and compared to existing locations in the USA. Temperature modeling revealed 23 % of the meteorological stations were considered favorable for urediniospore germination and less than 1 % of the stations were favorable for teliospore survival. Rainfall patterns greater than 1,000 mm annually, or 38 % of the locations, were favorable for disease outbreaks. Climate model results were mapped using Climex software based on three predicted areas of establishment categorized as unsuitable (25 % similarity), marginal (50 % similarity) and favorable (75 % similarity). Results from these models were validated with survey results from overseas locations published in the scientific literature. Based on this study with *Melampsora larici-populina*, climate modeling will enhance the risk assessment process for fungal pathogens. poster

Cripps, Cathy L. Plant Sciences and Plant Pathology Dept., Montana State University, Bozeman MT 59717, USA. CCripps@montana.edu. ***Amanita* in the Rocky Mountain alpine zone: Where mycorrhizal mushrooms tower over miniature forests.**

Amanita is an important ectomycorrhizal genus with a North American seat

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of diversity in the warm climates of the southeastern states. However, it occurs with limited diversity in the cold-dominated Arctic-alpine biome. Here, lofty sporocarps tower above miniature forests of dwarf willow in a stunning reversal of canopy strata. A number of arctic-alpine macromycetes have circumpolar distributions across northern mountain tops and arctic tundra. This is true for the *Amanita nivalis* group, while *A. arctica* and *A. groenlandica* appear more restricted. There are reports of Arctic-alpine Amanitas from North America (Alaska, Canada), but virtually nothing is known for the Rocky Mountain alpine zone south of the Canadian border. Our NSF sponsored survey of the Alpine Mycota of this region revealed one section of the genus (Vaginatae) above treeline, and we report several species: *Amanita nivalis* s.l., *Amanita vaginata* (rare) and a new species *Amanita absarokensis*. Interestingly, *A. nivalis* is recorded only from the southern Rockies thousands of miles from the arctic, *A. absarokensis* only from the northern Rockies (Beartooth Plateau, WY/MT), and distributions to not appear to overlap. Mycorrhizal hosts include dwarf willows *Salix reticulata*, *S. arctica*, and shrub willow *S. glauca*. Neither *A. nivalis* nor *A. absarokensis* are recorded with willows below treeline in the Rockies. contributed presentation

Davidson, Jennifer M.^{1*}, Maloney, Patricia E.², Fichtner, Elizabeth J.², Falk, Kristen, R.², Jensen, Camille², Kane, Sarah F.² and Lynch, Shannon C.². ¹Dept. of Zoology, University of Hawai'i, Honolulu HI 96822, USA; ²Dept. of Plant Pathology, University of California, Davis CA 95616, USA. jmd@hawaii.edu. **Long-term monitoring of inoculum production by *Phytophthora ramorum* in mixed-evergreen and tanoak-redwood forest in California.**

We tracked timing and levels of inoculum production by *Phytophthora ramorum* in two common forest types, mixed-evergreen and tanoak-redwood forest, in coastal, northern California during the past four years. Significant year-to-year variation in inoculum production occurred within and between forest types. In addition, timing of inoculum production tended to occur later in mixed-evergreen as opposed to tanoak-redwood forest. This lag may be due, in part, to a greater decrease in the inoculum reservoir in bay laurel (*Umbellularia californica*) leaves, the main source of inoculum, during the hot, dry summer months in mixed-evergreen forest. In support of this hypothesis, in 2002 and 2003, recovery of *P. ramorum* from attached, infected bay laurel leaves declined from over 90% at the beginning of the summer in both forest types to 25% in mixed-evergreen forest versus 60% in tanoak-redwood forest. Measurements taken at the end of summer in 2004 showed that bay laurel leaves from mixed-evergreen forest had significantly lower moisture content and water potential than bay laurel leaves from tanoak-redwood forest. Further studies are planned to address the influence of tree water potential on summer survival of *P. ramorum* in bay laurel leaves, and the corresponding effects on timing of inoculum production in these two forest types. contributed presentation

Davis, E. Christine and Shaw, Jon. Dept. of Biology, Duke University, P.O. Box 90338, Durham NC 27708, USA. christine.davis@duke.edu. **Surveys of liverwort-associated endophytes in North America, Europe, and New Zealand reveal unexpectedly rich fungal communities.**

Surveys of liverwort endophytes were conducted in North Carolina, the Pacific Northwest (Washington, Idaho, British Columbia), Germany, and New Zealand. Nearly 100% of the fungi cultured were Ascomycota. All major lineages of non-lichenized ascomycetes were recovered, however 50-80% of cultures were Xylariales. Species-accumulation curves reveal that most endophytic fungi encountered were singletons (found only once), and that liverwort endophytes are very diverse. There was no significant difference in species richness between North Carolina, the Pacific Northwest, Germany, or New Zealand. Extrapolation estimators indicate that North Carolina and New Zealand are likely to be significantly richer than Germany or the Pacific Northwest with larger survey sizes. This prediction is due to the increased frequency of uninfected hosts in both Germany and the Pacific Northwest, as well as decreases in richness and species shifts in the Xylarialean community. In both of these sample regions, the same species of *Nemania* was the commonest isolate encountered. This similarity is likely due to similarity in overall plant communities: conifers dominate both Germany and Pacific Northwest sample sites. Implications of this finding toward understanding the ecology of Xylariaceous endophytes are discussed. poster

Day, Melissa^{1*}, Gibas, Connie¹, Fujimura, Kei², Egger, Keith² and Currah, Randolph S.¹. ¹Dept. of Biological Sciences, University of Alberta, Edmonton AB T6G 2E9, Canada, ²Ecosystem Science and Management Program, University of Northern British Columbia, Prince George BC V2N 4Z9, Canada. mjday@ualberta.ca. **Root endophytic *Cryptosporiopsis* species from the Canadian High Arctic.**

Species of the hyphomycete genus *Cryptosporiopsis* have teleomorphs in *Pezizula* and *Fabraea* (Helotiales) and have been reported as either endophytes or pathogens in a wide range of plant species from temperate regions of the world. Recently, we isolated species of this genus from the roots of *Cassiope tetragona*, *Dryas octopetala*, *Salix arctica*, and *Saxifraga oppositifolia* collected from Ellesmere Island in the Canadian High Arctic (79 degrees N, 76 degrees W). Colonies are cream to light brown, sometimes causing dark brown discoloration of the medium. Straight to curved, cylindrical, hyaline macrospores 15-20 micrometers in length and filled with oil droplets were produced. Microconidia were absent. Molecular data indicates the presence of two species: *C. radiculara*

Kowalski & Bartnik and *C. ericaecea* Sigler. Prior reports of dark septate endophytes (DSE) in the roots of arctic or alpine plants refer to *Phialocephala fortinii* and *Leptodontidium orchidicola* but there are no reports of species of *Cryptosporiopsis* in these habitats. Like other DSE, the species seemed to have little host specificity. poster

De Meyer, Elsie M.^{1*}, De Beer, Z. Wilhelm¹, Vismer, Hester F.² and Wingfield, Michael J.¹. ¹Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, 0002, South Africa, ²PROMEC Unit, Medical Research Council, P.O. Box 19070, Tygerberg, 7505, South Africa. elsie.demeyer@fabi.up.ac.za. ***Sporothrix* spp. associated with utility pole decay in Southern Africa.**

Wooden utility poles are widely used in electricity distribution networks throughout Southern Africa. These poles are continuously degraded by microorganisms, particularly fungi. In a recent survey of the fungi responsible for decay of wooden poles in South Africa, several isolates of *Sporothrix* were collected. The aim of this study was to identify these isolates. Based on micro-morphology, growth studies, and sequences of the ITS 1 and 2 regions of the ribosomal DNA operon and part of the beta-tubulin gene, isolates from poles could be separated into two distinct groups. One of these groups included isolates with a morphology similar to *S. schenckii*. Sequences confirmed that these isolates were the same as environmental isolates of *S. schenckii*, previously shown to be distinct from clinical isolates. Growth studies showed that the environmental isolates of *S. schenckii*, including those from poles, grew significantly faster than clinical isolates of this fungus. Isolates in the other group from poles, were clearly distinct in morphology, growth characteristics and sequences from those in the *S. schenckii* group as well as from all other *Sporothrix* spp. included in the study. We conclude that the *Sporothrix* spp. from utility poles in South Africa represent two distinct species and these are currently being described. poster

De Vos, Lieschen^{1*}, Myburg, Alexander A.¹, Wingfield, Michael J.² and Wingfield, Brenda D.¹. ¹Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, S. Africa, ²Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, S. Africa. lbahlman@fabi.up.ac.za. **Genetic linkage analysis of pathogenicity in a unique cross between *Fusarium circinatum* and *F. subglutinans*.**

Fusarium isolates that are associated with the *Gibberella fujikuroi* species complex include at least nine different biological species (mating population A-I) that are reproductively isolated. In a recent study, a cross between *F. circinatum* and *F. subglutinans* (mating population H and E) was reported. The aim of this study was to generate a genetic linkage map of the two species as well as to identify possible Quantitative Trait Loci (QTLs) linked to pathogenicity of the pitch canker parent in an F2 backcross population. A framework map was constructed using 582 Amplified Fragment Length Polymorphism (AFLP) markers, the mating type (*MAT-1* and *MAT-2*) and histone (*H3*) genes. A total of 12 linkage groups were identified. The F2 backcross population was derived from an F1 hybrid isolate that was backcrossed to the pitch canker parent. Results of inoculations using 94 F2 backcross individuals on susceptible *Pinus patula* seedlings showed that lesion length had a heritability (H2) of 0.30. Although not high, this indicates an appreciable amount of genetic control for pathogenicity. AFLP analysis was performed on these backcross individuals using the same AFLP primer combinations previously used. Identification of QTLs will provide powerful tools to study the genetic architecture of interspecific differentiation of pathogenicity in the two parental genomes. contributed presentation

Dean, Ralph A. Center for Integrated Fungal Research, Dept. Plant Pathology, North Carolina State University, USA. ralph_dean@ncsu.edu. **The rice blast story: from genome sequence to function.**

Magnaporthe grisea is the causal agent of rice blast, the most devastating disease of rice world-wide. Because of its molecular genetic tractability the rice blast pathosystem has emerged as a seminal model to elucidate the basis of pathogen-host interactions. Over the past few years, international consortia were successful in obtaining complete genome sequences for both *Magnaporthe* and rice. Other recent initiatives have resulted in genome sequences for several other pathogenic and non-pathogenic filamentous fungi. With this wealth of new information, providing access to the raw components of the pathogen's offensive arsenal and host's defenses, how far have we come to understand the molecular basis of disease outcome? In my presentation I will discuss some of the novel discoveries that have only come to light as a result of having access to the genome sequences, such as novel classes of secreted proteins, surface receptors and large suites of enzymes involved in secondary metabolism that may play a role in the disease process. I will also highlight some of the limitations of the current state of knowledge, such as inadequate gene predictions, lack of sensible annotation of the majority of predicted genes and little knowledge of gene function. To address the latter I will discuss recent results from functional analyses including transcription profiling and gene knockout experiments. I will close with some thoughts on strategies and other resources needed to fully appreciate this host-pathogen interaction. symposium presentation

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Degawa, Yousuke. Kanagawa Prefectural Museum of Natural History, 499, Iryuda, Odawara, Kanagawa 250-0031, Japan. degawa@nh.kanagawa-museum.jp. **Taxonomic studies on the family Mortierellaceae.**

The family Mortierellaceae is one of the well-known soil fungi, including about 100 spp. The difficulties to maintain their sporulation and insufficient information on sexual reproduction prevented constructing a natural classification of the family. Direct field observation on their microhabitats enabled to establish a baiting method for selective isolation of each species, and a good condition for inducing the sexual reproduction. Using the dead bodies of arthropods as baits, new or rare species were repeatedly obtained. Six species of them belonged to the Section *Actinomortierella*, four of which were new. Five of them were heterothallic and showed new style of zygospore formation on the medium containing arthropods. Based on these ecological and morphological characters, the concept of the section was revised, and treated it as an independent genus. Five heterothallic species of the genus *Actinomortierella* were biologically isolated. Furthermore, within *A. capitata*, morphologically identical two intraspecific isolated mating groups were detected. They showed clear differences in geographical distribution (tropical and temperate area), and temperature ranges for mycelial growth and zygospore production. Molecular analysis on 18SrDNA ITS region suggested that each mating group should be treated as an independent species respectively. contributed presentation: **MSJ Research Encouragement Award Lecture**

Degawa, Yousuke^{1*} and Sato, Hiroki². ¹Kanagawa Prefectural Museum of Natural History, 499, Iryuda, Odawara, Kanagawa 250-0031, Japan, ²Kyushu Research Center, Forestry and Forest Research Institute, 11-16, Kurokami 4 chome, Kumamoto, Kumamoto 860-0862, Japan. degawa@nh.kanagawa-museum.jp. **How to clarify the true status of anamorphic Trichomycetes? -an approach based on the observation of its host animal behavior.**

The orders Asellariales and Eccrinales are anamorphic Trichomycetes, in which neither zygospore nor trichospore has been known. Do they lose these kinds of spores? Careful observations on the living hosts brought us invaluable hints for solving this question. In *Orchesellaria mauguioi* (Asellariales), trichospore-like spore formation was observed when the hosts (*Isotomurus* sp.) were keeping on the water in chamber. They often molted and their shed molts floated on the water. The fungal thalli were situated at the lower surface of the molts in water. Arthrospores germinated to produce short stalks penetrating the molt and bearing the thick walled, cylindrical spores on their tips. Each spore accompanied a bowling-pin-shaped thin walled cell with external long appendage, which reminds us the fructification of the genus *Orphella*. When the millipede (*Epanerchodus* sp.), a host of *Enterobryus* sp. (Eccrinales) was keeping in moist chamber, peculiar conidiophore with mushroom-shaped conidia often emerged on the accumulated dung of hosts. This fungus was identified as a rare hyphomycete, *Aenigmatospora pulchra* R. F. Castaneda Ruiz *et al.*, described from Cuba. The stalk of this fungus was constantly connected to the short cylindrical 2 or 3-celled hyphal segments, similar to the arthrospores of *Enterobryus* sp., buried in the dung. The implications of these newly found spores are discussed. symposium presentation

Dentinger, Bryn C.* and McLaughlin, David J. Plant Biological Sciences, University of Minnesota, St. Paul, MN 55108, USA. dent0015@umn.edu. **Homoplastic surgery: reconstructing the classification of two coral mushroom families (Clavariaceae and Pterulaceae).**

Club and coral fungi are a polyphyletic assemblage of hymenomycetous mushrooms. The clavarioid sporocarp has repeatedly evolved in the Homobasidiomycetidae (Pine *et al.* 1999), yet to what degree this morphology is homoplasious is still not completely known. We evaluated the systematics of the coral mushroom families Clavariaceae and Pterulaceae using DNA sequence data and multiple phylogenetic methods. We generated 35 sequences from the 5' region of the nuLSU rDNA spanning 10 genera and 19 species of clavarioid fungi. These sequences, plus 45 published sequences, were aligned to the dataset of Moncalvo *et al.* (2002) and analyzed under the parsimony criterion. Based on this analysis, subsets of *Clavaria* and Pterulaceae were evaluated separately to obtain better resolution within each group. Our preliminary results indicate that both Clavariaceae and Pterulaceae need to be revised in order to reflect a monophyletic classification. The genus *Clavaria* appears to be monophyletic, but also requires revision to include some species while excluding others. Several species of *Pterula* are identified within the G2 cultivar clade of fungus-farming ants for the first time. These results provide a preliminary view of the systematics of two core families of coral mushrooms, contribute to understanding the history of the ant-fungus mutualism, and present a framework for future investigation. poster

Desjardin, Dennis E.^{1*} and Hemmes, Don E.² ¹Dept. of Biology, San Francisco State University, San Francisco, CA 94132, USA, ²Dept. of Biology, University of Hawai'i, Hilo, Hawai'i 96720, USA. ded@sfsu.edu. **Agaricales of the native forests of Hawai'i.**

The Hawaiian Archipelago is the most isolated oceanic island group on earth. Constantly forming, migrating and subsiding, the volcanic chain has formed land that has remained above sea level continuously for the past 29 million years, resulting in terrestrial laboratories for the evolution of a diverse biota. Human

habitation over the past 2000 years has dramatically impacted the landscape. Currently, over 90 % of Hawaiian terrestrial habitats are dominated by introduced plants (>4600 spp.), whereas less than 10 % remains in undisturbed native forests. As a consequence of these factors, the Islands display some of the highest levels of endemism and extinction documented to date. The diversity of Hawaiian Agaricales also reflects these factors. Of the 335 species documented by us to date, 275 are associated with introduced plants in non-native habitats, whereas only 60 species (18 %) are known from native habitats and are considered by us as native species with 75 % endemism. Surprising observations include: the low diversity of native Agaricales; no native Hawaiian trees support ectomycorrhizae; native Hawaiian Agaricales are dominated by Tricholomataceae *s.l.* and Hygrophoraceae *s.l.*; there is very limited adaptive radiation within native agaric lineages. We will present data from 12 years of fieldwork, focused on the diversity and origins of native Hawaiian Agaricales. symposium presentation

Dickie, Ian A.^{1*}, Dentinger, Bryn C.⁴, Avis, Pete G.³, McLaughlin, David J.⁴ and Reich, P. B.² ¹Landcare Research - Manaaki Whenua, P.O. Box 69, Lincoln, Canterbury, New Zealand, ²Department of Forest Resources, University of Minnesota, Green Hall, 1530 Cleveland Ave. N., St. Paul, MN 55108, USA, ³Chicago Field Museum of Natural History, Botany Department, Roosevelt Rd. at Lakeshore Drive, Chicago, IL 60605, USA, ⁴Department of Plant Biology, University of Minnesota, 250 Biological Science Center, 1445 Gortner Ave, St. Paul, MN 55108, USA. dickiei@landcareresearch.co.nz. **Ectomycorrhizal fungi of North American oak savannas.**

Oak savannas, once a dominant ecosystem of Midwestern North America, have all but disappeared from the landscape. Although much of oak savanna has been lost to agricultural conversion, other areas have converted to oak woodlands due to suppression of fire. We compare the ectomycorrhizal fungal community of Minnesota oak savannas subjected to frequent fire as a restoration tool with former oak savannas that have converted to oak woodlands due to fire suppression. Ectomycorrhizal root tip surveys using RFLP analysis and sporocarp collections, and T-RFLP analysis of rhizosphere fungi gave somewhat different views of community composition, but all suggest an extremely high diversity of fungi in these systems (estimated at more than 250 species of ectomycorrhizal fungi), with the fungal community broadly dominated by *Cenococcum* and *Russula* spp., with more local dominance by other groups. The high diversity of fungi is remarkable, given the low diversity of ectomycorrhizal host plants (three to four species). Although we predicted that frequent fire might make savanna mycorrhizal communities more prone to invasion than oak woodland fungal communities, reciprocal bulk soil transfers between plots had idiosyncratic effects on fungal communities as measured by T-RFLP. Nonetheless, T-RFLP did distinguish between site differences and showed similar patterns of species dominance as root tip collections. contributed presentation

Douhan, Greg W.^{1*}, Martin, Darren P.² and Rizzo, David M.¹ ¹Department of Plant Pathology, University of California, Davis, CA, 95616, USA, ²Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, Observatory, 7925, South Africa. gwdouhan@ucdavis.edu. **Intragenic recombination within an actin locus of the ectomycorrhizal fungus *Cenococcum geophilum*.**

We have recently detected three divergent lineages of *Cenococcum geophilum* isolated from a California oak-woodland. One lineage contained two divergent subclades; within this lineage incongruent phylogenies of one mitochondrial and three nuclear genes suggested potential recombination, but only when isolates from outside of the studied population were included in the analysis. To further investigate recombination in our local population of this putative asexual fungus, additional loci were sequenced from 44 isolates. Phylogenetic incongruence between these 10 loci is consistent with recombination occurring within the local population. However, most of the incongruence was caused by potential recombinant sequence types within the actin locus (~240 bp). Additional sequence data from the actin locus (~1300 bp) were obtained from parental and recombinant sequence types. Recombination analyses (RDP, GENECONV, MAXCHI, CHIMAERA, SISCAN and BOOTSCAN) using the recombination detection program RDP2 detected intragenic recombination and a potential recombination breakpoint with the actin locus. However, the divergence between the two subclades suggests that the recombination event is ancient or was due to some type of horizontal gene transfer or parasexual event. Actin sequence data from a world-wide sample of *Cenococcum geophilum* may help to differentiate between these two hypotheses. poster

Douhan, LeAnn I., Andrews, John H., Douhan, Greg W. and Rizzo, David M. Department of Plant Pathology, University of California, Davis, CA, 95616, USA. lidouhan@ucdavis.edu. **Phyllosphere fungi associated with bay laurel trees in California.**

Phytophthora ramorum (Pr), causal agent of sudden oak death, is an emerging pathogen in coastal forests of CA and OR. Pr is a generalist that also causes leaf necrosis on many native hosts. In particular, bay laurel (*Umbellularia californica*) serves as a foliar host that supports high levels of sporulation by Pr and plays a key role in the spread of the pathogen. The presence of other leaf colo-

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nizing fungi on bay laurel, both epiphytes and endophytes, may influence the establishment of Pr on this host. To understand the diversity of the fungal community associated with bay laurel leaves, we are using both cultural and molecular methods. The primers ITS1F and LR3 were used to amplify a region that includes the highly variable ITS regions but also covers the conserved LSU-rDNA. Preliminary data has demonstrated a diverse assemblage of phyllosphere fungi based on clones derived from DNA extractions from adhesive tape strips applied to the leaf surface. We also found that most clones could not be identified because no close matches were found in the ITS regions and only the 5.8s region gave strong hits based on BLAST searches. However, the clones could be identified with better resolution based on LSU-rDNA. In contrast, most fungi cultured from leaf surfaces were represented in GenBank based on ITS. This suggests that the unidentified epiphytes are possibly unculturable using standard approaches and/or may be unknown taxa. poster

Dubey, Tara. AerotechP&K, 1220 Quarry Lane, Pleasanton CA 94566, USA. TDubey@aerotechpk.com. **Factors affecting the collection of air samples for spore counts.**

Spore trap analysis for counting fungal spores present in the air, serves as primary criteria for the detection of mold problem present inside a building. Severity of the mold problem inside a building is estimated by comparing the presence or absence of genera in outdoor samples and by comparing if indoor spore counts are higher than outdoor spore counts. In order to make these techniques more dependable, it is essential to understand the effect of various natural and technical factors influencing the spore distribution in outdoor environment. Air samples from outdoor air were analyzed to see fungal diversity and their distribution pattern during different hours of the day to see the effect of light, temp. humidity, wind and volume of the sampled air. Samples were collected for 5 minutes at different times of the day (8am, 12pm, 4pm, 8pm, 12 am, and 4am), and at 12 noon for different durations (5, 10, 30, and 60 minutes) with a rate of 15 liters/minute. A comparison of percent trace analyzed (15%, 25% and 100%) indicated the significant counts lost due to partial analysis of a trace. Over all, *Cladosporium*, *Penicillium/Aspergillus*. were most predominating spore types followed by *Alternaria*, *Rust/Smut* types of spores. Maximum spore count was seen during morning indicating the significant role of sunlight in spore releasing process. poster

Dulmer, Kristopher M. and Horton, Thomas R.* Environmental Forest Biology, State University of New York- Environmental Science and Forestry, Syracuse, NY 13210, USA. kdulmer@hotmail.com. **Evidence that American chestnut seedlings tap into existing ectomycorrhizal networks of non-chestnut hosts.**

The ectomycorrhizal (EM) communities of American chestnut (*Castanea dentata*) (AC) were explored in a forest setting in order to evaluate their potential for associating with EM networks of canopy trees. AC seed were planted in spring in three different red and white oak dominated sites in New York State and harvested 5 months later. Seedlings were harvested using a 10cm soil corer to include bulk soil with intermingling roots of canopy trees. The seedlings and bulk soil were cleaned and all of the ectomycorrhizae were morphotyped. Molecular techniques (PCR amplification and RFLP analysis) were used to compare and identify plant and fungal genotypes of all morphotypes. Fungal and plant specific ITS primers were used to identify the symbionts. There were 74 different fungal RFLP types found across the 30 soil cores. Of the 36 RFLP types found on AC, 28 were multi-host fungi, 8 were found solely on AC, four of which were represented by only one sample. There were 24 EM fungi found on AC and another host within the same core. Red oak was most commonly found sharing the same RFLP type with AC (23 times) followed by white oak and American beech (7 times each), and eastern hemlock, white pine and black birch (2 times each). These results suggest there is a high potential that AC seedlings are tapping into the EM networks supported by canopy trees. contributed presentation

Dunham, Susie M.* and Spatafora, Joseph W. Department of Botany and Plant Pathology, Oregon State University, Corvallis OR, 97331, USA. dunhams@science.oregonstate.edu. **Species diversity and encounter rates for mat forming ectomycorrhizal fungi in Douglas fir forests at the HJ Andrews experimental forest, Oregon, USA.**

Dense hyphal mats formed by ectomycorrhizal fungi can contribute up to 40% of the microbial biomass in Pacific Northwest forest soils. Past research has shown that ECM mats are formed by fungi from distinct clades of the Basidiomycota (e.g., Hysterangiales and Gomphales). To further define the diversity of fungi forming ECM mats we sampled and phylotyped 56 mats from 17 old growth (350+ yrs) sites and 37 mats from 14 second growth (40-60 yrs) sites. Sampling was restricted to forest sites dominated by Douglas fir (*Pseudotsuga menziesii*). Within each age class mats formed by *Piloderma* species were encountered most frequently with 61% and 53% of respective old growth and second growth mats belonging to this genus. We identified four total ITS sequence variants within *Piloderma* cf. *fallax* and cf. *byssinum*. Following *Piloderma* the second most commonly encountered genus in old growth was *Ramaria*, in second growth *Hysterangium*. All other species encountered were relatively uncommon. Overall, 18 mat forming species were encountered in old growth, 11 in second growth. Rarefaction analyses indicate that the diversity of mat forming species is significant-

ly lower in second growth stands. This research highlights the potential importance of *Piloderma* in forest soils and the need for a better taxonomic understanding of this genus. symposium presentation

Dunham, Susie M.^{1*}, Spatafora, Joseph W.¹ and Kretzer, Annette M.² ¹Department of Botany and Plant Pathology, Oregon State University, Corvallis OR 97331, USA, ²Faculty of Environmental and Forest Biology, SUNY College of Environmental Science and Forestry, Syracuse, NY 13210, USA. dunhams@science.oregonstate.edu. **The utility of genetic spatial autocorrelation analyses in fungal population biology.**

Cryptic growth habits make fungal individuals difficult to observe and hinders hypotheses testing about life histories of important species. Knowledge of within-population genetic structure can yield important insights into population dynamics and spatial analysis of genetic data has potential for contributing to this research area. We used spatial autocorrelation analysis to study genet size in two *Rhizopogon* sister species. Within this context analysis of genetic relatedness as a function of spatial distance provides an accurate measure of genet size estimated across all genets sampled. At larger spatial scales patterns of genetic isolation often are estimated with allele frequencies calculated from predefined sampling units. Precision of these statistics declines when sampling units encompass multiple random breeding units (neighborhoods) as the genetic variance among sampling units, relative to the total, declines and the power to detect genetic structure is lost. We analyzed the degree of genetic relatedness as a function of distance in the Pacific golden chanterelle (*Cantharellus formosus*) within a 50 ha forest stand. Significant fine-scale genetic structure was detected with genetic 'patches' approximating 400 m in diameter indicating spore dispersal limitations for this species. These results have important implications for population sampling and fungal ecology. contributed presentation

Eberhart, Joyce L.*¹, Luoma Dan L.¹, Abbott, Rick² and Moore, Andy². ¹Department of Forest Science, Oregon State University, Corvallis, OR 97331, USA, ²Umpqua National Forest, Roseburg, OR 97470, USA. joyce.eberhart@orst.edu. **Ten years of monitoring the effects of harvest techniques on American matsutake (*Tricholoma magnivelare*) production.**

The commercial harvest of American matsutake (*Tricholoma magnivelare*) has become a multi-million dollar industry in the Pacific Northwest. There is considerable controversy regarding how the resource should be managed, including concern over whether raking of surface soil layers to find mushrooms will reduce subsequent fruiting. The objective of this study is to evaluate the effects of several harvest techniques on matsutake production. In 1994 the study was established in the Oregon Cascades, selecting 18 similar shiros of matsutake. In 1995 six treatments were implemented: 1) No harvest (control), 2) Harvest with minimal disturbance (gentle rocking and pulling), 3) Raking litter and duff layers, sporocarp removal and NO replacement of the duff, 4) Raking litter and duff layers, sporocarp removal, and careful replacement of the duff, 5) Removal of the litter and duff layer and 10cm of mineral soil, sporocarp removal and NO replacement of duff and mineral soil, 6) Removal of the litter and duff layer and 10cm of mineral soil, sporocarp removal and replacement of duff and mineral soil. Mushroom production of the shiros has now been monitored for 10 years. Results indicate that careful harvest methods have no impact on sporocarp production, while raking without replacement of the duff has long-term negative impacts. Damage to shiros caused by repeated raking has not been tested. poster

Edwards, Sally M.* and Spiegel, Frederick W. Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville AR 72701, USA. smedwar@uark.edu. **Branch patterns and formation in the dictyostelids.**

The dictyostelid cellular slime molds are notable for several unusual components of their life cycles. Members of this group typically exist in humus, soil, or dung as free-living amoebae. When their bacterial food sources become scarce, the amoebae aggregate in response to a chemical signal. These aggregations of discrete cells, known as pseudoplasmodia, can form migratory slugs. Fruiting occurs once a suitable environment is reached; in many species, the anterior cells of the slug form a non-living cellular stalk while the posterior cells develop into the sticky spore mass, or sorus. However, many dictyostelids produce fruiting bodies which display elaborate branching patterns and multiple sori. The most familiar of these patterns are the Christmas tree-like whorls of *Polysphondylium*. However, other types of branching do occur, as in the irregular fruiting bodies of *Dictyostelium aureo-stipes* and the coreform formations of *D. polycephalum*. It has previously been difficult to illustrate the development of these more complex fruiting bodies due to limitations in photographic equipment. Using Auto-Montage with both a dissecting and compound microscope, in-focus photomicrographs were obtained for the successive stages of fruiting body formation. The taxonomic implications of developmental characteristics such as branching will also be discussed. poster

Elmore, Whitney C.*, Kimbrough, James W. and Benny, Gerald. Mycology Lab, University of Florida, P.O. Box 110680, Gainesville, FL 32611, USA. wcelmore@ufl.edu. **Arbuscular mycorrhizal fungal diversity and colonization of**

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production St. Augustine grass sod in North Central Florida.

The arbuscular mycorrhizal fungi colonizing 'Floratam' St. Augustinegrass on sod farms in North Central Florida was studied using percent colonization and spore density experiments. Sampling was performed on three sod farms in Bradford, Union, and Marion counties. St. Augustinegrass was chosen due to a lack of information concerning mycorrhizal colonization. Sod farm locations were chosen based on their continual production of sod for more than 10 years. The field soil was characterized as having low amounts of organic matter and having a slightly acidic to neutral pH. Roots from sod samples were cut from the crown and examined for percent colonization by root clearing and staining procedures. Spore densities of sample field soils were calculated for each location using spore staining and microscopic examination following trap plantings of sorghum-sudan grass and wet-sieving techniques. Identification of mycorrhizal species was completed with microscopic examination of spore wall(s), size, and color. Trap soil was a 50% (w/w) low phosphorous, sandy soil combined with a 50% field sample soil. Amplification of potentially cryptic species as well as increased spore production was accomplished by soil dilution. Phosphorous deficient soil was used to enhance mycorrhizal colonization since most species respond more favorably in these soils. Various arbuscular mycorrhizal species were discovered colonizing this cultivar of St. Augustinegrass with a range of colonization percentages between locations. The results of these studies are evidence of arbuscular mycorrhizal association with St. Augustinegrass. poster

Engkhaninun, Jintana¹, To-anun, Chaiwat², Ono, Yoshitaka³ and Kakishima, Makoto¹. ¹Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki, 305-8572, Japan, ²Department of Plant Pathology, Chiang Mai University, Chiang Mai, Thailand, ³College of Education, Ibaraki University, Mito, Ibaraki 310-8572, Japan. engjintana@yahoo.com. **Rust fungi newly recorded in Thailand.**

Eighty-six species in 23 telemorphic genera and 5 anamorphic species of rust fungi have been recorded in Thailand. Thailand is geographically, topographically and climatically diverse; and the diversities have created varieties of vascular plants inhabiting in Thailand. However, the number of rust fungi, that parasitize living vascular plants, reported for Thailand are less than those reported for several countries in Southeastern Asia. This indicates that Thailand has been under-explored. In the past years, the rust fungus surveys have intermittently undertaken and, recently, extensive surveys have been carried out in the northern part of Thailand, during which over 500 specimens were collected. We here report 17 species newly recorded in Thailand as follows: *Coleosporium plumeriae*, *C. paederiae*, *Endophyllum paederiae*, *Melampsora ricini*, *M. kusanoi*, *Phakopsora eletariae*, *P. cheoana*, *P. cingens*, *P. fici-erectae*, *P. tecta*, *P. zizyphulgaris*, *Puccinia oxalidis*, *P. hypoxidis*, *P. rhei-undulati*, *P. epilopii*, *Uredo clemensiae* and *Uromyces lespedizae-procumbentis*. poster

Ezawa, Tatsuhiro¹, Mori, Akinobu², Ohtomo, Ryo³ and Osaki, Mitsuru¹. ¹Graduate School of Agriculture, Hokkaido University, Sapporo 060-8589 Japan, ²Graduate School of Bioagricultural Science, Nagoya University, Chikusa, Nagoya 464-8601, Japan, ³National Institute of Livestock and Grassland Science, Nishinasuno, Tochigi 329-2793, Japan. tatsu@res.agr.hokudai.ac.jp. **Isolation of organelles involved in polyphosphate accumulation in arbuscular mycorrhizal fungi.**

Arbuscular mycorrhizal fungi form symbiotic associations with 80% of land. The fungi take up phosphate (Pi) from soil through extraradical hyphae and translocate to the host. In this process, Pi is condensed into inorganic polyphosphate (polyP) which is a linear chain of 3 to < 1,000 Pi linked by high-energy phosphoanhydride bonds and a major translocation form of Pi in the fungi. Although the metabolic pathway of polyP in prokaryotes has been clarified, that in eukaryotic microorganisms has not been elucidated. The objective of the present study is to isolate and characterize organelles involved in polyP synthesis and accumulation in arbuscular mycorrhizal fungi. Marigold (*Tagetes patula*) was inoculated with of *Glomus* sp. HR1 and cultured in a growth chamber for 5 weeks. Extraradical hyphae of the fungi were collected, homogenized on a mortar and fractionated in the continuous density gradient of Percoll. PolyP content of the fractionated organelles was determined by the polyphosphate kinase/luciferase method. PolyP was enriched in the layer 1 (specific gravity: 1.07 g mL⁻¹) and the layer 2 (sediment, specific gravity: >1.15 g mL⁻¹) at 10- to 15-fold. These fractions showed polyP synthesizing activity in the presence of ATP and Pi as substrate. Further purification and characterization are undergoing. poster

Farr, David. USDA, ARS, Systematic Botany & Mycology Laboratory, Beltsville MD 20705, USA. davef@nt.ars-grin.gov. **Managing and organizing bioinventory data.**

The broader the geographic area covered in biodiversity studies, the more significant the data become. The combining of data from different studies is an obvious way to expand the coverage of a biodiversity project. The Web is the perfect vehicle for the distribution of biodiversity data. Data can be compared and contrasted and hypotheses formulated to meet the needs of a diverse group of users - planners, ecologists, pathologists etc. However, to meet this goal two requirements must be considered: (1) the data must be incorporated into logically constructed databases, and (2) web access to the raw data - not just html pages for-

matted for a presentation - should be provided. Ways to achieve both these requirements will be presented and discussed. symposium presentation

Flores, Roberto*, Honrubia, M. & Morales, O. Depto. Microbiología, Facultad de CCQQ y Farmacia, Universidad de San Carlos de Guatemala. & Depto. Biología Vegetal, Facultad de Biología, Universidad de Murcia, Spain. rflores@yahoo.com, rflores@ceroble.edu. **A new variety of *Amanita hemibapha* in Guatemala.**

In Guatemala, Central America, we have found some possible new species and varieties of *Amanita*, including *A. hemibapha*. In the case of the latter one, we have seen differences from the type variety using molecular and microscopic analysis. Guatemala is a very interesting place for studying the diversity and evolution of macrofungi, especially those that are mycorrhizal. poster

Flores, Roberto. Depto. Microbiología, Facultad de CCQQ y Farmacia, Universidad de San Carlos de Guatemala. & Depto. Biología Vegetal, Facultad de Biología, Universidad de Murcia, Spain. rflores@yahoo.com. **Disjunct species of ectomycorrhizal fungi in Guatemala.**

The position of Guatemala as part of the Southern extreme of the Old North American Continent and its orographic relief with high elevations has permitted the development of many genera of ectomycorrhizal mushrooms that live in the Northern Hemisphere. These disjunct taxa include many of the well known species in Europe and North America (e.g., *Hydnum repandum*, *Cantharellus cibarius*, *Amanita muscaria*, etc.), while others have disjunct distributions from populations found in Asia & North America (e.g., *Lactarius indigo*, *L. rimosellus*, *Amanita smithiana*, *Cathartelasma ventricosa*, *Tricholoma portentosum*, etc.). Many species, however, seems to be endemic (e.g., *Boletus guatemalensis*, *B. luteoloincrustatus*, and many undescribed species). The number of species is still growing with the continuing local research. poster

Frisvad, Jens C. and Andersen, Birgitte. BioCentrum-DTU, B. 221, Technical University of Denmark, DK-2800 Kgs. Lyngby, Denmark. jcf@biocentrum.dtu.dk. **An extended phenotypic characterization of filamentous fungi is needed in future taxonomic research.**

Species descriptions and taxonomic revisions of fungi are usually based on core micromorphological features and few other features that have proven to be of value in a particular genus under consideration. If two species look superficially similar in a phenotypic sense, but have a significant number of DNA sequence differences in one or more genes, they are often called sibling species. In order to secure that such phylogenetic species are not just representatives of different populations, or that individual mutants are elevated to species level, several correlated phenotypic differences must be present in order to accept a species. We advocate a species model based on a unique combination of functional apomorphic features, i.e. diagnostic features. Such a species model is based on several gene clusters and in addition epigenetic features. This species model is operational if a minimum number of feature types are considered, including micromorphology, macromorphology, extrolites (including secondary metabolites, organic acids, volatiles and extracellular enzymes), water activity, temperature, and pH etc. More than one basal growth medium should be used to get full phenotypic expression. poster

Fujimura, Kei E.* and Egger, Keith N. Dept. Ecosystem Science and Management, University of Northern British Columbia, Prince George, BC V2N 4Z9, Canada. kfujimura@gmail.com. **Impact of directional, non-replacement succession on the root associated fungal community in the Canadian High Arctic.**

In directional, non-replacement succession, plant species are not replaced as the succession progresses, so plant diversity increases with age. This type of succession is opportune for examining how belowground diversity changes with plant community diversity. We examined the root associated fungal community at a High Arctic site on Ellesmere Island, Nunavut. Plots were placed in zones representing 10 year time intervals since deglaciation, with a control plot in an area that had not been glaciated since the Little Ice Age. For the youngest plot only two non-mycorrhizal plant species were harvested, but as succession continued more plant species were added for a total of six different hosts. T-RFLPs were used to describe fungal community diversity based on the ITS region of the nrDNA. Canonical correspondence analysis was used to test for time and plant host effects. Simple regression was used to test the temporal effect for each plant host. Results suggest that the mycorrhizal status of the plant host is the primary determinant of fungal community composition. Surprisingly, the species richness of the root endophytic community on non-mycorrhizal plant hosts was comparable to the diversity of mycorrhizal plants. contributed presentation

Fujimura, Kei E.*, Egger, Keith N.¹ and Henry, Greg H.R.² ¹Dept. Ecosystem Science and Management, University of Northern British Columbia, Prince George, BC V2N 4Z9, Canada, ²University of British Columbia, Vancouver, BC V6T 1Z4, Canada. kfujimura@gmail.com. **Impact of warming on the root associated fungal community from the Canadian High Arctic.**

We examined the impact of warming on the root-associated fungal com-

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munity of several arctic plants in the Canadian High Arctic. Warming was simulated using Open Top Chambers on three distinct sites. Three replicates of warming and ambient plots were studied for each site. Fungal communities were assessed using T-RFLP analysis of the nrDNA and by isolation of fungi from roots. T-RFLP analysis was conducted directly on *Salix arctica* roots, but cultures were isolated from three additional host plants. T-RFLP genotype frequency and diversity was examined for *S. arctica*. Ordination of a distance matrix generated from rDNA RFLP genotypes from cultures was used to examine patterns among the four host plants. Representative culture isolates were sequenced to identify taxa. The lowest genotype frequency and richness was found on a site with soils derived from dolomitic parent materials. Genotype frequency tended to be higher in warmed compared to ambient plots on all sites. Ordination analyses revealed that the fungal communities were determined primarily by site characteristics rather than by warming treatment or host (for cultures). The dominant species isolated was *Phialocephala fortinii*. poster

Fujitsuki, Kaori^{1*}, Fukuhara Shoji¹, Aimi Tadanori², Maki, Noboru² and Morinaga, Tsutomu¹. ¹Hiroshima Prefectural University, School of Bioresources, 562 Nanatsukacho, Shobara-city, Hiroshima 727-0023, Japan, ²Advanced Life Science Institute, Inc. 2-10-23 Maruyamadai, Wako, Saitama, 351-0112, Japan. ³Advanced Life Science Institute, Inc., 2-10-23 Maruyamadai, Wako, Saitama, 351-0112, Japan. tmorina@bio.hiroshima-pu.ac.jp. **DNA sequence of mitochondria in *Tricholoma matsutake*.**

In general, we know growth of *Saccharomyces cerevisiae* strain having the mutation in mitochondria genome becomes more slowly than wild strain and forms small colony. In *Neurospora crassa*, if mutation occurs in mitochondria genome, growth rate becomes slow. As these results, the mutation occurs in mitochondria genome, especially, deficiency of respiration, it's growth become very bad. By the way, the mycelium of *Tricholoma matsutake* grows only 3cm per one month. To clear the bad growth, we isolated mitochondria genome and sequenced. The total length of mitochondria genome of *Tricholoma matsutake* was 45.7 kbp. This size is almost same one of *Schizophyllum commune* known as a saprobe, has a mitochondria genome of 49.7 kbp. In the position of E404 to E407 fragment, gene of Cytochrome c oxidase subunit 1 protein was coded but this gene had the large insertion of 1240bp. This insertion had 63% homology to interon protein of *Agrocybe aegerita*. E711 fragment the homology to NADH dehydrogenase subunit 5 protein. This fragment also was cut by the large insertion. Now we already sequenced about 80% of mitochondria genome. Until this summer, we will show the complete sequence of mitochondria. poster

Fukasawa, Yu^{*}, Osono, Takashi and Takeda, Hiroshi. Laboratory of Forest Ecology, Graduate school of Agriculture, Kyoto University, Kyoto 606-8502, Japan. asobu@kais.kyoto-u.ac.jp. **Role of *Microporus affinis* in woody litter decomposition in a subtropical evergreen forest.**

Lignicolous fungi have an important role in woody litter decomposition in forest ecosystems. Identification of species and quantitative analysis of wood structural components of individual decay column is necessary to clarify the wood decay patterns of individual lignicolous fungi. In this study, decay columns of *Microporus affinis* in woody litter of *Castanopsis sieboldii* were identified and physical and chemical properties of the columns were measured. Relative density (RD) of logs were measured and used as an index of decay. Lignocellulose index (LCI) of wood in each decay columns were calculated as relative amount of carbohydrate in lignocellulose matrix. Relative volume of decay column of *M. affinis* in a log positively correlated with RD of logs. Lignin content and LCI of decay columns were constant among RD of logs, although density of decay columns positively correlated with RD of logs. Among logs with low RD, decay columns of other fungi had lower LCI than that of *M. affinis*. These results suggest that in decomposition of woody litter of *C. sieboldii*, lignin and carbohydrate were decomposed simultaneously by *M. affinis* in early phase of decomposition, then, carbohydrate was decomposed selectively by other fungi in late phase of decomposition. Poster

Fukihar, Toshimitsu^{1*} and Matsumoto, Taeko². ¹Natural History Museum & Institute Chiba, Aoba-cho 955-2, Chiba 260-8682, Japan, ²Toho Univ. Fac. of Sci., Miyama 2-2-1, Funabashi, Chiba 274-8510, Japan. fukihar@chiba-muse.or.jp. **Change in dominant ectomycorrhizal species during a 12-year period in *Carpinus-Quercus* dominated coppice woods in Chiba, Central Japan.**

Basidiocarp and ascocarp phenology, species composition and productivity were investigated in *Carpinus-Quercus* dominated coppice woods in Chiba, central Japan. *Carpinus-Quercus* dominated coppice woods were maintained over the centuries as secondary woods, traditional rural landscape in Kanto area, Central Japan. A quadrat (14 x 11 m) was made in the study site and investigated 114 times in 6 years (1990-1993, 1999, 2001). The fruiting season was observed twice: in summer (June, July) and in autumn (October). In each year, 18-50 species were observed, and a total of 106 species in 22 families were recognized in 6 years. The total number of species increased every year and the number was not saturated. Ectomycorrhizal species were dominant in every year (81 %-99 %; in total dry weight) such as Amanitaceae, Entolomataceae, Boletaceae, Russulaceae. The dominant families fluctuated in each year; Entolomataceae was dominant in 1990 (70.4 % in total dry weight), in 1991 (33.9 %), in 1992 (30.5 %) and

in 1993 (51.5 %). In 1999, Boletaceae (62.6 %) was dominant and in 2001, Amanitaceae (47.4 %) was dominant. The total mean productivity was 31.24 kg/ha (upper ground sporocarp; dry weight), the most productive year (62.79 kg/ha) was 12 times more productive than that in the least productive year (5.10 kg/ha). poster

Fukuda, Hideshi^{1*} and Sano, Akira². ¹Nihon Fukushi Univ., 26-2 Higashihaemicho, Handa-city, Aichi 475-0012, Japan, ²Mie Pref. Sci. Tech. Prom. Ctr., 3769-1 Nihongi Hakusan-cho, Isshi-gun, Mie 515-2602, Japan. fukuda@n-fukushi.ac.jp. **Propagation of *Urocerus japonicus*, a woodwasp with a fungal symbiont, in old felled Japanese cedar trees.**

Woodwasps are symbiotically associated with *Amylostereum* fungus spp. Adult females inoculate the fungus during oviposition on sapwood of host trees. Aided by fungal symbiosis, woodwasp larvae can digest sapwood with low nutritional value. *Urocerus japonicus*, a fungus-carrying woodwasp, oviposits selectively on freshly felled Japanese cedar trees that are presumed to be suitable for propagation of the fungal symbiont. We investigated the potential for growing *U. japonicus* in old trees by propagating *Amylostereum laevigatum* in the wood before woodwasp oviposition. Oviposition activity levels were higher on oviposited trees (fungus-inoculated by another woodwasp before oviposition) and on artificially inoculated trees (fungus-inoculated artificially before oviposition) than on control trees. Next-generation adults emerged from artificially inoculated trees but not from previously oviposited and control trees. These results suggest that *U. japonicus* can utilize fungus already propagating in wood. Moreover, we investigated the effect of inoculation season on fungus propagation in the wood. Clear wood discoloration was recognized in summer-inoculated trees but there was almost no discoloration in fall-inoculated trees. In summer-inoculated trees, fungus propagated mainly in discolored areas; in fall-inoculated trees, it propagated widely irrespective of discoloration. These results suggest that fall-inoculated trees would be best for growing these woodwasps. poster

Fukushima, Kazutaka^{*} and Chikamori, Minoru. Research Center for Pathogenic Fungi and Microbial Toxicoses, Chiba University, 1-8-1 Inohana, Chuo-ku, Chiba 260-8673, Japan. **A new hexose transporter (Hxt1) from *Cryptococcus neoformans*: molecular cloning and structural and functional characterization.**

We carried out a screen for *Cryptococcus neoformans* genes involved in resistance to copper ion toxicity and identified a new hexose transporter (Hxt) gene, *HXT1*. Hxt1 consists of 520 amino acids and functions to transport hexoses such as glucose and galactose. Although Hxt1 conferred copper resistance to *Saccharomyces cerevisiae*, disruption of the *HXT1* gene showed that Hxt1 is not necessary for copper resistance. In virulence test, a *hxt1* mutant strain showed 12% less phenoloxidase activity than the wild-type strain, and no difference in the ability to form melanin was identified. In addition, the *hxt1* mutant strain showed virulence similar to that of the wild-type strain in experiments with *Caenorhabditis elegans*. However, the *hxt1* mutant strain generated larger capsules than were generated by the wild-type strain. Thus, Hxt1 appears to be involved in capsule formation. poster

Fukushima, Kazutaka^{*}, Hashizume, Toko and Takizawa, Kayoko. Research Center for Pathogenic Fungi and Microbial Toxicoses, Chiba University, 1-8-1 Inohana, Chuo-ku, Chiba, 260-8673 Japan. kfuky@faculty.chiba-u.jp. **Identification and molecular phylogeny of dematiaceous fungi *Phialophora* species based on the D1/D2 domain of rDNA and their ubiquinone systems.**

Species in the deuteromycete genus *Phialophora* are ubiquitous and cosmopolitan and are important saprobes as well as plant and human pathogens. Accurate species identification is difficult because of the limited number of morphological characters and their pleomorphism. The present study was designed to explore the potential use of the D1/D2 domain of rDNA as a tool for species identification of *Phialophora* spp. and to perform phylogenetic analysis of the fungal taxa using the domain. Ubiquinone system being useful as a chemotaxonomic classification tool was also analyzed. 38 species of *Phialophora* including medically important species as *P. verrucosa* were used. Two kinds of ubiquinone (Q) molecules, Q-10 (7 species) and Q-10(H2)(31 species), were identified as the major Q and most of the 7 species with Q-10 were related to human diseases. The D1/D2 domain provided very significant information in species identification; it had adequate sequence difference for the identification of medically important species and suggested the necessity of reclassification between some species. The phylogenetic tree constructed by NJ method showed three clusters with following characteristics: I (all species with Q-10, most of human pathogens), II (species related to the genus *Cadophora*), and III (saprophytic species with strong variability in hyphal pigmentation). poster

Gallery, Rachel E.^{1*}, Dalling, James W.¹, Higgins, K. Lindsay², and Arnold, A. Elizabeth^{2,3}. ¹Department of Plant Biology, University of Illinois, Urbana, IL 61801, USA, ²Department of Biology, Duke University, Durham, NC 27708, USA, ³Current address: Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA.

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arnold@ag.arizona.edu. **Diversity and demographic impact of seed-infecting fungi: A case study with neotropical *Cecropia* spp.**

Community-wide recruitment limitation has been proposed as an important mechanism influencing patterns of tree regeneration, and potentially mediating plant species coexistence in tropical forests. For light-demanding tree species, which germinate from a soil-seed bank, infection by fungi can greatly reduce seed survival, and may therefore affect both recruitment success and adult distribution. Here we examine the interactions between seeds and communities of endophytic, saprophytic and putatively pathogenic fungi associated with four sympatric *Cecropia* species in Panama. Seeds were experimentally buried in forest soils, excavated after 5 months, surface sterilized, and subsequently incubated on 2% MEA. All isolates were sequenced at the nuclear ribosomal internal transcribed spacer region (nrITS) and grouped according to 90%, 95%, and 99% sequence congruence. Resulting groups were used as functional taxonomic units to compare fungal communities associated with seeds of each host species in terms of diversity, richness, taxon abundance, taxonomic composition, and whole-community similarity. Highly diverse taxa with known affinities to endophytes, saprophytes, and pathogens were recovered, including a large number of Eurotiomycetidae, Chaetothiomycetidae, Sordariomycetidae, and Dothideomycetidae, few Saccharomycetidae, and some Basidiomycota (including Ustilaginomycetes and Homobasidiomycetes). We discuss the potential for host affinity among seed infecting fungi to influence the survival and distribution of *Cecropia* spp. in tropical forests. poster

Gams, Walter^{1*} and Zare, Rasoul² ¹Centraalbureau voor Schimmelcultures, Utrecht, Netherlands and ²Dep. of Botany, Plant Pests & Diseases Res. Inst. Tehran, Iran. gams@cbs.knaw.nl. **New advances in *Verticillium* taxonomy.**

The largest section of *Verticillium*, sect. *Prostrata*, has been revised and its species re-classified in several genera (Zare & Gams, Nova Hedwigia, 2000-2001). Section *Verticillium* containing only *V. luteo-album* is distantly related to section *Nigrescentia* (Zare et al., Mycol. Res. 108: 576-582, 2004). The latter section comprising the important plant-pathogenic species *V. dahliae* and *V. albo-atrum* plus a few other, weaker plant pathogens, is retained as *Verticillium* in the strictest sense by designation of *V. dahliae* as the conserved type of the genus (Gams et al., Taxon, 2005). In a current project, the former section *Albo-erecta* with well-differentiated, erect conidiophores and mainly fungicolous species, and many so far unclassified taxa are being investigated using classical and molecular techniques. A large number of isolates obtained from all over the world and various substrata are examined. Morphological and molecular (sequences of ITS region, small subunit ribosomal DNA and translation elongation factor 1-alpha) data show an extensive variation among isolates examined; the observed relationships correlate with the ecology of the isolates, suggesting the need for further generic segregation. Four new genera are envisaged around *V. biguttatum*, *V. rexianum*, *V. leptobactrum* and some isolates from old polypores. No new teleomorphs are found yet. contributed presentation

Garbelotto, Matteo^{1*}, Olarte, R. ¹, Swiecki, Ted J. ² and Bernhardt, Elizabeth A. ² ¹Forest Pathology and Mycology, University of California, Berkeley, CA 94720, USA, ²Phytosphere research, Vacaville, CA 95687, USA. matteo@nature.berkeley.edu. **Microsatellite analyses reveal California wildland infestations by *Phytophthora cinnamomi* may have originated in neighboring agricultural settings.**

Although the presence of the exotic pathogen *P. cinnamomi* is well documented both in agricultural/horticultural situations and in wildlands in many regions of the world, its discovery in California wildlands is recent. Two manzanita species (*Arctostaphylos* spp.) in the Sierra Nevada are infected and seriously affected by this pathogen. The pathogen has also been isolated frequently from coast live oaks (*Quercus agrifolia*) in Southern California woodlands. Microsatellite analyses were performed on isolates representative of the most important lineages in the world, on isolates from Christmas tree farms in the Sierra Nevada foothills, and on one isolate from an avocado ranch in Southern California. Results from about 100 isolates indicated that 1)- The microsatellite analysis can differentiate all major lineages and can detect differences within lineages; 2)- the diversity of *P. cinnamomi* is large in manzanita, with at least three main clonal lineages detected and several genotypes; 3)- diversity is limited in coast live oak with a single clone. Two of the clones found on manzanita were also isolated from Christmas tree farms, and the clone on oaks was the same one as the clone found on avocados. The clone from avocado in California matched one of the three clones commonly found in avocados around the world, while the clones in Christmas tree farms matched clones associated with the horticultural/ornamental plants industries. The spatial pattern of distribution of clones in manzanita suggests at least two independent introductions occurred, and that the most disturbed areas contain the maximum genotypic diversity. contributed presentation

Garbelotto, Matteo^{1*}, Smith, A. ¹, Parrent, Jeri Lynn² and Gilbert, Gregory³ ¹University of California, Berkeley, CA 94720, USA, ²Duke University, Durham, NC 27708, USA, ³University of California, Santa Cruz, CA 95064, USA. matteo@nature.berkeley.edu. **Population differences in *Datronia caperata* between the Caribbean and Pacific coasts in Central America.**

Datronia caperata (Basidiomycotina) is a secondary pathogen of white

mangroves (*Languncularia racemosa*) in Central America. The genetic structure of this fungus in Panama has been recently studied using AFLP analyses. Results suggested populations over 60 km in distance experienced limited gene flow, while no clear distinction could be detected between the Pacific and Caribbean coastlines. Here, we present further results on the genetic structure of six populations of this fungal species, three from the Pacific and three from the Caribbean coasts, in Panama and Costa Rica, using genealogies of two mitochondrial and two nuclear loci. For each locus, alleles clustered in one of two clades, suggesting a clear allelic genealogical pattern. Results indicated a significant difference between populations on the two coasts: while populations on the Pacific coast were characterized by the presence of alleles belonging to both clades, Caribbean populations were characterized only by alleles belonging to one of the two possible clades for each locus. Implications of these results, including a combined analysis of all four loci, are discussed and presented not only to enhance our understanding of the evolution and population structure of this fungus, but also as potential useful data for the development of management guidelines to preserve the current biodiversity of threatened mangrove ecosystems. poster

García-Bustamante, Joslyn M. University of New Mexico, Biology Department, MSC03 2020, Albuquerque, NM 8713, USA. jozge@unm.edu. **Thermophilic Fungi of the Sevilleta National Wildlife Refuge.**

The goal of this research is to characterize thermophilic fungi from semi-arid grasslands of the Sevilleta National Wildlife Refuge (SNWR). The McKenzie Flats region of the SNWR represents a transition biome in central New Mexico. During summer months, daytime subsurface soil temperatures commonly reach greater than 60 °C. Little is known about microbial communities in this environment. Soil samples taken across different soil and vegetation types were plated onto five different media and incubated at 50-55 °C for 1 to 2 weeks. Fungi were identified by using a combination of molecular and classical methods. Species identified to date include *Thermoascus* spp., *Penicillium* spp., and *Thermomyces* (*Humicola*) *lanuginosa*. The frequency of recovery of the thermophilic fungi was highest during periods of higher soil moisture and in soils with increased C, N and P. Highest occurrence of thermophiles occurred at the Nunn Flats site, which also had highest C, N and P. Nunn Flats was subject to a prescribed burn in 2002. These results appear to represent one of the first demonstrations of thermophilic fungi responding to local factors in a natural environment.

Gargas, Andrea. Dept. of Botany, University of Wisconsin, Madison, WI, USA. agargas@wisc.edu. **ITS2 rRNA secondary structure and evolution.**

Conserved secondary structure of ITS2 rRNA allows the alignment of homologous ITS2 rDNA sequences regions from diverse fungi. Models for ITS2 rRNA secondary structures are presented for representatives of clades within the Lecanorales (Ascomycota), combined with phylogenetic hypotheses for structure evolution. poster

Geiser, Linda^{1*}, Dillman, Karen² and Laursen, Gary³. ¹USDA-Forest Service, Siuslaw National Forest, P. O. Box 1148, Corvallis, OR 97330, USA, ²USDA-Forest Service, Tongass National Forest, P.O. Box 309, Petersburg, AK 99833, USA, ³Dept. of Biology and Wildlife, P.O. Box 756100, 305A Bunnell Building, Fairbanks AK, USA. lgeiser@fs.fed.us. **Lichens of the Great Kobuk Sand Dunes in northwestern Alaska.**

We studied lichen communities of the Great Kobuk Sand Dunes of the Kobuk Valley National Park in northwestern Alaska (67.13 deg N, 159.04 deg W). The Dunes were created during the late Pleistocene era and consist of calcareous sands eroded from the Brooks Range by glaciers and transported to their present location by the Kobuk River and winds. A total of 75 genera and 170 taxa were recorded from the exposed, preserved dunes and from the surrounding boreal forest on degraded sand dunes. Partially vegetated, well preserved dunes occupied a very small proportion of the Dunes surface area while supporting a disproportionate number of calciphilous lichens unique to exposed sands and absent from the surrounding boreal forest. Monitoring and conservation strategies are needed to measure disturbance in these fragile, trampling-sensitive dune environments as tourism increases and climate change progresses. contributed presentation

Geml, József^{1*}, Laursen, Gary A. ¹, Lutzoni, François², Nusbaum, Harris C. ³ and Taylor, D. Lee¹. ¹Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks AK 99775, USA, ²Department of Biology, Duke University, Durham NC 27708, USA, ³Sequence and Analysis Program, Broad Institute, Cambridge MA 02141, USA. jgeml@iab.alaska.edu. **Phylogeography of basidiolichen-forming *Lichenomphalia* species in arctic, subarctic, and subantarctic regions.**

Species of the genus *Lichenomphalia* are restricted to arctic-alpine environments with the exception of *L. umbellifera* (syn. *Omphalina ericetorum*), which is also found in boreal forests and is considered the most broadly distributed and the most plastic species in the genus. Although *Lichenomphalia* species inhabit vast regions in several continents, no information is available on their genetic variation across geographic regions and the underlying population-phylogenetic patterns. We collected samples of *L. alpina* (syn. *Omphalina luteovittellina*), *L. hudsoniana* (syn. *Omphalina hudsoniana*), and *L. umbellifera* from arctic, subarctic,

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and subantarctic regions and conducted population genetic and phylogenetic analyses based on nucleotide sequences from the internal transcribed spacer (ITS) and the large subunit (LSU) regions of the nuclear rDNA repeat. Phylogenies based on LSU confirmed the monophyletic origin of the three species and revealed the existence of at least one unknown taxon collected from New Zealand that likely represents a sister species to *L. alpina*. While the ITS sequences could not be aligned unambiguously among species, specimens of *L. alpina* and *L. hudsoniana* sampled over broad geographical regions in the Arctic included only 1 and 2 ITS haplotypes, respectively. On the other hand, substantial variation was found in *L. umbellifera*. These results agree with previous suggestion that this species is the oldest and most diverse of all known *Lichenomphalia* species. Nested Clade Analysis indicated allopatric fragmentation between populations of *L. umbellifera* in the Southern and Northern Hemispheres. Although we found fourteen distinct ITS haplotypes in populations across the Arctic, the null hypothesis of no geographical association of haplotypes could not be rejected. Because our geographic sampling represented a wide range of areas, we conclude that extensive dispersal and gene flow are the most prevalent forces shaping northern high-latitude populations in all three species. This is also supported by the lack of polymorphism in *L. alpina* and *L. hudsoniana*. symposium presentation

Gibson, Cara M.* and Hunter, M.S. University of Arizona, Dept. of Entomology, 410 Forbes Building, Tucson, AZ 85721-0036, USA. cgibson@ag.arizona.edu. **Enigmatic yeasts in beneficial insects.**

Despite much recent interest in invertebrate-bacterial symbioses, fungal associations with insects have received relatively little attention. Even though some yeasts are intimately associated with economically important natural enemies, we know little about the contributions of these symbionts in natural populations, or whether symbiotic relationships are compromised during insectary-rearing, with subsequent decreases in biocontrol efficacy. Here we present research characterizing symbioses between yeasts and two types of natural enemies. The yeast symbionts of green lacewings, *Metschnikowia chrysoperlae*, *Candida pimensis* and *C. picachoensis*, were previously thought to provide missing amino acids from adult lacewings' primarily carbohydrate diet. Our data suggest that the yeasts themselves require some minimum quality diet before providing nutrients to adult lacewings. In addition, we present evidence that the yeasts in green lacewings are vertically transmitted; a novel finding that has important implications for the nature of the lacewing-yeast relationship. In a second system, we are examining the role of the vertically transmitted intercellular yeast symbionts in *Comperia merceti*, a specialist egg parasitoid of brownbanded cockroaches. These wasps have the potential to substantially suppress brownbanded cockroach populations in enclosed building settings, yet it is unclear what role the yeasts may have in this multipartite interaction. poster

Gilbert, Luz B.*, Chae, Lee, Kasuga, Takao, Townsend, Jeff, Glass, Louise and Taylor, John W. Department of Plant and Microbial Biology, U.C. Berkeley, Berkeley CA 94720-3102, USA. lgilbert@berkeley.edu. **Comparative Genomic Hybridization within the Genus *Neurospora*.**

Comparative Genomic Hybridization (CGH) is becoming a popular way to determine similarity among strains and even species. A growing trend is to use CGH data to assess evolutionary history by developing phylogenetic trees from differences in hybridization between isolates. As yet few have questioned the reliability of CGH data to correctly assess sequence differences in hybridization and therefore the ability of this type of data to determine evolutionary relationships. The study of a simple eukaryote, the filamentous fungus *Neurospora*, offers a unique opportunity to rigorously address these questions using both experimental and simulated data. The genus *Neurospora* consists of eight closely related conidiating species indistinguishable by morphology, as well as several non-conidiating species. An accurate phylogeny was published by Dettman *et al.* 2003. We have constructed a 70mer oligomer array for *Neurospora crassa* representing 10,000 genes. I have analyzed comparative genomic hybridizations for all eight conidiating species of *Neurospora* as well as a few non-conidiating isolates. These results were then compared to simulated data generated to mimic the design of the CGH experiment. The goal of the simulated data is to determine under what scenarios CGH data might accurately determine evolutionary relatedness. We have used both the simulated and empirical data to generate distance based dendrograms for the different species that we can compare to the known phylogeny and assess the utility of CGH data for testing evolutionary relationships. contributed presentation

Gilbertson, Robert L.* and Hemmes, Don E.² ¹Dept. of Plant Pathology, University of Arizona, Tucson, AZ 85721, USA, ²Biology Discipline, Univ. Hawai'i, Hilo, HI 96720, USA. rlg@ag.arizona.edu. **Wood-rotting basidiomycetes on conifers in the Hawaiian Islands.**

There are no native conifers in Hawai'i. Conifer plantations were established by the Hawaiian Division of Forestry beginning about 1930 so they have been present for a relatively short time. Major conifer genera are *Pinus*, *Cupressus*, *Cryptomeria* and *Araucaria*. Our field work over the last 15 years has yielded 428 species of wood-rotting basidiomycetes on all woody substrates in Hawai'i. Included are 130 basidiomycetes on 12 species of conifers on the islands of Kauai, Molokai, Lanai, Maui, and Hawai'i. Of these 130 fungi, 110 or almost

85 percent are also reported from North America. Species that cause brown rots total 28 or nearly 22 percent of conifer-inhabiting species known in Hawai'i. This percentage is about the same as that of brown rot fungi on conifers in North America. As they do in North America, brown rot fungi probably have important ecological functions in Hawaiian forest ecosystems. Nearly 58 percent of the basidiomycetes on conifers in Hawai'i are also known to occur on native or exotic woody angiosperms there, and may have been present long before conifers were introduced. When and how these fungi were initially introduced in Hawai'i will probably never be known as there is virtually no information available on lignicolous fungi present before the establishment of conifers on the Hawaiian Islands. symposium presentation

Glawe, Dean A.^{1*}, Ammirati, Joseph F.², Callan, Brenda E.³, Dugan, Frank M.⁴, Norvell, Lorelei L.⁵ and Seidl, Michelle T.⁶ ¹Washington State Univ., Puyallup, WA 98371, USA, ²Univ. of Washington, Seattle, WA 98195, USA, ³Natural Res. Canada, Pacific Forest. Cent., Victoria, BC V8Z 1M5 Canada, ⁴USDA-ARS, Pullman, WA 99164, USA, ⁵Pacific Northwest Mycol. Serv., Portland, OR 97229, USA, ⁶Envir. Microbiol. Lab., Inc., Bellevue, WA 98004, USA. glawe@wsu.edu. **The Pacific Northwest Fungi Project: developing a collaborative model for inventorying biodiversity on a regional basis.**

The Pacific Northwest Fungi Project was founded in 2002 to develop a new model for biodiversity surveying. Only about 70,000 of an estimated 1.5 million fungal species are known worldwide. Ignorance of 95% of fungal species impedes efforts to classify them, understand their phylogeny, biology, and ecology, and to assess economic impacts. Understanding this important part of the earth's biota will enhance our ability to cope with future challenges resulting from global climate change and the pressures on natural ecosystems caused by human populations. There is urgent need for new approaches for collecting, characterizing, and classifying the world's mycota as an alternative to traditional approaches dependent on national funding, print journals, and uncoordinated research. Project goals are to foster idea exchange among academic and field mycologists, develop collaborative projects, coordinate databases, develop the new online journal *Pacific Northwest Fungi* for information on the region's fungal natural history, and involve non-professional mycologists. Relying heavily on mutual collegial support, internet resources (web sites, an online journal, and email), teleconferences, and occasional face-to-face meetings, the Project actively develops, tests, and assesses approaches to biodiversity surveying that may succeed where past efforts have proven ineffective or too costly. poster

Glawe, Dean A.^{1*}, Dugan, Frank M.², Cerkauskas, R.F.³, du Toit, L.J.⁴, Mohan, S.K.⁵ and Liu, Y.⁶ ¹Dept. of Plant Pathology, Puyallup Res. and Ext. Center, Washington State Univ., Puyallup WA 98371, USA, ²USDA-ARS WRPIS, Washington State Univ., Pullman WA 99164, USA, ³Agriculture and Agri-Food Canada, Harrow, Ontario N0R 1G0 Canada, ⁴Washington State Univ., Mt. Vernon WA 98273, USA, ⁵Univ. of Idaho, Parma ID 83660, USA, ⁶Univ. of Washington, Seattle, WA 98195, USA. glawe@wsu.edu. **Leveillula taurica: An emerging plant pathogen in the Pacific Northwest.**

Leveillula taurica occurs on numerous host plants representing more than seventy families, including both dicots and monocots. North American reports date to 1906. The fungus has since been reported from Mexico and Ontario, as well as Texas, Florida, California, and Arizona. Within the Pacific Northwest (PNW), the conidial state first was reported from Idaho on cucumber (*Cucumis sativus*) and tomato (*Lycopersicon esculentum*) in 1989 and later on onion (*Allium cepa*) in 1995. It was reported from British Columbia on greenhouse pepper (*Capsicum annuum*) in 2003, and from central Washington State on onion and potato (*Solanum tuberosum*) in 2004. Both sexual and asexual states were found on greenhouse-grown seaside arrow grass (*Triglochin maritima*) in eastern Washington in 2004. The ITS sequence obtained from the strain on *T. maritima* was identical to sequences from strains on pepper in Australia and *Elaeagnus angustifolia* in Iran. With the confirmation of *L. taurica* on diverse hosts in the PNW, and the recent discovery of sexual state in the region, plant pathologists should be alert for potential impact of this pathogen causing economic losses in the PNW agriculture. The possible epidemiologic role of alternative hosts in the region may complicate control this pathogen. poster

Glawe, Dean A.^{1*} and Laursen, Gary A.² ¹Puyallup Res. and Ext. Cent., Washington State Univ., 7612 Pioneer Way E., Puyallup, WA 98371-4998, USA, ²Inst. of Arctic Biology, P.O. Box 756100, 305A Bunnell Bldg., Fairbanks, AK 99775, USA. glawe@wsu.edu. **Erysiphales of extreme environments: Subarctic powdery mildews in interior Alaska.**

With an area of more than 1.5 million square kilometers and six large physiographic/climatic regions, Alaska includes extraordinary geographic, climatic, and ecologic diversity. The occurrence of some species of obligately parasitic powdery mildew fungi (Erysiphales) in Alaska is noted in Amano's book on their global distribution and host ranges, and in Braun's world taxonomic monograph. However, there is almost no information available on the distribution, biology, or ecological relationships of Erysiphales within Alaska, particularly that assesses and compares such phenomena across the six different regions of the state. In

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2004, we began a study of Alaskan Erysiphales focusing initially on subarctic Erysiphales occurring in interior Alaska. Results of work thus far completed suggest that the diversity of Erysiphales in the region has been underestimated, both on native and introduced hosts. Consistent with Amano's and Braun's accounts, *Sphaerotheca* and *Erysiphe* (*sensu lato*) included most of the species collected. Species can differ significantly in host specificity, ranging from those associated with a single host genus to those occurring on hosts in multiple plant families. Teleomorphs appeared to be formed earlier and more consistently than is the case in the same or similar species observed in coastal Washington State where anamorphs frequently over-winter. Life cycles of Erysiphales in interior Alaska may be adapted for short growing seasons, reminiscent of the case in rust fungi occurring in similar regions. Some species, such as *Microsphaera palczewskii* appear to be recent arrivals on introduced host plants, while species occurring on native *Salix*, *Vaccinium*, and other host species appear ubiquitous and long-established. Observed associations included those of the powdery mildew fungus and host, but also powdery mildew-powdery mildew [coinfection of *Alnus crispa* by *Microsphaera* (*Erysiphe*) *alni* and *Phyllactinia guttata*], and powdery mildew fungus-mycoparasite (several Erysiphales species were found infected by *Ampelomyces quisqualis*). Alaska is expected to undergo profound ecological changes during the next century as a result of global warming. As climate change occurs, altered host distributions likely will affect significantly the distributions, life histories, and ecology of Erysiphales. It will be important to establish baseline information on the distribution and behavior of Erysiphales in the region in order to understand the effects of climate change on these fungi and their hosts, and to determine whether they may be used as indicators of change. Because of their superficial growth habit, relatively easy detection, and varied host relationships, Erysiphales may provide useful model systems for studying how plant-fungus interactions will be affected by climate change in extreme environs at high latitudes. symposium presentation

Gomi, Katsuya. Lab. of Bioindustrial Genomics, Graduate School of Agricultural Science, Tohoku University, 1-1, Tsutsumidori-Amamiyamachi, Aoba-ku, Sendai 981-8555, Japan. gomi@biochem.tohoku.ac.jp. **Recent developments in recombinant protein production by a filamentous fungus, *Aspergillus oryzae*.**

Aspergillus oryzae is an industrially important filamentous fungus in the Orient, especially in Japan, since it has been used for sake, soy sauce, and soybean paste manufacturing for more than a thousand years. In addition, *A. oryzae* has also been used for production of various commercial enzymes for food processing. Because of its safety proved by the long history of extensive use in food industries and its high capability of protein secretion, *A. oryzae* has been attracting much attention for a suitable host organism for industrial production of heterologous proteins. Actually, alkaline lipase of *Thermomyces lanuginosus* has been industrially produced by an *A. oryzae* recombinant strain. However, the amount of heterologous proteins produced has not been comparable to those of homologous or fungal proteins. To date, many attempts have been done to improve the productivity of foreign proteins in *Aspergilli*, and yield improvement has been accomplished mainly by the introduction of multiple copies of expressed genes, the use of strong promoters, and gene fusions to own well-secreted proteins. Recently, codon optimization of the foreign gene resulted in significant increase in secreted non-fungal protein yield caused by the increased mRNA level. This strategy may lead to stabilize heterologous mRNA. In addition to stability of mRNA, alternations in 5'-untranslated region of the gene to be expressed had a considerably beneficial effect on the translation efficiency owing presumably to promotion of translation initiation of the gene. Moreover, since degradation of heterologous proteins has been recognized to be caused by the action of own proteases, molecular genetically modified strains deficient in proteases have been constructed and the use of them has resulted in increased heterologous protein levels. symposium presentation

Goto, Yasuhiko^{1*}, Ando, Yoko¹, Maruyama, Kokichi¹, Sasaki, Hiromi¹, Masai, Toshiro², Orihara, Takamichi², Shimono, Yoshito², Fukihar, Hiroko³ and Osaku, Koichi³. ¹The Mycologist Circle of Japan, c/o Y. Goto, Abiko, Chiba, 270-1175 Japan, ²The Yokin-no-Kai, c/o K. Matsumura, Egawa, Shimamoto, Osaka 618-0013, Japan, ³The Chiba Mycological Club, c/o Natural History Museum & Institute Chiba, Aoba-cho, Chiba 260-8682, Japan. hattori@affrc.go.jp. **Poisonous mushrooms in Japan: their taxonomy, toxicology and folklore.**

In many regions of Japan, people enjoy hunting wild edible mushrooms. Certain regions have "professional mushroom hunters" and wild mushrooms are sold in local markets. On the other hand, poisonous mushrooms are occasionally eaten accidentally in Japan. In 2004, it was repeatedly reported that people undergoing kidney dialyses suffered serious encephalitis after eating *Pleurocybella porrigens*, that was supposed to be an edible mushroom and frequently eaten in certain areas of Japan. Some poisonous species such as *Amanita ibotengutake*, *Boletus rhodocarpus* and *B. venenatus*, are recently described from Japan. An undescribed species of *Tylopilus* was revealed to contain a deadly poison in 2002. Additionally, several poisonous species were originally described from Japan: *Clitocybe acromelalga*, *Galerina fasciculata*, *Omphalotus guepiniformis* (= *Lampteromyces japonicus*), and *Russula subnigricans*. We introduce the above species in addition to other important poisonous mushrooms, discussing their taxonomy, toxicology and folklore, and exhibit color photographs from the field. poster

Gotou, Takanobu*, Mizuno, Seiichi, Shinoda, Tadashi, Ohki, Kohji and Yamamoto, Naoyuki. Calpis Co., Ltd., 11-10, Fuchinobe 5chome, Sagamihara-shi, Kanagawa 229-0006, Japan. takanobu.gotou@calpis.co.jp. **Purification of proteolytic enzymes from *Aspergillus oryzae* needed in processing of antihypertensive peptide, Ile-Pro-Pro, in casein hydrolysis.**

Recently, a method to prepare antihypertensive peptides, Val-Pro-Pro and Ile-Pro-Pro from casein was newly developed with *Aspergillus oryzae* protease. However, there is no information about key enzymes which play important roles in the processing of the two peptides in *A. oryzae* protease. Therefore, we tried to identify proteinases and peptidases which can catalyze the processing of Ile-Pro-Pro from *A. oryzae* protease in the present study. We purified two types of proteolytic enzymes needed in the processing of Ile-Pro-Pro from *A. oryzae* extract by three steps of chromatographies. One of the enzymes that hydrolyze casein had an identical N-terminal amino acid sequence to that of Neutral protease I. The other enzyme had a similar N-terminal amino acid sequence to Leucine aminopeptidase reported from *Aspergillus sojae*. Ile-Pro-Pro was processed from casein by adding of these purified two enzymes but not by single enzyme. From these results, importance of these two enzymes of *A. oryzae* protease in processing of Ile-Pro-Pro was suggested. poster

Grubisha, Lisa C.* and Bruns, Thomas D. Department of Plant and Microbial Biology, 111 Koshland, University of California, Berkeley, CA 94720-3102, USA. grubishl@nature.berkeley.edu. **High levels of genetic differentiation are detected within island populations in two sympatric *Rhizopogon* species.**

We are investigating the relationship between genetic and geographic structure in two sympatric species of *Rhizopogon* on two of the California Channel Islands. *R. vulgaris* and *R. occidentalis* are hypogeous, ectomycorrhizal fungi associated with pines. Spore dispersal is by mammals that consume fruiting bodies, thus dispersal should be restricted by geographic barriers and distance between populations. *R. vulgaris* and *R. occidentalis* were sampled from native pine populations on Santa Cruz Island and Santa Rosa Island. Results from analysis of microsatellite data reveal that in both species populations separated by very short distances can exhibit a high degree of genetic differentiation if intervening areas do not contain suitable habitat. Within Santa Cruz Island, populations of both species showed a high degree of structure even though they were only separated by 11-18 km. Physical barriers, such as the lack of pines and a large dry valley, separated these populations, that were located on two mountain ranges. On Santa Rosa Island, *R. occidentalis* populations have extremely low levels of gene diversity possibly resulting from a bottleneck. These results are consistent with the idea that in isolated pine populations gene flow between populations of these fungi is restricted by the movement of the mammals that disperse their spores. contributed presentation

Gueidan, Cécile* and Lutzoni, François. Department of Biology, Duke University, Box 90338, Durham NC 27708, USA. cg19@duke.edu. **Molecular phylogeny of the Verrucariales (Fungi, Ascomycota) and the evolution of nutritional modes in the Chaetothyriomycetidae.**

Verrucariales is a poorly studied order of mostly rock-dwelling lichenized ascomycetes, found in varied habitats ranging from marine and fresh water to dry environments. Phylogenetic relationships among members of Verrucariales are mostly unknown and the morphology-based classification has never been tested with molecular data. The first goal of this project is to reconstruct a multilocus phylogeny for this order. Recent molecular phylogenetic studies showed the Verrucariales as sister to the Chaetothyriales. These two orders share a most common ancestor with members of the order Pyrenulales. Together, these three orders are recognized as forming the subclass Chaetothyriomycetidae. The order Chaetothyriales is strictly non-lichenized, whereas the orders Verrucariales and Pyrenulales contain both lichenized and non-lichenized taxa. The order Verrucariales includes non-lichenized taxa living on lichens as parasites, commensals or saprobes (lichenicolous fungi). The diversity of lifestyles within these three orders provides evidence that host-switches and changes in nutritional habits occurred frequently. The second goal of this project is to reconstruct ancestral states to test if lichenicolous lichens and fungi were transitional stages between mutualism and parasitism. contributed presentation

Hallen, Heather E.* and Trail, Frances. Department of Plant Biology, Michigan State University, East Lansing, MI 48824, USA. hallenhe@msu.edu. **Examination of sexual development in *Gibberella zeae* using Affymetrix GeneChip microarrays.**

Gibberella zeae (anamorph *Fusarium graminearum*) is the causal agent of Fusarium head blight, a serious disease of wheat and other cultivated crops. We have developed a genome-wide Affymetrix GeneChip microarray of *Gibberella zeae*. Our lab has used the first-generation GeneChips to investigate sexual development *in vitro*. We sampled from zero-hour (0H) vegetative hyphae, 24H wide dikaryotic hyphae, 48H unpigmented perithecial initials, 72 and 96H immature perithecia, and mature perithecia with ascospores (144H) (time points refer to time following induction of sexual development). We have performed from three to five biological replicates per time point; additionally, we have begun sampling

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the corresponding growth stages *in planta*. While analysis is still at an early stage, we have been able to identify several clusters of differentially regulated genes. We are particularly interested in genes that are upregulated during sexual development, and are focussing our further research efforts on these genes. poster

Hallen, Heather E.*, Guenther, John C. and Trail, Frances. Department of Plant Biology, Michigan State University, East Lansing, MI 48824, USA. hallenhe@msu.edu. **Two novel mutants in *Gibberella zeae* affect ascospore development and discharge.**

Gibberella zeae (anamorph *Fusarium graminearum*) infects wheat, corn and numerous other crop plants to inflict substantial economic losses worldwide. The primary inoculum is the ascospore, forcibly discharged from perithecia developed on crop debris. Consequently, ascospore discharge is of considerable interest in understanding the disease cycle of this fungus. We have been investigating the role of ion channels in ascospore discharge by performing targeted gene knockouts. Recently, we have generated two mutants which affect ascospore development and discharge. One produces apparently normal perithecia and asci, but lacks ascospores. Meiosis and reduction division apparently take place within the ascus, but spores are not fully developed. The second mutant produces ascospores but does not discharge them. The perithecia are considerably drier than wild type. contributed presentation

Hambleton, Sarah^{1*}, Seifert, Keith A.¹, Nickerson, Nancy L.², and Hill-Rickette, Grace³. ¹Biodiversity Theme (Mycology & Botany), Agriculture and Agri-Food Canada, Ottawa, Ontario K1A 0C6 Canada, ²Biodiversity Theme (Mycology & Botany), Agriculture and Agri-Food Canada, Kentville, Nova Scotia B4N 1J5 Canada, ³University of Alberta, Edmonton, Canada. hambletons@agr.gc.ca. **Chlamydozporic ascomycetes: an examination of relationships and variation among taxa with minimal or reduced morphology.**

Many fungi isolated from soil produce thick-walled, melanized, resistant structures called 'aleurioconidia' or 'chlamydozporic'. Some isolates also produce synanamorphs that facilitate identification, but others are simply described as humicola- or trichocladium-like on the basis of brown aleurioconidia produced laterally or terminally on minimally differentiated conidiophores. Our recent studies of fungi isolated from soil and plant roots recovered a number of chlamydozporic taxa that were distinct according to analyses of SSU and ITS rDNA sequences. Some were identified (eg. *Humicolopsis*) while others await names, or are newly described based on results of detailed morphological studies and comparisons with known genera of chlamydozporic fungi, including *Thermomyces*, *Humicola* and *Trichocladium*. Characters of the colony, conidium (germ pores, septation, ornamentation), conidium ontogeny, and synanamorph were useful for differentiating new taxa. Chlamydozporic production was inconsistent among isolates and sometimes required special incubation conditions. Analyses of new and existing sequence data highlighted the diverse phylogenetic relationships of these fungi allied to four Classes of Ascomycota. In some cases, closely related sequences from GenBank were for unnamed root-associated fungi. ITS data suggest that *Humicola* is a synonym of *Trichocladium*. contributed presentation

Gowland, Kelli M.^{1,2}, Clements, Mark A.², and Nicotra, Adrienne¹. ¹School of Botany and Zoology, Australian National University, Canberra, ACT 0200, Australia; ²Center for Plant Biodiversity Research, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia. kelli.gowland@csiro.au. **Detecting bias in host and fungal associates of three epiphytic *Aeridinae* orchids of Australia**

An epiphyte is an organism that utilizes another organism as a substrate upon which to live. Epiphytes derive no direct benefit from, nor do they confer any direct benefit to their host, thus most epiphytes are not host specific. Despite this, research on three epiphytic *Aeridinae* orchids of eastern Australia uncovered non-random distribution patterns within four disparate field sites. Two of the orchids, *Sarcophilus olivaceus* and *Plectorrhiza tridentata*, exhibited distinct host species preferences. All orchids depend upon a mycorrhizal fungus to germinate, thus it is intuitive that the host bias reflects a non-random fungal distribution. To test this hypothesis *Rhizoctonia*-like fungi were isolated from orchid roots from two field sites, pure cultures were obtained and the nuclear ribosomal ITS sequences of these isolates determined. The results suggest that these fungi are neither restricted to particular species of woody plants, nor to the different sites. They also demonstrate that these orchids associate with distinct clades of *Ceratobasidium* fungi and that their fungal associates correlate strongly with their ecological preferences. poster

Hanlin, Richard T.^{1*} and González, María C.² ¹Department of Plant Pathology, University of Georgia, Athens, Ga, 30602-7274, USA, ²Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México 04510, México. mcgv@ibiologia.unam.mx. **Fungal Philately.**

Fungal Philately, the collecting of postage stamps, is one of the most popular hobbies in the world. Postal services in many countries take advantage of this by designing stamps that will appeal to collectors, as well as serve their primary function as postage. For some smaller countries, the sale of postage stamps to collectors represents a significant percentage of their national income. The majority of philatelists are general collectors, but many others are thematic, or topical, col-

lectors, concentrating on stamps with a particular theme, such as birds, animals, flowers, etc. One such topic is mushrooms and other fungi. The first postage stamps depicting mushrooms were issued by Romania in 1958. Since then, about 160 countries have issued over 2,500 stamps depicting some 700 species of fungi. A notable exception is the USA. This number does not include souvenir sheets that have been produced by many countries. *Amanita muscaria* is the most common mushroom found on stamps, followed by *A. caesarea*, *A. phalloides* and *A. pantherina*. Other frequent genera include *Agaricus*, *Cantharellus*, *Coprinus*, *Hygroclype*, *Lactarius*, *Macrolepiota* and *Russula*. *Boletus edulis* is the most common bolete. Among the ascomycetes, *Morchella esculenta* is most common, along with a few cup fungi and *Xylaria* species. Most groups of fungi are represented by at least one stamp, including rusts, smuts, polypores, slime molds, lichens and hyphomycetes, especially *Penicillium notatum*, which is often shown with Sir Alexander Fleming, the discoverer of penicillin. poster

Hanna, John W.^{1,2*}, Klopfenstein, Ned B.¹, Kim, Mee-Sook¹, McDonald, GERAL I.¹ and Moore, James, A.² ¹USDA Forest Service-RMRS, 1221 South Main Street, Moscow, ID 83843, USA, ²Dept. of Forest Resources, University of Idaho, Moscow, ID 83844, USA. jhanna@fs.fed.us. **Phylogeographic structure of *Armillaria ostoyae* in the western United States.**

Direct-PCR was used to obtain sequences of nuclear rDNA regions (large subunit, internal transcribed spacer including 5.8S, and intergenic spacer) from *Armillaria ostoyae* genets collected in the western USA. Many genets contained heterogeneous sequences that indicate intragenomic variation and/or intraspecific hybridization. Intragenomic variation in rDNA regions was verified with the application of specific internal primers and visual analysis of sequence chromatograms. Bayesian inference methods defined three phylogenetic groups. Two phylogeographic groups were associated with the Rocky Mountain and Pacific Northwest regions of the USA. Additional analysis of *A. ostoyae* from outside the western USA indicates the presence of a circumboreal group with representation in Utah, USA. Individual genets containing heterogeneous sequence combinations from multiple groups were common in some geographic regions. Analysis of phylogeographic structure among these groups and hybrids allows for conjecture of paleogeographic and paleoclimatic influences. Hypothetically, groups may have physically converged after long-term geographic isolation. Subsequent hybridization events may have influenced evolution and contributed to variation in ecological behavior of *Armillaria* species. contributed presentation

Hasebe, Nobukatsu¹, Henkel, Terry W.¹ and Stephenson, Steven L.² ¹Department of Biological Sciences, Humboldt State University, Arcata, California 95512, USA, ²Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas 72701, USA. nhqri@earthlink.net. **Myxomycete communities of the Upper Potaro River, Pakaraima Mountains, Guyana.**

Myxomycete diversity in the rain forests of the Upper Potaro River area of Guyana's Pakaraima Mountains was investigated. Data from field collections and moist-chamber cultures of bark, aerial and ground substrata collected along transects in mixed and *Dicymbe* monodominant forests are discussed with respect to myxomycete distribution and microhabitats in the two forests. Putatively new species of *Lamproderma* are examined, and new distributional records for species in several genera are discussed. poster

Hasegawa, Eri^{1*}, Ota, Yuko¹ and Ito, Susumu². ¹Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan, ²157-62 Tsutsui-Yatsuhashi, Aomori 030-0944, Japan. haseg@ffpri.affrc.go.jp. ***Armillaria* isolated from herbaceous plant roots.**

We attempted to detect *Armillaria* on plants in abandoned rice fields in Aomori Prefecture, Japan. Sampling sites were seasonally inundated, though wet all year. Soil blocks containing plants were removed from the ground, the soil was washed off with water, and isolations were attempted from underground plant parts. *Armillaria* sp. was isolated from herbaceous plant species including *Carex* spp. The fungus was isolated from living roots 3-18 cm below ground, but not from rhizomes or dead roots. No mycelial mats or rhizomorphs were observed on roots. Most plants were not wilted or yellowed, and did not show other symptoms. There were no trees or bushes in the sampling sites and soil samples did not contain tree roots. The fact that *Armillaria* inhabits living roots of herbaceous plants other than achlorophyllous orchids without causing disease symptoms indicates new ecological characteristics of the fungus. poster

Hashimoto, Yasushi^{1*}, Kunishi, Ayako¹ and Hasegawa, Shigeaki². ¹Agro-environmental Science, Obihiro University of Agriculture and Veterinary Medicine, Inada-cho, Obihiro, Hokkaido 080-8555, Japan, ²Graduate School of Environmental Earth Science, Hokkaido University, N10W5, Sapporo, Hokkaido 060-0810, Japan. yhashi@obihiro.ac.jp. **Interspecific C transfers from *Larix kaempferi* Carr. to *Pyrola incarnata* Fischer by way of mycorrhizal fungi.**

Our knowledge of the function of *Pyrola* mycorrhizas in forest ecosystems has been limited. To confirm the interspecific C transfer from *Larix kaempferi* to *Pyrola incarnata* by way of mycorrhizal fungi, ¹³C tracer studies were performed. We fed ¹³CO₂ to *L. kaempferi* and measured the excess atom% of ¹³C

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in *P. incarnata* in experimental pots containing both plants species with field soil. To identify the mycorrhizal fungi, both plants mycorrhizas were collected from the experimental pots and compared for restriction fragment length polymorphisms (RFLP) of the amplified internal transcribed spacer (ITS) region in nuclear rDNA and ITS sequences. In the experimental pots, significant levels of 13C were detected from leaves of *P. incarnata*. Furthermore, the results on PCR-RFLP and ITS sequences suggested the same species of fungi were colonized on both mycorrhizal roots of *P. incarnata* and *L. kaempferi* that were collected from the experimental pots. One of those fungi was identified as *Thelephora terrestris* by ITS sequence. These results indicate that there are interspecific C transfer from *L. kaempferi* to *P. incarnata* via their common ectomycorrhizal and *Pyrola* mycorrhizal hyphal connection. poster

Hatai, Kishio¹, Muraosa, Yasunori¹, Morimoto, Kyoko¹, Sano, Ayaka², Nishimura, Kazuko² and Fujimoto, Kayo³. ¹Division of Fish Diseases, Nippon Veterinary and Animal Science University, Musashino, Tokyo 180-8602, Japan, ²Research Center for Pathogenic Fungi and Microbial Toxicoses, Chiba University, Chiba 260-8673, Japan, ³Chiba Prefectural Fisheries Research Center, Chiba 295-0024, Japan. hatai@scan-net.ne.jp. **A new fungus isolated from abalone with white nodules in Japan.**

In January 2004, some abalones died from an infection after being imported from South Africa. Several moribund abalones of about 64 g in body weight were examined. White nodules were present on the surface of the body parts. A lower fungus was observed in the nodules under the microscope. To isolate the fungus, a part of nodule was inoculated onto PYGS agar containing streptomycin sulfate and ampicillin. After three days on incubation at 15C, a single fungus was observed growing on the plates that appeared similar to the fungus first observed under the microscope. The fungus (a strain, NJM 0451) grew well at 15C, but not at 30C. The fungus was obligate marine fungus, because it only grew on the PYGS agar. The fungus looked like the fungi of the order Lagenidiales from some morphological characteristics. Namely, the shape of zoosporangium was like the middle between the genera *Halocrusticida* and *Haliphthoros*. The zoospores were released from the top of discharge tubes developed from a zoosporangium. The size of zoospores was bigger than that of the two genera. The phylogenetic tree inferred from 18S rDNA partial sequence using the isolate NJM 0451 and some related fungi showed that the isolate NJM 0451 was a new genus in the order Lagenidiales. poster

Hattori, Tsutomu. Forestry and Forest Products Research Institute, Tsukuba 305-8687, Japan. hattori@affrc.go.jp. **Overview of fungal diversity studies in Japan: toward the establishment of a new RDB.**

The Japanese Ministry of the Environment (ME) published the first comprehensive red data book (RDB) of non-vascular plants, including 91 species of fungi, in 2000. It was great first step in fungal conservation, but several common species were involved in the list while some important, rare ones were missed. ME plans to revise the red list (RL) every 5 years and the RDB every 10 years, and has organized the Committee for Selection and Evaluation of Threatened Wildlife of Japan to propose a revised RL in late 2006. For revision of the RL, the mycology team under the Committee listed macrofungi whose occurrences and/or known distribution are extremely limited, or whose occurrences are restricted to environments or hosts that are extremely reduced or undergoing reduction. Mapping of the listed fungi in addition to those in the last RDB is now in process in cooperation with amateur mycologists from various areas of the country. Some other research activities may enhance the scientific values of RLs and RDBs. Some mycological clubs are recording occurrences of macrofungi in certain sites over the long-term. Such activities are expected to result in complete species lists at the local level, while detecting chronosequential reductions of certain species at the sites. There are already some inventories of host and environmental ranges of some taxa in certain regions. Such information should be collected for the establishment of a comprehensive ecological catalog of fungi. Some mycologists are currently monitoring some rare fungi intensively to detect their distribution, as well as environments and hosts on which they depend. symposium presentation

Hattori, Tsutomu. Forestry and Forest Products Research Institute, Tsukuba 305-8687, Japan. hattori@affrc.go.jp. **Host recurrence among wood-inhabiting Aphyllophoraceous fungi in a cool temperate area of Japan.**

In order to reveal host recurrences among wood-inhabiting Aphyllophoraceous fungi, I established a 200 x 300 m plot at an old growth forest in a cool temperate area of Japan, and recorded fungi within the plot. I marked all the coarse woody debris (CWD) > 20 cm in diameter within the plot. I recorded DBH or basal diameter, tree species, and fungal species occurred on each CWD. Decay class was also recorded for each CWD belonging to three major tree genera in the forest, *Quercus*, *Castanea* and *Fagus*. To test for host recurrence of the fungi, I calculated the probability (P) of observing ? the recorded number of a particular species on the most frequently occurred host tree genus. The following species were restricted on *Quercus* and *Castanea*: *Daedalea dickinsii*, *Hymenochaete rubiginosa*, *Melanoporia castanea*, *Piptoporus soloniensis*, *Xylobolus frustulatus*. The following species showed high recurrence on *Fagus* spp. (P<0.001) though their occurrences were not always restricted on *Fagus* spp.: *Elmeria holophaea*, *Fomes fomentarius*, *Antrodiaella hoehnelii*. Among the species frequent on oaks

and chestnuts, *D. dickinsii*, *Inonotus xeranticus*, *M. castanea*, and *X. frustulatus* were highly recurrent on larger substrata (P<0.001, x square tests). I suggest that species recurrent on beeches as well as those on oaks with large diameter may be lost in young forests where no beech trees and huge oak trees exist. poster

Hattori, Tsutomu^{1*}, Fukiharu, Toshimitsu² and Goto, Yasuhiko³. ¹Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan, ²Natural History Museum & Institute Chiba, Aoba-cho, Chiba 260-8682, Japan, ³The Mycologist Circle of Japan, Abiko, Chiba, 270-1175 Japan. hattori@affrc.go.jp. **Mycological activities by mycological clubs in Japan.**

There are over 80 mycological clubs consisting of mainly amateur mycologists in Japan. Some of them hunt edible mushrooms, but many of the clubs are also active in pure mycology. Among these clubs' activities, first and foremost is contribution to local inventories of macrofungi. The Yokin-no-Kai and the Mycologist Circle of Japan inventory macrofungi monthly at sites in Kyoto and Kanagawa respectively. The Chiba Mycological Club holds mycological forays all over Chiba Prefecture. Such activities result in spatial mappings and records of chronosequential fluctuations for certain species. These clubs also train and educate amateurs and students. In fact, many professional mycologists were trained to identify macrofungi within such clubs in their school days, because there are few mycological courses for macrofungi in Japanese colleges. Many amateur members of these clubs publish books on mushrooms designed for amateur mycologists as well as mushroom hunters. Additionally, some amateurs actively report species of macrofungi new to science or new to Japan. Amateur mycologists are a part of the MSJ membership. Many of them participate in MSJ annual meetings and make poster and oral presentations for newly recorded fungi, introduction of rare fungi, etc. poster

Hazard, Chris M.¹, Horton, Thomas R.^{1*}, Leopold, Don J.¹ and Lilleskov, Erik A.² ¹Dept. of Environmental and Forest Biology, State University of New York College of Environmental Science and Forestry, Syracuse NY 13210, USA, ²USDA Forest Service, Houghton MI 49931, USA. thorton@esf.edu. **Mycorrhizal ecology of pinedrops (*Pterospora andromedea*) in the Northeastern United States: is the plant rare because the fungus is rare?**

Pinedrops (*Pterospora andromedea*, Monotropoideae) are common in the Western United States, but rare in the Northeast. An explanation for this regional rarity could be that its mycorrhizal symbiont is uncommon in the Northeast. As a myco-heterotrophic plant, pinedrops are unable to fix carbon, and thus parasitize mycorrhizal fungi for energy. In the Western United States several haplotypes of pinedrops exist, which are specific to one of two common ectomycorrhizal fungi within the genus *Rhizopogon* subgenus *Amylopogon*, both which associate with members of Pinaceae. We hypothesize that in the Northeastern United States pinedrops are also associated with *Rhizopogon*, and that the autotrophic plant host is eastern white pine (*Pinus strobus*). Further, we hypothesize that these fungi are rare in the Northeast. We have sampled wild populations of northeastern pinedrops and have characterized the plant haplotypes and fungal symbionts with molecular techniques; these data were compared to those from the West with phylogenetic analyses. We found only one haplotype/fungal symbiont pair. The haplotype was not unique to the Northeast, unlike the fungal symbiont, which may be a new species within *Amylopogon*. Bioassays with eastern white pine planted in field soils are being used to assess the distribution and rarity of this fungus further. contributed presentation

Henk, Daniel A.* and Vilgalys, Rytas J. Department of Biology, Box 90338, Duke University, Durham, NC 27708, USA. dah@duke.edu. **Host specificity and population structure in species of *Septobasidium*.**

Septobasidium is a genus of fungi that infects scale insects. These fungi have been thought to primarily disperse with their host insects, yet there are numerous putative host generalist *Septobasidium* species suggesting that these species must occasionally disperse independently of host insects. We developed an approach to quantify specificity using a phylogenetic measure, which we applied to ten common species of *Septobasidium*. We used DNA sequence data to infer a phylogeny for the host insects, and used this phylogeny to assess fungal host specificity. We then examined the population structure of host specialist, host generalist, and intermediate specialist *Septobasidium* species from an overlapping geographic range in the southeastern U.S. In the host generalist *S. ramorum*, we recovered a strong signal of geographic subdivision but no evidence of subdivision based on host species. However, we did detect some correlation between *S. ramorum* genetic structure and genetic structure of its primary host insect species, *Chionaspis nyssae*. Unlike the host generalist, we have not yet found evidence of geographic or host associated population structure in either the host specialist, *S. fumigatum*, or the intermediate specialist, *S. sinuosum*. We conclude that in *Septobasidium*, codispersal is not the underlying cause or necessarily a result of specificity. symposium presentation

Henkel, Terry W.^{1*}, Aime, M. Catherine², Chin, M.³ and Andrew, C.⁴ ¹Department of Biological Sciences, Humboldt State University, Arcata, California 95521, USA, ²USDA-ARS, Systematic Botany and Mycology Lab, Beltsville,

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Maryland 20705, USA, ³1089 A Street, Arcata, California 95521, USA, ⁴Kanawapai Village, Upper I, Guyana. twh5@humboldt.edu. **Edible mushrooms used by the Patamona Amerindians of Guyana.**

Mushrooms are a seasonally important food for the indigenous Patamona Amerindians of the rain-forested Pakaraima Mountains of Guyana. In collaboration with the Patamona, we have documented at least 17 species of edible fleshy fungi. The majority of these fungi are undescribed species, and many are ectomycorrhizal associates of leguminous *Dicymbe* spp. (Caesalpinaceae). A number of these fungi belong to groups that are infrequently collected for the table by North Americans (e.g., Clavulinaceae, Sarcoscyphaceae, Amanitaceae) whereas groups which contain highly prized culinary mushrooms by north temperate standards (e.g., Cantharellaceae) are shunned by the Patamona. The Patamona have incorporated mushrooms into their pantheon of edible wild foods. The breadth of wild organisms in other taxonomic groups (e.g. vertebrates, invertebrates, plants) used by the subsistence Patamona is wide, and mushrooms appear to play a seasonally important dietary role. Ectomycorrhizal fungi associated with regionally-restricted *Dicymbe* spp. present a unique fungal resource to the Patamona, previously unrecorded in Amazonian ethnomycology. The fact that not all locally available edible mushrooms are utilized by the Patamona may reflect the evolving state of their knowledge regarding mushrooms, in which known edible species are condoned and others remain unknown, and therefore taboo. poster

Henkel, Terry W.^{1*}, James, Tim Y.², Miller, Steven L.³, Aime, M. Catherine⁴ and Miller, Orson K., Jr.⁵ ¹Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA, ²Department of Biology, Duke University, Durham, NC 27708, USA, ³Department of Botany, University of Wyoming, Laramie, WY, USA, ⁴USDA-ARS, Systematic Botany and Mycology Lab, Beltsville, MD, USA, ⁵Virginia Polytechnic & St. University, P.O. Box 858, McCall ID 83638, USA. twh5@humboldt.edu. **The mycorrhizal status of *Pseudotulostoma volvata* (Elaphomycetaceae, Eurotiales, Ascomycota).**

Pseudotulostoma volvata O.K. Mill. & T. W. Henkel is a morphologically unusual member of the otherwise hypogeous Elaphomycetaceae due to its epigeous habit, and its spore-bearing mazaedium borne on an elevated stalk at maturity. Field observations and plot studies in Guyana indicated that *P. volvata* was restricted to tropical rain forests dominated by ectomycorrhizal (EM) *Dicymbe corymbosa* Spruce ex Benth. (Caesalpinaceae), suggesting an EM nutritional mode for the fungus. An EM status for *P. volvata* would corroborate its placement in the ectotrophic Elaphomycetaceae. Here we confirm the EM status of *P. volvata* with a combination of morphological, molecular, and mycosociological data. contributed presentation

Herrera, Jose*, Omodon, Melvin E. and Dillavou, Clayton. Division of Science, 100 E. Normal, Truman State University, Kirksville, MO 63501, USA. jherrera@truman.edu. **Assessment of fungal infection on borate-treated cellulose insulation.**

Cellulose insulation has rapidly gained a large market share among home builders and buyers. Recent concern regarding health effects of high concentrations of fungi within indoor environments ("sick building syndrome") has promoted concern about susceptibility of building materials including wood products (in general), and cellulose insulation (specifically) to fungal attack. This study reports a decrease or absence of fungal infection in cellulose insulation made from recycled paper and treated with varying concentrations of sodium polyborate (Boron 10TM; CAS # 183290-63-3) within 7-scale wall units exposed to variable and high ambient temperatures and relative humidities throughout the summer. Our results suggest that cellulose insulation treated with sodium polyborate almost completely eliminated five common fungal species sprayed onto cellulose within the wall units and is likely having a cytotoxic or sporocidal effect on many, if not all, fungal species. These results suggest that cellulose insulation treated with sodium polyborate, when properly applied and installed, is resistant to fungal infection for at least 124d at high temperatures and relative humidities. poster

Hibbett, David S.* and Costanzo, Janine. Biology Department, Clark University, Worcester MA 01610, USA. dhibbett@black.clarku.edu. **Measuring fungal discovery: a survey of recent progress in the homobasidiomycetes.**

Fungal systematists face the daunting challenge of describing all the species of the Mycota on Earth. Fungal ecologists have traditionally been consumers of taxonomic research, which provides them with tools for identification. In recent years, however, fungal molecular ecologists have started to make their own unique contributions to the discovery of biodiversity. We are surveying depositions of ITS and nuc-lsu rDNA sequences of homobasidiomycetes to GenBank in an attempt to quantify the acquisition of sequences, and the contribution of environmental studies to the discovery of new species. There are about 8000 homobasidiomycete ITS sequences in GenBank, of which 96% were deposited since 1998. In 2004, about 660 ITS sequences of homobasidiomycetes were deposited, and 11% of these were from environmental studies. About 10% of the environmental sequences were less than 90% identical to sequences that were in GenBank at the time that they were deposited. Data for nuc-lsu rDNA are comparable. To complete the catalog of extant fungal diversity, it will be necessary to integrate the data emerging from environmental studies with those produced by traditional taxonomy. This will require new phyloinformatics tools, as well as changed attitudes about the requirements for species description. contributed presentation

Higgins, K. Lindsay^{1*}, Arnold, A. Elizabeth^{1,2}, Miadlikowska, Jolanta¹ and Lutzoni, François¹. ¹Department of Biology, Duke University, Durham, NC 27708, USA ²Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA. khl15@duke.edu. **Diversity, species composition, and evolution of fungal endophytes across three major plant lineages.**

Although associated with all plants, fungal endophytes represent an unknown proportion of fungal diversity, and little is known about the phylogenetic affinity of these symbiotic microfungi. To date, most surveys of endophytes associated with foliage have focused on the temperate zone, such that boreal and arctic endophytes are poorly known. We used a culture-based approach to survey endophytic fungi from healthy photosynthetic tissues of three host species (*Huperzia* sp., *Picea mariana*, and *Dryas octopetala*) representing three major lineages of land plants (lycophytes, conifers, and angiosperms, respectively) in boreal and arctic sites. Phylogenetic analyses of the nuclear large and small ribosomal subunits (LSUrDNA, SSUrDNA) were used to examine the diversity, phylogenetic placement, and host affinity of forty-six endophyte species, which represented all major lineages of nonlichenized, filamentous Ascomycota. Special focus was placed on endophytes which, based on preliminary BLAST searches of nrITS data, appeared to represent the Dothideomycetidae, a lineage of particular interest because it contains endophytes as well as many plant pathogens. Together, these data provide evidence for greater than expected diversity of endophytes at high-latitude sites, and provide a framework for assessing the evolution of these poorly known but ubiquitous symbionts of living plants. poster

Hirooka, Yuuri*, Kobayashi, Takao and Natsuaki, Keiko, T. Lab. of Tropical Plant Protection, Tokyo University of Agriculture, 1-1-1, Sakuragaoka, Setagaya-ku, Tokyo 156-8502, Japan. 70040001@nodai.ac.jp. **Re-examination of *Nectria sensu lato* in Japan.**

Bionectria (Ascomycetes, Hypocreales) has white to yellow perithecia, 1-septate ascospores and *Clonostachys* anamorph. In Japanese mycoflora, this genus includes *B. bysicola*, *B. capitata*, *B. compactiuscula*, *B. epichloë*, *B. oblongispora*, *B. ochroleuca* and *B. pseudostrata*. In this study, one new species of *Bionectria* sp. h116 and its anamorph *Clonostachys* sp. h116 on dead twigs were collected in Okinawa and Kagoshima Pref. Surface of ascospore was warts arranged in striate. Present taxa, *Bionectria* species with warts arranged in striate was only *B. pseudostrata* Schroers (Anamorph: *C. pseudostrata* Schroers) from Schroers (2001). However, *Bionectria* sp. h116 and its anamorph differed from *B. pseudostrata* (Anamorph: *C. pseudostrata*) in the surface structure of perithecia [warted vs. smooth], color of perithecia [whitish-orange vs. orange-brown to brown], size of ascospores [15-21 X 5-7.5 µm vs. 9-17 X 3-6 µm], and size of conidia [3-16 X 2-4 µm vs. 3.6-8 X 2-3.8 µm]. This species belongs to the subgenus *Bionectria* (Schroers 2001). Two other species of this genus also have been collected from Japan for the first time; *B. grammicospora* Schroers & Samuels (Anamorph: *C. grammicospora* Schroers & Samuels) in Miyagi Pref. and *B. sporodochialis* Schroers (Anamorph: *C. sporodochialis* Schroers) in various parts of Japan. poster

Hirose, Dai. Graduate school of life and environmental science, University of Tsukuba, Sugadaira Montane Research Center, Sugadaira, Nagano 386-2201, Japan. daihiro@sugadaira.tsukuba.ac.jp. **Ecology of ectomycorrhizal fungi: population structure and biogeography.**

Population structures of ectomycorrhizal (ECM) fungi in various ecosystems have been studied extensively using molecular ecological methods. These studies have showed the propagation manners of various ECM fungi in natural ecosystems. It is important to select a proper fungal species in studying the population of ECM fungi, since a host tree is always associated with diverse ECM fungi. We have studied the ecology of *Stiellus pictus* which colonizes and forms ectomycorrhizas on fine roots of Japanese five-needled pine species. This fungus is suitable for the study of population ecology of ECM fungi. The reasons are as follows. (1) It is a dominant ECM fungus colonizing on fine roots of the pine species, (2) forms macroscopic tubercle mycorrhizas which can be easily identified and isolated, and (3) has a narrow host range in nature like as other *Stiellus* spp. that have been widely studied from ecological and ecophysiological view points. In addition, the host pines are distributed in relatively high altitude places in isolation in Japan. We studied following subjects on this fungus: (1) its host range in experimental conditions, (2) distribution pattern in a plantation stand, (3) population structures in natural forest stands, and (4) comparison of local populations in Japan. Based on the results of these studies, we discuss ecological characteristics of *S. pictus*, and its biogeography. symposium presentation

Hirotschi, Sato^{1*}, Takakazu, Yumoto² and Noriaki, Murakami¹. ¹Lab of Plant Taxonomy and Evolution, Department of Botany, Graduate School of Science, Kyoto University, Oiwake-cho, Kitashirakawa, Sakyo-ku, Kyoto-shi, Kyoto, 606-8502 Japan, ²Research Institute of Humanity and Nature, National Institutes for the Humanities, Inter-University Research Institute Corporation, 335 Takashima-cho, Marutamachi-dori Kawaramachi nishi-iru, Kyoto 602-0878, Japan. kuritake@fj8.so-net.ne.jp. **Cryptic species and host specificity in the ec-**

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tomycorrhizal genus *Strobilomyces*.

The degree of host specificity is one of the most important factors when understanding symbiosis between ectomycorrhizal fungi and their host plants. It has been supposed that most of ectomycorrhizal fungi, especially tropical, subtropical or warm temperate fungi, lack host specificity and that common mycorrhizal networks are made among forest trees by sharing those generalist fungi. However, the species classification of fungus is very behind due to the scarcity of the useful morphological characters for taxonomy. Therefore, existence of cryptic species of ectomycorrhizal fungi might make us underestimate their host specificity. Nevertheless, few researchers tried to examine this possibility so far. In this research, we tried to recognize cryptic species of the ectomycorrhizal genus *Strobilomyces*. Although low host specificity of the fungal genus was supposed, we found several races (possibly cryptic species) with high host specificity. We found 5 host specific races toward the plant subgenus *Cyclobalanopsis* (*Quercus-Fagaceae*) out of 11 races in Japanese ever-green forests. The result of this research clarified that the underestimation of the host specificity in ectomycorrhizal fungi was made by the existence of cryptic species, and strongly suggests possibility that high host specificity of ectomycorrhizal fungi might be common. poster

Hofstetter, Valérie^{1*}, Gueidan, Cécile¹, Reeb, Valérie¹, Miadlikowska, Jolanta¹ and Lutzoni, François¹. ¹Department of Biology, Duke University, Durham, NC 27708, USA. valh@duke.edu. **Molecular phylogenetics of lichen-forming fungi: ribosomal genes versus protein-coding genes.**

The collaborative project, titled Assembling the Fungal Tree of Life (AFTOL), is sampling eight molecular regions (nSSU, nLSU, ITS, mtSSU, *RPB2*, *RPB1*, *EF1*-alpha and *ATP6*) for 1500 species to contribute toward a comprehensive phylogenetic hypothesis of the Fungi. The resolving power of ribosomal RNA genes and associated non-coding regions is fairly well understood throughout the ascomycete tree. However, only few studies have used protein-coding genes to infer phylogenetic relationships among lichen-forming fungi. The two multilocus phylogenetic studies that included a protein-coding gene for a broad taxon sampling across Ascomycota (Reeb *et al.*, 2004; Lutzoni *et al.*, 2004) have shown that *RPB2* used in combination with ribosomal data recovered multiple deep relationships within Ascomycota that were never revealed previously, or were revealed with only low support values in prior studies. Here we present phylogenetic analyses for six of these eight loci, individually and in combination, across a large number of lichen-forming and allied fungal species. The resolving power of each locus will be assessed at different taxonomic levels, ranging from closely related species to taxa classified in different orders. Putative causes of inconsistencies among gene trees will be explored. The minimum combination of genes with the highest level of resolution and support will be investigated. We hope this study will form the foundation necessary to guide the selection of loci for future evolutionary studies on lichen-forming and allied ascomycetes. contributed presentation

Honan, Amy H.* and Desjardin, Dennis E. Department of Biology, San Francisco State University, San Francisco CA 94132, USA. ahonan@sfsu.edu. **A preliminary monograph of *Tetrapyrgos* based on morphology and ITS sequence data.**

The saprotrophic genus *Tetrapyrgos* (Basidiomycota, euagarics) currently consists of 16 species worldwide, two of which appear morphologically to be conspecific. Recent collecting trips have yielded over 100 specimens from Thailand, Malaysia, Indonesia, Brazil, and California. These collections provide new reports of *Tetrapyrgos* and indicate two new species belonging to this genus. Morphological and molecular sequence data (ITS region) from the recent collections, type specimens, and other representative exsiccata are analyzed to delimit taxonomic relationships within this genus. poster

Honda, Yoichi*, Watari, Junko, Sakatoku, Naofumi, Watanabe, Takahito and Watanabe, Takashi. Gokasho, Uji, Kyoto, Japan 611-0011. yhonda@kuwri.kyoto-u.ac.jp. **Cloning of *gpd* and construction of transforming vectors in *Ceriporiopsis subvermispora*.**

A selective white rot basidiomycete, *Ceriporiopsis subvermispora* is a promising microorganism effective as a biocatalyst to degrade plant cell wall lignin in industrial processes, including pulp and paper manufacture, and conversion of lignocellulosic biomass to various compounds. Extracellular oxidizing enzymes and metabolites have been the focus of intense research interests and the genes for these enzymes have been characterized. However, there is no report on development of DNA-mediated transformation in this fungus. In the present work, we successfully clone and characterize a gene encoding glyceraldehyde-3-phosphate dehydrogenase from *C. subvermispora* and demonstrated the gene is actually expressed in the fungus. The expression of the gene was controlled by glucose in the medium. We also constructed transforming vector plasmids containing the promoter and terminator sequences from *gpd* gene combined to a heterologous drug resistant marker gene such as hygromycin B phosphotransferase (*hph*) and bialaphos resistance gene (*bar*). poster

Hong, Soon Gyu^{1*}, Halonen, Marilyn² and Pryor, Barry M.¹ ¹Division of Plant Pathology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA, ²Arizona Respiratory Center, University of Arizona HSC, Tucson, AZ 85724, USA. polypore@email.arizona.edu. **Diversity of *Alternaria* species**

in the Sonoran Desert revealed by morphological, molecular, and immunological characterization.

Alternaria is a major fungal allergen source and is strongly associated with the development of asthma, especially in children raised in desert environments. To examine the diversity of *Alternaria* species in the Sonoran Desert, molecular, morphological, and immunological characterizations were carried out for isolates recovered from soil and plant debris collected from urban and desert areas around Tucson, AZ. AFLP fingerprinting analysis revealed that most isolates clustered within the alternata species-group, which includes *A. alternata*, *A. arborescens*, and *A. tenuissima*. Isolates were divided into 16 clusters by the 70% similarity criteria, and showed considerable morphological diversity in conidium size, shape, and catenation. Groupings based upon morphological features were not strongly correlated with groupings based upon AFLP data. Allergens were detected by hybridization with serum from patients with or without asthma development and with either positive or negative skin prick test responses based upon standard *Alternaria* extracts. Six major allergens were shared by most isolates. In addition, some isolates had minor allergens which were shared by only a few isolates. Groupings by allergen profile were not strongly correlated with groupings by either morphology or AFLP data. contributed presentation

Horn, Bruce W. National Peanut Research Laboratory, USDA-ARS, Dawson, GA 39842, USA. bhorn@nprl.usda.gov. **Effect of fungal competition on the colonization of wounded peanut seeds by *Aspergillus* section *Flavi* from natural soil populations.**

The effect of fungal competition on the colonization of wounded peanut seeds by *Aspergillus* section *Flavi* species in soil was examined. Viable peanut seeds were wounded and inoculated with 20 soils differing in composition and density of *Aspergillus* species, then incubated for 14 d at 37 °C (seed water activity = 0.92). Maximum percentages of seed colonization by section *Flavi* species were well below 100% despite high species densities in some soils. Furthermore, less than half of the viable propagules in soil at the wound site resulted in seed colonization by section *Flavi* species. Significant interactive effects ($P < 0.0001$) between soil densities of individual section *Flavi* species and potentially competing *Aspergillus* species (other section *Flavi* species and *A. niger*) suggest that competition is responsible for suppressing seed colonization by section *Flavi* species. Other fungal species were capable of invading peanut seeds only with soils from fallow fields and forested locations where the densities of section *Flavi* species and *A. niger* were low. poster

Hosaka, Kentaro^{1*}, Castellano, Michael A.² and Spatafora, Joseph W.¹ ¹Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA, ²US Forest Service, PNW Research Station, Corvallis, OR, 97331, USA. hosakak@science.oregonstate.edu. **Global biogeography of Hysterangiales (Basidiomycota): a Gondwanan origin?**

Hysterangiales is an order of ectomycorrhizal Basidiomycota that forms truffle-like sporocarps. It is distributed globally, both in the Northern and Southern Hemispheres, but each species is restricted to well-defined areas of endemism. Truffle-like fungi are mostly assumed to be incapable of long distance dispersal as their spores are only spread via small animal mycophagy. Based on both the high occurrence of endemism and limited spore dispersal, we hypothesized that the distribution of the order may be strongly influenced by vicariance. Multigene phylogenies resolved 3 major clades within the order that are composed exclusively of the Southern Hemisphere taxa, and they form a basal paraphyly, supporting a Hysterangiales origin in the Southern Hemisphere. The results of ancestral area reconstructions are consistent with the hypothesis of an east Gondwanan, i.e. Australian, origin of the order. Although the topologies of some more terminal clades are consistent with vicariance (e.g., a sister relationship of New Zealand and New Caledonian taxa), some areas (e.g., Australia) are in several different subclades of the order, which is in conflict with a strict vicariant scenario. Based on these patterns, we propose an east Gondwanan origin and diversification of the order prior to the breakup of Pangaea followed by vicariance as well as several dispersal and/or extinction events. symposium presentation

Hoshino, Tamotsu. Research Institute of Genome-Based Biofactory, National Research Institute of Advanced Industrial Science and Technology (AIST), 2-17-2-1, Tsukisamu-higashi, Toyohira-ku, Sapporo, Hokkaido 062-8517, Japan. tamotsu.hoshino@aist.go.jp. **Ecophysiology of snow mold fungus, *Typhula ishikariensis* in the Arctic.**

Snow mold fungi are psychrophilic or psychrotrophic fungal pathogens of perennial grasses and winter cereals in the Northern Hemisphere. However, there are few records of those fungi in non-agricultural regions such as the Arctic. We attempted to find snow mold fungi, especially *Typhula* species (*T. incarnata* and *T. ishikariensis*) in the Arctic. *Typhula ishikariensis* was divided two genetic types as biological species I (BS-I) and II (BS-II) based on mating and morphological experiments. BS-I was widely distributed in Eurasia. However, the geographical distribution of BS-II was limited. We did not find BS-II between the Baltic countries and central Siberia. Dominant isolates of BS-I from the Arctic, such as from Greenland, have an optimum growth temperature at 4°C and showed irregular

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growth at 10°C on potato-dextrose agar medium (optimum growth temperature of typical strains of *T. ishikariensis* BS-I was 10°C). However, dominant isolates from the Arctic had higher frost resistance than isolates from cool regions, such as from southern Norway. Results suggest that dominant isolates of *T. ishikariensis* in the Arctic lost growth ability at relatively high temperature (10°C), but developed in frost resistance. The biological characteristics seen in 'cold hardiness' in Arctic isolates are important factors favoring ecological adaptation under Arctic environmental conditions. symposium presentation

Hosoya, Tsuyoshi^{1*} and Sakuma, Daisuke². ¹National Science Museum, Tokyo, Japan, ²Osaka Museum of Natural History, Osaka, Japan. hosoya@kahaku.go.jp. **Current status of fungal inventory and database establishment in Japan.**

Due to regional broadening in the South and North, Japan embraces a wide diversity of organisms. Fungi are no exception. In spite of a relatively long history of mycobiota inventories in Japan, begun in 1905 (Shirai, 1905), much information remains to be added to the fungal inventory in Japan. Currently, the newest inventory of fungi in Japan is being edited by Dr. Katamoto, revising the most recent inventory by Hara (1954). Inventories require the mass accumulation of information, and advances in information technology and database software have contributed greatly to progress in this regard. To support such information, the preservation of specimens and appropriate curatorial works are required. The National Science Museum (TNS) is working on generating a database of its own specimens, but more extensive information based on fungal materials collected in a wide area of Japan, is required to support information on a wide diversity of Japanese mycobiotas. GBIF (Global Biodiversity Information Facility), an international project begun in 2002, has provided a good opportunity to integrate information of specimens kept in major mycological herbaria in Japan. Until now, some 23,000 records of fungal specimens have been archived, and can be accessed through the TNS homepage (<http://svrsh2.kahaku.go.jp/fungal/>). contributed presentation

Hsieh, Huei-Mei^{1*}, Ju, Yu-Ming¹ and Rogers, Jack D.² ¹Institute of Botany, Academia Sinica, Nankang, Taipei 115, Taiwan. ²Department of Plant Pathology, Washington State University, Pullman, Washington 99164-6430, USA. monicah@gate.sinica.edu.tw. **Molecular phylogeny of *Hypoxyton* and related genera.**

Sequences of two nuclear protein-encoding genes, beta-tubulin and actin, were selected to infer the phylogenetic relationships among the new genus *Annulohypoxyton* (formerly *Hypoxyton* sect. *Annulata*), *Biscogniauxia*, *Daldinia*, and *Hypoxyton*. Four major xylariacean genera with *Nodulisporium* or nodulisporium-like anamorphs. 109 cultures and 3 specimens of 83 taxa were included in the analyses, including 16 taxa of *Annulohypoxyton*, 14 of *Biscogniauxia*, 11 of *Daldinia*, and 42 of *Hypoxyton*. *Biscogniauxia* taxa form a monophyletic clade, which represents the earliest segregate from the other three genera. The next branch is composed of taxa belonging to *Annulohypoxyton*, which also forms a monophyletic clade. The third branch include taxa from *Hypoxyton* and *Daldinia*, with the latter branched off as a coherent group within the former. *Hypoxyton* is provisionally accepted as a paraphyletic genus and is now restricted to include only those taxa previously placed in *Hypoxyton* sect. *Hypoxyton*. poster

Hubbard, Michelle* and Kaminskyj, Susan. Dept. Biology, Univ. Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada. Michelle.Hubbard@usask.ca. **Distribution and motility of *Aspergillus nidulans* Golgi equivalents.**

Filamentous fungi including *Aspergillus nidulans* grow by highly polarized tip growth, which involves directed secretion of the endomembrane-derived vesicles. Fungal endomembrane systems include the endoplasmic reticulum, Golgi equivalents (GEs), vacuoles. Putative GEs can be localized *in vivo* using a GFP-tagged sodVIC strain, created by Susan Assinder (Univ. Wales, Bangor), who has shown that GEs congregate at future branch sites. Tip growth is defective in the temperature sensitive *A. nidulans* hyphal morphogenesis mutant *hypA1*. If *hypA1* cells are grown at 42°C they lack normal polarity; when 'downshifted' to 23°C these cells polarize and begin wildtype tip growth. We compared the dynamics of the putative GEs in a *hypA1* strain containing GFP-tagged sodVIC, grown at 23°C, 42°C, and during repolarization after downshift. Putative GEs are more abundant at hyphal tips than in basal regions, even in poorly polarized cells grown at 42°C. Putative GEs are motile in all growth temperature regimes. This motility is largely tip directed even when growth is slow. Tip-directed GE motility rate correlates with tip growth rate, both increasing as *hypA1* cells established polarity after downshift; both were significantly higher still in hyphae grown overnight at 23°C. In contrast, retrograde and lateral GE motility rates were similar for all growth temperature regimes. I am using inhibitors and selective fluorescent probes to clarify the mechanisms underlying distribution and motility of GEs and other endomembrane compartments. contributed presentation

Hughes, Monica* and Weir, Alex. 226 Illick Hall, SUNY-ESF, Syracuse, NY 13210, USA. mohughes@syr.edu. **Diversity and host utilization of New Zealand Laboulbeniales.**

New information is improving our understanding of the evolution and biogeography of New Zealand Laboulbeniales. Similar to other fungal biodiversity studies, a high number of species in our collection are uncommon, with a newly estimated lower bound of 300 species, revised upward from an earlier estimate of

200. A number of common genera (*Laboulbenia*, *Dimeromyces*, *Corethromyces*, *Peyritschiella*, *Monoicomyces*, *Stigmatomyces*, *Rhachomyces*) are about equally represented in comparison with the northern hemisphere. Conspicuous differences in New Zealand include a diverse *Diphymyces* component on Choleviniae, the total absence of Ceratomycetaceae, perhaps due to the paucity of aquatic hosts inhabiting still water, the lack of any species on hydrophiloids, and an under-representation of *Rickia*. Overall host utilization patterns are similar: hosts are primarily mycophagous, predacious, or saphrophagous. Differences include a comparatively low utilization of Carabidae, the discovery of four new host families in Diptera and Coleoptera, and a potentially more important role for coleopteran families such as Tenebrionidae. Here we compare and contrast patterns of Laboulbeniales diversity and host utilization between north and south temperate regions, and also provide preliminary information and comparison of their seasonality and exploitation rate. poster

Hughes, Monica* and Weir, Alex. 226 Illick Hall, SUNY-ESF, Syracuse, NY 13210, USA. mohughes@syr.edu. **New species of Laboulbeniales from New Zealand.**

Published information on the Laboulbeniales of New Zealand (26 described species) compares unfavorably with well-studied north temperate regions such as Poland (179 described species). This is especially surprising in light of the long isolation of these islands and the highly endemic nature of the New Zealand entomofauna. Over the past six years we have carried out intensive surveys throughout New Zealand and have increased the number of known species to 190. This figure includes several new genera and approximately 100 undescribed species. The extent of novelty discovered in this group of arthropod-associated fungi compares with similar estimates for other fungal groups in relatively unexplored locales, and adds further support to the idea that we currently know only a small fraction of the total global mycota. Here we present micrographs illustrating some of New Zealand's Laboulbeniales. poster

Hyde, Kevin D.*, Vijaykrishna, Dhanasekaran and Jeewon, Rajesh. Centre for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Hong Kong SAR, PR China. kdhyde@hkucc.hku.hk. **Origins of freshwater ascomycetes.**

Theories concerning the origins of freshwater ascomycetes have been based on ecological studies, suggesting that they have originated from terrestrial fungi. In this study, 18S rDNA sequences from major groups of fungi and basal animals are used to date the evolutionary origins of freshwater ascomycetes. Due to the lack of convincing fossil evidence and differences in evolutionary rates the Bayesian relaxed-clock method under five calibration points were utilized. Phylogenies show that freshwater ascomycetes occur in only three classes (Dothidiomycetes, Leotiomycetes and Sordariomycetes). Morphological and molecular studies indicate that freshwater and marine Halosphaeriales have terrestrial ancestors. Molecular data also indicates that the family Annulatascaceae and other unitunicate ascomycetes (e.g. *Pseudohalonectria*) are polyphyletic and have a terrestrial origin. Unitunicate freshwater ascomycetes appear to have evolved several times independently from the terrestrial environment. Both terrestrial and freshwater loculoascomycetes (e.g. *Boerlagiomyces*, *Lophiostoma*, *Massarina*) are morphologically alike and they also share similar phylogenetic histories. However, whether marine representatives of these genera evolved from terrestrial or freshwater ancestors is unknown and it would be interesting to investigate this evolutionary aspect by incorporating taxa from these ecologically and geographically different habitats in future molecular studies. poster

Inaba, Shigeki* and Harayama, Shigeaki. NITE Biological Resource Center (NBRC), Department of Biotechnology, National Institute of Technology and Evaluation (NITE), 2-5-8, Kazusakamatari, Kisarazu-shi, Chiba 292-0818, Japan. inaba-shigeki@nite.go.jp. **A new saprotrophic species of the genus *Myzocytiopsis* (Oomycetes) in Japan.**

A saprotrophic species of *Myzocytiopsis* (Myzocytiopsidales, Oomycetes) was isolated from a soil sample obtained in Nagano Prefecture, Japan. It was isolated from pieces of floating snakeskin used as a bait in a mixture of the soil sample and sterilized distilled water. It grew well on peptone-yeast extract-glucose (PYG) agar plate. On dead human skin, it formed thalli that were coarse, septate, extensively developed and frequently branched. Moreover, they appeared beaded, and were in some cases slightly, while in some other cases quite markedly, constricted at their septa. The sporangia vary in shape and form one exit tube. The content emerges fully and forms a vesicular mass in which zoospores are differentiated and discharged. The zoospores are monoplanetic and either pyriform, reniform or ellipsoidal in shape, having the size of 7-10 ~10-13 micrometers. Sexual reproduction was not observed. The species is similar to *Myzocytiopsis humana* in its habitat, but clearly distinguishable from it by the shape of thalli, size of zoospores, and lack of an organ for sexual reproduction. Sequence analysis of the mitochondrially-encoded *cox2* region showed its clustering with *M. humana* and *Lagenidium giganteum*, but it shared only 96.4 and 95.3 % similarities, respectively, with these species. Based on these observations, we propose that it is a new species of the genus *Myzocytiopsis*. poster

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MSA ABSTRACTS

Ishiguri, Maki*, Arima, Toshihide and Morinaga, Tsutomu. 562 Nanatsukacho, Shobara-city, Hiroshima 727-0023, Japan. tmorina@bio.hiroshima-pu.ac.jp. **Mechanism of fruiting body formation in *Polyporus arcularius*.**

Polyporus arcularius is basidiomycetous fungus and there are many papers in respect to photo-induction of fruiting and nutritional aspects of mycelium. But, there are no studies about the mechanism of fruiting body formation of this fungus. Since Leonard (1971) showed that phenoloxidase (PO) was related to form the fruiting body in *Schizophyllum commune*, there had been many papers about PO of another mushrooms. But, it was not clear yet. We already reported about the mutants that had not PO activity in *Polyporus arcularius*. These mutants were called PO-TA-1 and PO-TA-2, respectively. PO-TA-1 and PO-TA-2 were homokaryon and had the opposite mating type against to each other. Also, these mutants were crossed with wild type homokaryon having an opposite mating type and could make the fruiting body. But, after the crossing between these we could not find. Namely, these homozygous PO-less dikaryon could not produce fruiting body. Therefore, we did the cloning of this P.O. gene and sequenced. And, now by using this clone, we tried northern analysis and RT-PCR after light irradiation. poster

Jackson, Kimberland, Bashir, M.E. and Gunasekaran, M.* Dept. of Biology, Fisk University, Nashville, TN 37208, USA. mguna@fisk.edu. **An *in situ* assay for glutathione reductase from permeabilized cells of *Candida albicans*.**

A procedure is described which allows the rapid permeabilization of yeast cells. *Candida albicans* for quantitative *in situ* assay of glutathione reductase (GSSGR, EC 1.6.4.2) activity. GSSGR is a flavoprotein that catalyzes the reduction of GSSG to reduced GSH using NADPH as an electron donor. It is a key enzyme in the GSH-ascorbate cycle, which provides protection against oxidation stress. *Candida* cells are permeabilized by incubation in buffer containing different solvents: toluene, xylene, diethyl ether, ethanol and their combinations to examine their effect on membrane permeability. In addition the effect of various temperatures and time on permeabilization was investigated. The results obtained by *in situ* assay were compared with standard GSSGR assay carried out with cell-free extracts. Based on the results we feel that the permeation method of *in situ* assay is highly sensitive, specific and less time consuming. This procedure is equally applicable to fresh and frozen samples. poster

Jacobson, David^{1,3*}, Cornelia Boesl², Shahana Sultana², Till Roenneberg², Martha Merrow², Rachel Adams³, Jeremy Dettman³, Margarida Duarte⁴, Isabel Marques⁴, Alexandra Ushakova⁴, Patricia Carneiro⁴, Amaldo Videira⁴, Laura Navarro-Sampedro⁵, Maria Olmedo⁵, Luis M. Chorrochano⁵, Natvig, Donald O.⁶, and John Taylor³. ¹Dept. of Biological Sciences, Stanford University, Stanford, California, USA. ²Institute for Medical Psychology, University of Munich, Germany. ³Dept. of Plant and Microbial Biology, University of California, Berkeley 94720, USA. ⁴Instituto de Biologia Molecular e Celular, Porto, Portugal. ⁵Departamento de Genética, Universidad de Sevilla, Spain. ⁶Dept. of Biology, University of New Mexico, Albuquerque NM, USA. djacob@stanford.edu. **New findings of *Neurospora* in Europe and comparisons of diversity in temperate climates on continental scales.**

Neurospora was previously considered primarily a tropical or subtropical genus. However, recent field surveys found *Neurospora* occupying an entirely new ecological niche under the bark of fire-damaged trees in dry and cold habitats within a new geographic range, western North America, from New Mexico (34°N) to Alaska (64°N) (Jacobson *et al.* 2004 *Mycologia* 96:55-74). Isolates from these sites were composed predominantly (95%) of a single species, *N. discreta*, heretofore the least common species of *Neurospora* collected. In 2003 and 2004, a multinational effort surveyed southern Europe for *Neurospora* after unusually devastating wildfires. *Neurospora* was found from southern Portugal and Spain (37°N) to Switzerland (46°N). Species collected included *N. crassa*, *N. discreta*, *N. sitophila*, and *N. tetrasperma*. Although the latitude, climate and vegetation are similar to western North America, species distribution and spatial dynamics were quite different. Rather, these characteristics are more similar between southern Europe and semitropical Florida, where four different species are also present over very small spatial scales (Powell *et al.* 2003 *Mycologia* 95:809-819). These differences in regional diversity will form the basis of testable hypotheses, furthering the value of this model organism as a subject for studying fungal ecology. poster

James, Timothy Y.^{1*}, Vilgalys, Rytas J.¹, Longcore, Joyce E.², Mozley-Standridge, Sharon E.³, and the Assembling the Fungal Tree of Life Working Group. ¹Dept. of Biology, Duke University, Durham, NC 27708 USA, ²Dept. of Biol. Sciences, U. Maine, Orono, ME 04469 USA, ³Dept. of Plant Sciences, U. Georgia, Athens, GA 30602 USA. tyj2@duke.edu. **Early diverging lineages on the fungal tree of life: novel endoparasitic clades of Chytridiomycota.**

The basal branches on the fungal tree consist of a heterogeneous mix of taxa possessing ancestral characters such as coenocytic hyphae, reproduction through sporangia, and motile spores. How these basal taxa are related to each other and to the major radiation of the terrestrial fungi (Dikaryofungi) is unclear. Among these basal lineages are endoparasitic Chytridiomycetes with extremely reduced morphology, such as *Olpidium* and *Rozella*. In this study we address the phylogenetic arrangement of the basal lineages of Fungi and address the phylogenetic

position of *Olpidium* and *Rozella* using molecular sequence data from six gene regions (nuclear 18S and 28S rRNA genes, ATP6, EF1-alpha, RPB1, and RPB2). Both the Zygomycota and Chytridiomycota appear paraphyletic in most analyses. The Blastocladales are highly diverged from the other four orders of Chytridiomycetes. *Olpidium* and *Rozella* were recovered as separate lineages in the fungal phylogeny, both distinct from previously sampled clades of chytrids. *Rozella* spp. are well supported as the earliest diverging lineage in rDNA and RPB1+RPB2 phylogenies. This placement of *Rozella* renders the Chytridiomycetes paraphyletic. contributed presentation

Jeewon, Rajesh*, Yeung, Quin SY and Hyde, Kevin D. Dept. Ecology & Biodiversity, University of Hong Kong, Pokfulam Road, Hong Kong SAR, China. rrjeewon@hku.hk. **Molecular profiling and phylogenetic diversity of fungal communities associated with pine needles.**

Fungal communities undoubtedly contribute immensely to plants ecosystem. This study investigates fungal diversity and succession from Pine needles (*Keteleeria fortunei*, *Pinus eliottii* and *Pinus massoniana*) based on morphological comparison coupled with a molecular approach based on DGGE and phylogenetics. Morphological and culture dependent studies showed that about 80% of fungi were anamorphic, with *Trichoderma* and *Cladosporium* being dominant. Others include *Bostrichonema*, *Gliocladium*, *Glioccephalotrichum* and *Paecilomyces*. Two hyphomycetes, *Cancellidium pinicola* and *Thozetella pinicola*, new to science were also recorded. 40 different fungal operational taxonomic units (OTU) recovered from DGGE bands were sequenced and analysed. Phylogenies based on partial 18S rDNA sequences indicate that 32 are bitunicate ascomycetes, 4 are phylogenetically related to mitospore Letiomycetes, 2 are members of Trichocomaceae and another 2 belong to the Hypocreales and Lecanorales (lichens) respectively. Most of these fungi have not been recovered from morphological and cultural methodologies as well as from previous endophytic studies reported elsewhere. It is highly possible that many of them are very important in the decomposition process but are morphologically and culturally undetected. These findings have important scientific implications in biodiversity and ecological studies. poster

Jewell, Kelsea A.* and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. jewell.kels@students.uwlax.edu. **The possible biocontrol of pathogenic *Candida albicans* using the killer yeast *Candida glabrata* Y55.**

Candida albicans is responsible for both minor and serious mycoses, commonly termed candidiasis. These infections are difficult to treat due both to the ineffective nature of antifungal drugs and the emergence of resistant strains. It is increasingly important to identify novel antifungal therapies. One area of possible exploitation is killer yeasts. The term "killer yeasts" includes fungi in Ascomycota, Basidiomycota, or deuteromycetes that produce extracellular fungicidal or fungistatic toxins due to internal viral infections. We have performed a series of competition experiments between several clinical isolates of *C. albicans* against a killer strain of *Candida glabrata*. These experiments have been aimed at determining the fungicidal and dimorphism-inhibiting ability of a killer *Candida* strain against *C. albicans*. Killing activity was determined by plating killer strains in lawns of *C. albicans* on media containing methylene blue dye. This dye is taken up by the yeast and released upon cell death; killing activity is indicated by areas of increased pigmentation. Killing activity was verified using the LIVE/DEAD stain under epifluorescence microscopy. Inhibition of dimorphism is determined by the changing total protein ratios of yeast and hyphal growth forms. Results indicate that there is antagonism between various strains of *C. albicans* and *C. glabrata*. contributed presentation

Johnson, Desirée*, Sung, Gi-Ho and Spatafora, Joseph W. Oregon State University, Dept. of Botany & Plant Pathology, Corvallis, OR 97331, USA. johnsode@onid.orst.edu. **Systematics of the genus *Torrubiella*.**

Torrubiella is a genus of ~60 species of arthropod pathogenic fungi that primarily includes pathogens of spiders and scale insects. It is characterized by the production of superficial perithecia and the absence of a stroma. Like much of the Clavicipitaceae, *Torrubiella*'s asci are cylindrical with thickened apices and ascospores are filiform and either remain intact or disarticulate into partspores according to species. The most common anamorphs linked to the genus include *Akanthomyces*, *Gibellula*, *Paecilomyces* and *Verticillium*. The phylogenetic relationship of *Torrubiella* to the rest of the Clavicipitaceae is poorly understood with leading hypotheses suggesting a link between *Torrubiella* and species of *Cordyceps* that produce superficial perithecia on poorly formed stroma (e.g., *C. tuberculata*). Phylogenetic placement of *Torrubiella* and its relationship to other members of the Clavicipitaceae were investigated via multigene phylogenetic analysis of five gene regions including SSU nrDNA, LSU nrDNA, RPB1, RPB2 and tef 1-alpha. Taxon sampling included teleomorphic and anamorphic isolates and a broad representation of the Clavicipitaceae. The monophyly of *Torrubiella* was rejected with three main groups inferred by these analyses. The relationships of *Torrubiella*, and its anamorphs, to *Cordyceps* and the Clavicipitaceae will be discussed. poster

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MSA ABSTRACTS

Johnston, Peter R. Landcare Research, Private Bag 92170, Auckland, New Zealand. johnstonp@landcareresearch.co.nz. **Estimating fungal diversity - answers from the subantarctic.**

The number of fungal species in the world remains an intriguing question in mycology. Given the level of alpha-taxonomic knowledge in most regions, this number needs to be estimated indirectly. Data from intensively surveyed sites in the temperate Northern Hemisphere has been used to suggest that fungal diversity can be estimated by a comparison with plant diversity. A ratio of 6 fungal species to each plant species is often used. However, the highest levels of plant diversity are in tropical regions. Does the ratio between plant and fungal diversity estimated from temperate regions also hold for tropical regions? What is the impact of changing levels of plant diversity on the 6 fungal:1 plant species ratio? The subantarctic islands of New Zealand, with strong gradients in latitude and plant species diversity, will be used to address this question. Catalogues of fungi for these islands remain hopelessly incomplete, making it impossible to use all-species lists to compare fungal diversity between islands. This talk will discuss a phylogenetic approach to estimating fungal diversity, using data that suggests alpha-taxonomic knowledge in the New Zealand region for one intensively surveyed family, the Rhytismataceae, is close to complete. This data will be used to assess the impact that changing levels of plant diversity might have on estimates of fungal diversity. symposium presentation

Johnston, Peter R. Landcare Research, Private Bag 92170, Auckland, New Zealand. johnstonp@landcareresearch.co.nz. **Pacific journeys – the dispersal and evolution of *Metrosideros*-associated fungi.**

The rapid dispersal of *Metrosideros* across the Pacific Ocean over the last 2-3 million years provides an opportunity to address questions about the dispersal and evolution of fungal communities. The widely dispersed *Metrosideros* communities of the Pacific are thought to have radiated out from the New Zealand. *Metrosideros* in New Zealand is associated with a large and distinctive fungal biota. Some fungi are known to have the ability to disperse over long distances. Have the *Metrosideros*-adapted fungi of New Zealand followed along behind *Metrosideros* as it has dispersed? Alternatively, has *Metrosideros* evolved a series of novel, independent forest communities at each of the island's where it has established? Preliminary observations of fungi associated with ohia in Hawaii suggest that the second scenario may be correct. Ohia does have a set of distinctive and characteristic fungi. Where did they come from? How did they become adapted to life on ohia? What opportunities does the arrival of a new host plant present to fungi already present at a locality? contributed presentation

Jumpponen, Ari. Division of Biology, Kansas State University, Manhattan, KS 66502, USA. ari@ksu.edu. **Pitfalls and utilities of using molecular detection of fungi.**

Molecular tools are becoming more popular in studying the ecology of fungi. Comparisons of a sporocarp survey, on site or bait-seedling mycorrhiza assays, and direct amplification of soil DNA indicate that all but sporocarp survey methods provide largely congruent views of the mycorrhizal community at a low-diversity study site. Although results using different methods appear congruent, example data sets indicate that studies sequencing PCR amplicons from environmental samples are burdened by chimeric molecules that constitute up to 30% of all obtained data. Similarly, choice of primers can have a substantial impact on the inferred community structure. Regardless of these potential shortcomings, two case studies show that environmental DNA data can provide novel insights to fungal community dynamics. 1) A study on soil-inhabiting fungal communities in tallgrass prairie demonstrated a vast species richness of fungi and identified a group of potentially novel Ascomycetes that occurred more frequently in soil than therein imbedded roots. 2) A study of arbuscular mycorrhizal fungi (AMF) colonizing tallgrass prairie plant communities showed a community level response to nitrogen amendment, although root colonization by AMF was affected only minimally. symposium presentation

Kageyama, Stacie A.*, Bottomley, Peter J., Cromack, Kermit and Myrold, David D. Oregon State University, Corvallis, OR 97331, USA. stacie.kageyama@oregonstate.edu. **Changes in soil fungal communities across meadow-forest transects in the western Cascades mountains of Oregon, USA.**

Molecular analysis of ectomycorrhizal root tips and collection of sporocarps in Pacific Northwest coniferous forests indicate that fungal communities are spatially heterogeneous. The goal of this study was to use molecular techniques to examine changes in the total belowground fungal community along forest-meadow transects. We collected soil cores along three transects at two paired high montane forest-meadow sites at the H. J. Andrews Experimental Forest in the Western Cascade Mountains of Oregon, USA. We used fungal ITS rDNA primers with length heterogeneity PCR amplification of DNA extracted from soil. Our results agree with earlier root tip and sporocarp studies that indicate that the forest communities are spatially heterogeneous. In contrast, the meadow fungal communities exhibit much more homogeneity in their composition. poster

Kajimura, Hisashi. Lab. of Forest Protection, Graduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya 464-860, Japan. k46326a@nucc.cc.nagoya-u.ac.jp. **Symbiotic secrets in ambrosia beetle-fungal systems.**

About 3400 species of ambrosia beetles are found in 10 tribes of two sub-families of the Curculionidae, the Platypodinae and the Scolytinae. Ambrosia beetles vary in life history, but all carry and maintain ectosymbiotic "ambrosia" fungus spores in specialized organs termed mycangia. They bore tunnels (galleries) mainly in the sapwood of recently killed trees, disseminating the spores over the wall of gallery system. They are considered to have species-specific associations with primary ambrosia fungi (PAF), on which larvae feed for their development. Many of ambrosia fungi are placed in the anamorph genera *Ambrosiella* or *Raf-faelea*. However, the fungal symbionts of only a small percentage of the ambrosia beetles have been isolated, and it is not clear if the isolated fungi are the PAF. Few studies also have elucidated relationships between the beetles and the fungi: how do they encounter and how do they act each other, in spite of great importance to comprehending the symbiotic associations. I review the current state of knowledge on ambrosia beetle-fungal interactions, particularly in the Scolytinae of Japan. I also present recent data on the contributions of the fungi to the beetle success, and lay a special emphasis on the fact that PAF associated with one species of ambrosia beetles could have a nutritional potential as food resource for larvae of other beetle species. symposium presentation

Kamada, Takashi. Dept. of Biology, Fac. of Science, Okayama University, Okayama 700-8530, Japan. kamada@cc.okayama-u.ac.jp. **Genomic studies in the homobasidiomycete *Coprinus cinereus*.**

The homobasidiomycete *Coprinus cinereus* has been used as a model to study fungal development and regulation, because of its ease of cultivation, its amenability to genetic analysis, rapid development of its multicellular structure, the mushroom, and its naturally synchronous meiosis in the mushroom. This fungus has a total genome size of ~37.5 Mb, which is organized into 13 chromosomes, ranging in size from 5 to 1 Mb. The genome project on this fungus has been done as part of the Fungal Genome Initiative in the Whitehead Institute and the 10X sequence assembly of the genome of *C. cinereus* strain Okayama-7 has been released. Also, a BAC library of Okayama-7, component clones of which have been positioned on the sequence assembly, as well as chromosome-specific cosmid libraries, is available. These lines of information, coupled with a wealth of developmental mutants identified and existing molecular techniques such as efficient DNA-mediated transformation, RNAi and detailed gene mapping using RAPD markers, will facilitate both forward and reverse genetics of development and regulation in this fungus. symposium presentation

Kaminskyj, Susan¹ and Dahms, Tanya E.S.² ¹Dept. Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada, ²Dept. Chemistry and Biochemistry, University of Regina, 3737, Wascana Parkway, Regina, Saskatchewan, S4S 0A2, Canada. susan.kaminskyj@usask.ca. **Probing life at the hyphal tip: adventures in microscopy.**

What we observe and how we interpret it depends on our vantage point. Since the late 1500s, the development of and subsequent technological improvements in microscopy have changed the fundamentals of biology. Microscopy is important for mycology due to the small size of fungal organisms and/or their taxonomically diagnostic parts, and is relevant to cell biology in general particularly as fungi are superb model systems. Until the late 1950s, improvements to microscopy were mostly in resolution (better optical systems, development of electron microscopy), contrast control (differential staining, optical contrasting methods such as DIC) and information capture (photography). More recently, antibody tagging (fluorescence and gold), molecular tagging (GFP and chemically-selective probes), computer enhanced epifluorescent imaging (confocal) and electronic image capture and analysis have combined to provide *in situ* identification and monitoring of dynamic biological processes. We are combining established and newer imaging methods to extend our understanding of tip growth in *Aspergillus nidulans* hyphae. For example, atomic force microscopy (AFM) can image at high resolution (comparable to SEM, and better for depth discrimination) and also examine surface properties by force spectroscopy. Notably, we have used AFM on growing hyphae, imaging and collecting data on wall properties during tip growth. Consistent with general models, we demonstrate that the walls at growing hyphal tips and branches are more significantly more force compliant than mature regions. symposium presentation

Kaneko, Shuhei. Fukuoka pref. Forest Res. & Exten. Center Japan 1438-2 Toyoda Yamamoto Kurume-city Fukuoka 839-0827, Japan. shu-k@try-net.or.jp. **Cultivation of *Pholiota adiposa* in the Sugi (*Cryptomeria japonica* saw dust based media).**

Cultivation of the edible mushroom, *Pholiota adiposa* in the Sugi (*Cryptomeria japonica*) saw dust based substrate containing Sugi saw dust, cotton hull, corn-cob meal and rice bran (Sccr) was investigated. The optimal temperature range for mycelial growth of *P. adiposa* wild strains was 20-30 C and the optimal temperature was around 26 C. Growth did not occur at 40 C and all but one strain named Oninome-B died after 5 days. The optimal initial pH value of the cultivation medium was around 6.5 and various initial pH values converged to 3.5-5.5 after cultivation. The C/N ratio and pH value of the Sugi saw dust based substrate (Sccr) were suitable for mycelial growth and fruit body formation of *P. adiposa*.

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Adding cotton hull and corn-cob meal were effective to improve the water balance and increase the pH value respectively. Packing 500g of the Sugi saw dust based substrate (Scer) into the Nameko bottle (800ml), cultivating at 22.5 C under dark conditions for about 10 weeks, germinating at 14 C with over 95% RH and under around 700Lx, a yield of over 150g of fruit bodies was attained by flushing twice. Although less than the Buna (*Fagus crenata*) saw dust based substrate, the Sugi saw dust based substrate is considered to be available for cultivating *P. adipesa* due to its' low cost. poster

Karasawa, Toshihiko*, Takebe, Masako and Okazaki, Keiki. National Agricultural Research Center for Hokkaido Region, 1 Hitsujigaoka, Toyohira-ku, Sapporo 062-8555, Japan. tkarasaw@affrc.go.jp. **Management of indigenous arbuscular mycorrhizal fungi to reduce P fertilizer application in soybean-based cropping systems.**

The effects of preceding cropping on the growth, P uptake, arbuscular mycorrhizal (AM) colonization and yield of soybean were examined at 22, 44, 66 or 88 kg/ha of P application levels (recommended rate for soybean being 66 kg P/ha in this field) in order to clarify the appropriate rate of P application for soybean grown after respective preceding crop species. Growth, P uptake and AM colonization of soybean after wheat (AM host) cropping were superior to those after following or radish (nonhost) cropping at all P levels. It was therefore thought that the effect of wheat cropping on soybean is mainly caused by a larger AM fungal population in the soil, which improves AM colonization and P uptake of soybean, since AM fungi are obligately symbiotic fungi that need hosts to survive and multiply. Growth of soybean after nonhosts was accelerated with increase in P application levels, though that after AM host did not respond to P fertilization at more than 44 kg P/ha. The yield of soybean after AM host cropping was greater than that after nonhost cropping at 22 and 44 kg P/ha, but no effect of preceding cropping was observed at P/ha of 66 kg or more. The yield of soybean after AM host cropping did not respond to P fertilization at more than 22 kg P/ha. The results suggested that 44 kg P/ha is sufficient to secure both good growth and a high yield of soybean after AM host cropping. poster

Kasuya, Taiga^{1*} and Retnowati, Atik². ¹College of Agrobiological Resources, University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan, ²Herbatium Bogoriense, The Research Center for Biology, The Indonesian Institute of Sciences, Bogor, Java 16001, Indonesia. s0310849@ipe.tsukuba.ac.jp. **Four species of the genus *Calvatia* (Lycoperdaceae) from Indonesia.**

The genus *Calvatia* comprises 35 taxa and widely distributed in the world. This genus is characterized by large, subglobose to turbinate basidiomata, fragile, tough endoperidium and *Lycoperdon*-type capillitium. Species diversity of *Calvatia* were intensively studied in Europe and North America, but it is far from completely known in the tropical Asia. Although some species of *Calvatia* were fragmentally reported in several papers on fungal flora of Indonesia, this genus has not yet been comprehensively studied. We examined the specimens of *Calvatia* deposited in Herbarium Bogoriense, Bogor (BO), and 4 species were recognized. Among them, *Calvatia malukuensis* Kasuya et Retnow., ined., collected from Maluku Islands, Eastern Indonesia is described as a new species. This species has subpyriform basidiomata, bronze to reddish brown endoperidium and subglobose, warty basidiospores. *Calvatia rosacea* Kreisel, known from Ecuador also has bronze to reddish peridium, but *C. malukuensis* is distinguished from *C. rosacea* by apedicellate, subglobose basidiospores. The other 3 species, *C. boninensis* S. Ito et Imai, *C. craniiformis* (Schwein.) Fr. and *C. cyathiformis* (Bosc) Morgan are newly recorded from Indonesia. poster

Kauff, Frank*, Cox, Cymon J. and Lutzoni, François. Duke University, Dept. of Biology, Box 90338, Durham, NC 27708, USA. fkauff@duke.edu. **A data management framework for AFTOL (Assembling the Fungal Tree of Life).**

The "Assembling the Fungal Tree of Life (AFTOL)" project seeks to enhance our understanding of the evolutionary history of Fungi by bringing together a wide diversity of mycological and phylogenetic expertise. AFTOL Bioinformatics provides an efficient way of storing and analyzing the molecular data (targeting eight gene loci for c. 1500 taxa) and facilitates the communication between participants worldwide. An SQL database serves as the main storage facility for the data and is accessible through the WWW. An automated analysis subjects the raw sequence data to basecalling, contig assembly (using phred/phrap), and a local blast against a custom database to verify sequence identity. All intermediate and final results are available to the authors for verification with the possibility to make manual adjustments. Once verified, the final gene sequences for each locus are added to their respective alignments, which are then tested for topological congruence among loci. As a result, conflict-free matrices for different combinations of loci are provided to the users for further investigation, or forwarded to external collaborators of the Tree Of Life project for phylogenetic analysis. The system also provides a blast search against the AFTOL database, public access to sequence data (<http://ocid.nacse.org/research/aftol>), and formatting of sequence data for genbank submission. poster

Kawagishi, Hirokazu. 836 Ohya, Shizuoka 422-8529, Japan. achkawa@agr.shizuoka.ac.jp. **Body-function regulating compounds from the mushroom *Herichium erinaceum*.**

Body-function regulating compounds from the mushroom *Herichium erinaceum* will be discussed as follows. 1. Stimulators of NGF-synthesis: stimulators of NGF-synthesis have been expected to become medicines for degenerative neuronal disorders such as dementia. First naturally occurring stimulators, hericenone A to F and erinacines A to I, have been isolated from the fruiting bodies or mycelia of the fungus. Recently we isolated new analogs of hericenones and erinacines from the fungus. 2. Inhibitors of cytotoxicity of amyloid-beta-peptide: inhibitors of cytotoxicity of amyloid-beta-peptide have been expected to prevent or cure Alzheimer's disease. We found the very strong inhibitory effect of the extracts of the fruiting bodies of the fungus and succeeded in isolation and structure determination of one of the active principles from the mushroom. 3. Anti-MRSA compounds: methicillin-resistant *Staphylococcus aureus* (MRSA) is currently one of the most prevalent pathogens in nosocomial infections. We succeeded in isolation of some anti-MRSA substances from the fruiting bodies and the mycelia of the fungus. 4. Clinical test: clinical tests of the mushroom *Herichium erinaceum* have been done in a hospital in Japan. As a result, some symptoms of patients with dementia were improved and MRSA in some patients disappeared by eating this mushroom. symposium presentation

Kawamura, Fuminori^{1*}, Yamada, Akiyoshi¹ and Babasaki, Katsuhiko². ¹Faculty of Agriculture, Shinshu University, Minami-minowa, Nagano 399-4588, Japan, ²Forestry and Forest Products Research Institute, Tsukuba, Ibaraki, 305-8687, Japan. akiyosh@gipmc.shinshu-u.ac.jp. **Assessment of mycorrhization ability in the genetically modified saprotrophic mushroom, *Lentinula edodes*.**

Japanese government has validated the Cartagena protocol in the biodiversity agreement since 2003. Within this, treatment of Living Modified Organisms (LMO) is strictly defined. In the basidiomycetous mushroom fungi, LMO has already been constructed at the laboratory experimental level in the fungal taxa such as *Lentinula*, *Flammulina* and *Coprinus*. These LMOs have recently been addressed to the safety against wild organisms under natural environmental condition. In this study we focused on the confirmation of the absence of mycorrhization ability in LMOs of *Lentinula edodes* as same as the wild strains. Seven LMO and two wild strains of *L. edodes* were cultured and inoculated to the sterile seedlings of *Pinus densiflora* under the customary mycorrhiza synthetic conditions. As the positive and negative controls, 64 strains of ectomycorrhizal fungi and 11 strains of saprotrophic ones also were tested in their mycorrhization. While most strains of mycorrhizal mushrooms formed typical ectomycorrhizas, no strain of saprotrophic mushrooms did. In *L. edodes*, both LMO and wild strains showed no sign of mycorrhization. These results suggest that there is no evidence at present that saprotrophic LMO mushrooms accidentally express the mycorrhization ability. poster

Keirle, Matthew^{1*} and Mueller, Gregory². ¹The Committee on Evolutionary Biology, University of Chicago, Chicago, IL 60637, USA, ²The Field Museum of Natural History, Chicago, IL 60605, USA. mkeirle@uchicago.edu. **Covariance patterns in basidiome morphology revealed through multivariate analysis of selected *Laccaria* species.**

Historically, multivariate analyses of fungal morphology have been applied to reveal structure associated with delimiting discrete boundaries for cryptic taxa. Prior investigations have failed to examine patterns of covariance between basidiome morphological traits. In the current study, R-mode analyses of twelve morphological traits are carried out for 39 collections representing exemplar *Laccaria* specimens from locations across the United States and Canada embodying the taxonomic breadth of the genus. SAHN cluster, MDS polar ordination, principal components, path, and factor analyses are applied to reveal the underlying directionality of variance and covariance in the data set. Although no strong directional trend in a single principal component axis was found, factor and path analyses support the existence of latent macro-morphology and spore production factors. Aspects of the spore production factor suggest that the positioning of basidiospores in crowded form on the tips of the sterigmata creates a correlation between basidium shape and spore width which is independent of spore length. Interestingly, factor analysis provides little support for a latent overall mushroom stature factor or for latent factors which predict a correlation between the two major dimensions of the basidium and the basidiospore. poster

Kennedy, Allison* and M. Catherine Aime. USDA-ARS, Systematic Botany and Mycology Laboratory, Beltsville, MD 20705. allison@nt.ars-grin.gov. **Cultural studies *Moniliophora roreri*, an important cacao pathogen.**

The basidiomycetous plant pathogen *Moniliophora roreri* (Marasmiaceae), causal agent of the Frosty Pod Rot of *Theobroma cacao*, the source of chocolate, is currently in an invasive phase in Central and South America. Prior nucleotide sequence data has indicated the presence of three genetic groups: a basal genotype found on *Theobroma* and *Herrania* species in northwestern South America, a primarily Central American genotype spreading northward on *T. cacao*, and a third, derived genotype confined to *T. gileri* in northern Ecuador. Cultural studies were undertaken to address the following questions: (1) Do the genotypes fall into corresponding somatic compatibility groups? (2) Are there any measurable phenotypic data that correlate with the different groups? Preliminary

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results have shown evidence of reproductive isolation between genotypes, and that certain cultural characteristics are consistent between strains. However, no difference in growth rate, hyphal diameter or spore size was found. Evidence for A-B-C type speciation is discussed. poster

Kennedy, Louis E.¹, Hallen, Heather E.^{2*} and Henkel, Terry W.¹ ¹Department of Biological Sciences, Humboldt State University, Arcata, CA 95512, USA, ²Department of Plant Biology, Michigan State University, East Lansing, MI 48824, USA. hallenhe@msu.edu. **HPLC analysis of *Amanita* species from Guyana.**

The mushroom genus *Amanita* is known worldwide for its toxins. *Amanita* toxins include the hallucinogenic ibotenic acid and muscimol (*Amanita* section *Amanita*, e.g. *A. muscaria* and *A. pantherina*), and the cyclic peptide amatoxins and phallotoxins (*Amanita* section *Phalloideae*, e.g. *A. phalloides* and the *A. bisporigera* species complex, the death cap and destroying angels). Amatoxins are responsible for upwards of 90% of fatal mushroom poisonings in humans. We used high-performance liquid chromatography (HPLC) to assess 21 individuals, in 20 species, collected during the past two years from tropical rain forests in Guyana. The majority of these are undescribed species. One species is eaten by indigenous people; the remainder are avoided. Neither amatoxins nor phallotoxins were detected in nineteen of the collections sampled. Two Guyana collections yielded HPLC peaks consistent with amatoxins and phallotoxins; the presence of these toxins was subsequently ruled out for one of these collections by mass spectrometry. poster

Kennedy, Peter G.* and Bruns, Thomas D. Department of Plant and Microbial Biology, 321 Koshland Hall, University of California, Berkeley, Berkeley, CA 94720, USA. pkennedy@berkeley.edu. **The role of interspecific competition in ectomycorrhizal interactions.**

Competition is often considered a fundamental process influencing the structure of species assemblages, yet little is known about competition among ectomycorrhizal (EM) fungi. We examined competitive interactions between *Rhizopogon occidentalis* and *Rhizopogon salebrosus* in a six-month microcosm study. *Pinus muricata* seedlings were grown in three EM treatments: *R. occidentalis*, *R. salebrosus*, and *R. occidentalis* and *R. salebrosus*. At two, four, and six months, five seedlings per treatment were harvested and EM root tip biomass of each species was determined. Root tips in the two-species treatment were identified using molecular techniques. *R. occidentalis* had similar EM root tip biomass when grown alone or in the presence of *R. salebrosus*. In contrast, *R. salebrosus* had significantly lower EM root tip biomass when grown with *R. occidentalis* than when grown alone, indicating it was a competitive inferior under the conditions tested. Competition was driven by differences in timing of colonization resulting in a strong priority effect for *R. occidentalis*. Our results, together with two earlier studies, indicate competition may play a more important role in EM interactions than previously recognized. contributed presentation

Kerekes, Jennifer F.* and Desjardin, Dennis E. Dept. of Biology, San Francisco State University, San Francisco, CA 94132, USA. kerekesj@yahoo.com. **A monographic treatment of the genus *Crinipellis* from Southeast Asia.**

In this monographic treatment, the diversity, geographic distribution and phylogenetic relationships of species in the genus *Crinipellis* (Basidiomycota, euagarics) in Southeast Asia will be documented. To date, only fourteen species of *Crinipellis* have been reported from the region, although many more occur there. We have collected seventy specimens from Indonesia, Malaysia and Thailand, and these are compared to numerous type specimens and herbarium exsiccata. Taxonomically significant macro- and micromorphological characteristics are documented and analyzed. *Crinipellis* is distinguished morphologically from the allied genera *Marasmius* and *Chaetocalathus* by stipitate basidiomes with pileipelli composed of thick-walled, dextrinoid, hair-like hyphae. To understand better the infrageneric classification of *Crinipellis* and its relationship with allied taxa (such as *Chaetocalathus*), molecular sequence data from the nuclear ribosomal Internal Transcribed Spacer (ITS) region is analyzed using species of *Marasmius s.s.* as an outgroup. poster

Kerekes, Jennifer F.^{1*}, Christensen, Catherine², Tanner, Kimberly¹, Stubbs, John¹ and Desjardin, Dennis E.¹ ¹Dept. Biology, San Francisco State Univ., San Francisco, CA 94132, USA, ²3151 Ortega St., San Francisco CA 94122-4051, USA. kerekesj@yahoo.com. **K-12 Educational Partnership: Bringing FUNgi into the Classroom.**

Would you like to share your enthusiasm for science and fungi with young people? Presented here is an example of educational outreach to a San Francisco urban middle school classroom on fungi developed between a 7th grade life science teacher and a graduate student involved with the National Science Foundation GK-12 Fellowship program. The original hands-on and inquiry-based lessons provide an introduction to the kingdom fungi, the ecological and economic importance of fungi, and the diversity of fungi. The lessons allow students to experience science research and to be a mycologist for a day. Analyzed data of written student responses before and after the lessons are presented. poster

Kerrigan, Julia^{1*}, Stone, Jeffrey¹, Manter, Daniel K.² and Winton, Loretta M.³ ¹Department of Botany and Plant Pathology, Oregon State University, Corvallis,

OR 97701-2902, USA, ²Soil Plant Nutrient Research, USDA Agricultural Research Service, Fort Collins, CO 80526, USA, ³Subarctic Agricultural Research Unit, USDA Agricultural Research Service, Fairbanks, AK 99775, USA. kerriju@science.oregonstate.edu. **Microfungi and canopy biology: The distribution of an endemic foliar pathogen and its effects on carbon dioxide flux.**

Phaeocryptopus gaeumannii, causal organism of the foliar disease Swiss needle cast of Douglas-fir, is endemic to the Pacific Northwest and widely distributed throughout the natural range of its host. The fungus produces fruiting bodies, pseudothecia, which emerge through and occlude stomata. To contribute to an understanding of how canopy fungi influence canopy processes, we measured the distribution of *P. gaeumannii*, determined the identity of fungal lineages, and assessed the effects of different colonization levels on gas exchange in the Wind River Experimental Forest in Washington, USA. Incidence of *P. gaeumannii* in young stands averages approximately 2-5 times greater than in mature and old-growth stands. Population genetic studies have shown that *P. gaeumannii* is two genetically differentiated, non-recombining sympatric lineages. We found that both lineages are present in the Wind River stands sampled, and that both lineages may occur within the same tree and same needle. One lineage is widespread while the second lineage had only been found in western Oregon prior to this study. A positive linear relationship between the amount of pseudothecia present and a decline in carbon dioxide assimilation rates was recorded. Declines in whole-tree carbon dioxide assimilation rates, ranging from 5-45%, are attributed to colonization by this microscopic fungus. contributed presentation

Kerrigan, Richard W.^{1*}, Callac, Philippe², Guinberteau, Jacques², Challen, Michael P.³ and Parra, Luis A.⁴ ¹Sylvan Research, 198 Nolte Dr., Kittanning, PA 16201, USA, ²INRA, MYCSA (Mycologie et securite des aliments) BP 81, 33883 Villenave d'Ornon cedex, France, ³Warwick HRI, Univ. of Warwick, Wellesbourne, Warks, CV35 9EF, UK, ⁴Avda. Padre Claret no 7, 5º G, 09400 Aranda de Duero, Burgos, Spain. rwk@sylvaninc.com. **A phylogenetic reconstruction of *Agaricus* section *Xanthodermatei*.**

Agaricus section *Xanthodermatei* comprises a group of species allied to *A. xanthodermus* and generally characterized by basidiomata having phenolic odors, transiently yellowing discolorations in some parts of the basidiome, Schaeffer's reaction negative, and mild to substantial toxicity. The section has a global distribution, while most included species have distributions restricted to regions of single continents. Using specimens and cultures from Europe, North America, and Hawai'i, we analyzed DNA sequences from the ITS1+2 region of the nuclear rDNA to identify and characterize phylogenetically distinct entities and to construct a hypothesis of relationships, both among members of the section and with representative taxa from other sections of the genus. 61 sequences from affiliated taxa, plus 20 from six (or seven) other sections of *Agaricus*, and one *Micropsal-liota* sequence, were evaluated under distance, maximum parsimony and maximum likelihood methods. We recognized 21 discrete entities in *Xanthodermatei*, including 14 established species and 7 new ones, three of which are described elsewhere. Four species from California, New Mexico, and France deserve further study before they are described. Section *Xanthodermatei* formed a single clade in most analyses, indicating that the traditional sectional characters noted above are good unifying characters that appear to have arisen only once within *Agaricus*. Deep divisions within the sequence-derived structure of the section could be interpreted as subsections in *Xanthodermatei*; however, low species richness and a lack of unifying characters in these relatively basal lineages led us to refrain from proposing new supraspecific taxa. The nearest neighbors of section *Xanthodermatei* are in section *Duploannulati*. contributed presentation

Keyhani, Nemat O. University of Florida, Microbiology and Cell Science, Gainesville, FL 32611, USA. keyhani@ufl.edu. ***Beauveria bassiana* versus ticks (Acari:Ixodidae): molecular mechanisms of fungal pathogenicity.**

The entomopathogenic fungus, *Beauveria bassiana*, displays varying degrees of virulence towards several important disease-agents carrying tick species including *Ixodes scapularis*. The overall process of infection involves many steps most of which remain unknown particularly at the molecular level. These include complex systems for: (1) adhering to the exoskeletal substrata, (2) evading host defenses, (3) penetrating and degrading the cuticle, (4) transporting to the cytoplasm and catabolizing necessary nutrients, and (5) dispersing from the catabolized host(s). The proteins and toxic compounds that contribute to this process include glycosidases, proteases, lipases, adhesion factors, transporters, developmental regulators, fungal arthropod toxins, oxalic acid, and numerous other secondary metabolites. These factors can be secreted, found in the cell envelope, in vesicles, vacuoles, and the cytoplasm. Furthermore, during the infection process, fungi produce specialized structures, such as germ tubes, appressoria, penetrant pegs, plates, hyphae, and hyphal bodies. Finally, once inside the host hemolymph, fungi differentiate into *in vivo* blastospores, which may help the organism evade the host immune response. These processes can be viewed as a developmental program coordinated by intricate regulatory mechanisms. *B. bassiana* is presented as a model organism for studying these processes. As part of our studies, a series of cDNA libraries were constructed from *B. bassiana* cell types and a robust expressed sequence tagged (EST) dataset has been generated. symposium presentation

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Kikuchi, Kensuke*, Matsushita, Norihisa and Suzuki, Kazuo. Laboratory of Forest Botany, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan. kiku@fr.a.u-tokyo.ac.jp. **Genotyping of mycorrhizas synthesized by spore inoculation of *Suillus bovinus*.**

In previous studies, we have developed SSR (simple sequence repeat) markers from *Suillus bovinus* and mycorrhizal ability of monosporous strains of *S. bovinus* was confirmed. In this study, seedlings of *Pinus densiflora* were inoculated with spores of *S. bovinus* and genotyping of mycorrhizas formed were conducted with SSR marker. The result is discussed in relation with reproduction of *S. bovinus*. poster

Kim, Mee-Sook^{1*}, Hanna, John, W.^{1,2}, McDonald, GERAL I.¹ and Klopfenstein, Ned B.¹ ¹USDA Forest Service-RMRS, 1221 S. Main St., Moscow, ID 83843 USA. ²Dept. of Forest Resources, University of Idaho, Moscow, ID 83844, USA. mkim@fs.fed.us Characterization of North American *Armillaria* species: **Genetic relationships determined from nuclear rDNA (IGS, ITS, and large subunit) sequences and AFLP markers.**

Genetic relationships among 10 North American *Armillaria* species were analyzed using sequence data from nuclear rDNA (intergenic spacer, internal transcribed spacer including 5.8S, and large subunit: LSU) and Amplified Fragment Length Polymorphism (AFLP) markers. Phylogenetic analyses of the rDNA sequences suggested the occurrence of interspecific hybridization between *A. ostoyae* and *A. gemina*. Several *Armillaria* species (i.e., *A. calvescens*, *A. sinapina*, *A. gallica*, NABS X, and *A. cepistipes*) clustered together based on rDNA sequence data; however, AFLP data provided delineation among these species. AFLP analysis supported current taxonomic classification established by conventional methods (e.g., morphology and interfertility tests). Both LSU sequence and AFLP marker data indicate that *A. mellea* and *A. tabescens* are genetically distant from the other *Armillaria* species of North America. poster

Kim, Seong Hwan^{1*}, Kim, Jae-Jin², Breuil, Colette² and Kim, Gyu-Hyeok³. ¹Department of Microbiology, Dankook University, Cheonan, Chungnam, 330-714 Korea. ²Dept. of Wood Science, University of British Columbia, Vancouver, B.C. V6T 1Z4, Canada. ³Dept. of Forest Resources and Environmental Sciences, Korea University, Seoul, Korea. **Differentiation of sibling species *Ophiostoma piceae* and *Ophiostoma quercus* using beta-tubulin gene derived PCR primers.**

Ophiostoma piceae and *O. quercus* are sibling species and members of *O. piceae* complex. These two species are found worldwide on conifer and hard wood and cause sapstain problems. Since the two species are genetically closely related and morphologically very similar, it is not easy to identify them. To find a fast and reliable method for their identification, we amplified by PCR and sequenced the beta-tubulin gene from isolates of *O. piceae* and *O. quercus* from different geographical origins. Sequence variations between the two species were clearly observed. Potential nucleotide sites in the variable region of beta-tubulin gene were selected and used for the designation of *O. piceae* and *O. quercus* specific primers. Specificity tests of the designed primers to the known isolates of *O. piceae* and *O. quercus* showed that they could easily differentiate the two species. With the beta-tubulin gene derived primers, we could also detect the two species present on pinewood. poster

Kinjo, Noriko^{*1} and Zang, Mu². ¹College of Liberal Arts and Sciences, Tokyo Medical and Dental University, 2-8-30, Kojinodai, Ichikawa-shi, Chiba 272-0827, Japan. ²Kunming Institute of Botany, Academia Sinica, Kunming Yunnan 650204, P.R. of China. k.kinjo@spn2.speednet.ne.jp. **Cultural and microscopical studies on *Cordyceps sinensis*.**

Cordyceps sinensis has attracted many people due to its peculiar characteristics of fruiting on the host caterpillar. The fungus was used as a tonic for court cuisine from the middle of the Qing dynasty, and has become one of most famous and esteemed traditional Chinese medicines. The fungus has been noted for its medicinal potential, hence extensive pharmaceutical studies have been carried out and reported in China and Japan. The fungus is endemic in the alpine shrub-meadow zone of high mountains in the southernwestern China. We have explored its habitats in these regions and reported the results of the expeditions, morphological and genetic studies of the fungus (Kinjo and Zang, 2001). Our result also inferred that the anamorph of *C. sinensis* is closely related to *Hirsutiella sinensis*. Here we present the result of culturing study on *C. sinensis*, and the direct observation of the teleomorphic state developing into its anamorph. The ascospores dropped on a SBA plate were germinated to produce hyphae or conidiogenous phialides from 10 days after inoculations. Conidia were ovoid, ellipsoid and brown coloured. Two or three, occasionally much more conidia were aggregated together in a slime head, as a cultural period progressed. These morphological characters were similar to *H. sinensis*. Other cultural characteristics also will be also presented at the meeting. poster

Kinoshita, Akihiko^{1*}, Satomura, Takami² and Horikoshi, Takao³. ¹Graduate School of Biosphere Sciences, Hiroshima University, 1-7-1, Kagamiyama, Higashi-Hiroshima 739-8521, Japan. ²Center for Ecological Research, Kyoto University, 2-509-3, Hirano, Otsu 520-2113, Japan. ³Faculty of Integrated Arts and Sciences, Hiroshima University, 1-7-1, Kagamiyama, Higashi-Hiroshima 739-

8521, Japan. akisita@hiroshima-u.ac.jp. **Fungal biomass in ectomycorrhizas of seedlings and adult trees of four tree species.**

In order to estimate the role of ectomycorrhizal fungi in carbon cycling of forest ecosystems, it is needed to quantify their biomass. Usually fungal biomass of ectomycorrhizas was quantified by multiplying the amount of mycorrhizal tips by fungal mass in each tip. It has been suggested that ectomycorrhiza comprises 20-40% of fungal tissues. However, it is considered that fungal contents may variable with the differences of plant species and their growth stages. In this study, we compared fungal sheath area (FSA; %), as an indicator of fungal contents of ectomycorrhizas, between seedlings and adult trees of *Abies firma*, *Pinus densiflora*, *Fagus crenata* and *Quercus serrata* in temperate to cool temperate forests of western Japan. Roots of seedlings and adult trees of each species were sampled in autumn 2002-2004. Fifteen -25 mycorrhizal tips of each species were randomly selected, and sectioned by hand transversely. Mycorrhizal and fungal sheath thicknesses were measured for 2-4 sections for each tip. Then FSA was calculated using these values. In addition, the tips were classified to reveal mycorrhizal types. Large numbers of mycorrhizal types were found in adult trees than seedlings in all species. FSA was almost similar both seedlings and adult trees. Therefore the range of fungal contents in ectomycorrhizas is from 20-40%, irrespective of differences of plant species, growth stages and the number of mycorrhizal types. poster

Kiyuna, Tomohiko^{1*}, An, Kwang-Deuk¹, Kigawa, Rika², Sano, Chie², Miura, Sadatoshi² and Sugiyama, Junta³. ¹NCIMB Japan Co., Ltd., Research Center, 330 Shimizu Nagasaki, Shizuoka-shi, Shizuoka-ken 424-0065, Japan. ²Tokyo National Research Institute of Cultural Properties, Tokyo, Japan. ³NCIMB Japan Co., Ltd., Kanda Office, Sudacho Towa Bldg. 6F, 2-2-4 Kanda Sudacho, Chiyoda-ku, Tokyo 101-0041, Japan. tkiyuna@suruga-g.co.jp. **Mural-paintings in the Takamatsu-zuka and Kitora tumulus: The current status of mycoflora and the roots of their fungi.**

The discovery of Takamatsu-zuka Tumulus in Asuka-mura, Nara Pref. was in 1972. The tomb is dated near end of later period of the Tumulus age (late 7c.). The most striking findings were the mural-paintings on the plaster adorning the inner walls of the stone chamber in this tumulus. Since then the mycoflora in the stone chamber, including inner walls and paintings, and the adjacent room has been investigated at regular intervals. The mycoflora was stable till the end of 1990s. The situation of fungi on inner walls in the stone chamber suddenly changed in 2001; the appearance of fungi occurred frequently and they grew onto colorful paintings. Also, similar situation has recently occurred in the Kitora Tumulus' stone chamber (late 7c.) discovered in 1983. In order to contribute the preservation of mural-paintings in the stone chamber, we have recently investigated the mycoflora and searched the identity and roots of fungi. As a result, the major fungi relating to the biodeterioration of mural-paintings were assignable to the anamorph genera *Fusarium*, *Trichoderma* and *Penicillium*. In the study, we have clarified the identity of *Fusarium* and *Trichoderma* isolates using the integrated analysis of phenotypic characters (mainly morphology) and genotypic ones (28S rDNA D1/D2 and EF 1-alpha). The roots and lineages of these fungi will be polyphasically discussed. poster

Kiyuna, Tomohiko¹, An, Kwang-Deuk¹, Harada, Yukio² and *Sugiyama, Junta³. ¹NCIMB Japan Co., Ltd., Research Center, Shizuoka-ken, Japan. ²Hirosaki University, Faculty of Agriculture & Life Science, 3 Bunkyo-cho, Hirosaki, Aomori-ken, Japan. ³NCIMB Japan Co., Ltd., Kanda Office, Sudacho Towa Bldg. 6F, 2-2-4 Kanda Sudacho, Chiyoda-ku, Tokyo 101-0041, Japan. jsugiyam@suruga-g.co.jp. **Identity of *Taphrina farlowii* Sadebeck ('Archiascomycetes') based on a new collection: searching from morphological and molecular characters.**

The isolate CBS 376.39 preserved as *Taphrina farlowii* has been identified as the ascomycetous yeast *Pichia guilliermondii* from both the molecular phylogenetic and phenotypic comparisons by Sjamsuridzal *et al.* (1997) and subsequently by Ogawa *et al.* (2003). The purpose of this study is to do collect and isolate "true" *T. farlowii* and polyphasically investigate the identity. In June 2004 one of the authors (Y. H.) collected a fresh material of a fruit pocket fungus that parasitized *Prunus ssiiori* ("Shiuri-Sakura") in Hirosaki, Aomori Prefecture. Physiological and chemotaxonomic characterization, and molecular phylogenetic analyses of 18S rDNA and ITS-5.8S rDNA sequences, in addition to observations of morphological characters, have been made for both the specimen and living isolate. As a result, morphological and habitat characteristics of this fungus were well agreed with those of Mix's description for *T. farlowii* Sadebeck in 1949. Besides, the molecular phylogenies have suggested that the closest relatives of our *T. farlowii* are *T. confusa* on *P. alabamensis*, *P. virginiana*, etc. and *T. padi* on *P. padus*. This placement using the molecular phylogenetics was agreeable to Mix's opinion based on the traditional taxonomy. Polyphasic comparisons between "false" *T. farlowii* isolate, and "true" *T. farlowii* specimen and isolate will be fully demonstrated. poster

Klich, Maren A. USDA/ARS/Southern Regional Research Center, New Orleans, LA 70124, USA. mklich@src.ars.usda.gov. **Aflatoxin production and long-**

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term survival of *Aspergillus flavus*.

Eight strains of *Aspergillus flavus* varying in aflatoxin production were inoculated onto YES and PDA agar media and incubated at 37 C. *A. flavus* generally produces more aflatoxin on YES than on PDA. All four of the high-producing isolates survived for at least 2.5 years on YES, whereas only one of the isolates on PDA survived over 2.5 years. Only one of the four low/non-producing isolates survived 2.5 years, and that was on YES. The study included high and low aflatoxin-producing strains derived from one isolate. Of these, only the high-producing substrain on YES survived 2.5 years. In a second experiment, two sets of the eight isolates were incubated on YES at 25 C for two weeks and then one set was placed in a 47 C incubator. All of the isolates incubated at 25 C were viable after 1.5 years, but only two of the strains survived 1.5 years at 47 C. Both of these were high-producing strains. Under the conditions considered, presence of high levels of aflatoxin is associated with long-term survival of *A. flavus*. poster

Ko, Han-Gyu^{1*}, Park, Hyuk-Gu², Kim, Seong Hwan¹ and Park, Won-Mok¹. ¹School of Life Sciences and Biotechnology, Korea University, Seoul 136-701, Korea, ²Department of Microbiology, Dankook University, Cheonan, Chungnam, 330-714, Korea. mushroom@korea.ac.kr. **Analysis of sequences expressed during the primordial and basidiome stages by Suppression Subtractive hybridization in *Hericium erinaceum*.**

The suppression subtractive hybridization (SSH) technique is an efficient method for detecting genes that are differentially expressed among different cells or among cells under modified conditions. In an effort to understand fruit body differentiation during in *Hericium erinaceum*, an edible and medicinal mushroom, we grew *H. erinaceum* KUMC 1008 on oak sawdust medium supplemented with rice bran and harvested its primordia and basidioma. RNA was extracted from the harvested samples and differentially expressed sequences were investigated by SSH. We obtained 139 cDNA clones from primordial library and 149 cDNA clones from basidioma library, respectively. The size of the insert ranged from 50 to 1300 bp with an average of 299 bp for primordial and 366 for basidioma clones. Sequencing of the clones and BLASTX search of through GenBank database showed that there were many unknown genes. Further analysis of the sequence obtained will be presented. poster

Ko, Han-Gyu^{1*}, Park, Hyuk-Gu², Kim, Seong Hwan³, Sung, Jae-Mo¹ and Park, Won-Mok¹. ¹School of Life Sciences and Biotechnology, Korea University, Seoul 136-701, Korea, ²Department of Microbiology, Dankook University, Cheonan, Chungnam, 330-714, Korea, ³Department of Applied Biology, Kangwon National University, Chuncheon, Gangwon-Do. 200-701, Korea. mushroom@korea.ac.kr. **RAPD analysis of *Cordyceps* species and design of specific primers for *C. militaris*.**

Genetic relationship of 27 isolates containing five *Cordyceps* species and two entomopathogenic species from different geographical area was assessed in order to develop a *Cordyceps militaris* specific molecular marker. For this, random amplified polymorphic DNA (RAPD) analysis was performed using Operon primers set against the genomic DNA of the species tested. The sizes of amplified DNA fragments ranged from 100 to 5,000bp. Among the tried primers, OPA-01, OPA-10 and OPA-13 primers amplified DNA fragments of 300 to 3,000bp. A dendrogram based on UPGMA analysis of the RAPD band patterns showed that *C. militaris* could be separated from *C. scarabaecicola*, *C. pentatomi*, *C. yongmoonensis*, *C. longissima*, *Shimizuomycea paradoxa*, and *Paecilomyces tenuipes*. A DNA band likely unique to *C. militaris* was cut and its nucleotide sequence was determined. A PCR primer pair was designed based on the determined sequence and tested against all the isolated used in this study. The primer pair amplified the target DNA only from *C. militaris*, suggesting that the primers set could be used for the detection of *C. militaris*. poster

Kobayashi, Hisayasu¹, Yamada, Akiyoshi², Tokumasu Seiji³ and Kakishima, Makoto⁴. ¹Ibaraki Prefectural Forestry Research Institute, Naka, Ibaraki 311-0122, Japan, ²Faculty of Agriculture, Shinshu University, Minami-minowa, Nagano 399-4588, Japan, ³Sugadaira Mountain Research Center, University of Tsukuba, Sanada, Nagano 386-2201, Japan, ⁴Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki 305-8577, Japan. hkoba@agri.pref.ibaraki.jp. **Mycorrhizal morphology in Rosaceae and Ulmaceae produced by entolomatoid fungi in Japan.**

Fruit bodies of entolomatoid fungi were found on the ground around 16 species of trees in Japan. Soil blocks associated with fruit bodies were taken for collecting mycorrhizas from their roots. A total of 22 mycorrhizal samples were collected from the soil blocks around *Prunus mume* (1 sample), *P. yedoensis* (1), *P. speciosa* (1), *P. sargentii* (1), *P. verecunda* (1), *P. jamazakura* (1), *Kerria japonica* (1), *Rosa multiflora* (5), *Rubus hirsutus* (1), *Pyracantha coccinea* (1), *Sorbus commixta* (1), *Malus domestica* (2), *M. toringo* (2), *Pyrus pyrifolia* var. *culta* (1), *Ulmus davidiana* var. *japonica* (1) and *Zelkova serrata* (1). Among them, samples collected around *Prunus mume* and *Rosa multiflora* were identified as mycorrhizas formed by *Entoloma saepium* and *E. clypeatum* f. *hybridum*, respectively. However, fruit bodies connected with other samples could not be identified to species. Microscopic observations showed that all samples were morphologically similar each other. The surfaces of mycorrhizas were silvery white in color, simple, flask-like shaped, 2-5 mm in long and 1-2 mm in diame-

ter and fungal hyphae were observed between the apical root cells. The apical root cells were finally disappeared and replaced by the hyphae. These characteristics are different from those of mycorrhizas produced by other group of fungi. poster

Koide, Roger T. Dept. of Horticulture, Penn State University, University Park, PA 16802, USA. rxxk13@psu.edu. **Temporal and spatial partitioning in ectomycorrhizal fungal communities.**

We have shown that in a *Pinus resinosa* plantation, ectomycorrhizal fungal communities are structured in space and in time. For example, we have shown that the hyphae of species of ectomycorrhizal fungi partition the forest floor according to layers (litter, F-layer, H-layer, mineral soil). Our experiments suggest that partitioning of this kind occurred as a consequence of variability in level of substrate decomposition, and as a consequence of variation in depth in the forest floor. Significant negative and positive correlations also occurred among hyphae of various species in small samples (0.25 ml) of F-layer. Ectomycorrhizal fungi also partition the forest floor in time; significant negative correlations among species pairs occurred throughout a 13 month time course. Significant positive temporal correlations also existed for other species pairs, suggesting a lack of temporal partitioning among those species. Temporal and spatial partitioning occurred independent of each other. symposium presentation

Kretzer, Annette M. SUNY-ESF, Faculty of Environmental and Forest Biology, 1 Forestry Drive, Syracuse, NY 13210, USA. kretzera@esf.edu. **Prospects of parentage analysis in basidiomycetes.**

Parentage analysis has become a popular tool for many plant and animal studies, but has so far been rarely used in fungi. One of the powerful promises that parentage analysis holds for fungi is that it can trace paths of spore dispersal and establishment, even if the direction cannot readily be determined in most basidiomycetes. I have used 6 and 7 medium polymorphic microsatellite markers (average expected heterozygosities ~0.4) and Goodnight & Queller's likelihood ratio test to identify probable parent/offspring pairs in *Rhizopogon vinicolor* and *Rhizopogon vesiculosus* (Boletales, Basidiomycota) collected from three intensively sampled plots in the Oregon Coast Range. Across both species, 1012 and 568 genotyped pairs could not be excluded as possible parent/offspring pairs, but only 7 and 4 had a significantly ($\alpha = 0.001$) higher likelihood of being related as parent and offspring than being unrelated. Of these, only two *R. vinicolor* genets were still supported as parent and offspring ($\alpha = 0.05$) when tested against the alternative hypothesis of being full siblings; they were located approx. 45 m and 28 m apart from each other. Methods and challenges of parentage analysis in basidiomycetes will be discussed. contributed presentation

Kropp, Bradley R.^{1*} and James M. Trappe². ¹Dept. of Biology, Utah State University, Logan, UT 84322, USA, ²Dept. of Forest Science, Oregon State University, Corvallis, OR 97331, USA. brkropp@biology.usu.edu. **Phylogenetics of *Gigasperma* based on partial nuclear large subunit rDNA sequences.**

Gigasperma is a small genus with species characterized by unusual, smooth, large, thick-walled, globose to subglobose basidiospores and a hypogeous habit. Two species are currently assigned to the genus: *G. cryptica* from New Zealand and *G. americanum* from the western United States. A phylogenetic study based on nuc-lsu rDNA sequences shows the unusual spore form shared by the two species is homoplastic. The results indicate that both *G. cryptica* and *americanum* are derived from agaricoid ancestors but are otherwise not closely related. poster

Kubota, Mayumi and Hyakumachi, Mitsuro. Faculty of Applied Biological Sciences, Gifu University, 1-1 Yanagido, Gifu 501-1193, Japan. mayumik@cc.gifu-u.ac.jp. **Colonization preference and morphology of arbuscular mycorrhizal fungi.**

While AM fungi are thought to have wide host range, number of studies has showed that there is specific compatibility between plants and AM fungi. In this study, colonization preference of AM fungi was investigated in order to elucidate how and why AM fungi select plants. A Japanese woody plant, *Clethra barbinervis* (Ericales), and two crop plant species, cucumber and tomato, were used as test plants. Soils were collected from 6 different vegetation sites and used as AM fungal inoculum. Test plants were grown with AM fungal inoculum for 6 weeks. Morphology of AM fungi colonizing plant roots was observed. In *C. barbinervis*, only *Paris*-type morphology was observed. In cucumber, *Arum*-type morphology was dominantly observed. In tomato, both *Arum*- and *Paris*-types were observed. DNA was extracted from roots of the test plants and colonizing AM fungi were determined using PCR with Glomales specific primers. Various AM fungal families were frequently detected from roots of tomato and *C. barbinervis* grown in throughout soil samples. In contrast, Glomaceae and Paraglomaceae/Archaeosporaceae were frequently detected from roots of cucumber. These suggest that rather than the soil type, plant selects AM fungi and the selection manner depends on plant species i.e. cucumber has strong selectivity and tomato and *C. barbinervis* do not. Influence of neighbor plants for selection of AM fungi was further investigated. *C. barbinervis* greatly increased Acaulospora colonization in cucumber when they were grown where *C. barbinervis* was dominant. Diversity

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of AM colonization in *C. barbinervis* decreased when *C. barbinervis* grown where cucumber was dominant. These suggest that plant species affect selection of AM fungi in neighbor plants. Influence of plant root exudates on AM colonization was discussed here. symposium presentation

Kuga-Uetake, Yukari. Faculty of Agriculture, Shinshu University, Minami-Minowa, Nagano 399-4598, Japan. ykuga@shinshu-u.ac.jp. **Diversity and similarity in the structure of mycorrhizas.**

Most plant species establish symbiotic organs called mycorrhizas, structures formed between plant roots and fungal hyphae. The organs are sites of exchange of nutrients between two organisms, and to date, seven types are recognized based on their structure. Except for ectomycorrhiza, arbuscular, ectendo-, monotropoid, arbutoid, ericoid, and orchid mycorrhizas establish intracellular hyphae. The intracellular hyphae are, however, always separated from host cells by host membrane continuous with the plasma membrane and cell wall materials derived from the host. Ecto-, ectendo-, arbutoid, and monotropoid mycorrhizas develop hyphal layers intercellularly, which is called a Hartig net, and around the root tip called a mantle. Host microtubule (MT) arrays change accompanying intracellular fungal colonization in arbuscular, orchid, ectendo- and monotropoid mycorrhizas. MTs were always closely associated with the membrane surrounding the fungal hyphae. Recently in ecto-, ectendo- and monotropoid mycorrhizas, modified cortical MTs were also observed for the first time in host cells adjacent to Hartig net hyphae. The seven mycorrhizal types are distinctive in the structures but share a common feature of the presence of host MTs on membranes closely associated with fungal structures. symposium presentation

Kunishi, Ayako* and Hashimoto, Yasushi. Agro-environmental Science, Obihiro University of Agriculture and Veterinary Medicine, Inada-cho, Obihiro, Hokkaido 080-8555, Japan. yhashi@obihiro.ac.jp. **Mycorrhizal colonization and structure of *Pyrolytic incarnata* Fischer growing in a Japanese larch forest.**

Pyrolytic L. is known to form arbutoid mycorrhiza, but details of morphology and ecology of *Pyrolytic* mycorrhizas are not clear. To investigate the seasonal change of quality and quantity of *Pyrolytic* mycorrhizas, the roots of *Pyrolytic incarnata* Fischer were collected from a Japanese larch (*Larix kaempferi* Carr.) forest. These mycorrhizas were divided into morphological types by details of mycorrhizal surface. Each type was sectioned for observation of mycorrhizal fungal structures. Some dominant types of *Pyrolytic* mycorrhizas and ectomycorrhizas of *L. kaempferi* collected from a forest site were analyzed for restriction fragment length polymorphisms (RFLP) of the amplified internal transcribed spacer (ITS) region in nuclear rDNA. *Pyrolytic* mycorrhizal colonization rate and number of types were increased from spring to summer. A total of 11 types were present in *Pyrolytic* mycorrhizas. Observations of the sections of mycorrhizas showed that two types have only intracellular hyphae with no organized fungal sheath and one type have only the sheath. The other types were typical arbutoid mycorrhiza that have organized sheath, Hartig net and intracellular hyphae. ITS-RFLP pattern of the most dominant type of *Pyrolytic* mycorrhizas had the same pattern of ectomycorrhizas of *L. kaempferi*. Thus the fungi that colonized on these dominant types were identified as Thelephoraceae by ITS sequences. poster

Kurihara, Yuko^{1*}, Ogawa, Yoshio², Degawa, Yousuke³ and Tokumasu, Seiji¹. ¹Sugadaira Montane Res. Cent., Univ. of Tsukuba, 1278-294, Osa, Sanada, Nagano 386-2201, Japan, ²Coll. of Pharmacy, Nihon Univ., 7-7-1, Narashinodai, Funabashi, Chiba 274-8555, Japan, ³Kanagawa Pref. Museum of Natural History, 499, Iryuda, Odawara, Kanagawa 250-0031, Japan. kurihara-yuko@nite.go.jp. **A proposal for the division of the order Kickxellales based on the comparison with its related orders.**

The order Kickxellales Benjamin 1979 has been regarded as a close relative of Harpellales, and most of the species are saprobes and inhabit in soil or on dung of omnivorous or herbivorous mammals. Though the current classification system of the order lacks consistency due to the inclusion of newly added taxa after Benjamin (1959), no comprehensive taxonomic studies have been made after his work. To construct a more consistent taxonomic system of Kickxellales, the following strategy was used. First, all Kickxellales genera were classified into groups based on the optical microscopic morphology. Second, these groups were evaluated based on the septal ultrastructure and 18S and 28S rDNA sequence analysis, respectively. From these results, a taxonomical conclusion was drawn. Three groups; *Coemansia* group, *Spiromyces* group, and *Ramicandelaber* group were recognized in Kickxellales, and they were morphologically and phylogenetically distinct enough from each other and from any other fungal groups including Dimargaritales and Harpellales. Thus, each of the three groups would be regarded as an independent order, that is, Kickxellales *sensu* Benjamin 1979 would be divided into three orders. This treatment makes the range of Kickxellales recur to the original one that has been stretched out gradually. symposium presentation

Kurihara, Yuko^{12*}, Machida, Ryuichiro³ and Fukui, Makiko³. ¹Dept. of Biotech., Nat. Inst. of Tech. and Eval., Kazusakamatari, Kisarazu, Chiba 292-0818, Japan, ²Mycol. & Metabol. Divers. Res. Cent., Tamagawa Univ. Res. Inst., Machida, Tokyo 194-8610, Japan, ³Sugadaira Mont. Res. Cent., Univ. of Tsukuba, Osa, Sanada Nagano 386-2201, Japan. kurihara-yuko@nite.go.jp. **Fungi isolated from proturans under rearing.**

Protura is one of the most primitive hexapod orders, and all the species live in soil. Fungal parasites of soil arthropods including proturans were scarcely investigated while entomopathogenic fungi of Pterygota have been relatively fully studied and already applied for industry. To develop a new isolation source of industrially useful fungi, we studied fungi isolated from *Baculentulus densus* (Acferentomidae, Protura). Proturans were extracted from litter and soil collected at Shinko-ji, Sanada, Nagano, Japan with a Tullgren funnel, and kept in rearing containers with a small amount of litter in laboratory. Fungi were isolated from dead/intact bodies of proturans after rearing. As a result, *Acremonium kiliense*, *Lecanicillium psalliotae* and other *Verticillium sensu lato* species, and *Conidiobolus coronatus* dominantly appeared from them. A strain of *A. kiliense* showed an antifungal activity. *Lecanicillium psalliotae* has been shown to be phylogenetically close to *Isaria* spp. (Luangsa-ard *et al.* 2004), and *C. coronatus* is known as a biological-control agent. These results suggest that proturans and other soil arthropods would provide us industrially important fungi as Pterygota. poster

Kwan, Hoi-Shan*, Chum, Wing Yan, Bian, Xue-Lin, Xie, Wei-Jun, Ng, Zhang, Leung, Grace, Sze Wan. Department of Biology and Food and Nutritional Sciences Programme, The Chinese University of Hong Kong, Hong Kong SAR, China. hoishankwan@cuhk.edu.hk. **Gene expression profiles of Shiitake mushroom *Lentinula edodes* revealed by Differential Display, cDNA Microarray and Serial Analysis of Gene Expression (SAGE).**

Fruit body development is an important area in mushroom biology and has recently been studied at the molecular level. We aim to characterize gene expression profiles during fruit body development of Shiitake mushroom *Lentinula edodes*. First, we used the differentially display method RNA fingerprinting with arbitrarily primed polymerase chain reaction (RAP) to isolate genes differentially expressed during fruit body development. RAP is powerful in isolating gene fragments but requires tedious down-stream works to isolate full-length for further analysis. Over 100 genes were isolated and sequenced. Fifteen were studied further. Second, RAP products were used as probes to hybridize to cDNA macroarray membranes to identify and sequenced over 100 differentially expressed genes. Third, the cDNA clones from a cDNA library of primordium were randomly picked and sequenced to generate over 500 unique Expressed Sequence Tags (ESTs). Differential expressions of ESTs were analyzed by dot-blot hybridization and cDNA microarray analysis using total cDNA from mycelium and primordium as probes. From the above analysis, only relative levels of differentially expressed genes were obtained. To determine the proportion of each mRNA among total transcripts in mycelium and primordium, we used Serial Analysis of Gene Expression (SAGE) which reports the number of transcripts for each gene. About 20,000 transcripts were counted from five developmental stages and 110 genes could match to our ESTs. Examination of the kind of genes abundantly and differentially expressed in primordium indicated that at the initiation of fruit body, the following occurred: (1) specific sets of genes are expressed in primordium, (2) mycelium-specific genes are suppressed, (3) different sets of structural proteins appear in different stages, (4) protein turn-over increases, (5) protein synthesis increases, and (6) specific signal transductions occur. Gene expression profiles revealed by different approaches were compared and were generally consistent. contributed presentation

Lam, Wing Hon^{1*}, Taylor, Paul W.J.², Jeewon, Rajesh¹ and Hyde, Kevin D.¹ ¹Centre of Research in Fungal Diversity, Department of Ecology & Biodiversity, University of Hong Kong, Hong Kong SAR, China, ²Bio Marka, Joint Centre for Crop Innovation, Institute of Land and Food Resources, University of Melbourne, Vic, 3010, Australia. winghon@hkusua.hku.hk. **Molecular phylogeny of the pathogenic falcate-spored *Colletotrichum* species.**

Colletotrichum and its teleomorph *Glomerella* are important plant pathogens that cause a disease known as anthracnose. The economic impact due to the damage of crops by this disease is huge. Species concepts in *Colletotrichum* have been mainly based on morphological and cultural criteria, until recently molecular phylogenetics were utilized to study the relationship of some of the agricultural important species e.g. *C. gloeosporioides*, *C. acutatum*, *C. musae*. In our study, we focused on the pathogenic falcate-spored *Colletotrichum* species, including those infecting grasses and the non-graminicolous ones. The morphological characters in these species are often highly variable and have caused a lot of confusions in the differentiation of species. Using the internal transcribed spacer (ITS) region of the nuclear ribosomal DNA and beta-tubulin (tub2) gene, we tried to elucidate the interspecific relationships between the selected isolates. We have also examined the type materials of *C. capsici*, *C. caudatum*, *C. falcatum* and *C. trichellum*. Fresh isolates were also obtained from the original collection locations and epitypes/lectotypes were designated in order to stabilize the application of species names. poster

Landis, Frank C.^{1*} and Gargas, Andrea². ¹University of Akron, Akron OH, USA, ²University of Wisconsin-Madison, Madison, WI, USA. flandis@uakron.edu. **ITS2 secondary structure defines species-specific probe regions for fungi.**

We designed prototype DNA microarrays including 183 ITS2 rDNA sequences from 162 fungal species known to inhabit soil, with representative

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species from each of the five Eumycota phyla plus Oomycota. Probes were based on 20 nt segments of each ITS2 sequence, with microarrays containing all possible 20 bp segments. Arrays were designed to detect multiple fungal species from soil samples. Initial results provided substantial insight into designing eukaryotic rDNA microarray detectors, as these microarrays were compromised by two design limitations: 1) 55% of the probes were shared among two or more species. This is understandable, as ITS2 regions contain substantial phylogenetic information, suggesting that a number of 20-nt oligonucleotide segments should be similar or identical among species. 2) Most seriously, prototype design also proved susceptible to spoofing, responding to fungi not represented on the array. For example, one test species hybridized with single-copy probes from seven different species, although supposedly it was not represented in the array. Since most soil fungal species are unidentified, probes designed to detect known taxa must also have safeguards against responding to unknown taxa. Fortunately, one significant result potentially overcomes both limitations. Analysis of probe duplications against 119 of the array sequences showed that unique sequences tended to occur most often around nt position 40 of ITS 2, where 67% of probes were unique, and duplicates were confined to near relatives. Position 40 corresponds precisely with loop 2 of the ITS2 folding structure, a folding structure repeated in all 119 sequences. Our findings suggest that probes based on loop 2 sequences would a priori be close to taxon-specific and therefore resistant to spoofing. More generally, analysis of secondary structure folding patterns in rapidly evolving sequences holds promise for the design of taxon-specific oligonucleotide probes. poster

Landolt, John C.^{1*}, Slay, Michael E.² and Stephenson, Steven L.³ ¹Dept. of Biology, Shepherd University, Shepherdstown WV 25443, USA, ²Ozark Highlands Office, The Nature Conservancy, Fayetteville AR 72701, USA, ³Dept. of Biological Sciences, University of Arkansas, Fayetteville AR 72701, USA. jlandolt@shepherd.edu. **Dictyostelium rosarium and other cellular slime molds from Ozark caves.**

Samples of "soil" material were collected from 33 caves in Arkansas, Missouri and Oklahoma. These samples were processed in the laboratory using standard isolation procedures for dictyostelid cellular slime molds. These organisms were recorded from 18 of the 33 (55%) caves. In addition to the fairly cosmopolitan species *Dictyostelium mucoroides*, *Polysphondylium pallidum* and *P. violaceum*, five other species were recovered, including numerous isolates of *D. rosarium* from 12 different caves. Based upon these data and an earlier study of West Virginia caves, *D. rosarium* appears to have a preference, or at least a particular tolerance, for cave environments. In general, the pH values of soil samples from Ozark caves were more acidic than those from the West Virginia caves sampled previously. This project was supported in part by the National Science Foundation, the University of Arkansas, Shepherd University, and The Nature Conservancy. poster

Landolt, John C. Dept. of Biology, Shepherd University, Shepherdstown WV 25443, USA. jlandolt@shepherd.edu. **Studies of Alaskan cellular slime molds.**

In the 1990's, the results of several studies of cellular slime molds (CSM) of high-latitude regions of Alaska were published in the journal Arctic and Alpine Research. Additionally, a number of other studies were carried out and one project is still ongoing. This presentation summarizes the results of this work on Alaskan CSM, published and unpublished. Although occurring at low levels of species richness in high latitudes regions of western and central Alaska, measured densities of CSM sometimes rival those of lower latitudes. One probable new species has been recovered, and some interesting patterns of ecological succession in CSM communities are suggested by the data obtained from the various study sites. This work has benefited from the efforts of Dr. S. L. Stephenson, logistical support and funding from Dr. G. A. Laursen (UAF/National Park Service research grants Nos. PX9830-93-062, PX9830-92-385, PX9830-0-0451, PX9830-0-0472, and PX9830-0-0512) and from contributions provided by a number of students and technicians, particularly Woody Wingate and Bess Morrison. Dr. Glen Juday was instrumental in setting up the study that allowed data to be collected from the Columbia Glacier region. Thanks also to personnel of the U.S. National Park Service, funding provided by the National Geographic Society (NGS grant #3974-88), and logistical support from Shepherd University. symposium presentation

Laursen, Gary A.^{1*}, Horak, Egon² and Taylor, D. Lee³. ¹UAF, Inst. of Arctic Biology, P.O. Box 756100, 305A Bunnell Bldg., Fairbanks, AK 99775, USA, ²ETH Zentrum, University of Zurich, Zurich, SZ, Switzerland, ³UAF, Inst. of Arctic Biology, 311 Irving I, Fairbanks, AK, 99775, USA. ffgal@uaf.edu. **Galerina patagonica Singer from Gondwanian Mainland AU and NZ, their Subantarctic Islands, and Patagonia.**

Twenty-eight collections (*Galerina patagonica* Singer) were examined from the Subantarctic Islands (SAIs) of Macquarie (540 S., AU), Campbell (520 S, NZ) and Auckland (500 S., NZ), but not yet recorded from other SIAs, and from mainland NZ and AU. SAI substrates included peaty soil, vascular plant litter of *Poa foliosa*, *Stilbocarpa polaris*, *Pleurophyllum hookeri*, *Dracophyllum longifolium*, *D. scoparium*, *Metrosideros umbellata* and mosses. The biodiversity of island agaric floras show affinities with Patagonia (S.Am.) 2700 km NE. *G. patagonica* Gondwanian distribution strongly supports long-distance wind and/or bird dispersal mechanisms. To investigate the systematic and phylogeography of

G. patagonica, the internal transcribed spacer (ITS) was sequenced in addition to part of the RPB1 gene in a subset of 13 specimens. Data analyses revealed two clades within *G. patagonica* that were congruent across the two genes, robust to methods of phylogenetic inference and strongly supported. We suggest the presence of two cryptic species within the currently recognized species. Clade 1 was found in material from both mainlands as well as Auckland and Macquarie Islands. Clade 2 was found on all three Subantarctic islands, but not on the two mainlands. Identical sequences were often found in multiple localities indicating recent long-distance dispersal of both cryptic species. Minor sequence variation within clade 2 was partitioned between the islands however, and suggests genetic isolation between clade 2 populations. symposium presentation

Lee, Hyang B.^{1*}, Kim, Youngjun², Jin, Hui Z.³, Lee, Jung J.³, Kim, Chang-Jin³, Park, Jae Y.¹, Park, Chae H.¹ and Jung, Hack S.¹ ¹Department of Biological Sciences, Seoul National University, Seoul 151-747, Korea, ²Division of Biotechnology, The Catholic University of Korea, Puchon 420-743, Korea, ³Korea Research Institute of Bioscience and Biotechnology (KRIBB), Post office Box 115 Yusong, Taejeon 305-600, Korea. minervas@snu.ac.kr. **A new *Hypocrea* strain producing harzianum A cytotoxic to tumor cell lines.**

A new fungal strain producing a trichothecene metabolite, harzianum A, was isolated and its cytotoxicity to tumor cell lines was evaluated. The strain was identified as a new *Hypocrea* strain based on morphological characteristics and ITS rDNA sequence data. Harzianum A was isolated from wheat bran culture by 50% acetone extraction, silica gel chromatography, Sephadex LH-20 chromatography and HPLC. The chemical structures were determined by ESI- or HRFAB-MS and ¹H and ¹³C-NMR analyses. Harzianum A showed cytotoxicity to HT1080 and HeLa cell lines with IC₅₀ values of 0.65 and 5.07 µg ml⁻¹, respectively. Harzianum A with a chemical formula of C₂₃H₃₈O₆ showed moderate to strong cytotoxicity to human cancer cell lines. This is the first report on the production of cytotoxic harzianum A by a new *Hypocrea* strain. poster

Lee, Jin S.^{1*}, Sung, Ha Y.¹, Lim, Young W.² and Jung, Hack S.¹ ¹Department of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea, ²Department of Wood Science, Faculty of Forestry, University of British Columbia, Vancouver, BC V6T 1Z4, Canada. minervas@snu.ac.kr. **Phylogenetic analyses of *Perenniporia* and *Ganoderma* based on molecular sequences.**

Perenniporia s. l., characterized by the ellipsoid to distinctly truncated spores usually with thick walls of variable dextrinoid reaction, is a large heterogeneous group that overlaps with several other generic concepts and makes the classification difficult at present. Phylogenetic relationships of 48 taxa of *Perenniporia* and related genera were studied by comparing differences among phylogenetic trees inferred from ITS1 rDNA, partial 28S rDNA, and 6-7 regions of RPB2 DNA sequences. It showed that the species of *Perenniporia* s. l. did not form a monophyletic group and were divided into six subgroups: *Abundisporus* (*A. fuscopurpureus*, *A. sclerosetosus*, *Loweoporus pubertatis*, *L. violaceus*), *Loweoporus* (*L. lividus*, *L. roseoalbus*, *L. tephroporus*), *Perenniporia* s. s. (*Perenniporia medulla-panis*, *P. narymica*, *P. subacida*), *Perenniporiella* (*Perenniporiella micropora*, *P. neofulva*), *Truncospora* (*Perenniporia aurantiaca*, *P. ochroleuca*, *P. ohienensis*), and *Vanderbylia* (*Perenniporia delavayi*, *P. fraxinea*, *P. latissima*). Besides, another subgroup *Ganoderma* (*G. applanatum*, *G. meredithiae*, *G. lucidum*, *G. resinaceum*, *Perenniporia robinophilina*) with truncate thick-walled spores as a common character was included in *Perenniporia* s.l. together. poster

Lee, Soo Chan* and Shaw, Brian D. Program for the Biology of Filamentous Fungi, Department of Plant Pathology and Microbiology, Texas A&M University, College Station, Texas, 77803, USA. sclee@tamu.edu. **The role of protein myristoylation in cell morphogenesis in *Aspergillus nidulans*.**

N-myristoylation increases hydrophobicity to allow cytoplasmic proteins to associate with membranes. This modification is mediated by *N*-myristoyl transferase (NMT). In *Aspergillus nidulans*, the mutation in NMT encoding gene (*swf1*) results in abnormal morphogenesis during spore germination and establishment of hyphal growth at restrictive temperature. Six suppressors of *swf1* (*ssf*) mutants have been identified through UV mutagenesis. Genetic analysis has shown that all six mutations are extragenic to *swf1* and all mutated proteins are downstream of Swf1. These secondary mutations enable the *swf1* mutant to recover from the loss of cell polarity axis. All *ssf* mutants have been separated from *swf1* strain by backcross with wild type. Interestingly *ssfB*, *ssfC*, and *ssfD* produced a red pigment, which could be ascocouanoine, which is produced during ascospore germination, or norsolorinic acid, a precursor of sterigmatocystin. The distinguishable colonial phenotype of *ssf* mutants at 42C enables us to clone each gene by complementation. Through the step, *ssfD* has been found to encode one subunit of the 26S proteasome, which is likely to interact with another proteasome subunit protein, which is predicted to be myristoylated. Subsequent analysis of *ssfD* is ongoing. The analysis of these mutants is in progress and will be discussed. contributed presentation

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Liang, YingMei^{1*}, Tian, ChengMing^{1,2} and Kakishima, Makoto¹. ¹Graduate School of Life and Environmental Sciences, University of Tsukuba, Ibaraki 305-8572, Japan, ²College of Natural Resources and Environment, Beijing Forestry University, Beijing 100083, China. ymeilt@hotmail.com. **Phylogenetic analysis of *Pucciniastrum* species in Japan.**

Pucciniastrum is a large, cosmopolitan genus of Pucciniastraceae. About 24 species are known in the world and all species have heteroecious life cycles which alternate between species of Pinaceae (*Abies*, *Picea* and *Tsuga*) and dicotyledonous plant species (16 families, 26 genera) (Hiratsuka 1958, Cummins and Hiratsuka 2003). Among these species, 21 species have been reported in Japan (Hiratsuka *et al.*, 1992) and are classified into 4 morphological groups based on the structure of ostiolar cells of peridia in the uredinia. Among 4 groups, one group has smooth ostiolar cells and contains 16 species. They were separated into different species mainly based on their host plants, because of the morphological similarities of uredinial and telial stages among these species. However, their taxonomic identity and phylogenetic relationships were still unknown. 43 specimens from 14 species with smooth ostiolar cells were collected from different areas in Japan and their phylogenetic relationships were analysed by molecular methods. Sequence data obtained from D1/D2 region of nuclear large subunit rDNA, 5.8S rDNA and their internal transcribed spacers, ITS1 and ITS2 regions were used to infer phylogenetic relationships of these species. The NJ tree constructed from D1/D2 region showed that *P. circaeae* and *P. epilobii* formed a single clade with high bootstrap support. This tree also indicated that *P. fagi*, *P. hikosanense*, *P. boehmeriae*, *P. kusanoi*, *P. actinidiae*, *P. corni*, *P. styracinum*, *P. yoshinagai*, *P. miyabeianum* and *P. tiliae* formed a single clade, whereas *P. fagi*, *P. hikosanense* and *P. tiliae* were monophyletic and formed different clades from the other 7 species in the NJ tree from ITS region. The both NJ trees from D1/D2 and ITS regions showed that *P. hydrangeae-petiolearis* and *P. coryli* were monophyletic with high bootstrap support. symposium presentation

Lickey, Edgar B.*, Hughes, Karen W. and Petersen, Ronald H. Dept. of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN, 37996 USA. elickey@utk.edu. **Surveying the mushroom-forming mycota of the Great Smoky Mountains National Park for the ATBI.**

A three year effort to catalog the basidiomycete taxa, particularly the mushroom-forming fungi, of the Great Smoky Mountains National Park (GSMNP) was initiated in the summer of 2004 as part of the ongoing All Taxa Biodiversity Inventory. The goal of this project is to collect, identify, and voucher specimens. DNA is being extracted from each specimen and the nuclear ribosomal ITS region is being amplified and sequenced. The sequences will be deposited into the sequence database GenBank. Finally, an easily accessible web-page will be created for each species, complete with description, photos, location and habitat data. Field sampling consists of weekly forays and periodic "bio-blitzes" involving experts in certain taxonomic groups. The floristic richness and geologic diversity of the GSMNP provides the ingredients for an extremely rich mycota. At present (15 January 2005), approximately 1000 specimens comprising about 500 species have been collected. Several represent species new to science, and many represent new park records and range extensions. symposium presentation

Lim, Young Woon*, Kim, Jae-Jin, Lu, Monica and Breuil, Colette. Department of Wood Science, University of British Columbia, BC, V6T 1Z4, Canada. ywlim@interchange.ubc.ca. **Determining fungal diversity on *Dendroctonus ponderosae* and *Ips pini* affecting lodgepole pine using cultural and molecular methods.**

Several beetles (Coleoptera: Scolytidae) and their fungal associates cause severe damage to lodgepole pine in Western Canada and the Northwestern United States. The fungal diversity from the surface of two bark beetle species, *Dendroctonus ponderosae* Hopkins (mountain pine beetle) and *Ips pini* Say (pine engraver), was surveyed using cultural and molecular methods. Nine fungal taxa were recognized by morphological characterizations. All nine taxa were isolated from the mountain pine beetle whereas only seven of the nine taxa were isolated from the pine engraver. The identification was based on cultural morphology and high sequence similarities of the internal transcribed spacer (ITS) and large subunit ribosomal DNA (LSU rDNA) region to sequences of known fungi. Fungal ITS regions were amplified from DNA directly extracted from the beetle surface. The PCR products were cloned and 250 clones were classified by their restriction pattern with *HaeIII* and *RsaI*. A total of 26 RFLP types were identified and subsequently sequenced. Among them, 15 RFLP types were identified as being present in mountain pine beetle and 14 were present in pine engraver. Sequence analysis of the RFLP types showed that 23 ascomycetes and 3 basidiomycetes were represented in the clone libraries, whereas the isolates from the cultural method represented 7 ascomycetes and 2 basidiomycetes. We found that yeast and non-staining filamentous Euscomycetes fungi were detected efficiently using a molecular approach, while the major sapstaining fungi and decay fungi were best detected using cultural methods. symposium presentation

Limkaisang, Saranya^{1*}, Furtado, Edson L.², Liew, Kon W.³, Salleh, Baharuddin³, Sato, Yukio⁴, Fangfuk, Wanwisu⁵, To-anun, Chaiwat⁵, Khodapost, Seyed A.⁶, Cunningham, James H.⁷ and Takamatsu, Susumu¹. ¹Faculty of Bioreources, Mie University, Kamihama-cho, Tsu, Mie 514-8507, Japan, ²Dept. of Productio Veg-

etal/FCA-UNESP, P.O. Box 237, 18603-970, Botucatu/SP, Brazil, ³School of Biological Sciences, Universiti Sains Malaysia, Penang 11800, Malaysia, ⁴Toyama Prefectural University, Kosugi-Cho, Toyama 939-0398, Japan, ⁵Dept. of Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiangmai 50200, Thailand, ⁶Dept. of Plant Protection, College of Agriculture, Gilan University, Rasht, Iran, ⁷Dept. of Primary Industries- Knoxfield, Private Bag 15, Ferntree Gully Delivery Centre, Victoria, 3156, Australia. limkaisang@yahoo.com. **Phylogenetic relationship of *Oidium anacardii*, *O. bixae*, *O. citri*, *O. heveae*, *O. mangiferae* and allied species inferred from the ITS and 28S rDNA sequences.**

The powdery mildew fungi that occur on several tropical/subtropical trees, i.e., *Acacia*, *Anacardium*, *Bixa*, *Citrus*, *Hevea*, and *Mangifera*, are mitospore *Oidium* species sharing a *Pseudooidium* anamorph. Although the fungal species are described as *Oidium anacardii*, *O. bixae*, *O. citri*, *O. heveae*, and *O. mangifera*, their identification and phylogenetic placements are still uncertain due to the absence of the teleomorphic state. We performed phylogenetic analyses of these fungi collected in Asia, Australia and South America using the ITS and 28S rDNA sequences. Both ITS and 28S rDNA sequences indicated that they are identical or closely related to one another with only a few sequence substitutions. The sequences of these fungi are also identical or closely related to the sequence of *Erysiphe* sp. on *Quercus phillyraeoides*, and are grouped into a distinct clade together with strong bootstrap support. There is no apparent conflict in morphological characteristics among the fungi. These results suggest that the powdery mildew fungi on these tropical/subtropical trees are conspecific and may be an anamorph of *Erysiphe* sp. on *Quercus phillyraeoides*. Cross-inoculation tests are required to substantiate this possibility. contributed presentation

Lindahl, Björn D.*, Ihrmark, Katarina, Stenlid, Jan and Finlay, Roger D. Swedish University of Agricultural Sciences, Dept. of Forest Mycology & Pathology, Box 7026, SE-75 007 Uppsala, Sweden. bjorn.lindahl@mykopat.slu.se. **Fungal succession in the forest floor of a North European *Pinus sylvestris* forest.**

Rapid progress in the development of new molecular techniques greatly improves our possibilities to study microbial communities in soil. PCR amplification of soil derived DNA and cloning of PCR products into *E. coli* enable ITS sequencing and identification of fungi from within mixed communities. By combining cloning and sequencing with community fingerprinting techniques such as T-RFLP (terminal restriction fragment length polymorphism), complex communities may be analysed in large sample sets. We have studied fungal communities in soil samples from of a North European *Pinus sylvestris* forest and investigated the vertical distribution of fungal taxa throughout the litter-, humus- and upper mineral horizons of the podzol. Community composition data was correlated with C/N ratio, 13C content and 15N content of the soil samples, in order to evaluate the contribution of fungal communities to organic matter decomposition and nitrogen delivery to plants. Needle endophytes and saprotrophic fungi predominated in the surface litter. In more decomposed litter and humus the saprotrophs were replaced by ericoid- and ectomycorrhizal fungi. In mineral soil samples unidentified ascomycetes dominated. Colonisation by saprotrophic fungi decreased the C/N ratio while the relative abundance of 15N was stable, indicating respiration of litter carbohydrates and retention of litter nitrogen in fungal mycelium. Colonisation by mycorrhizal fungi increased the C/N ratio as well as the relative abundance of 15N, suggesting removal of nitrogen powered by root-derived carbohydrates. symposium presentation

Lindley-Settlemyre, Lora A.*, Spiegel, Frederick W. and Silberman, Jeffrey D. Department of Biological Sciences, SCEN 632, University of Arkansas, Fayetteville, Arkansas 72701, USA. lalindl@uark.edu. **Molecular phylogeny of the protostelids.**

Protostelids are free-living amoebae that form simple fruiting bodies. They are among the simplest of fruiting amoebae. Their fruiting bodies usually consist of a stalk and one or more spores. Based on amoebal morphology, it is not clear that all organisms described as protostelids are closely related. If so, then some of these fruiting protists may be examples of morphological and life-cycle convergence. At the molecular level, very little is known about relationships among different species of protostelids. Additionally, little is known about the shared evolutionary history of the protostelids, dicytostelids, and myxomycetes (Eumycetozoa). Because of the limited number of morphological, developmental, and life-cycle characters, and because the plasticity of these characters is largely unknown, we have chosen to do a molecular phylogenetic analysis of the protostelids. We are sequencing and constructing phylogenetic trees from alpha tubulin, beta tubulin, and heat shock protein 90. contributed presentation

Lindner Czederpiltz, Daniel L.^{1*}, Banik, Mark T.¹, Micales, Jessie A.¹ and Trummer, L.² ¹Center for Forest Mycology Research, USDA-FS Forest Products Laboratory, One Gifford Pinchot Drive, Madison, WI 53726, USA, ²USDA-FS State & Private Forestry, 3301 C Street, Suite 202, Anchorage, AK 99503, USA. dlindner@wisc.edu. **The effect of mortality agent on fungal succession and decay rate in Lutz spruce.**

Lutz spruce (*Picea x lutzii*) on the Kenai Peninsula of Alaska often die from

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attack by spruce bark beetle (*Dendroctonus rufipennis*) and occasionally from wind-throw during storms. Dead trees represent a significant fire danger, so it is important to know how long it takes these trees to decay, and whether different mortality agents affect the composition of the fungal community and thereby the rate of decay. To investigate the effects of mortality agent, 5 snags and 15 logs in various stages of decay were sampled from a site on the Kenai Peninsula. Five of the trees had been uprooted by wind, while the remaining 15 trees were killed by bark beetles. Stress wave decay measurements were taken at three locations within each log, and the fungal community was sampled by collecting fruiting bodies, culturing wood samples, and analyzing sequences of rDNA extracted directly from 50 drilled-wood samples per log. Initial results indicate that bark beetle-killed trees decay faster, and that decay progresses from the base of the tree toward the top in beetle-killed trees, while decay proceeds from the top of the tree toward the base in wind-throw trees. Preliminary analysis of the fungal community suggests that *Fomitopsis pinicola* occurs more commonly in the base of beetle-killed trees, and that wind-throw trees have less fungal colonization in general at the base. poster

Liu, Mindy and *Hodge, Kathie T. Dept. of Plant Pathology, Cornell University, Ithaca NY 14853, USA. kh11@cornell.edu. **Transoceanic dispersal and origins of the orange-spored *Aschersonia* species, *A. aleyrodias* and *A. placenta*.**

Morphologically similar taxa with disjunct distributions might be the same species, sister species, or distantly related species. Overwhelming similarities between two tropical fungal taxa, *Hypocrella libera* (anam. *Aschersonia aleyrodias*) and *H. raciborskii* (anam. *Aschersonia placenta*) from the Old World and the New World raise the question about the nature of the relationship between them. Based on DNA sequence data (RPB2, EF1-a and b- tubulin), we intend to investigate whether or not there is genetic subdivision between Old World and New World isolates. If so, are these two geographically disjunct taxa indeed phylogenetically close relatives? What historical events might have contributed to the present disjunction? We conducted a nested clade analysis, statistical tests and phylogenetic analyses which revealed significant geographically-related subdivision between Old world and New World haplotypes. Further phylogenetic analysis with extensive sampling has confirmed their sister relationship. Through a phylogenetic area- cladogram and by using a coalescent approach we estimated the polarity of historical transoceanic dispersal. poster

Lodge, D. Jean^{1*}, Baroni, Timothy J.² and Lindner Czederpiltz, Daniel L.³ ¹Center for Forest Mycology Research, USDA Forest Service, Forest Products Laboratory, Luquillo PR 00773-1377, USA, ²Department of Biological Sciences, State University of New York, College at Cortland, Cortland, NY 13045, USA, ³Center for Forest Mycology Research, USDA Forest Service, Forest Products Laboratory, One Gifford Pinchot Dr., Madison, WI 53726-2398, USA. djlodge@caribe.net. **Fungi from a lost world in Belize: Doyle's Delight.**

More than 30 new species (including 7 Entolomataceae, 7 Hygrophoraceae, and 8 Tricholomataceae) were recently discovered in a cloud forest on the highest peak in Belize, Doyle's Delight. The peak was named by Dr. Sharon Matola (Director of the Belize Zoo and avid naturalist) and colleagues in reference to Sir Arthur Conan Doyle's book, "The Lost World". Several apparently undescribed species of corticioid fungi were also found, including a *Dichostereum* sp., a *Phlebia* sp., a *Protodydium* sp. and an unusual merulioid *Phanerochaete* sp. Numerous collections were also made of a striking daedaleoid polypore with magenta stains, which is currently being described by L. Ryvarden and M. Mata as *Daedalea rosea*. Some taxa were characteristic of neotropical cloud forests, including a new species of *Arthrosporella*. A few species of *Hygrocybe* and *Myceina* represent disjunct populations of taxa known previously only from the Amazon Basin and may indicate the presence of relictual, ancient populations of these fungi. Except for a tsunami originating in the Gulf of Mexico near the Yucatan Peninsula at the Cretaceous/Tertiary boundary 65 million years ago, Doyle's Delight and neighboring highlands have remained above sea level for over 300 million years, making this area a good candidate for an ancient refugium. poster

Long, Melissa* and Shaw, Brian D. Program for the Biology of Filamentous Fungi, Department of Plant Pathology and Microbiology, Texas A&M University, College Station, Texas 77803, USA. mmlong@ag.tamu.edu. **A mutation in *Aspergillus nidulans* chaperonin subunit, *cctA* results in a tip splitting, polarity maintenance phenotype.**

The *Aspergillus nidulans* *cctA1* temperature sensitive mutant is defective in polarity maintenance when grown at restrictive temperature (39C). The conidia of *cctA1* germlings swell isotropically and can establish a primary germ tube but over time the mutant can no longer maintain polarity and dichotomously branches at the growing tip when incubated at 39C. The mutant is complemented by a plasmid containing a gene encoding a chaperonin subunit. Transposon insertion within this gene disrupts the ability of the clone to complement the *cctA1* phenotype. The chaperonin is a large barrel shaped protein composed of two stacked rings made of eight subunits each and assists in the folding of approximately 10% of newly synthesized proteins. Though the exact make up of the substrates of this complex is not fully understood, the best studied to date are the cytoskeletal proteins, actin and tubulin. Homologs of all eight *S. cerevisiae* chaperonin subunits are found in the *A. nidulans* genome. It is hypothesized that a cytoskeletal defect

leads to the *cctA1* dichotomously branching phenotype. Analysis of this hypothesis will be discussed. contributed presentation

Luk, Wing-Yan*, Cheung, Man-Wai, Leung, Ping-Chung and Chiu, Siu-Wai. Dept. of Biology and Institute of Chinese Medicine, The Chinese University of Hong Kong, and Dept. Medicine, University of Hong Kong, Hong Kong SAR, China. SWChiu@cuhk.edu.hk. **Estrogenicity and anti-breast cancer effects of *Ganoderma lucidum*, *G. tsugae* and their artificial hybrid.**

Both *Ganoderma tsugae* and *G. lucidum* are categorized as red lingzhi and commercially produced. An interspecific hybrid of these lingzhi was created by protoplast fusion. This study verified the anti-proliferative effects on human estrogen-dependent breast cancer cells MCF-7 and estrogen-independent cells MDA by cytotoxicity MTT method and viability assay using Trypan Blue staining. Lingzhi enhanced the apoptosis pathway as revealed by RT-PCR using specific primers of anti-apoptotic gene bcl-2, pro-apoptotic gene bax and tumor suppressor gene p53. Both terpene and polysaccharide fractions contributed to the anti-cancer property of lingzhi. Reconstitution of these active ingredients even showed higher potency than the aqueous hot-water extracts. The physiological stage of lingzhi also modulated this bioactivity; aqueous extracts from basidiospores were ineffective while the submerged fermented lingzhi biomass was the most effective. The interspecific hybrid showed hybrid vigor with the highest potency than its parents. Besides, this is the first report on the estrogenicity of lingzhi by *in vitro* E-screen test and estrogen receptor competitor binding assays. The terpene fraction accounted for this bioactivity. Further, lingzhi stimulated proliferation of bone cells. Thus lingzhi is a favourable dietary supplement for women with menopause problem or osteoporosis. contributed presentation

Lumbsch, H. Thorsten. The Field Museum, Department of Botany, Chicago IL, USA. tlumbsch@fmnh.org. **Phylogenetic relationships of the lichen-forming order Agryales.**

The Agryales is a small order of crustose, lichen-forming fungi that is characterized by hemiangiocarpous ascoma development and an ascus with an amyloid ascus wall and non-amyloid tholus. The circumscription of Agryales is unclear. Families, such as Anamylopsoraceae, which were included based on morphological evidence, appear to be distantly related in molecular trees. Also the phylogenetic position of the order is poorly understood. While some molecular studies place the Agryales close to Ostropales (it was even suggested to merge these orders), the order is a sister-group to Pertusariales in other studies. The phylogenetic position and circumscription was re-investigated using sequence data of the nuclear LSU and mitochondrial SSU rDNA, and the protein-coding RPB-1 gene. contributed presentation

Luoma, Daniel L.* and Eberhart, Joyce L. Department of Forest Science, Oregon State University, Corvallis, OR 97330. USA. luomad@fsl.orst.edu. **Forests, Fire, and Fungi.**

A massive forest fire that burned through southwest Oregon in 2002 impacted a research site where we have gathered data on ectomycorrhizae (EM) and ectomycorrhizal fungus (EMF) sporocarp production since 1992. Two of three blocks of the regional long-term ecosystem productivity (LTEP) experiment were burned. Experimental tree harvest treatments were applied to the blocks in 1997. All treatments were established in 80- to 100-yr-old, naturally regenerated stands chosen for homogeneity of initial stand and soil conditions. All treatments in one block burned with medium to high intensity. Most of a second block burned less intensively. A third block was spared. After disturbance, survival of ecto- and VA- mycorrhizal inoculum is critical for many shrubs and trees. These legacies, along with charred logs and snags, likely affect ecosystem development after fire. We sampled EM and EMF sporocarps in the spring and fall of 2003 in order to document the immediate effects of fire on the overlay of the original LTEP experimental treatment effects. No sporocarp production was found in heavily burned areas. Sporocarp production was associated with light to medium burns only in the LTEP control treatment areas. Ectomycorrhizae were similarly reduced in response to the interaction of burn severity and LTEP treatment, one year after fire. poster

Lutzoni, François* and Reeb, Valerie. Dept. of Biology, Duke University, Durham NC 27708, USA. flutzoni@duke.edu. **Topological conflict, methodological artifact, or misinterpretation of results?**

The use of Bayesian MCMC methods has transformed the field of phylogenetics. Concomitant with the increased popularity of this approach, came a higher level of apparent conflicts among gene phylogenies and phylogenetic studies in general. These topological discrepancies have been attributed to poor analytical practices, e.g., using nucleotide sites that are saturated by changes compared to amino acid data. However, low amount of data, and misinterpretation of support values (including bootstrap proportions and posterior probabilities) can be misleading. In this presentation we will demonstrate that most differences among published fungal topologies are not hard conflicts, but are mostly due to the lack of data and to limitations in the current implementation of Bayesian MCMC methods. contributed presentation

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Machida, Masayuki^{1*}, Sano, M.², Terabayashi, Y.¹, Kumagai, T.³, Yamane, N.¹, Takase, K.¹, Tanaka, T.⁴, Terai, G.⁵, Galagan, J.⁶, Nierman, W. C.⁷, Denning, D.⁸, Ohashi, S.², Abe, K.⁹, Asai, K.³ and Gomi, K.⁹ ¹BRF, Natl. Inst. of Advanced Ind. Sci. and Technol. (AIST), Central 6, 1-1, Higashi, Tsukuba, Ibaraki, 305-8566, Japan, ²Kanazawa Institute of Technology, ³CBRC, Natl. Inst. of Advanced Ind. Sci. and Technol. (AIST), ⁴Natl. Inst. of Technol. and Eval., ⁵INTEC Web and Genome Informatics, ⁶Broad Inst. of MIT and Harvard, ⁷Inst. for Genomic Res., ⁸Wythenshawe Hospital, ⁹Tohoku University, Japan. m.machida@aist. **Analyses of genome structure and gene expression of *Aspergillus oryzae*.**

Aspergillus oryzae is extensively used in Japanese traditional fermentation industries and in enzyme productions by modern biotechnology. The whole genome sequencing of *A. oryzae* has been almost completed at the end of 2004 (in submission). Approximately 12,000 genes with longer than 100 amino acids in length were predicted from the *A. oryzae* genome of 37.6 Mb in size. Comparison of the number of genes in each COG functional category revealed that *A. oryzae* had genes more redundant specifically for those concerning to metabolism than *Aspergillus fumigatus*, *Aspergillus nidulans* and *Neurospora crassa*. Synteny analysis among *A. oryzae*, *A. fumigatus* and *A. nidulans* showed that *A. oryzae* had significantly more synteny breaks than between *A. fumigatus* and *A. nidulans* and that *A. oryzae* genome had a mosaic structure consisting of *A. oryzae*-specific and common loci among the three species. Mapping of ESTs to the genes on each chromosome revealed that the expression of the genes on the *A. oryzae* specific-loci was obviously lower than those on the loci common to the three *Aspergilli*. Based on the genome sequence, the DNA microarray consisting of 11,000 oligonucleotides were prepared. The fluorescence intensity of the microarray supported the lower expression of the genes on the *A. oryzae*-specific loci. The transcriptional regulation of the metabolic pathways by the microarray is under progress. symposium presentation

Maekawa, Nitaro. Faculty of Agriculture, Tottori University, 4-101 Koyama-Minami, Tottori, 680-8553, Japan. kin-maek@infosakyu.ne.jp. **Corticoid fungi in subtropical islands of Japan.**

Mycogeographic relationships of the corticoid fungi (homobasidiomycetes with effused and skin-like basidiomata) between two subtropical areas, Ogasawara Islands and the Ryukyu (Loochoo) Islands, are presented. Ogasawara Islands (also known as the Bonin Islands), located about 1,000 km south (26-27N, 142E) of Tokyo, have a characteristic forest ecosystem with many endemic species of trees and small woody plants because the islands are "oceanic islands". On the other hand, the Ryukyu Islands, located about 1,600 km west (24-27N, 124-128E) of Ogasawara Islands at almost the same latitude as the latter, are "continental islands" and have a tree flora similar to that of Taiwan and mainland China. During a floristic study of the corticoid fungi in the two subtropical areas, more than 500 specimens were collected. Morphological analyses of these specimens revealed that 51 species belonging to 26 genera and 64 species belonging to 32 genera were distributed on Ogasawara Islands and the Ryukyu Islands, respectively. Taxonomic and specimen details will be discussed for some of the interesting species belonging to the genera *Asterostroma* and *Haloaleurodiscus*. symposium presentation

Maier, Wolfgang F.A.^{1*}, Crane, Patricia E.² and Wingfield, Brenda D.¹ ¹Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa, ²Forest Research, Sala Street, Private Bag 3020, Rotorua, New Zealand. wolfgang.maier@fabi.up.ac.za. ***Chrysomyxa weirii* is more closely related to *Melampsora* than to *Chrysomyxa*.**

Chrysomyxa weirii Jackson is an autoecious microcyclic rust fungus attacking several spruce species (*Picea engelmannii*, *P. glauca*, *P. mariana*, *P. rubens*, *P. sitchensis*), mainly in northwestern North America. It has also been reported to cause severe problems in nurseries of *P. pungens* in the eastern United States. A special feature of the species is its one-celled water-dispersed teliospores that germinate to produce two-celled basidia. Here we present a phylogeny based on nuc LSU ribosomal DNA sequences that clearly shows that *Chrysomyxa weirii* is not associated with *Chrysomyxa* but with *Melampsora*. This is supported by both high bootstrap and Bayesian a posteriori probabilities. The affinities to *Melampsora* are also reflected by teliospore morphology because the teliospores of *Melampsora weirii* are elongated and thin-walled like the teliospores of other representatives of *Melampsora*, and the basidium germinates through a pore in the teliospore cell wall, which has also been observed for several *Melampsora* species. Therefore a new combination for the species will be proposed. poster

Mandyam, Keerthi* and Jumpponen, Ari. Ackert Hall, Kansas State University, Manhattan, KS 66502, USA. kgm9595@ksu.edu. **Diversity and function of fungal endophytes of a tallgrass prairie.**

Arbuscular mycorrhizal (AM) fungi are important mutualists in the grasslands. However, a two-year monthly sampling in a tallgrass prairie ecosystem showed that root colonization by dark septate endophytes (DSE) may exceed AM colonization. To identify the DSE fungi, root-inhabiting fungi were isolated and root endophytes identified via Koch's postulates. As much as 45% of the isolates belonged to the genus *Periconia* and formed typical DSE structures without any damage to the host. *Periconia* species were metabolically characterized by testing their

ability to utilize complex C sources and organic N sources. The results show that *Periconia* species can use complex C sources and organic N sources. The host range of the DSE fungi was tested by inoculating a number of native grasses and forbs. While most species were colonized, the native grasses were more heavily colonized than forbs. Colonization by *Periconia* species resulted in positive, neutral or negative growth responses in the native species. These responses suggest that DSE fungi may control plant community structure. The function of these fungi remains unclear. We will present preliminary results on the role of *Periconia* species in drought tolerance and host N uptake facilitation. symposium presentation

Marshall, Wyth L.^{2*} and Berbee, Mary L.¹ ¹University of British Columbia, Department of Botany, Vancouver, B.C. Canada, ²Bamfield Marine Sciences Center, Bamfield, B.C. V6T 1Z4, Canada. wythmarshall@yahoo.ca. **Spherical mesomycetozoans, members of a newly discovered lineage at the fungus/animal split, are common in marine invertebrate guts.**

Unicellular heterotrophs reproducing via flagellated zoospores are abundant and successful within aquatic environments. These include thraustochytrids (Stramenopiles), achlorophorous algae, chytrid fungi and mesomycetozoans. The unicellular ancestor of fungi and animals may also have shared many of these characteristics and was most likely marine. Several new lineages near the animal fungal divergence have been described recently and continued sampling for marine heterotrophs will lead to an increase in the known biodiversity within these groups and may even reveal new clades. Marine invertebrate guts are an understudied, microbe rich environment favourable for heterotrophic organisms. Nearly a dozen animal species were collected along the Western Coast of Canada and their gut contents were cultured on several media. Colonies producing sporangia were sub-cultured and identified as either mesomycetozoans or thraustochytrids based on their SSU sequences. Thraustochytrid isolates were diverse and belonged to a variety of clades or genera. Mesomycetozoans were found in most animals and most were closely related to *Pseudoperkinsus tapetis* and *Sphaeroforma arctica*, two species isolated from marine invertebrates. Some host animals had mesomycetozoans of more than one phylotype, suggesting that this clade of mesomycetozoans is common within marine invertebrate guts. contributed presentation

Massoumi Alamouti, Sepideh* and Breuil, Colette. Dept. of Wood Science, University of British Columbia, Vancouver BC V6T1Z4, Canada. alamouti@interchange.ubc.ca. **Morphological and molecular identification of staining fungi associated with the northern spruce engraver, *Ips perturbatus* (Eichhoff).**

Staining fungi were isolated from *Ips perturbatus* beetles and their galleries collected from spruce logs in northern British Columbia and the Yukon Territory. Fungal isolates were identified using morphological characteristics, nuclear rDNA and partial beta-tubulin gene sequences. A number of staining fungi were consistently isolated from the beetles and their galleries, while others seemed to be rather sporadic or ubiquitous associates. Ten morphological and phylogenetic species were recognized among these fungi. Three species were identified as *O. bicolor*, *O. manitobense* and *L. abietinum* while seven fungi were recognized as undescribed species. The undescribed fungi were morphologically and genetically different from the species reported in the literature, which suggested that they are new species being reported for the first time. poster

Masuya, Hayato* and Ichihara, Yu.² ¹Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan, ²Tohoku Research Center of Forestry and Forest Products Research Institute, Morioka, Iwate 020-0123, Japan. massw@ffpri.affrc.go.jp. ***Ceratocystiopsis alba* should be treated as a species of *Ophiostoma*.**

During the course of survey of ophiostomatoid fungi in Japan, we found an ophiostomatoid fungus on the bark of *Ulmus laciniata*. This fungus was characterized by hyaline perithecia, evanescent asci, and elliptic, fusiformed ascospores without septa, and considered to be a *Ceratocystiopsis*-type *Ophiostoma* species. Morphological characteristics of this fungus were identical to those of *Ceratocystiopsis alba*. Molecular comparison of the fungus with *Ceratocystiopsis*-type *Ophiostoma* showed that the fungus was closely related to *Ceratocystiopsis alba*. The genus *Ceratocystiopsis* is now treated as a synonym of *Ophiostoma*, excluding *C. alba*. Phylogenetic analyses based on partial LSU rDNA sequence showed that the fungus was not related to *Ophiostoma* species. Analyses based on SSU rDNA, on the other hand, indicated that the fungus was phylogenetically related to Ophiostomataceous fungi. It was not included in the group of typical *Ceratocystiopsis*-type *Ophiostoma*, but placed in the sister clade of the genus *Ophiostoma*. This fungus was not related to the other ophiostomatoid fungi, such as *Ceratocystis*, *Pyxidiophora*, *Kathistis*, and *Sphaeronaemella*. Tolerance to cycloheximide, which is an important character of the genus *Ophiostoma*, was lacking in this fungus. However, some *Ophiostoma* species also lack cycloheximide tolerance. Thus, morphological and physiological similarities of this fungus with some *Ophiostoma* species position it within the range of this genus, despite of some discrepancy in the facts from molecular analyses. Our present conclusion is that this fungus should be treated as a member of *Ophiostoma*. poster

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Matheny, P. Brandon Dept. of Biology, Clark University, Worcester MA 01610, USA. pmatheny@clarku.edu. **Phylogeography of the Inocybaceae (euagarics): evidence for multiple biogeographic hypotheses.**

The Inocybaceae, a species-rich family of ectomycorrhizal euagarics, is distributed world-wide in various ectotrophic habitats and phylogenetically is one of the more well-studied clades of euagarics. As a result, the group represents an excellent model for phylogeographic research of ectomycorrhizal fungi. Area optimization cladograms using a parsimony method support relatively recent dispersal events to tropical and temperate South America and to New Zealand. Extinctions are minimized under this scenario. In contrast, accommodating ancient vicariance events and allowing for no dispersal must account for many extinctions, which proves to be a less parsimonious explanation for the current distribution of the family. However, tropical and southern hemisphere taxa express a strong degree of species-level and higher-level endemism and vicariance cannot be ruled out in all cases. Endemic taxa include many Australian, African, and South American species and higher-level groups. In contrast, some north temperate species are believed to be wide-spread geographically across Asia, Europe, and North America. Phylogeographic relationships of South American and Australian taxa are heterogeneous. For example, a South American *Nothofagus* associate is basal to a north temperate Pinaceae-associated clade, but another *Nothofagus* associate is related to Australian Myrtaceae symbionts. In addition, a new genus, *Auritiella*, is proposed to accommodate African and Australian lineages with elongated cheilocystidia, necropigmented basidia, and/or evolution of a sequester habit. Molecular clock dating techniques using nLSU-rDNA and *rpb2* genes suggest a late Cretaceous split (about 90 Mya) between the African and Australian clades of *Auritiella*. Recent dispersal between these two continents for this genus is firmly rejected. symposium presentation

Matheny, P. Brandon^{1*}, Aime, M. Catherine², Ammirati, Joseph F.³, Aoki, T.⁴, Baroni, Timothy J.⁵, Binder, M.¹, Crane, Patricia E.⁶, Curtis, J.¹, de Nitis, M.¹, Dentinger, Bryn C.⁶, Frøslev, T.⁸, Ge, Z.W.⁹, Halling, Roy¹⁰, Hosaka, K.¹¹, Hughes, Karen W.¹², Kerrigan, Richard W.¹³, Kropp, Bradley R.¹⁴, Langer, G.E.¹⁵, Matsuuru K.¹⁶, McLaughlin David J.⁶, Nilsson R.H.¹⁷, Nishida H.¹⁸, Padamsee M.⁶, Petersen Ronald H.¹², Piepenbring, M.¹⁹, Seidl, Michelle T.³, Slot, Jason¹, Vauras, J.²⁰, Vellinga, E.C.²¹, Wang, Zheng¹, Wilson, A.¹, Yang, Z.L.⁹, and Hibbett, David S.¹ ¹Biology Dept., Clark Univ., 950 Main St., Worcester, MA 01610 USA; ²Systematic Botany & Mycology Lab, 10300 Baltimore Ave., Beltsville, MD 20705-2350 USA; ³Biology Dept., Box 351330, Univ. of Washington, Seattle, WA USA 98195; ⁴National Inst. Agrobiological Sciences, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan; ⁵Dept. Biological Sciences, Box 2000, State Univ. New York - College at Cortland, Cortland, NY 13045 USA; ⁶Dept. Plant Biology, Univ. of Minnesota, St. Paul, MN 55108-1095 USA; ⁷Northern Forestry Centre, Canadian Forest Service, 5320 - 122 Street, Edmonton, AB Canada T6H 3S5; ⁸Botanical Inst., Univ. of Copenhagen, Øster Farimagsgade 2D, DK-1353 Copenhagen, Denmark; ⁹Kunming Inst. Botany, Chinese Academy of Sciences, Heilongtan, Kunming 650204, P. R. China; ¹⁰Inst. Systematic Botany, The New York Botanical Garden, Bronx, NY 10458-5126 USA; ¹¹Dept. Botany & Plant Pathology, Oregon State Univ., Corvallis, OR 97331; ¹²Botany Dept., Univ. of Tennessee, Knoxville, TN 37996-1100; ¹³Sylvan Research, 198 Nolte Dr., Kittanning, PA 16201 USA; ¹⁴Dept. Biology, Utah St. Univ., Logan, UT 84322 USA; ¹⁵Univ. Kassel, FB 18 Naturwissenschaften, FG Oekologie, Heinrich-Plett-Str. 40, D-34132 Kassel; ¹⁶Dept. Organismic & Evol. Biology, Harvard Univ., 26 Oxford St., Cambridge, MA 02138 USA; ¹⁷Göteborg Univ., Botaniska Inst., Box 460, SE 405 30 Göteborg, Sweden; ¹⁸Inst. Molecular & Cellular Biosciences, Univ. Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-0032, Japan; ¹⁹Botanisches Inst., J. W. Goethe-Univ., Senckenberganlage 31-33, D-60054 Frankfurt; ²⁰Herbarium, Biology Dept., Univ. of Turku, SF-20500 Turku, Finland; ²¹Plant & Microbial Biol. Dept., Univ. of California at Berkeley, 111 Koshland Hall, Berkeley, CA 94720-3102 USA. pmatheny@clarku.edu. **Progress towards assembling the tree of life for the Basidiomycota.**

The phylogeny of the Basidiomycota has been addressed in a limited way from analysis of nucleotide data. Most studies have relied primarily on single gene analyses of nuclear ribosomal RNA genes (18S or 25S). Confidence measures have been generally inadequate in such studies despite efforts at dense taxon sampling. As part of the the Assembling the Fungal Tree of Life (AFTOL) project, our laboratory is generating multi-locus datasets for resolving higher-level phylogenetic relationships of Basidiomycota. We present results from a nuclear rDNA data set (3.5 kb) for 200 AFTOL basidiomycetes, a protein-coding data set of *rpb2*, *rpb1*, and *tef1* (1350 amino acids) for 85 taxa, and a combination of these data into a 6-locus data set (18S, 25S, 5.8S, *rpb2*, *rpb1*, and *tef1*). rDNA sequences support a sister relationship between the Ustilaginomycetes (true smut fungi) and the Hymenomycetes (mushroom-forming fungi), a relationship consistent with several ultrastructural and biochemical characters. However, a combination of rDNA and protein-coding genes suggests the Urediniomycetes (rusts and allies) could be the sister group to the Hymenomycetes. Spliceosomal intron placement might support this view. The Microbotrymycetidae (a diverse group including anther smuts and diverse yeasts) appears sister to the Urediniomycetidae with strong measures of support. rDNA Bayesian and *rpb2* parsimony analyses, however, fail to support the monophyly of the Exobasidiomycetidae. Basal nodes in the Hymenomycetes are well-resolved and moderately supported in the most

gene-rich data sets. In the 6-locus data set, the cantharelloid clade represents the most ancient branch among the Homobasidiomycetes. The trechisporoid and gomphoid-phalloid clades represent a monophyletic group with moderately high bootstrap support. Distal homobasidiomycete clades also receive moderate to high bootstrap support. Examples include: the inclusive monophyly of the atheloid and bolete clades; the sister position of the russuloid clade to the euagarics, atheloid, and bolete clades; and a sister relationship between the theleporoid and polyporoid clades. contributed presentation

Matsuda, Yosuke*, Noguchi, Yuuta, Nakanishi, Kenichi and Ito, Shin-ichiro. Laboratory of Forest Pathology and Mycology, Faculty of Bioresource Sciences, Mie University, Tsu 514-8105, Mie, Japan. m-yosuke@bio.mie-u.ac.jp. **Ectomycorrhizal associations of naturally grown *Pinus thunbergii* seedlings in a coastal pine forest.**

To identify ectomycorrhizal (ECM) fungi associated with naturally regenerated *Pinus thunbergii* seedlings grown at coastal areas, we sampled 15 current-year-old and 14 more than 1-year-old seedlings at a coastal pine stand. ECM roots were first morphotyped by microscopy, and were then classified as RFLP-types analyzing the rDNA of the internal transcribed spacer region digested with two enzymes, *Alu* I and *Hin* f I. RFLP-types were directly sequenced to identify fungal species. In total, 13 species were found and *Cenococcium geophilum* was identified morphologically. For current- and more than 1-year-old seedlings, *C. geophilum* and *Lactarius* sp. were either the most or the second most dominant species in terms of both the number of ECM roots and the frequency of occurrences per seedling. The number of ECM roots colonized by *C. geophilum* or *Lactarius* sp. was positively correlated with the shoot dry weight of seedlings, and the correlation coefficient of the latter species was higher than that of the former. These results indicate that multiple species of ECM fungi are involved in the ECM formation on *P. thunbergii* seedlings and a few dominant species may be important for the growth and survival of the seedlings at the coastal area. poster

Matsumoto, Naoyuki^{1*} and Hoshino, Tamotsu². ¹National Institute for Agro-Environmental Sciences, Tsukuba 305-8267, Japan. ²National Institute of Advanced Industrial Science and Technology (AIST), Sapporo 062-8517, Japan. nowmat@affrc.go.jp. **Adaptations of snow mold fungi, *Typhula ishikariensis* and *T. incarnata*, to diverse winter climates.**

Typhula ishikariensis consists of two biological species, each including several endemic taxa adapted to local environments. Freezing tolerance of mycelia at -20C is a common trait in some taxa of both biological species existing in Moscow, Saskatchewan, and coastal regions in north Norway and Greenland. Their growth at 10 to 12 C becomes irregular due presumably to high respiration because free radical scavengers improve growth. Such a trait coincides with DNA sequence in the large mitochondrial subunit. *T. ishikariensis* biotype B is distributed in localities differing in the number of days with snow cover ranging from 40 to 150 days p.a. Its sclerotia become smaller and virulence increases with decreasing snow cover days. The population in the least snowy locality is practically soilborne and seldom develops sporocarps. Soil environment is more stable than the habitat under snow cover in such a changeable habitat. *T. incarnata* populations from diverse localities are similar in sclerotium size as well as in virulence: a single isolate of *T. incarnata* covers a broad variation in sclerotium size comparable to that in the *T. ishikariensis* complex. They, however, differ in the number of days required for carpogenic sclerotium germination. In the less snowy habitats, when persistent snow cover starts is difficult to predict. Populations in such a habitat are "prudent" in this respect. symposium presentation

Matsuura, Kenji. Laboratory of Insect Ecology, Graduate School of Environmental Science, Okayama University, 1-1-1 Tsushima-naka, Okayama 700-8530, Japan. kenjiJPN@cc.okayama-u.ac.jp. **Termites and a termite-egg-mimicking fungus: a novel insect-fungus interaction.**

Mimicry has evolved in a wide range of organisms encompassing diverse tactics for defense, foraging, pollination, and social parasitism. Egg protection is an essential behavior in social animals. Here I report an extraordinary case of egg mimicry by a fungus, whereby the fungus gains competitor-free habitat in termite nests. The phenomenon of termites harboring brown fungal balls alongside their eggs was found recently in the Japanese termite *Reticulitermes speratus*. When workers recognize the eggs laid by queens, they bring the eggs together and heap them up in order to take care of them. Brown fungal balls, named "termite balls," are frequently found in egg piles of *Reticulitermes* termites in Japan and the US. The brown ball was identified as the sclerotium of a corticioid fungus, *Fibularhi-zoetonia* sp. nov. Although termite balls promote egg survival under certain experimental conditions, the relationship is not always symbiotic but is sometimes parasitic or pathogenic. Dummy-egg bioassays using glass beads showed that both morphological and chemical camouflage were necessary to induce tending by termites. Scanning electron microscopic observation revealed sophisticated mimicry of the smooth surface texture. These results provide clear evidence that termite balls mimic termite eggs. This finding suggests that mimicry is a diverse and widespread tactic even in fungi. symposium presentation

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Mayor, Jordan R.^{1*}, Henkel, Terry W.¹ and Aime, M. Catherine². ¹Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA, ²USDA-ARS, Systematic Botany and Mycology Lab, Beltsville, Maryland 20705, USA. jrm46@humboldt.edu. **Ectomycorrhizae accelerate calcium acquisition from leaf litter in a monodominant *Dicymbe corymbosa* (Caesalpinaceae) forest in Guyana.**

We tested the hypothesis that ectomycorrhizae (EM) alter mineral nutrient concentrations and decomposition of leaf litter within a monodominant forest of the ectomycorrhizal, canopy tree *Dicymbe corymbosa* Spruce ex Benth. in Guyana. A root-exclusion experiment and a reciprocal transplant experiment were performed to determine how the exclusion of ectomycorrhizae would influence decomposition of *D. corymbosa* leaves. Mass loss of *D. corymbosa* leaf litter was determined on three occasions during a 12 month period, and was unaffected by the presence of ectomycorrhizae. Elemental analysis of N, P, K, Ca, and Mg was performed on the residual *D. corymbosa* leaf litter after 12 months. Both experiments demonstrated that, at 12 months, leaf litter Ca concentrations were significantly reduced in the presence of ectomycorrhizae. These results suggested an ectomycorrhizal enzymatic mode of Ca mobilization which may facilitate continued root growth and domination of litter layers by ectomycorrhizae. Additionally, saprotrophic fungi that specialize on *Dicymbe* leaves have been identified through multi-year plot sampling; these foliicolous specialists may facilitate rapid decomposition of *D. corymbosa* leaves within monodominant forests and, in conjunction with ectomycorrhizae, contribute to rapid mineral nutrient recycling in the system. poster

McAlpin, Cesaria E. and *Wicklow, Donald T. USDA, ARS, National Center for Agricultural Utilization Research, Peoria IL, USA. wicklodt@ncaur.usda.gov. **DNA fingerprinting analysis of *Petromyces alliaceus* section *Flavi*.**

The objective of this study was to evaluate the *Aspergillus flavus* pAF28 DNA probe's ability to produce DNA fingerprints for distinguishing among genotypes of *Petromyces alliaceus* section *Flavi*, a fungus considered responsible for the ochratoxin A contamination that is occasionally observed in California fig orchards. *Petromyces alliaceus*, *P. albertensis* and 7 species in *Aspergillus* section *Circumdati* were analyzed by DNA fingerprinting using a repetitive sequence DNA probe pAF28 derived from *A. flavus*. The presence of hybridization bands with the DNA probe and the *P. alliaceus* or *P. albertensis* genomic DNA indicates a close relationship between *A. flavus* and *Petromyces alliaceus* section *Flavi*. Twelve distinct DNA fingerprint groups or genotypes were identified among 15 isolates of *Petromyces*. Species belonging to *Aspergillus* section *Circumdati* hybridized only slightly at the 7.0 kb region with the repetitive DNA probe, suggesting very little DNA homology. The pAF28 DNA probe offers a tool for typing and monitoring specific *P. alliaceus* clonal populations and for estimating the genotypic diversity of *P. alliaceus* in orchards, vineyards or crop fields. poster

McKay, Doni^{1*}, Jennings, Tara² and Smith, Jane E.¹. ¹USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR 97331, USA, ²Department of Forest Science, Oregon State University, Corvallis, OR 97331, USA. dmckay@fs.fed.us. **Life in red soils: Investigating forest recovery after wildfire.**

Post-fire forest recovery is dependent on functioning soil fungal communities. To examine effects of burn severity on soil recovery we are measuring total fungal diversity and nutrients from soil from the 2003 Booth & Bear Butte fire complex in the Cascade Range of Oregon. Soil samples were collected immediately after fire and 3 times during the post-fire year from 24 paired plots of detrimentally (severely) and moderately burned soils. Using TRFLP techniques, we show that soil fungal diversity is low for the detrimentally burned soils and typically higher in the moderately burned soils. The detrimentally burned soils were higher in pH than the moderately burned soils, whereas the moderately burned soils had higher measures of ammonium, nitrate, carbon, total nitrogen and phosphorus, and CEC. Soils were also collected for a microcosm seedling bioassay. Roots were assessed for percent colonization of dark septate and ectomycorrhizal fungi (EMF); molecular PCR methods were used to identify EMF and assess fungal community recovery. Our results show that fires resulting in large areas of detrimentally burned soil decrease nutrient availability, reduce mycorrhizal colonization of regenerating seedlings, and negatively impact post-fire site productivity. poster

McLaughlin, David J. Dept. of Plant Biology, University of Minnesota, St. Paul, MN 55108, USA. davem@umn.edu. **The Advance of the Basidiomycota: The View across the Plasma Membrane**

During the last 50 years there have been remarkable advances in our knowledge of evolution within the Basidiomycota, new concepts of the basidium and basidiospore release, and an expansion in both taxonomic and structural diversity. But we remain a long way from a complete understanding of evolutionary relationships within the phylum, and further still from a full elucidation of basidiomycete structure and its functional significance. This review of subcellular structure will begin with the basidium and ballistosporic mechanism. Subcellular characters have aided us in establishing monophyletic classes, and have been used to assess relationships between the Ascomycota and Basidiomycota. I will discuss the latter by reviewing the origin of the Uredinales, mitosis in ascomycetous and

basidiomycetous yeasts, and Woronin bodies. The availability of molecular sequence data in the 1990's made possible genetic assessment of phylogenies, provided guidance on interpretation of subcellular characters, and made possible the integration of molecular and subcellular characters in phylogenetic analysis. Now the development of bioinformatic databases of both molecular and structural characters will permit the analysis of ever larger data sets. These databases also reveal the scarcity and incompleteness of structural studies and provide guidance in filling gaps in the data. I will consider cystidia as an example of understudied structures with potential phylogenetic utility. In analyzing the Basidiomycota both evolutionary and cell biologists need to look across the plasma membrane, the former to understand the implications of cell diversity for explaining organismal function, and the latter to recognize the value of comparative studies in understanding cell function. **MSA Presidential Address**

McLenon, Terri^{1*}, Skillman, Jane¹, Taylor, Jonathan¹, Provart, Nicholas¹ and Moncalvo, Jean-Marc^{1,2}. ¹University of Toronto, Department of Botany, 25 Willcocks Street, Toronto, ON M5S 3B2, Canada, ²Royal Ontario Museum, Department of Natural History, Mycology, 100 Queens Park, Toronto, ON M5S 2C6, Canada. terri.mclenon@utoronto.ca. **Documenting fungal communities in soil: DNA sampling strategies and development of bioinformatic tools for automated phylogenetic identification.**

We have compared bulked and point sampling methods for assessing fungal diversity and community structure in coniferous forest soil from southern Ontario. Ten nLSU clone libraries were generated to produce at least 50 sequences per library for a total of ca. 800 sequences. Similar sequencing effort recovered a greater number of distinct nLSU sequences from bulked sampling than from point sampling; however, similar phylogenetic groups were recovered from each library, although with very little species overlap. Sampling curves did not show any sign of saturation after sequencing 148 clones from a single PCR amplification nor when all the data were pooled together. Overall, our results suggest that while a vast sequencing effort is needed to fully document the community of fungi in a forest plot, limited sequencing efforts may be sufficient to quickly document the presence of dominant phylogenetic and ecological groups in a soil horizon at a given time. We present the prototype of a novel bioinformatic tool (FungID) that addresses some of the known difficulties with these types of analyses by automatically integrating an unknown sequence and its top BLAST hits into their corresponding clade in the fungal tree of life. We also discuss how phylogenetically-based comparative methods may overcome problems associated with species (or OTU) circumscription. symposium presentation

Medina, Cristina^{1,2*}, González, María C.¹, Cifuentes, Joaquín², Vidal, Guadalupe², Sierra, Sigfrido² and Medina, Pedro³. ¹Universidad Nal. Aut. México, Instituto de Biología, Depto. Botánica, México, DF 04510, México, ²Secc. Micología, Herbario FCME, Facultad de Ciencias, México DF 04510, México, ³Univ. de Guadaluajara, Centro Univ. de la Costa, Depto. Ciencias, Puerto Vallarta, Jalisco, CP 48280, Mexico. megv@ibiologia.unam.mx. **Preliminary study of gorgonian fungi from Marietas Islands coral reef, Mexico.**

Some microscopic fungi associated with *Gorgonia* sp. from Marietas Islands coral reef are reported. The mycota associated with coral reef ecosystems has been little explored and only few studies have been conducted about fungi associated with pathogenic disease symptoms in various host organisms, usually in the form of tissue necrosis or biomineralisation. Fungi have been observed inhabiting several coral species including gorgonians in the Caribbean and South Pacific. A sample of *Gorgonia* sp. was collected via SCUBA from Burbuja Cave. Each sample was placed wet into a sterile plastic bag and transported to the laboratory. Sections of 0.5 square cm were excised from each sample unit. Cut sections (4 per plate) were surface-sterilised and then were placed onto Petri dishes containing selective media prepared with sea water with added antibiotics to diminish bacterial contamination. The inoculated plates were incubated 15 d at room temperature and with ambient light and each plate was checked daily for the emergence of fungal hyphae, which were transferred to fresh media and purified. The fungal isolates were grouped according to 10 morphological characters and then each distinctive isolate was chosen for taxonomic identification. Some recorded fungi were *Aspergillus*, *Cladosporium*, *Epicrococcum*, *Paecilomyces* and *Penicillium*. poster

Miadlikowska, Jolanta^{1*}, Arnold, A. Elizabeth², Higgins, K. Lindsay¹, Sarvate, Senehal³, Gugger, Paul⁴, Way, Amanda¹, Hofstetter, Valérie¹ and Lutzoni, François¹. ¹Duke University, Durham, NC, USA, ²University of Arizona, Tucson, AZ, USA, ³University of Virginia Health System, Charlottesville, VA, USA, ⁴University of Minnesota, St. Paul, MN, USA. jolantam@duke.edu. **Endolichenic fungi: random inhabitants or symbiotic partners.**

Studies of lichenicolous fungi (secondary fungi associated with lichen thalli) have been restricted, almost exclusively, to fungal species with visible reproductive structures on lichen surfaces. These visible fungi are abundant in nature and taxonomically diverse. However, the potential for fungi to occur asymptotically within thalli (i.e., as endolichenic fungi, analogous to endophytes of plants) remains mostly unexplored. We used a gradient of surface-sterilization to

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examine fungal communities associated with asymptomatic thalli of foliose lichen genera (*Lobaria*, *Nephroma*, *Peltigera*, and *Umbilicaria*) representing different habitats (terricolous, epiphytic and saxicolous) in neotropical, temperate, boreal, and arctic sites. Based on the sequences of the entire ITS region obtained from all cultivable fungal isolates, we explored diversity, taxon composition, geographic structure and host specificity of endolichenic fungi. Phylogenetic placement and affiliation of selected endolichenic fungi, endophytes isolated from different plant lineages, and representatives of major lineages of Ascomycota were explored based on combined data from the small and large nuclear ribosomal subunits, and provide the basis for a discussion of the evolution of the endophytic and endolichenic habits. contributed presentation

Mihail, Jeanne D.* and Bruhn, Johann, N. Division of Plant Sciences, University of Missouri, Columbia, MO 65211, USA. mihailj@missouri.edu. **Bioluminescence patterns among *Armillaria* spp., other fungi, and oomycetes.**

The phenomenon of bioluminescence among *Armillaria* spp. is widely recognized, although the details and their ecological significance are poorly understood. We examined temporal patterns of bioluminescence of 3 sympatric *Armillaria* spp. which differ in parasitic ability and foraging strategy. Luminescence of mycelia of 4 genets of *A. gallica*, *A. mellea*, and *A. tabescens* was examined in response to environmental illumination and mechanical disturbance. Temporal dynamics of luminescence were assessed for these 12 genets in time series for mycelia growing on agar vs root wood disks. Luminescence of saprotrophic *A. gallica* was enhanced by environmental illumination and mechanical disturbance. In contrast, luminescence of parasitic *A. mellea* and *A. tabescens* was quenched by environmental illumination and less responsive to disturbance. Differences among *Armillaria* spp. suggest that luminescence has been shaped by differing selective pressures. Luminescence of *Armillaria* spp. was compared with that of fungi in the Phyla Zygomycota (2 genera), Ascomycota (6 genera), and Basidiomycota (3 genera), and filamentous heterotrophs in the Phylum Oomycota (2 genera). Luminescence was more common than expected, raising the possibility that fungal bioluminescence plays a greater ecological role than previously appreciated. contributed presentation

Miki, Satoko. The University of Shiga Prefecture, 2500 Hassaka-cho, Hikone-shi, Shiga 522-8533, Japan. toki43@hotmail.co.jp. **Cultivation of *Pleurotus eryngii* on madake (*Phyllostachys bambusoides*).**

Bamboo was a useful material as household goods and building materials in Japan. However those demands gradually decrease and bamboo grove is being desolated. Alternative way to use bamboo should be searched since bamboo is a renewable resource and has a function as carbon fixation. This study was conducted to examine the possibility of bamboo as substrates of mushroom cultivation. Madake, *Phyllostachys bambusoides*, refined to cotton was used in the present study. Four substrates were prepared by mixing bamboo, sugar cane bagasse and rice bran at (a) 90 : 0 : 10, (b) 67.5 : 22.5 : 10, (c) 45 : 45 : 10 and (d) 0 : 90 : 10 ratio, respectively. A 300 g of substrates were filled in 850 ml culture pottles for mushroom production and sterilized. After cooling them, the spawns of *Pleurotus eryngii* were inoculated. Spawn running days were 30±5 on (a), 32±3 on (b), 32±5 on (c) and 28±2 on (d). Average fruitbody yields were 39±9.1 g on (a), 42.0±10.3 on (b), 42.0±15.2 on (c) and 32.1±12.7 on (d). These results suggested that refined bamboo are available for substrates of mushroom cultivation. poster

Miller, Orson K., Jr. Biology Department, Virginia Tech, Blacksburg VA 24061, USA. orsonk@frontiernet.net. **Interactions of host plants and arctic higher fungi.**

Arctic plant communities have evolved close associations with higher fungi. The associations involve ectomycorrhizal, ericoid, and basidiolichen mutualism. There are also bryophyte and decomposer associations which appear to be very specific to either hosts or litter quality. The arctic tundra in Alaska has ectomycorrhizal taxa, including 16 species of *Salix*, *Betula nana*, *Dryas octopetala*, *Arctostaphylos alpina*, and *Cassiope tetragona*, with 41 associated EM fungi. Three basidiolichens, species of *Botrydina*, are associated with omphaloid agarics. Four moss genera, *Drepanocladus*, *Calliergon*, *Campylium* and *Oncophorus*, along with *Sphagnum* are associated with five species of *Galerina* and *Phaeogalera stagnina*. These genera make up 70% of the bryomass, but only 4 of 11 genera of pleurocarpus mosses are associated with species of *Galerina*. Decomposers such as *Lepista multifforme*, *Marasmius epidryas*, and species of *Hygroclybe* and *Hypholoma* are associated closely with specific plants or groups of arctic plants. These close associations have allowed arctic communities to become established with ease following climate change and the emerging of new landscapes. Examples of these associations will be presented and discussed. symposium presentation

Miyakawa, Sachie*, Osaki, Mitsuru and Ezawa, Tatsuhiro. Graduate School of Agriculture, Hokkaido University, Sapporo 060-8589, Japan. s-miya@chem.agr.hokudai.ac.jp. **Arbuscular mycorrhizal fungi colonizing pioneer plants grown in acid sulfate soil in Rankoshi-cho, Hokkaido, Japan.**

Acid sulfate soil is formed by oxidation of sulfur-rich minerals. Revegetation of the soil is difficult due to low pH and poor nutrient availability. However, some pioneer plants in symbiosis with microorganisms survive and grow under

such an extreme environment. The objectives of the present study are i) to characterize arbuscular mycorrhizal (AM) fungi in extreme environment and ii) to investigate diversity of the fungi to understand significance of the fungi. The experimental site is a disturbed area in Rankoshi-cho, Hokkaido island, Japan. Scattered vegetation of *Phragmites australis*, *Betula platyphylla* var. *japonica*, *Polygonum sachalinense* var. *giganteus* was observed. AM fungal spore was isolated from rhizosphere of *Pe. japonica* var. *giganteus* and identified as *Glomus* sp. RF1 based on the 18S rDNA sequence. *Glomus* sp. RF1 belonged to the cluster of *Gl. manihotis* and *Gl. clarum*, and interestingly, the sequence and spore morphology were highly similar to those of *Glomus* sp. HR1 which was also isolated from acid sulfate soil in Aichi pref. in the main island of Japan. The rhizosphere soils of several pioneer plants were collected, and the same (or closely related) species was cultured to investigate AM fungal diversity based on the 28S rDNA sequence. The involvement of diversity of AM fungi in the growth of pioneer plants was discussed. poster

Miyamoto, Toshizumi¹, Campos, Daniela T. S.², Coelho, Irene S.², Araújo, Elza F.² and Kasuya, Maria Catarina M.² ¹Hokkaido University, Graduate School of Agriculture, Division of Environmental Resources, Sapporo, Japan, ²Federal University of Viçosa, Department of Microbiology, Viçosa, MG, Brazil. tmiyamot@for.agr.hokudai.ac.jp. **Morphological and molecular characterization of *Cordyceps australis* and its anamorph.**

Cordyceps australis was found parasitizing ants (*Dinoponera* sp., Hymenoptera; Formicidae). Clavus growing from the ant and synnemata formed in PDA were characterized morphologically. Clavus stipe blackish-brown in the base and orange near head, 42 mm long. Head orange, 2.7 x 2.1 mm. Oblique perithecia, hyaline, becoming brownish-yellow near to the ostioles, 0.93-1.25 x 0.15-0.25 mm, immersed, curved neck. Ostioles slightly projecting. Asci cylindrical, c.a. 390-600 x 5-6 µm, with depressed globose apex 6-7 µm, 8-spored. Ascospores multiseptated, hyaline, filiforme, easily separated as part-spores. Part-spores fusiform, slightly attenuated, truncated apices, 6.2-11.5 x 0.6-0.8 µm. Mycelium isolated from Clavus stipe, fast growth, forming synnemata after 45 d on PDA, at 25 °C. Synnema stipe dark brown, simple, cylindrical, 15-40 x 0.5 mm. Fertile head, white, 3-6 x 0.5-0.6 mm. Central part of head reddish when young, brownish with age. Conidiogenous cells emerging from hymenium-like layer. Conidia hyaline, aseptate, fusiform, 6-7 x 1.2-1.4 µm. Anamorphic morphological characteristics show this fungus belongs to the genus *Hymenostilbe*. Pure culture was used for molecular characterization and ITS sequences have been prepared to be deposited in the Gen-Bank database. This fungus presents high homology to *Hymenostilbe odonatae*, the anamorphic phase of *Cordyceps odonatae*, and *Cordyceps forquignoni*, *Cordyceps nutans* and *Cordyceps myrmecophila*. Poster

Mohatt, Kate* and Cripps, Cathy L. Plant Sciences and Plant Pathology, 119 Ag-BioScience Facility, P.O. Box 173150, Bozeman, MT 59717-3150, USA. mohatt@montana.edu. **Preliminary results on the ecology and diversity of ectomycorrhizal fungi associated with whitebark pine seedlings inside and outside the canopy zone of Greater Yellowstone forests.**

Whitebark pine (*Pinus albicaulis*) is a keystone subalpine species in the western USA, and has declined 40-90% throughout its range. The trees provide nuts to endangered grizzly bears, colonize inhospitable terrain, provide habitat for flora and fauna, and are important in watershed relations. Decline is attributed to white pine blister rust, fire suppression, bark beetles, and global climate change. Efforts are underway to restore forests by out-planting seedlings. Inoculation with native mycorrhizal fungi is known to increase seedling survival, yet little is known of the mycorrhizal symbionts crucial to whitebark pine. This project is discovering the mycorrhizal fungi with seedlings, and determining if seedlings outside the canopy zone host a less diverse, more generalist set of fungi than those below mature trees. This comparison is of particular interest for learning how seedlings gain mycorrhizal fungi because birds are the main dispersal agent of seeds. Molecular methods including ITS sequencing and virtual RFLP analysis are used to identify fungi on roots and morphotyping to ascertain diversity. Preliminary results with ITS sequences have revealed a diversity of fungi on seedlings, including *Cenococcum*, *Rhizopogon*, and *Gautieria*. Further results of the molecular analyses, diversity, ecology, and distribution of ectomycorrhizal fungi with whitebark pine will be presented. poster

Momany, Michelle. Dept. of Plant Biology, Univ. of Georgia, Athens, GA 30602, USA. momany@plantbio.uga.edu. **Genomic approaches to polarity.**

Multicellular filamentous fungi and unicellular yeast both grow in a polar manner. In the budding yeast *Saccharomyces cerevisiae* polarity requires three steps: establishment of cortical markers specifying the site of bud emergence, the relaying the bud site information via a Rho GTPase module and recruitment of the morphogenetic machinery needed for cell surface growth at the specified site. Comparison of the genomes of *S. cerevisiae* and *A. nidulans* show that the cortical markers are absent or poorly conserved, while the Rho GTPase signaling module and the morphogenetic machinery are highly conserved. Approaches combining genomics and genetics to study polarity will be discussed. symposium presentation

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Moore, Geromy and Taylor, Josephine*. Department of Biology, Stephen F. Austin State University, Nacogdoches TX 75961, USA. jtaylor@sfasu.edu. **Infection of *Cuscuta gronovii* by *Aureobasidium pullulans*.**

Aureobasidium pullulans was isolated from necrotic stems of *Cuscuta gronovii* Willd., commonly known as swamp dodder. Conidia from two-week old cultures of *A. pullulans* were used to inoculate healthy dodder tendrils under greenhouse conditions. Necrosis was produced within 48 hours, at which time the fungus had thoroughly colonized the dodder stem surface. Transmission electron microscopy revealed the presence of both intercellular and intracellular hyphae within cortical cells of the dodder stem. *A. pullulans* holds promise as a potential mycoherbicide to treat dodder infestations. poster

Morgenstern, Ingo*, Klopman, Shlomit and Hibbett, David S. Department of Biology, Clark University, Worcester MA 01610, USA. imorgenstern@clarku.edu. **Diversity and phylogenetic relationships of class II fungal heme peroxidases in homobasidiomycetes.**

Heme containing peroxidases are common enzymes occurring in all living organisms. Mostly, they are used in response to various kinds of oxidative stress, but in white rot fungi belonging to the homobasidiomycetes they play an important role in lignin degradation. According to structural and biochemical features ligninolytic fungal peroxidases are placed in class II of the superfamily of plant peroxidases. Manganese peroxidases (MnP), lignin peroxidases (LiP), and the more recently described versatile peroxidases (VP) are members of this class. Fungi producing a white rot do not necessarily secrete all of these enzymes. However, if a type of heme peroxidase is present it usually occurs in a series of multiple isoforms. We have performed phylogenetic analyses using complete amino acid sequences from published sources which reveal that class II fungal peroxidases share evolutionary roots with class I (peroxidases of prokaryotic origin) and class III (classical plant peroxidases) of the superfamily plant peroxidases. We have also generated partial MnP gene sequences, which we have combined with the published full-length sequences for phylogenetic analyses focused on evolutionary relationships within the fungal peroxidases. Finally, we have performed tree reconciliation analyses between gene trees and species trees to elucidate the diversity and phylogenetic relationships of these enzymes. The results of these analyses indicate that there have been many gene duplications in class II fungal peroxidases, including ancient and recent events. contributed presentation

Morita, Atsushi* and Tanaka, Chihiro. Laboratory of Environmental Mycology, Graduate School of Agriculture, Kyoto University, Kyoto, 606-8502, Japan. poet50@kais.kyoto-u.ac.jp. **Identification and characterization of NRPS-like gene *EmMaa1* in *Exserohilum monoceras*.**

Exserohilum monoceras is a fungal pathogen of *Echinochloa* weed species, and now used as a bioherbicide for them in Japanese paddy fields. However, as yet little has known about its virulent factor or pathogenic mechanism. We have investigated the functions of non-ribosomal peptide synthetases (NRPSs) in *E. monoceras*, for that some peptide compounds are characterized as host specific toxins in phylogenetically related species (e.g. *Cochliobolus* and *Alternaria*). Using PCR with degenerate primers we have obtained several putative NRPS gene fragments of *E. monoceras*. In this study, we report the cloning and functional analysis of *EmMaa1*. Sequence analysis of *EmMaa1* revealed that it was a homolog of *Maa1* originally identified in *Leptosphaeria maculans* genome, and also indicated that *EmMaa1* was an NRPS-like gene with single adenylation domain, thiolation domain but no condensation domain. In *L. maculans* *Maa1* disruptant was identical to wild type with respect to growth and pathogenicity. Targeted disruption of *EmMaa1* also resulted in no phenotypic alteration in pathogenicity between mutant and wild type. However *EmMaa1* disruptant showed relatively slower growth and more aerial hyphae production than wild type. This suggests *EmMaa1* is not involved in the pathogenicity of *E. monoceras*, but has something to do with its vegetative growth. poster

Mouriño-Pérez, Rosa R.¹*, Roberson, Robert W.² and Bartnicki-García, Salomón¹. ¹Department of Microbiology and Division of Biological Experimentation & Application, Center for Scientific Research of Ensenada (CICESE), Km. 107 Ctra. Tijuana-Ensenada, Baja California, México, ²School of Life Sciences, Arizona State University, Tempe, AZ, USA. rmourino@cicese.mx. **Dynamics of the microtubular cytoskeleton during growth and branching in *Neurospora crassa*.**

By confocal microscopy, we analyzed microtubule (MT) behavior during hyphal growth and branching in a *Neurospora crassa* strain whose microtubules were GFP-tagged. Images were assembled in space and time for a precise picture of the 3-D organization of the microtubular cytoskeleton and a clear view of its dynamics. Cytoplasmic MTs are mainly arranged longitudinally along the hyphal tube. Straight segments are rare; most MTs show a distinct helical curvature with a long pitch and a tendency to intertwine with one another to form a loosely braided network throughout the cytoplasm. This study revealed that the microtubular cytoskeleton of a hypha advances as a unit: as the cell elongates, it moves forward by bulk flow. Nuclei appeared trapped in the microtubular network and were carried forward in unison as the hypha elongated. During branching, one or more MTs became associated with the incipient branch. Branch MTs are continuous with a set of adjacent MTs from the parent hypha. Originally transverse in the incipient branch, MT orientation turned longitudinal as the branch elongated and the

length and number of MTs increased. Although a full account of the origin of branch MTs remains an open question, the recorded evidence indicates both bulk insertion of parent-hypha MTs as well as de novo extension by anterograde polymerization. The latter conclusion was supported by FRAP studies showing evidence of MT assembly in the growing tip of the developing branch. Nuclei entered the branch entrapped in the advancing network of MTs. contributed presentation

Mozley-Standridge, Sharon* and Porter, David. Department of Plant Biology, University of Georgia, Athens, GA 30602, USA. emozley@plantbio.uga.edu. **Chytrid fungi in the "Nowakowskiella" clade (order Chytridiales, phylum Chytridiomycota): determination of generic limits using 18S small and 28S large ribosomal subunit nuclear gene sequences.**

Multiple classification schemes exist for members of the Chytridiomycota based on different uses of morphological, developmental, and ultrastructural characters. Addition of molecular characters from multiple genes has provided support for the most recent order level classification scheme based primarily on ultrastructural characters. For chytrid fungi in the recently identified "Nowakowskiella" clade (order Chytridiales), ultrastructure has been sampled for several genera with few distinguishing differences between genera. On the other hand, combined analysis of 18S and 28S ribosomal genes has provided a better idea of generic limits for members of the clade and can be used as a framework for comparison of morphological and developmental characters in a phylogenetic context. Included in this study are suggestions for taxonomic revision of *Allochytridium*, *Catenochytridium*, *Cladochytrium*, *Nowakowskiella*, *Nephrochytrium*, and *Septochytrium*. poster

Mueller, Gregory M. Department of Botany, The Field Museum, Chicago, IL 60605, USA. gmueller@fieldmuseum.org. **Overview of fungal biogeography.**

Until recently, the prevailing notion was that ancient organisms with easily dispersed spores like fungi would be broadly distributed with few interesting biogeographic patterns. There were exceptions, such as the distribution of *Cytaria* with *Nothofagus* and potential temperate East Asian / Eastern North American disjuncts. For the most part, distribution patterns were listed only as secondary information in monographs or discussed with a pathogen's host distribution. Pairing studies to implement the biological species concept necessitated sampling multiple individuals over the entire geographic range for the first time, and the repeated discovery of discrete, genetically isolated populations of supposedly cosmopolitan species sparked an interest in understanding biogeographic patterns of fungi. Rigorous testing awaited the development of molecular data and the computational techniques and theory needed to analyze the data. We now know that many species of fungi have discrete distribution ranges, often congruent with patterns seen in animals and plants. While much progress has been made, numerous questions remain, including the importance of the role spores play in dispersal, the constraints or drivers which determine diverse organismal distribution patterns, and the age-specific information that is provided by distribution patterns for fungal clades. symposium presentation

Mullaney, Edward J.* and Ullah, Abul H. J. Southern Regional Research Center, ARS, USDA, New Orleans, LA 70124, USA. emul@srcc.ars.usda.gov. **Conservation of an eight-cysteine motif in fungal histidine acid phosphatases.**

A survey of known amino acid sequence of a number of fungal histidine acid phosphatases (HAP) has revealed a conserved eight-cysteine motif (8CM). Typically, conserved amino acid sequences have been associated with catalytic or structurally essential components for the functionality of a protein. The catalytic mechanism of HAPs is known, and no cysteines are involved in catalysis. Therefore, the HAP's 8CM appears to have been conserved because they are involved in the formation of key disulfide bridges. X-ray crystallographic data of *Aspergillus niger* myo-inositol hexakisphosphate and a few other fungal HAPs have revealed that all eight cysteines are components of disulfide bridges. While 3-D molecular models for all fungal HAPs are not available, the unique pattern of conservation supports a similar critical role for these amino acids in all these HAPs sequences. A different 8CM has recently been reported from a survey of plant databases. Almost 500 different plant polypeptides having various functions all shared a unique cysteine motif, which like the HAP cysteines has no catalytic function. Rather, it appears that both the plant and the HAP 8CM have been conserved to provide the essential tertiary structure of the molecule for maintaining both a functional active site and a substrate-binding domain. poster

Munkacsí, Andrew¹* and May, Georgiana². ¹Plant Biological Sciences Graduate Program, University of Minnesota St. Paul, MN, USA. ²Department of Ecology, Evolution and Behavior, University of Minnesota, USA. munk0009@umn.edu. **A phylogenetic and population genetic reconstruction of *Ustilago maydis*.**

Maize was domesticated in southern Mexico from a teosinte 10,000 years ago, and exported to the United States 2,000 years ago and to South America 5,000 years ago. *Ustilago maydis* only infects maize and the teosintes. We tested the popular hypothesis that *U. maydis* originated on a teosinte in Mexico and followed maize as maize was traded to new locations. We collected DNA sequence

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data from four protein-coding genes (*ATP6*, *COX3*, *GPD3*, *EF-1alpha*) of select Ustilaginales taxa, and via phylogenetic analyses, identified *Sporisorium reilianum* and *Ustilago scitaminea* as the closest relatives of *U. maydis*. The DNA sequence data were then translated and aligned among taxa representative of major Eukaryote lineages, which allowed for phylogenetic-based tests of time to infer whether *U. maydis* arose before maize. Coeladogenesis analyses between the plant and fungal phylogenies were also conducted to deduce whether the number of substitutions in *U. maydis* could have occurred since maize arose. To identify the number of populations of *U. maydis* along the initial migration route of maize, we genotyped 1000 collections of *U. maydis* teliospores from the United States, Mexico, and South America using 10 microsatellite markers. Five populations of *U. maydis* were identified, one which was comprised solely of isolates on one teosinte population in Mexico. The divergence times of the five populations will be compared to the dates estimated for the domestication and movement of maize. contributed presentation

Muraguchi, Hajime^{1*}, Kamada, Takashi² and Yanagi, O. Sonoe¹. ¹Akita Prefectural University, Department of Biotechnology, Shimoshinjo nakano, Akita, 010-0195, Japan, ²Okayama University, Department of Biology, Tsushima Naka 3-1-1, Okayama, 700-8530, Japan. muraguchi@akita-pu.ac.jp. **BAC contig map of *Coprinus cinereus*.**

We constructed a BAC library of *Coprinus cinereus* strain Okayama-7, which was used for the genome project by the Broad Institute and its draft sequence assembly is now available. We performed fingerprint analysis of the BAC clones using the Image and FPC software and used the draft sequence assembly to assign the BACs to the chromosomes. The Image software produces 'sizes' files, which contain information about the restricted fragments from the BAC clones. Analysis of this information by the BACFinder assigned part of the BAC clones to a specific region in the published sequence. For the BACs that could not be assigned by the BACFinder, we performed end-sequencing to map them on the published sequence. FPC contigs could be anchored on the published sequence, if only part of their component clones could be assigned to specific regions in the published sequence. These lines of information about BAC positions on the sequence was put together in an Excel file and processed by a macro program written in Visual Basic for Applications (VBA) to depict the positions of BAC clones on the chromosomes. The BAC tiles on the chromosomes will facilitate gene cloning by complementation of a mutant phenotype with a BAC clone following genetic mapping of the mutation onto an existing linkage map of RAPD markers. poster

Murakami, Yasuaki^{1*}, Hadano, Eiji and Hadano, Atsuko². ¹Oita Mushroom Research Inst., Akamine 2369, Bungo-Ohno, Oita 879-7111, Japan, ²Ryogo 325, Oita 870-0883, Japan. murakami-yasuaki@pref.oita.lg.jp. **Re-discovery of luminescent mushroom, *Pleurotus eugrammus* Mont. Dennis var. *radiciocolus* Corner in southern islands of Japan.**

In 2004, *Pleurotus eugrammus* (Mont.) Dennis var. *radiciocolus* Corner was re-discovered. The species was first recognized by Yata Haneda. He collected the species in Yap, Palau, and Borneo islands. Seiichi Kawamura named it *Pleurotus lumailustris* Kawamura according to the specimens collected by Y. Haneda though he did not make description of the species. Finally Y. Haneda gave information and specimens to Dr. E.J.H. Corner who used to collect mushrooms together with Y. Haneda in Malaya. E.J.H. Corner (1981) regarded the species as a variety of *Pleurotus eugrammus*. This species was discovered in Ishigaki and Iriomote islands, Japan by Gensuke Miyagi of Ryukyu University in 1962. We could re-discover the species in the same area in 2004. Characteristics of species are as follows. Pileus 10-30mm in diameter, surface smooth, white with greenish brown spots. Flesh thin, white, taste and smell none. Gills decurrent, white. Stipe short, white. Spores white in mass, oblong, 4-6 x 3-5 μ m. Luminescent in whole basidiocarp. Dead tree trunk is proposed as a new habitat of this variety. poster.

Murata, Yoshiteru, Sano, Ayako*, Nishimura, Kazuko and Kamei, Katsuhiko. Department of Pathogenic Fungi, Research Center for Pathogenic Fungi and Microbial Toxicoses, Chiba University, 1-8-1, Inohana, Chuo-ku, 260-8673 Chiba, Japan. Aya1@faculty.chiba-u.jp. **The first isolation of *Arthrographis kalrae* from the oral cavity of a canine in Japan.**

Arthrographis kalrae (Tewari et Macpherson) Sigler et Carmichel 1976 is an environmental saprophyte fungus, and is one of the causative agents of emerging fungal infections in human and animals. *Arthrographis kalrae* causes not only superficial but also deep mycoses. The fungal disease is found world widely. We isolated a white mycelial fungus from the oral cavity of an 11-year-old sprayed female dog during a survey of oral fungal flora of house-holding pets. The colony on potato dextrose agar at 25C was white cottony producing arthroconidia, blastoconidia and chlamyospores, with a light brown glabrous part at the center, and a slight yellowish reverse. The isolate could grow at 37C while failed at 42C. The DNA sequences of internal transcribed spacer (ITS) 1-5.8S-ITS2 and D1/D2 regions of ribosomal RNA genes were identical more than 98 and 99% in homology with those of *A. kalrae* type strain deposited in GenBank as AB116536 and AB116544, respectively. In conclusion, this is the first report on *A. kalrae* isolation from Japan. poster

Murayama, Y. Somay^{1*}, Hanazawa, Ryo², Shibuya, Kazutoshi² and Ubukata, Kimiko¹. ¹Laboratory of Infectious Agents Surveillance, Kitasato Institute for Life Sciences, Kitasato University, 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan, ²Department of Surgical Pathology, Toho University School of Medicine, 6-11-1 Ohmorinishi, Ohta-ku, Tokyo 143-8541, Japan. somay@lisci.kitasato-u.ac.jp. **A case of invasive pulmonary aspergillosis caused by combined infection of *Aspergillus fumigatus* and *A. niger* confirmed by both histopathological examination and *in situ* hybridization.**

Invasive aspergillosis has become one of the serious opportunistic infection in patients with induced immunosuppression. In the paper, a case of pulmonary aspergillosis caused by two different species is described with a detailed histopathological and molecular biological examination. A patient, 68 year-old, male, showed the diffuse interstitial shadow in his both lungs on chest X ray photograph with a progression of respiratory distress after finishing of chemotherapy for his advanced lung cancer in the right lower lobe. Whereas a steroid pulse therapy was carried out, his status was not recovered. He was dead in pulmonary failure. The consequent autopsy study revealed a widespread invasive pulmonary aspergillosis in both lungs. To confirm the diagnosis, *in situ* hybridization employing three different probes; 18S rRNA gene (panfungal), alkaline proteinase gene (ALP; *Aspergillus* spp.-specific), and *Afut1* (*A. fumigatus*-specific), was carried out on paraffin sections from the lesions of both lungs. Filamentous fungi appeared in the right lesion were positive with both ALP and *Afut1* probes, but those from the left indicating characteristics of *A. niger* confirmed by consequent histological examination exhibited a negative signal with *Afut1* probe. Consequently, the patient was diagnosed as invasive aspergillosis caused by combined infection of *A. fumigatus* and *A. niger*. poster

Murrin, Faye. Department of Biology, Memorial University of Newfoundland, St. John's, NL A1B 3X9, Canada. fmurrin@mun.ca. **The tip of the iceberg: a five-year study of mycorrhizal biodiversity in the boreal forest of coastal Newfoundland.**

Terra Nova National Park (TNNP) is Canada's most easterly national park and it protects the northern remnants of the ancient Appalachian Mountains alongside the Atlantic ocean. While increasing environmental stress and the accompanying changes in biodiversity are expected to result in a decline in world-wide ecosystem stability, predictions from studies on global warming suggest that TNNP temperatures will remain more stable than those of other Canadian parks due to its maritime location. To lay the groundwork for future quantitative ecological studies on change in the park, we completed a five-year inventory of ectomycorrhizal basidiomycetes by examining fruiting bodies from sites dominated by black spruce (*Picea mariana*), balsam fir (*Abies balsamea*) and red pine (*Pinus resinosa*). Over 150 species have been identified from 10 sites and approximately 1290 collections over the study period. Species of the families Cortinariaceae, Russulaceae and Boletaceae were the most commonly encountered. We present here a summary of our findings including the first regional key to the species. The information acquired during this study contributes to climate-change inventory and biodiversity concerns, defines previously unidentified natural resources in the area, and lays the groundwork for future quantitative ecological studies on the macrofungal communities in Terra Nova National Park. It also adds significantly to our knowledge of the mushroom flora of the island of Newfoundland. poster

Nakagiri, Akira* and Okane, Izumi. Biological Resource Center (NBRC), Department of Biotechnology, National Institute of Technology and Evaluation, 2-5-8, Kazusakamatari, Kisarazu, Chiba 292-0818, Japan. nakagiri-akira@nite.go.jp. **Phylogeny, taxonomy and ecology of *Halophytophthora spinosa* (marine Oomycetes).**

Halophytophthoras are Pythiaceae oomycetes inhabiting marine and brackish water mangroves as the first colonizer of the submerged fallen mangrove leaves. Among *Halophytophthora* species, two varieties of *H. spinosa* (var. *spinosa* and var. *lobata*) are unique in forming a dehiscence tube from semi-papillate apex of the spined zoosporangium. In the phylogenetic tree of Oomycetes based on 28S rDNA D1D2 sequences, the varieties of *H. spinosa* clustered with *Sapromyces* (Rhipidiales, Rhipidiomycetidae *sensu* Dick, 2001) apart from other species of the genus *Halophytophthora* nesting within the Peronosporomycetidae, which suggests transferring the species to a new genus. Each of the two varieties is distinct in the manner of zoospore release, shape of dehiscence tube and condition for inducing release. Difference was also found in the substrate preference, i.e., var. *spinosa* has been isolated only from submerged fallen leaves of *Rhizophora mangle*, but var. *lobata* from those of various mangroves, which is reflected in their different geographical distribution. Molecular data (G + C mol%, sequences of 28S rDNA D1D2, ITS1 and ITS2) as well as the phenotypic characters showed a large gap between the two varieties, which may warrant that their taxonomic status should be ranked up to the species level. poster

Nakamura, Tomoyuki^{1*}, Akiyama, Yukihito¹ and Kawagishi, Hirokazu². ¹Applied Fungi Institute, IBI Corporation, 7841 Anayama-cyo, Nirasaki-shi, Yamanashi 407-0263, Japan, ² Faculty of Agriculture, Shizuoka University, 836 Ohya, Shizuoka 422-8529, Japan.

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n-tomo@eps4.comlink.ne.jp. **Genetic analysis and various pharmacological effects in *Phellinus linteus*.**

Phellinus linteus (Berk. et Curt.) Teng is a polypore of the hymenomycetes family and a heart-rot fungus occurring especially in groves of *Morus bombycis* Koidz. This fungus is known as a Chinese medicine, Souou, and the mycelia of the fungus show antitumor activity. However, their other pharmacological effects have not been known yet. Then, at first, genetic analysis of naturally occurring *P. linteus* was performed, and this species was identified as *P. linteus*. Next, we found some biological activities in the extract of the mycelia and succeeded in isolation and structure-determination of the active principles in the extract. Scavenging activity of superoxide anion radicals of the extracts was detected. As a result, caffeic acid was isolated as an antioxidant. Anti-allergic activity of the extracts was demonstrated by *in vivo* assay using NC/Nga/mice. Anti-tumor activity of the extracts using Sarcoma 180/mice, *p.o.* were examined. As a result, an alpha-1,3-glucan-protein complex was obtained as the most active component. poster

Nakashima, Chiharu. Faculty of Bioresources, Mie University, Mie pref. 514-8507, Japan. chiharu@bio.mie-u.ac.jp. **Cercosporoid fungi in subtropical islands of Japan and pacific countries.**

The genus *Cercospora* was established by Fresenius in 1863. Most of the species are known plant pathogens causing leaf spots of plants and are considered host specific. This hypothesis led to the description of a very large number of species (more than 3,000). It is common knowledge that countries of the Pacific Rim region have a diverse plant and fungal flora. Cercosporoid fungi that are strongly dependent on the host plant are expected to be diverse in these areas, too. However, research on Cercosporoid fungi in Asian countries including Japan has not been sufficient in comparison with Europe. This study discusses issues related to clarifying the diversity of Cercosporoid fungi in the Pacific rim countries (subtropical Islands of Japan, Thailand, Indonesia and Fiji) by Deighton*, using new criteria based on morphological characteristics that were revised by Braun. As a result, numerous new species have been found with the indigenous and cultivated plants in these countries. In addition, an expansion of the distribution of Cercosporoid fungi has been observed in the region in recent years, following the movement of the plants. symposium presentation

Narimatsu, Maki. Iwate Prefectural Forestry Technology Center, 560-11, dai3-chiwari, Kemuyama, Yahaba-cho, Shiwa-gun, Iwate 028-3623, Japan. m-narimatsu@pref.iwate.jp. **Development of inoculation method of *Tricholoma matsutake* to the fine roots in the forest.**

Tricholoma matsutake (Matsutake) is an ectomycorrhizal fungus and the most valuable wild mushroom in Japan. Cultivation of Matsutake by an artificial method is very difficult, and hence an effective method for construction of ectomycorrhizae of Matsutake has been needed. The objective of this study is to develop a new inoculation method of Matsutake to the fine roots of the living pine trees in the forest. Method: Mycelia of Matsutake grew for 30 days on the chemical fiber sheets which were soaked in modified MYPG liquid media (patent pending). The sheets covered with the mycelia were used for inoculation to the fine roots of young Japanese red pine (*Pinus densiflora*) trees. The root samples collected after 6 months from inoculation were used for microscopic observation and for PCR using Matsutake specific ITS primers. Results: Dark brown-black colored and dichotomously branched ectomycorrhizae with hartig-net shaped like a palm were observed by microscopy. From 33% of root samples and hyphae collected near roots, a specific DNA fragment of Matsutake was detected. These results indicate that this method is effective for inoculation of Matsutake to the forest. poster

Neda, Hitoshi*. Matsunosato, Tsukuba, Ibaraki, 305-8687, Japan. neda@ffpri.affrc.go.jp. **Agaricoid fungi in subtropical islands of Japan.**

The Nansei islands (Kagoshima pref. and Okinawa pref.), and the Bonin islands (Tokyo met.) are lying at 24°–29° north latitude (about the same as the Midway Islands and Florida). The Nansei islands are near to the Asian Continent and the main islands of Japan, while the Bonin islands are 1000 km south of Tokyo and far from the continent and other islands. Agaricoid fungi (Agaricales sensu Singer 1986) in the area have been studied since the middle of the 19th century. Two hundred and forty species have already been reported. Since 1984, I have collected fungal specimens in the area, adding 29 species to the list. 1) Forty-seven species (17%) are regarded as tropical of which 33 reach their northern limit on these islands. 2) There are 196 saprophytic and 66 mycorrhizal species in the area. 3) Only 8 mycorrhizal species (5.2%) occur on the Bonin islands. These mycorrhizal species are also distributed on the Nansei islands. They associated with *Pinus luchuensis* Mayer. This pine is not native to the Bonin islands, but was introduced from the Nansei islands. 4) The fruiting season of temperate species in the area is November to March (winter). The temperature of this period is equal to the temperature in spring and autumn on the Japanese main islands. However, 109 species have not been collected again in the area for the last 60 years. Many species are treated as doubtful species or misidentified records. Further, there are many unnamed species. symposium presentation

Nelsen, Matthew P. and Gargas, Andrea*. Department of Botany, University of Wisconsin-Madison, Madison, WI 53706-1381, USA. mpnelsen@wisc.edu. A

phylogenetic assessment of the use of secondary chemistry as a taxonomic character in the lichen genus *Thamnolia* (Icmadophilaceae).

Differences in secondary chemistry are frequently used to separate species in lichen taxonomy. It has been hypothesized that *Thamnolia* contains either two chemically distinct species (baeomycesic and squamatic acids vs. thamnolic acid) or a single chemically variable species. In an effort to assess the value of secondary chemistry as a species delimiter, we sequenced the ITS and partial IGS, RPB2 and mtLSU regions and tested whether chemical variants formed monophyletic groups. Based on our analyses, the two chemical variants do not form monophyletic groups, suggesting that secondary chemistry is not a good indicator of phylogenetic relationships in *Thamnolia*, and therefore, not a valid character for species delimitation. Furthermore, we investigate whether these loci provide evidence for cryptic recombination in this asexual lineage. poster

Nishimura, Kazuko^{1*}, Kamei, Katsuhiko¹, Sano, Ayako¹, Miyaji, Makoto¹ and Kawai, Genshiro². ¹Research Center for Pathogenic Fungi and Microbial Toxicosis, Chiba University. 1-8-1 Inohana, Chuo-ku, Chiba 260-8673, ²Food Research Laboratory, Asashimatsu Foods Co., Ltd., 1008 Dashina, Iida, Nagano, 399-2561 Japan. nishik@faculty.chiba-u.jp. **Mating behavior of *Schizophyllum commune* isolated from patients with bronchopulmonary mycosis in Japan.**

The basidiomycetous fungus *Schizophyllum commune* has recently emerged as a new causative agent of human mycosis. Since 1994, we have identified 34 isolates from 32 patients with allergic bronchopulmonary mycosis and related diseases as being the basidiomycete. Most isolates formed white to buff, felt or floccose colonies with a methane-like odor and a few formed a slow-growing, light brown, leathery colony on PDA plates. Hyphae were partially tuberculate in 30 isolates and bizarrely zigzag in two of the non-tuberculate four. Eight of the 34 isolates developed clamped hyphae, reproduced small, gilled, fan-like and/or medusoid or coralloid basidiocarps and dikaryotized the monokaryotic testers. Hyphae of the other 26 were not clamped and made monokaryotic testers develop clamped hyphae and then basidiocarps. Most of them were also dikaryotized by dikaryotic testers. Based on these results, the eight clamped and the 26 non-clamped were the dikaryon and monokaryon of *S. commune*, respectively. Although one monokaryotic and ten dikaryotic isolates of *S. commune* were reported as pathogens mainly for nasal sinusitis or sinus fungus ball from western countries, it is likely that basidiospores of the fungus are inhaled to cause bronchopulmonary infection. Both mono- and dikaryons of *S. commune* are important as one of the pathogens for bronchopulmonary mycosis. poster

Niwa, Rieko*, Osaki, Mitsuru and Ezawa, Tatsuhiro. Graduate School of Agriculture, Hokkaido University, Sapporo, 060-8589, Japan. niwarieko@hotmail.com. **Assessment of germination of *Plasmiodiphora brassicae* resting spore in rhizosphere of the host by nuclear-cell wall double staining.**

Clubroot disease of cruciferous plants is caused by a soil-borne pathogen, *Plasmiodiphora brassicae*, and difficult to control because the pathogen survives in soil for a long time as resting spore. We found disease-suppressive soil in the experimental field of Nagoya University and suggested that an increase in soil pH by accumulation of Ca might involved in suppression of the disease. The objective of the present study is to understand the mechanism of the disease suppression at the levels of germination. In the primary infection process, the resting spore germinates in rhizosphere of the host plant and loses nucleus due to the release of primary zoospore which infects the root hair of the host plant. We have established methods to collect the resting spores from the rhizosphere and bulk soils and to assess the presence or absence of nucleus in the spore by nuclear staining. The influence of soil pH on the spore germination and root hair infection was investigated. poster

Norvell, Lorelei L. PNW Mycology Service, Portland OR 97229-1309, USA. lnorvell@pnw-ms.com. **A return to the elusive *Phaeocollybia*: I. Key to western North American species.**

Phaeocollybia (*Cortinariaceae*) has ~80 species worldwide and has been reported from Eurasia, Australasia, and the Americas. Subterranean pseudorhizae, brown ornamented basidiospores, and mycelial tibiiform diverticula characterize the genus, while spore & cheilocystidial morphology, presence of clamp connections, pileipellis structure, pseudorhizal form, and syringaldazine reactivity help diagnose species. The ectomycorrhizal agaric genus reaches its highest diversity and abundance in the temperate rainforests of northern California, Oregon, Idaho, Washington, and British Columbia. From 1991-2004, over 1300 collections of 24 species were made in the region. During the past decade, the USA Northwest Forest Plan flagged *P. attenuata*, *P. californica*, *P. dissiliens*, *P. fallax*, *P. gregaria*, *P. kauffmani*, *P. lilacifolia*, *P. olivacea*, *P. oregonensis* (+ its synonym, *P. carmanahensis*), *P. piceae*, *P. pseudofestiva*, *P. scatesiae*, *P. sipet*, and *P. spadicea* as endemics or old-growth indicators; Oregon Natural Heritage will soon list the rare *P. radicata*. The naming of 9 new species (*P. ammiratii*, *P. benzokauffmani*, *P. luteosquamulosa*, *P. phaeogaleroides*, *P. pleurocystidiata*, *P. redheadii*, *P. rufiflipes*, *P. rufotubulina*, *P. tibiikauffmani*) since 1998 underscores the need for a workable key to the species of the Pacific Northwest. poster

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MSA ABSTRACTS

Novick, Rachel S. Yale University, Department of Ecology and Evolutionary Biology, New Haven, CT 06511, USA. rachel.novick@yale.edu. **Phylogeny and cospeciation in cedar rust fungi.**

The cedar apple rusts (*Gymnosporangium* spp. and associated form genera) are a group of about 60 parasitic species that have a broad range of hosts, life histories, and degrees of specialization. Most species alternate between telial and aecial hosts, while some either complete the entire life cycle on the telial host or reproduce asexually by repeating aecia or uredinia. Species infect from one to thirteen host genera. Little is known about the evolutionary relationships within this group, so that the following questions, relevant to parasite evolution in general, remain unanswered: First, how has cospeciation with multiple hosts impacted parasite speciation? Second, are asexual species evolutionary dead ends? Third, does specialization tend to be a derived trait and if so, can this trend be reversed? To address these questions, I am building a molecular phylogeny for the cedar apple rusts. I am using reconciliation analysis to compare parasite and host phylogenies and ancestral state reconstruction methods to trace the evolution of life cycles and specialization. My results to date suggest that both cospeciation and host-switching have played some role in the evolution of cedar apple rusts, that while asexual species may be derived, it seems possible to regain life stages that have been lost, and that a trend toward host specialization may exist in this group. symposium presentation

O'Donnell, Kerry¹*, Weber, Nancy S.², Rehner, Stephen A.³ and Rooney, A. P.¹ ¹NCAUR-ARS-USDA, Peoria, IL 61604, USA, ²Oregon State University, Corvallis, OR, USA, ³USDA/ARS/BARC, Beltsville, MD, USA. odonnekl@ncaur.usda.gov. **Molecular systematics and phylogeography of the true morels (*Morchella*).**

True morels (*Morchella*) are among the most highly-prized macrofungi collected by mycophiles during the spring in temperate regions of the northern hemisphere. The few species recognized in field guides are generally thought to be cosmopolitan in their distribution, but this assumption has never been tested rigorously. To address this question, we used multilocus DNA sequence data from parts of three loci [ITS and 28S rDNA, translation elongation factor (1- α), and RNA polymerase (RPB1)] to investigate species limits and their biogeography. Maximum parsimony analysis of the combined data provided a nearly fully resolved phylogeny in which a monophyletic *Morchella* comprised two sister clades: *Esculenta* (yellow-tan-grey morels) and *Elata* (black morels). Ancestral lineages of the *Esculenta* and *Elata* clades are confined to Eastern and Western North America, respectively. This, coupled with the finding that North America was most phylogenetically diverse area studied, indicates that the ancestral area of *Morchella* may be North America. The high continental endemism observed within *Morchella* suggests that long distance dispersal via airborne ascospores is rare, thereby facilitating historical biogeographic studies within this genus. symposium presentation

O'Reilly, Bernadette D.* and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. oreilly.bern@students.uwlax.edu. **The exploitation of mycorrhizal association to induce fruiting in *Morchella esculenta*.**

Morel mushrooms are notoriously difficult to produce commercially. This may be because *Morchella* sp. are facultatively mycorrhizal, an association that is difficult to establish and maintain in the laboratory. It has been shown that sclerotia are the key intermediate in the fruiting of morels. Past cultivation methods attempted to go directly from mycelia to sclerotia to fruiting bodies without exploiting the mycorrhizal stage. Elm seeds were asexually germinated, then planted in low nutrient soil and allowed to grow to several centimeters in height. Compatible *Morchella* strains were inoculated in an adjacent container of low nutrient soil. The mycelium from the low nutrient soil grew across the gap, crossing into the container with the photosynthetic elms. According to the 1988-1989 patents of Ower *et al.*, when morel mycelia inoculated in low nutrient soils reaches nutrient rich media, the nutrients will be translocated back to the nutrient-starved original mycelium, and sclerotia will be formed in this low nutrient soil. Previous experiments showed certain microbes have potential to induce fruiting in morels. These microbes were added to the sclerotia, the containers separated and the morels exposed to fruiting conditions. Pictures and data will be presented at the meeting. contributed presentation

Obase, Keisuke, Tamai, Yutaka*, Yajima, Takashi and Miyamoto, Toshizumi. Laboratory of Forest Resource Biology, Research group of Forest Resource Science, Division of Environmental Resources, Graduate school of Agriculture, Hokkaido University, Kita-9, Nishi-9, Kita-ku, Sapporo city, Hokkaido, 060-8589, Japan. oba-suke@for.agr.hokudai.ac.jp. **Ectomycorrhizal fungal flora on the volcano Usu, deforested by 2000 eruptions.**

We investigated underground ectomycorrhizal (ECM) fungal community associated with pioneer woody plant species in devastated areas derived from 2000 eruption on Mt. Usu, using ECM morphotyping and molecular analysis. About 4 ha research site around several craters where natural vegetation was disappeared just after 2000 eruption, was established. From June to September 2003 and 2004, we randomly selected 1 to 12 seedlings of each of all woody plant species observed there, and a part of lateral roots of them were sampled. Presence or absence of mycorrhizal association in each woody plant species was observed.

And then, we morphotyped ectomycorrhizas in roots of ECM woody plant species by morphological characterizations and PCR-RFLP analysis of the ITS region of the rRNA gene. ECM colonization and frequencies were examined. All morphotypes classified by both approach was subject to identification by sequence. Almost all seedlings of 8 woody plant species, including *Larix*, *Salix*, *Betula* and *Quercus*, were associated with ECM fungi. Number of ECM morphotypes per woody plant species was 1-6 and per seedling was 2 in average. 17 ECM fungi were identified in total and 11 of them were observed in only one woody plant species. *Laccaria*, *Hebeloma* and Thelephoraceae were observed many woody plant species and presented high relative colonization. poster

Ocasio-Morales, Roberto G.¹*, Tsopelas, Panagiotis² and Harrington, Thomas C.¹ ¹Department of Plant Pathology, Iowa State University, Ames IA 50011, USA, ²NAGREF-Institute of Mediterranean Forest Ecosystems Terma Alkmanos, 11528 Athens, B. O. 14180, Greece. rocasio@iastate.edu. **Microsatellite analysis suggests that *Ceratocystis platani* (?*C. fimbriata* f. *platani*) was recently introduced to Greece from Italy.**

Ceratocystis platani (?*C. fimbriata* f. *platani*) is a plant pathogenic fungus that causes cankers and wilt disease in *Platanus* species. It has caused significant economic losses in plantations in the USA and in ornamental plantings in Europe and the USA. Earlier studies of genetic diversity showed that the eastern USA population of *C. platani* is native to that region and that the southern European population was from an introduction of a single genotype through Italy. Recently, the disease was reported from southwestern Greece (Messinia Prefecture), where it is killing oriental plane (*Platanus orientalis* L.) of different ages and sizes along rivers and streams and in residential areas. Alleles of eight polymorphic microsatellite markers of 15 isolates from 13 locations in Greece were analyzed. Of the 15 isolates, 14 had the same microsatellite alleles as the most common genotype from Italy. The evidence suggests that the pathogen was introduced from Italy, most likely on live plant material. One Greek isolate showed a new microsatellite allele, probably due to a recent mutation. poster

Ogawa, Yoshio¹* and Tokumasu, Seiji². ¹College of Pharmacy, Nihon University, Narashinodai, Funabashi, Chiba 274-8555, Japan, ²Sugadaira Montane Research Center, University of Tsukuba, Sanada, Nagano 386-2201, Japan. y-ogawa@pha.nihon-u.ac.jp. **Correlation between genetic variations of nrDNA and morphological variations in *Umbelopsis ramanniana*.**

Umbelopsis ramanniana is one of the most widespread species in this genus and distributes from the polar regions to tropical regions. Furthermore, shapes of its sporangiospores are divergent and vary from subglobose to rounded oblong. These ecological and morphological characteristics of *U. ramanniana* imply that the genetic variations occur in the sequences of the nuclear ribosomal DNA (nrDNA) in isolates of the fungus. For the isolate of *U. ramanniana* collected from Japan and Europe, internal transcribed spacer (ITS) regions and D1/D2 regions of 28S nrDNA were sequenced and the results were analyzed related to the morphological characteristics. Neighbor joining and parsimony analyses on the sequences showed that these isolates were split into several intra-specific groups. Precise examination of the morphological characteristics showed that the isolates of those respective groups were different each other in length/width ratios of the sporangiospores. The present study suggests that the variations in the sequences of the nrDNA of *U. ramanniana* correlate with those in length/width ratios of sporangiospores. *Umbelopsis ramanniana* seems to be an assemblage of genetically and morphologically divergent strains. poster

Ohkubo, Masaru^{*1}, Abe, Jun-ichi P.¹, Shibata, Hisashi², Kakishima, Makoto¹ and Nakamura, Toru¹. ¹University of Tsukuba, Graduate School of Life and Environmental Science, 1-1, Tennoudai 1 chome, Tsukuba, Ibaraki 305-8572, Japan, ²Yamanashi Forest Research Institute, 2290-1, Saishouji, Masuho, Yamanashi 400-0502, Japan. ave@sakura.cc.tsukuba.ac.jp. **Hypogeous ascomycetes *Tuber* spp. in eastern Japan.**

The distribution of hypogeous ascomycetes *Tuber* spp. and their habitat were studied in different locations in eastern Japan for a better understanding of their ecology. In 2004, two study sites each in Saitama, Kanagawa and Tochigi Pref. and one each in Ibaraki and Yamanashi Pref. were chosen, for a total of eight sites. *Tuber indicum* was found in all locations except for Ibaraki and one of two Tochigi sites, making it the most geographically widespread species studied in eastern Japan. *T. oligospermum* was restricted to Ibaraki Pref. alone. In one of the Tochigi sites, an unknown species (*Tuber* sp. B) was found and is described as followed: Ascomata excavate, grayish brown to orange-brown, warted. Warts 1.1-2 mm across, pyramidal, flattened at the apex. Asci (1-) 2-7(-8)-spored. Ascospores 18-33 x 13-20 μ m, spiny-reticulate. Spines 3-11 μ m high. Although this *Tuber* sp. B resembled *T. pseudoexcavatum* based on the above morphological features, it differed in having smaller warts. Based on our and previous investigations, *T. indicum* seems to be dominant throughout Japan. Further, this fungus was found under *Carpinus japonica*, *C. laxiflora*, *Quercus myrsinaefolia*, *Q. dentata* and *Q. serrata*. The range of soil pH was 5.9-7.4, soil water percentage ranged between 18-44%. These results may reveal that *T. indicum* is adapted to a wide range of different environmental conditions. poster

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MSA ABSTRACTS

Okada, Gen^{1*}, Takematsu, Akiko¹, Ogawa, Hiroyuki², Wakabayashi, Keiko², Goto, Keiichi², Attili de Angelis, Derlene³ and Canhos, Vanderlei P.³ ¹Microbe Division / Japan Collection of Microorganisms, RIKEN BioResource Center, 2-1 Hirosawa, Wako, Saitama 351-0198, Japan, ²Laboratory of Beverage Development, Food Research Laboratories, Mitsui Norin Co., Ltd., 223-1 Miyahara, Fujieda, Shizuoka 426-0133, Japan, ³Andre Tosello Foundation, Rua Latino Coelho, 1301, Campinas 1889, SP, Brazil. okada@jcm.riken.jp. **Undescribed anamorphic basidiomycete producing white synnemata and dikaryotic blastoconidia.**

White synnematous hyphomycete with basidiomycetous affinities was collected and isolated from dead inflorescence of palm (*Phoenix rupicola*) in Sao Paulo, Brazil on October 1993 (Specimens GO 1675 & 1676; cultures JCM 12448 & 12449). Synnemata were white and indeterminate with parallel stipe and loose fertile zone. Hyphae were hyaline, septate, and lacking clamp connections. Conidia were produced basally in dry chain, hyaline, non-septate, subglobose, and dikaryotic. Conidiogenesis superficially looks like those of the anamorphs of *Botryobasidium*: (e.g., *Haplotrichum*, *Parahaplotrichum*), though the hyphae and conidia were completely hyaline and thin-walled. Based on 18S and 28S (D1/D2) rDNA sequence data, however, the fungus probably belongs to the Sebaciniales phylogenetically far from *Botryobasidium*. Although its phylogenetic position has not yet decided clearly, we think that a new genus should be established for this undescribed anamorphic basidiomycete. poster

Okane, Izumi* and Nakagiri, Akira. Biological Resource Center (NBRC), Department of Biotechnology, National Institute of Technology and Evaluation, 2-5-8, Kazusakamari, Kisarazu, Chiba 292-0818, Japan. okane-izumi@nite.go.jp. **Studies on xylariaceous fungi from plant leaves and other substrates.**

Xylariaceous fungi are known mainly as decomposers of angiosperms, and a few species have been reported to be plant pathogens. Some species have been found to live within living plant tissues, and considered as important endophytes. In this study, we surveyed diversity of the xylariaceous fungi from symptomless leaves of various vascular plants. Some strains were obtained from the fruit bodies on the pieces of wood, soil, and the nests of termites to investigate the wide range of xylariaceous fungi. We carried out taxonomical studies on isolates from leaves and other substrates by investigating morphology and molecular phylogeny. As a result, a sequence analysis based on the ITS regions of rDNA showed that the isolates from leaves were separated into two groups, namely *Nemania* and *Xylaria* clades, and two isolates from a nest of termite were included in the former clade. A cluster in the *Nemania* clade consisted of many isolates from various plants (evergreen-woody plants, orchids and pteridophytes) and two strains of *Nemania bipapillata*, whose data were derived from DNA database. All isolates from leaves in the cluster were similar in their colony appearances on media. These results suggested that most of the xylariaceous fungi inhabiting various vascular plants belong to the genus *Nemania* and *Xylaria*. It was confirmed that some species behave as not only saprophytes, but also endophytes. Fresh plants and termite-living environment must be important materials to investigate on biodiversity of xylariaceous fungi. poster

Okazaki, Koei* and Niwa, Osami. Kazusa DNA Research Institute, 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan. kokazaki@kazusa.or.jp. **Molecular mechanisms for the conjugate division: analysis using the fission yeast dikaryon.**

Many basidiomycetes use clamp connection to maintain the two different nuclei during mitotic division. However, the dikaryons of some basidiomycetes such as *Ustilago maydis* and ascogenous hyphae of the filamentous ascomycetes do not form the clamp connection. This suggests that basic mechanisms for the conjugate division underlie before the clamp connection have evolved. We found that the fission yeast *Schizosaccharomyces pombe* could propagate as a dikaryon in a manner to guarantee maintaining heterokaryon. Using this model organism and video microscopy, we are now analyzing the mechanism for nuclear pairing, communication between the two mitotic spindles, coupling of the two mitotic spindles to the single cytokinetic ring, and other mechanisms for dikaryon. We identified the minus-end directed kinesin as a motor protein responsible for nuclear pairing. Without this kinesin, the binucleated cell underwent mitosis and septation at two distant places, which produced a central binucleated cell and two monokaryons at the ends. The septation initiation network (SIN) proteins are known to localize asymmetrically at the spindle poles. Distribution of Cdc7, a member of SIN, suggested that the two spindles are arranged in a head-to-head orientation. poster

Okuda, Toru^{1*} and Bennett, Joan W.² ¹Tamagawa University Research Institute, 6-1-1 Tamagawa-Gakuen, Machida, Tokyo 194-0041, Japan, ²Department of Cell and Molecular Biology, Tulane University, New Orleans, LA 70118, USA. torula@lab.tamagawa.ac.jp. **Exhibition of Dr. Jokichi Takamine sponsored by Sankyo Co., Ltd. (APPENDIX to Special Symposium on Industrial Mycology).**

Filamentous fungi in the genus *Aspergillus* are involved in our daily life. Koji mold, *A. oryzae* is used for producing miso, soy sauce and sake by growing the fungus on steamed rice. Currently, *Aspergillus* is applied to the production of various enzymes and organic acids. Enzymes are particularly essential for industrial production of cereal food, detergents, forest products, textiles, feed, and beverages. Dr. Jokichi Takamine for the first time applied the enzymatic activity of

A. oryzae to modern industry. A hundred years ago, he recognized the diastatic activity of *A. oryzae*, patented the first microbial enzyme in USA, and launched Taka-diastase. The substance is still sold today as a digestive aid. He then hired Dr. Uenaka and together they isolated adrenalin (epinephrine), the first modern wonder drug. Dr. Takamine became increasingly wealthy, developed strong trade positions in several Japanese industries, and founded three companies including Sankyo Co. in Tokyo. As a private diplomat between US and Japan, he helped defray the cost of the now famous cherry trees planted in Washington, D. C. On this commemorative occasion of MSA/MSJ Joint Meeting, it is worthwhile to exhibit a number of historical photographs and materials related to Dr. Takamine, which are reproduced by the courtesy of The Great People of Kanazawa Memorial Museum in Kanazawa and Sankyo Co., Ltd., Japan. symposium presentation

Ono, Yoshitaka. College of Education, Ibaraki University, Mito, Ibaraki 310-8512, Japan. herb-iba@mx.ibaraki.ac.jp. **Life cycle and host specificity in *Ochropsora* and *Aplopsora* species.**

Species in rust genera *Aplopsora* and *Ochropsora* are presumed to have a macrocyclic heteroecious life cycle; however, only *O. ariae* and *O. kraunhiae* have been proven to be heteroecious. None of *Aplopsora* species is known its full life cycle. Species in the two genera produce a sessile, one-celled, thin-walled probasidium (teliospore), producing a metabasidium without dormancy; and the two genera differ only in the mode of metabasidium production (germination of teliospores). However, the difference in the mode of metabasidium production is a matter of degree of apical elongation of the probasidium during maturation. Thus, the taxonomic separation of the two genera has been questioned. In addition, three species in a poorly circumscribed genus *Cerotelium* have been suggested to belong to *Aplopsora* because of the similarity in probasidium morphology and a mode of metabasidium production. These necessitate the revision of classification of *Aplopsora*, *Ochropsora* and their allies with species distinction by their life cycle and host specificity, i.e., circumscribing species by the reproductive isolation. Artificial inoculation experiments over ten years have revealed macrocyclic, heteroecious nature of the life cycle in two *Aplopsora*, one *Ochropsora* and one *Cerotelium* species in addition to two *Ochropsora* and one *Cerotelium* species, whose full life cycle was previously known. Thus, one *Ochropsora* and two *Cerotelium* species produces spermogonia/aecia on species of *Corydalis/Dicentra* (Fumariaceae), while spermogonia/ aecia of two *Aplopsora* and two *Ochropsora* species are produced on *Anemone* (Ranunculaceae). Each of the species has unique spermogonia/aecial host species. These results indicate that seven reproductively isolated species constitute a single genus with two subgroups that have differentiated in the spermogonia/aecial host preference during the course of evolution. symposium presentation

Orihara, Takamichi^{1*}, Sawada, Fumiko², Ikeda, Shiho³, Yamato, Masahide³ and Iwase, Koji³. ¹ Dept. For. Sci., Fac. Agr., Kyoto Pref. Univ., 1-5 Shimogomahangicho, Sakyo-ku, Kyoto 606-8522, Japan, ²2-11-12 Tsujido-taiheidai, Fujisawa 251-0044, Japan, ³Biol. Environ. Inst., KANSO Technos Co., Ltd., 8-4 Ujimatsumi, Uji 611-0021, Japan. h_berg_f@io.ocn.ne.jp. **Taxonomical reconsideration of *Octaviania columellifera* (Japanese name, jagaimo-take) and its phylogenetic relationship to Boletaceae.**

The semi-sectoid truffle-like fungus, *Octaviania columellifera* (Japanese name, jagaimo-take, literally means potato fungus) is an endemic species in Japan. It was originally described by Dr. Yoshio Kobayashi in 1936, but, since then, has not been authentically described. On the other hand, it has been suspected that the species which was described under the name of *Octaviania asterosperra* (Japanese name, Kurama-no-jagaimo-take, literally means potato fungus in Kurama) since 1972 in Japan corresponds to *O. columellifera*. It was clarified in this study that these two species are identical, by examining ITS regions of the nuclear rDNA as well as other chemical, morphological and ecological features. It was also revealed that the species is phylogenetically close to some groups in Boletaceae. Moreover, *O. columellifera* was placed in different lineage from other *O. spp.* in Boletales. In case of chemical reactions, the change of the length of the spore ornamentation in various reagents, which was previously described in *Octaviania cyanesces* (Trappe & Castellano, 2000), was also recognized, although this finding might be inconsistent to the results of molecular analysis. poster

Osono, Takashi. Laboratory of Forest Ecology, Graduate School of Agriculture, Kyoto University Kyoto 606-8502, Japan. fujijun@kais.kyoto-u.ac.jp. **Role of phyllosphere fungi of forest trees in the development of decomposer communities and decomposition processes of leaf litter.**

The phyllosphere is the living leaf as a whole and includes the surface (phylloplane) and internal tissue. Phyllosphere fungi include epiphytes and endophytes that colonize the phylloplane and internal tissue, respectively, of living leaves. Phyllosphere fungi have been reported from a variety of plants including forest tree species. They have been studied intensively in terms of their ecological relationships with plants and other microorganisms on living leaves. In contrast, the ecology of phyllosphere fungi on leaf litter has received little attention even though they occur on various litters at initial stages of decomposition. At the leaf death, phyllosphere fungi can persist and have the advantage of gaining access to

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substrates in leaf litter prior to fungi that colonize after litter fall. Thus, phyllosphere fungi may have certain roles as saprophytes in the development of decomposer fungal communities and in decomposition processes of leaf litter. In this study, I review the role of phyllosphere fungi of forest trees, mainly temperate ones, in the development of decomposer communities and decomposition processes of leaf litter. Emphasis is placed on (1) occurrence of phyllosphere fungi on leaf litter, (2) origin and development of early colonizers, (3) succession and persistence until later stages of decomposition, (4) substrate utilization and decomposing ability, and (5) roles in the accumulation and decomposition of soil organic matter in forests. It is clear from the review that several of the common phyllosphere fungi are primarily saprotrophic litter-decomposing fungi and play significant roles in community development and decomposition processes. poster

Ota, Yuko^{1*}, Hattori, Tsutomu¹ and Banik, Mark T.² ¹Hokkaido Forestry Research Institute, Higashiyama, Koshunai-cho, Bibai, Hokkaido 079-0198, Japan, ²Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan. yuota@ffpri.affrc.go.jp. **Characterization of the *Laetiporus sulphureus* complex in Japan using phylogenetic analyses, morphological characteristics and single spore isolate incompatibility.**

Phylogenetic analyses, morphological studies and incompatibility tests were conducted to define the taxa in the Japanese *Laetiporus sulphureus* complex. Phylogenetic analyses based on the nucleotide sequences of the internal transcribed spacer (ITS) regions of the nuclear ribosomal DNA and beta-tubulin gene suggest that Japanese *Laetiporus* spp. are divided into three groups (A-C). Single spore isolates from groups A, B and C were incompatible each other as well as with single spore isolates of 4 North American *Laetiporus* species. However, some inter-continental single spore combinations showed unclear reactions. ITS sequence analysis supports the differentiation of the Japanese groups from the North American species. A European population of *L. sulphureus* is also clearly distinct from the Japanese groups based on DNA analyses. Collections with in each Japanese group share similar morphological characteristics and host range (conifers vs. hardwoods). contributed presentation

Otsuki, Kunihiko^{*}, Okada, Kazuhisa¹, Kusumoto, Koji² and Sandou, Hideyuki³. ¹Wakayama Research Center of Agriculture, Forestry, Fisheries, Forestry Experiment Station, 1504-1, Ikuma, Kamitonda-cho, Nishimuro-gun, Wakayama pref., Japan, ²Kusumoto Koji Photo Office, 2059, Shingu, Shingu City, Wakayama pref., Japan, ³Wakayama Prefectural Research Center of Environment and Public Health, 3-3-45, Sunayama-Minami, Wakayama City, Wakayama pref., Japan. otsuki_k0001@pref.wakayama.lg.jp. **Ecological characterization of the luminous fungus *Mycena lux-coeli* in a southern part of the Kii peninsula of Japan.**

Mycena lux-coeli is a fascinating luminous fungus that has been found in several discrete areas of Japan, e.g. the Izu islands, the Ogasawara islands, a southern part of the Kii peninsula and Kyushu. We have investigated ecological characteristics of the species in a southern part of the Kii peninsula, the largest area of its habitat distribution. The area of distribution extends about 80 kilometers along the coast, including one city and seven towns. The main habitats are coastal broad-leaved forests with big trees of *Castanopsis cuspidata* ver. *sieboldii*. The hosts are mostly *Castanopsis cuspidata* ver. *sieboldii* and exceptionally *Elaeocarpus sylvestris* ver. *Ellipticus* for two cases. The fruiting period in the years 2002 - 2004 was from May through October. At the beginning of the rainy season in early summer, numerous immature fruitbodies appeared suddenly and grew up in unison. Then many fruitbodies grew up one after another in succession. The immature fruitbodies opened their pilei and grew up into mature fruitbodies in 1 or 2 days. The period of the immature or mature fruitbody emitting relatively strong light was about 2 to 3 days. Thereafter the fruitbodies withered up in a period of 2 to 4 days while the light was getting weaker gradually. poster

Padamsee, Mahajabeen¹, Celio, Gail J.¹, Dentinger, Bryn C.¹, McLaughlin, David J.¹, Hibbett, David S.², Lutzoni, François³, Spatafora, Joseph W.⁴ and Vilgalys, Rytas J.³. ¹Dept. of Plant Biology, University of Minnesota, St. Paul, MN 55108, USA, ²Biology Dept., Clark University, Worcester MA, USA, ³Dept. of Biology, Duke University, Durham NC 27708, USA, ⁴Dept. of Botany & Plant Pathology, Oregon State University, Corvallis, OR, USA. pada0003@umn.edu. **Phylogenetic exploration and data-mining of the AFTOL non-molecular database.**

Subcellular characters have been shown to be phylogenetically informative at phylum and lower taxon levels. Septa, polar structures, and nuclear characters from the Assembling the Fungal Tree of Life non-molecular database were used to evaluate evolutionary relationships between selected taxa. Our methods involved separate analyses of septa and nucleus associated characters within and among phyla. We explored various effects of using character manipulations and constraint trees on the tree topology and measurements. Using septal characters in an analysis of the Basidiomycota, character selection was effective in reconstructing the known phylogeny based on molecular data. These analyses allow us to explore character evolution and help reevaluate character coding and description. contributed presentation

Palmer, Jonathan M.* and Volk, Thomas J. Dept. Biology, University of Wisconsin - La Crosse, La Crosse, WI 54601, USA. palmer.jona@students.uwlax.edu. **Molecular characterization of mycorrhizal 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. 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 fungi associated with the chestnuts. 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?" 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" sites. Over 700 collections have been identified to species, about 75 being putatively mycorrhizal with chestnut. Since many mycorrhizal fungi rarely fruit, a below-ground study of the mycorrhizal community was done using PCR/RFLP analysis and DNA sequencing techniques. 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*, both otherwise unknown from western Wisconsin. These data will be used in efforts to return chestnuts to their former dominance in their native Appalachian range. poster

Park, Chae H.* and Jung, Hack S. Department of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea. minervas@snu.ac.kr. **Phylogeographic study of *Irpex lacteus* using ITS sequences and f-AFLP markers.**

Irpex lacteus is one of the most common polypores and is widely distributed as a saprotroph on dead wood in Korea. For the analysis of *I. lacteus* populations from five provinces and three islands of Korea, genetic structure and phylogeographic pattern were examined using nuclear ribosomal ITS1-5.8S-ITS2 sequences and f-AFLP fingerprinting markers. Phylogenetic trees constructed by ITS sequences and f-AFLP markers respectively indicated that the isolates of *I. lacteus* from different geographical habitats were not so variable. The present geographical distribution of *I. lacteus* was dominantly influenced by the dispersal of basidiospores, while ecological habitat differences did not seem to be so important in determining the genetic structure of the species. Although two phylogenetic trees showed incongruent topologies each other, the tree generated by f-AFLP markers developed more resolution for the phylogenetic relationships of *I. lacteus* isolates, suggesting that the analysis using multiple loci is more useful to discriminate closely related taxa. poster

Park, Ju-Young^{1*}, Inaba, Shigeki¹, Manguwardoyo, Wibowo², Kanti, Ati³, Widayastuti, Yantyati³ and Ando, Katsuhiko¹. ¹NITE Biological Resource Center (NBRC), Department of Biotechnology, National Institute of Technology and Evaluation (NITE), 2-5-8, Kazusakamatari, Kisarazu-shi, Chiba Pref., 292-0818, Japan, ²University of Indonesia, Depok 16424, Indonesia, ³Indonesian Institute of Science, Jalan Ir. H. Juanda 18, Bogor 16002, Indonesia. paku-juyoung@nite.go.jp. **New and interesting fungi isolated in Indonesia.**

Tropical rain forests contain more than a half of the total species of the world's entire biota, despite that they cover only 7% of the Earth's terrestrial surface. In Indonesia, tropical rain forests occupy 57% of its territory, resulting in Indonesia to possess the world's second largest tropical forest with rich biodiversity. To study microbial diversity in Indonesia, our institute has been collaborating with three Indonesian governmental institutes and two universities, namely BPPT, DEPTAN, LIPI, IPB and UI. In 2004, 51 soil and 35 litter samples were collected from three sampling sites in Indonesia, i.e. Purwodadi Botanical garden (East Java), Cibinong Science Center and its surrounding (West Java), and Bukit Sari Botanical Garden (Jambi, Sumatera). A total of 1,203 fungi were isolated from the soil samples using the dilution and UV irradiation methods and 160 fungi were isolated from the litter samples using the manipulation method, which were classified into 76 and 19 genera, respectively. Some of the new and interesting fungi are: (1) *Bloxamia* sp. which is characteristic of showing holoblastic development of thick-walled and dark brown chlamydospores; (2) *Xenobotrytis acaducospora*; (3) two interesting *Aspergillus* spp. showing 97% homology with *A. anthodesmisi* in the D1/D2 region and characteristic of having big vesicles (up to 92.0 μm) and stipes trailed by mycelia. poster

Park, Keun A.*, Kim, Kung M. and Jung, Hack S. Department of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea. minervas@snu.ac.kr. **Phylogenetic analyses of *Piptoporus* based on ITS and 28S ribosomal DNA sequences.**

To study the phylogenetic relationships of *Piptoporus*, ITS and partial 28S regions of nuclear ribosomal RNA genes were sequenced from nine species of *Piptoporus* and ten related species. Phylogenetic analyses indicated that *Piptoporus* was heterogeneous and its members were divided into six distinct groups. *Piptoporus betulinus* (the type species of *Piptoporus*) was clustered with the

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members of *Fomitopsis* (*F. pinicola*, *F. palustris*, *F. feei*, *Piptoporus cretaceus*, *P. portentosus*, *P. officinalis* and *P. elatinus*) formed one major *Piptoporus* group, which was positioned paraphyletically to *Antrodia* spp. including *A. albida* (the type species of *Antrodia*). *Piptoporus soloniensis* was clustered with *A. serialis* and *A. variiformis* at the basal position of *Fomitopsis* group composed of *F. africana*, *F. dochmia* and *F. spraguei*. *Buglossoporus pulvinus* with the synonyms of *P. paradoxus* and *P. quercinus* was clustered with *F. africana* of *Fomitopsis* group. *Piptoporus australiensis* formed one group with *Spongipellis spumeus* and *A. sitchensis*. *Piptoporus pseudobetulinus* and *P. betulinus* have similar microscopic morphologies but phylogenetic positions of two species were different, showing that rot type could be an important character to discriminate between morphologically confused species. Although more taxonomic and phylogenetic studies with additional related species need to be achieved, our phylogenetic results apparently indicated that *Piptoporus* was composed of artificial taxa and certain species need to be newly transferred into several different genera like *Antrodia*, *Fomitopsis*, *Polyporus* and *Datronia*. poster

Parrent, Jeri L.*; Mao, Alison and Vilgalys, Rytas J. 139 Biological Sciences Bldg. Dept. of Biology. Duke University. Durham, NC 27708, USA. jlp13@duke.edu. **Guess who's coming to dinner? Actively foraging mycorrhizal fungi and their contribution to soil carbon storage.**

Although our understanding of ectomycorrhizal fungal (EMF) communities is greatly enhanced by the wealth of root tip and fruiting body surveys, knowledge regarding contributions of particular EMF species to host nutrient acquisition and hyphal biomass in soil remains limited. In this study, we used an ingrowth core approach designed to exclude roots and saprophytes to sample actively foraging EMF hyphae and ask: 1) Is community structure surveyed using this method congruent with that sampled from colonized root tips; 2) Is EMF biomass in soil greater in plots enriched in CO₂? To address these questions, cores were buried in control and elevated CO₂ plots at the FACTS-I research site, Duke Forest, NC. Clone libraries were constructed and ITS and LSU sequences were generated. Ergosterol was measured to estimate EMF hyphal biomass in cores and soil. This method successfully selected against saprophytes; only 5% of samples were non-mycorrhizal. Community composition overlapped between root tip and core samples, but several species abundant in cores were rarely encountered as mycorrhizas, suggesting incongruence between colonization and foraging abilities of certain species. Ergosterol content highlights the dominance of fungi in the soil microbial community, and the importance of considering EMF hyphal biomass when examining C dynamics and storage associated with increased CO₂. contributed presentation

Peay, Kabir G.¹*, Beneman, Chris² and Kennedy, Peter G.² ¹Division of Ecosystem Sciences, UC Berkeley, CA 94720, USA, ²Dept. of Integrative Biology, UC Berkeley, CA 94720, USA. kpeay@nature.berkeley.edu. **The role of ectomycorrhizal fungi in mediating drought stress during the early establishment of *Pinus muricata*.**

In the classic view of the mycorrhizal symbiosis plants provide photosynthetically derived sugars to the fungi in exchange for nutrients such as nitrogen or phosphorus. However, in coastal California, *Pinus muricata* (Bishop Pine) regenerates in a post-fire setting where nutrients are not limiting. In this setting, water may be the most important limiting resource as plants experience significant water deficit during summer establishment. In this study, we tested the ability of ectomycorrhizal (EM) fungi to protect seedlings of *P. muricata* from experimentally induced drought. We use a fully factorial design including four EM species *Rhizopogon occidentalis*, *R. salebrosum*, *R. evadens*, and *Tomentella subilliacina* and two drought treatments. We measured seedling photosynthetic rates, water use efficiency, above and below ground biomass, ¹³C stable isotope composition and % EM colonization. These measures are related to the ability of ectomycorrhizae to confer drought avoidance or tolerance on their host. contributed presentation

Pennanen, Taina* and Korkama, Tiina. Finnish Forest Research Institute, Vantaa Research Centre, P.O.B. 18, FIN-01301 Vantaa, Finland. taina.pennanen@metla.fi. **Structure of ectomycorrhizal communities and development of Norway spruce seedlings.**

The impact of tree genotype on the susceptibility to diseases is well established in plant pathology. However, it is unclear if formation ectomycorrhizal (ECM) symbiosis is dependent on a host tree genetic background. We utilized a clonal Norway spruce (*Picea abies*) trial planted on the clear-cut spruce forest site to investigate how the genetic variation of a host tree influences the ECM species composition and soil microbial communities. Eight healthy spruce clones were selected to represent various growth performances since outplanting in 1994. We found that structures of the ECM communities were different in slowly and fast growing spruce clones. Further, Shannon diversity index correlated positively to the growth of the trees, which was rather due to the greater evenness of the ECM communities in the fast growing clones than differences in ECM richness. In a same way, PLFA analysis indicated differences in humus microbial community structure between fast and slowly growing spruce clone plots. Our results imply that genetic variation of host tree may have a role in generating patchiness of microbial communities in boreal forest soils typically dominated by a single tree

species but thousands of ECM species. A selection of ECM isolates found to be common in well growing spruces is utilized in studying the early development of the spruce seedlings. symposium presentation

Perry, Brian A.*; Hansen, Karen and Pfister, Donald H. Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA. bperry@oeb.harvard.edu. **Phylogenetic relationships in the Pyrenomataceae (Ascomycota, Pezizales).**

Of the families of the Pezizales, the Pyrenomataceae (including Otideaceae) remains the least well studied or characterized. 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 Pyrenomataceae include taxa with a wide diversity of both morphological features and nutritional modes. Recent molecular phylogenetic studies indicate that the Pyrenomataceae is part of a lineage composed of the Sarcosomataceae, Sarcoscyphaceae, Ascodesmidaceae, and Glaziellaceae. The goal of this investigation is to generate a multiple gene phylogeny of the Pyrenomataceae 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 and RNA polymerase II sequence data will be presented and discussed. contributed presentation

Petersen, Ronald H.* and Hughes, Karen W. University of Tennessee, Knoxville, TN 37996-1100, USA. repete@utk.edu. **The Pacific and its rim: crossroads of mushroom distributions.**

Early identification of macrofungi from Pacific Ocean landmasses came from the capitals of Europe (i.e. the British Empire, French Indochina, Dutch East Indies, etc.). After the age of empires, national mycology began, but mushroom taxonomy has been subjugated to applied mycology (i.e. plant pathology, commercialization of edibles, etc.). Nonetheless, some patterns of macrofungal distributions have been elucidated, namely Gondwanaland, pantropical, east Asia/eastern North America and the like. To these can be added the following: pantropical (*Pleurotus djamor* and its variations), eastern North America/ tropical Pacific landmasses (*Gloeocantharellus*, *Ramaria zipellii*, *Sarcodon atroviride*), north Pacific rim (*Flammulina rossica*), endemic northeast Asia (*Pleurotus citrinopileatus*, *Oudemansiella brunneomarginata*, *Pleurotus abieticola*), Gondwanaland (*Conchomyces bursaeformis*, *Flammulina* with stratified pileus context) and endemic South Pacific (spiny-spored *Clavaria* species). Mushrooms with unexplained distributions include *Pleurotopsis longinqua*, Chilean *Flammulina velutipes*, and the apparent California halophiles *Flammulina velutipes* var. *lupinicola* and darkly pileate *Pleurotus ostreatus*. Thus, the Pacific Ocean landmasses and the Pacific Ocean rim include a myriad of ecomiches, climates, altitudes and island biogeographies, and support a macrofungal mycota just as varied. symposium presentation

Peterson, Stephen W.¹*, Vega, Fernando E.², Posada, Francisco² and Nagai, Chifumi³. ¹USDA, 1815 N. University St., Peoria, IL 61604, USA, ²IBL, USDA, Beltsville, MD 20705, USA, ³HARC, Aiea, HI 96701, USA. peterssw@ncaur.usda.gov. ***Penicillium coffeae*, a new endophytic species isolated from a coffee plant and its phylogenetic relationship to *P. fellutanum*, *P. thiersii* and *P. brocae* based on parsimony analysis of multilocus DNAs.**

Penicillium coffeae is described as a novel endophyte isolated from a *Coffea arabica* L. plant in Hawaii. The species is slow growing with short, vesiculate, nonverticillate conidiophores. Phylogenetic analysis using three loci shows that *P. coffeae* forms a strongly supported clade with *P. fellutanum*, *P. charlesii*, *P. chermesinum*, *P. indicum*, *P. phoeniceum* and *P. brocae*. Phenotypically these species are quite similar but can be distinguished. The EF-1alpha; gene from *P. fellutanum*, *P. charlesii*, *P. chermesinum* and *P. indicum* lack introns, *P. coffeae* and *P. phoeniceum* have a previously unknown intron at codon 20 and *P. brocae* and *P. thiersii* isolates have a single intron at codon 26. The most parsimonious interpretation of intron changes on the strongly supported phylogenetic tree requires the gain of a novel intron at position 20 and loss of intron 26 to arrive at the current distribution of introns in this gene. This is one of only a few examples of intron gain in genes. poster

Pfaff, Bridget L.^{1,2}* and Volk, Thomas J.² ¹University of Wisconsin La Crosse and ²Gundersen Lutheran Healthcare, 1900 South Avenue (C03-004), La Crosse, WI 54601, USA. blpfaff@gundluth.org. **Water, water everywhere: preliminary studies in medical document recovery following water infiltration.**

It is important to prevent damage by fungal growth on paper since paper medical records must be saved for a minimum of ten years in most states. Documents are often stored in basements and other areas prone to water and fungal damage due to space limitations. Water intrusion is commonly caused by clean water from sprinkler-heads and plumbing fixtures, and dirty water from sewer back-ups and river flooding, followed by varying degrees of mold growth. The need for practical document recovery is pertinent not just in health-care facilities, but in libraries and government agencies as well. Current recommendations for

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document remediation after flooding indicate freeze-drying as the ideal remediation; however, it is unclear if this poses subsequent exposures to destructive fungal spores. Although mold damage is visually obvious and often generates odors, it is unclear which fungi are commonly associated with document damage. This study proposes to evaluate recovered documents for the presence of fungal DNA to determine the fungal species that commonly cause damage. Control documents were compared to documents recovered from a river-flooded clinic and a clinic that was infiltrated by clean water. This study intends to determine which species elicit damage and if there are more effective remediation techniques. poster

Porras-Alfaro, Andrea*, Dvorachek, William H. and Natvig, Donald O. Department of Biology, The University of New Mexico. Albuquerque, NM 87131-0001, USA. aporras@unm.edu. **Fungal community associated with roots of two closely related grasses, *Bouteloua gracilis* and *B. eriopoda*.**

Studies of fungi associated with grasses have focused largely on above-ground tissues. However, fungal endophytes are also recovered from roots. This study examined fungi associated with roots of two dominant grasses, *Bouteloua gracilis* (blue grama) and *B. eriopoda* (black grama), collected from the Sevilleta National Wildlife Refuge in New Mexico. In part, this study reflects a long-term interest on the part of plant ecologists to understand the distributions of these two grass species. Plants were collected from areas where either one or the other grass was dominant, as well as from an area where the two species coexist. The diversity of fungi associated with roots was surveyed by direct PCR, cloning and sequencing of the internal transcribed spacer (ITS) of nuclear rDNA. Clones were sequenced and grouped using phylogenetic analysis. Among 140 clones sequenced, we observed more than twenty fungal species representing diverse basidiomycetes and ascomycetes. The fungi observed included several that appear to be closely related to species reported as either endophytes or plant pathogens. Most of these have not been reported previously from arid grasslands. There were no significant differences between the fungal groups associated with blue and black grama. The ecological significance of this diverse fungal assemblage is a subject ripe for additional study. poster

Porras-Alfaro, Andrea^{1*} and Bayman, Paul². ¹Department of Biology, The University of New Mexico, Albuquerque, NM 87131-0001, USA, ²Department of Biology, University of Puerto Rico, P.O. Box 23360, San Juan, PR 00931-3360, USA. aporras@unm.edu. **Mycorrhizal fungi of *Vanilla*: specificity, phylogeny and effects on seed germination and plant growth.**

Mycorrhizal fungi (MF) are essential for the germination of orchid seeds. However, the degree of specificity of this symbiosis and the effects of fungi on orchid growth are poorly understood. It is unclear if all MF are functionally equivalent for orchids, or if some are better than others at promoting seed germination and plant growth. The aims of this research were to: 1) identify the MF in *Vanilla*, 2) determine if these relationships are general or specific, and 3) compare the effects of different MF on germination and plant growth. Cultured and uncultured MF were identified by sequencing the internal transcribed spacer region of nuclear rDNA (nrITS) and part of the mitochondrial ribosomal large subunit (mtLSU), and by counting number of nuclei in hyphae. Our results show that at least three genera of *Rhizoctonia*-like fungi colonize *Vanilla*: *Ceratobasidium*, *Thanatephorus* and *Tulasnella*. We found differences (consistent and significant) in the effects of fungi on seed germination and plant growth. Effects of MF were related to phylogeny. A clade of *Ceratobasidium* had a consistently positive effect on plant growth and seed germination. However, isolates in another clade of *Ceratobasidium* exhibited contrasting effects on plant growth and germination. poster

Pringle, Anne¹ and *Vellinga, Else C.² ¹Department of Organismic and Evolutionary Biology, Harvard University, Cambridge MA, 02138, USA, ²Department of Plant and Microbial Biology, University of California, 111 Koshland Hall, Berkeley, CA 94720-3102, USA. apringle@berkeley.edu. **Last chance to know? Using literature to explore the biogeography and invasion biology of the Death Cap mushroom *Amanita phalloides*.**

The biogeography of fungi is poorly understood. Using the literature of *Amanita phalloides* as a case study we illustrate the utility and difficulty of using the historical record to describe the biogeography of ectomycorrhizal (EM) fungi and to establish a species as introduced or invasive. *A. phalloides* is deadly; it is a notorious fungus and a rich medical and mycological literature records the mushroom's distribution in North America. The earliest American record of *A. phalloides* dates to 1832, and four different authors identify the species as growing in California, Minnesota, Pennsylvania, North Carolina, and Maryland before 1910. But by mid-century field guides list *A. phalloides* as rare on the West Coast and absent from the East Coast. In modern American literature *A. phalloides* is described as a recently introduced and currently invasive species. The contradictions raise two questions, first, is *A. phalloides* an exotic to North America? Second, can the historical record be used to delineate the native distribution of any EM fungus? poster

Rajguru, Satyendra N.^{1*}, Margaritescu, Simona², Moncalvo, Jean-Marc², Silberman, Jeffrey¹ and Stephenson, Steven¹. ¹University of Arkansas, Department of Biological Sciences, Fayetteville, AR 72701, USA, ²Royal Ontario Museum and

University of Toronto, 100 Queens Park, Toronto, Ontario M5S2C6, Canada. srajgur@uark.edu. **Molecular phylogeny of plasmodial slime molds based on EF1A sequences.**

Myxomycetes (also known as plasmodial slime molds or myxogastriids) constitute one of the three major subgroups of the Mycetozoa. These organisms are characterized by a plasmodial stage, which under favorable conditions develops into mature sporophores. Previous phylogenetic studies of myxomycetes have been based on ultrastructure or morphological characters. Very little data exist on their molecular phylogeny. The phylogenetic relationships among the various taxa are being investigated using EF-1 alpha sequences from the type species within each described genus. Genomic DNA has been isolated from specimens obtained from moist chamber cultures or field collections. "Slime mold" specific primers have been designed to amplify EF-1 alpha sequences. Phylogenetic analyses are being carried out to assess the higher-order molecular phylogeny of the taxa for which sequences are available. (Research supported in part by two grants from the National Science Foundation.) contributed presentation

Rajguru, Satyendra N.^{1*}, Silberman, Jeffrey¹, Stephenson, Steven¹ and Landolt, John². ¹University of Arkansas, Department of Biological Sciences, Fayetteville, AR 72701, USA, ²Shepherd University, Department of Biology, Shepherdstown, WV 25443, USA. srajgur@uark.edu. **Genetic variation of *Dictyostelium rosarium* based on ITS sequences: a preliminary investigation.**

Dictyostelids (also called cellular slime molds) are members of the Mycetozoa that are commonly found in the soil as free living amoeba. These amoebae aggregate to form multicellular pseudoplasmodia and then fruiting bodies. *Dictyostelium rosarium*, commonly found in "soil" of cave environments, is a morphologically distinctive species characterized by the presence of lateral sori. The degree of genetic variation that may exist among *D. rosarium* isolates from different localities is unknown. In the present study, we investigated the extent of genetic variation that exists for *D. rosarium* isolates obtained from diverse geographical localities. These isolates were cultured and DNA extracted using a 5% chelex solution. Primers were designed to amplify both ITS regions of rDNA. Sequence analysis indicated that *D. rosarium* contains an ITS1-5.8S-ITS2 region of approximately 900bp. Preliminary results indicate some degree of variation among the isolates. Sequencing of additional isolates is currently ongoing. (Supported in part by two grants from the National Science Foundation.) poster

Redhead, Scott A.^{1*}, Cushion, Melanie T.², Frenkel, Jacob K.³ and Stringer, James R.² ¹ECORC, Agric. & Agri-Food Canada, Ottawa, ON, K1A 0C6, Canada, ²Univ. Cincinnati College of Medicine, 231 Albert Sabin Way, Cincinnati, OH 45267, USA, ³Univ. New Mex., 1252 Vallecita Dr, Santa Fe, NM 87501, USA. redheads@agr.gc.ca. ***Pneumocystis* nomenclature.**

The enigmatic fungal genus *Pneumocystis*, causal agent of so-called 'opportunistic' pneumonia (PCP) in immunocompromised individuals, has defied classification. Its initial discovery led it to be included in the lifecycle of the protozoan *Trypanosoma cruzi* causing Chaga's Disease. After the two were separated, *Pneumocystis* was still believed to be a protozoan, hence its name was covered by the zoological code. Only two codes of nomenclature, botanical and zoological, cover eukaryotic organisms resulting in bizarre nomenclatural situations when the two kingdom system is applied to microorganisms, e.g. rumen chytrids, mycetozoa, microsporidians. After molecular based phylogenies revealed new relationships, such organisms can 'switch' kingdoms, resulting in cascading nomenclatural changes. *Pneumocystis* exemplifies an extreme case because of the combination of 'misclassification' in the 'animal' kingdom and its initial inclusion in the lifecycle of a protozoan, leading to the description of a genus, *Schizotrypanum*, and a species, *T. cruzi*, based upon elements from both kingdoms. Reduced, yet highly characteristic morphology and obligate host-specific parasitism, including human hosts, have challenged classification at the subgeneric level leading to debate concerning the name for the human pathogen, *P. jirovecii*, often called *P. carinii*. Nomenclatural resolutions are detailed. poster

Rehmeyer, Cathryn¹, Kusaba, Motoaki³, Li, Weixi², Staben, Chuck², Birren, Bruce⁴, Dean, Ralph⁵ and Farman, Mark¹. ¹Department of Plant Pathology and ²Department of Biology, University of Kentucky, Lexington, KY, USA, ³Faculty of Agriculture, Saga University, Saga, Japan, ⁴The Broad Institute of Massachusetts Institute of Technology and Harvard University, Cambridge, MA, USA, ⁵North Carolina State University, Raleigh, NC, USA. cjrch2@uky.edu. **Structure and dynamics of *Magnaporthe grisea* telomeres.**

We describe the structural organization of all fourteen chromosome ends in the reference strain of the plant pathogenic fungus *Magnaporthe grisea*. Bioinformatic analysis of data from the *M. grisea* Genome Project enabled us to identify telomere-containing fosmid clones, which we then sequenced to completion. Aside from yeast, this represents the only complete characterization of telomeres in any organism. The most terminal portion of the *M. grisea* chromosomes exhibit a significant level of genetic redundancy; 11 ends have the same basic organization, consisting of a single RecQ helicase gene embedded in a region containing varying numbers of short tandem repeats. Some of these repeats contain short iterations of the TTAGGG motif, suggesting that they may interact with the termi-

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nal array to participate in telomere function and/or maintenance, possibly by regulating expression of the RecQ helicase gene. Internal to the RecQ-associated repeat region, each of the eleven ends possesses its own unique sequences which tend to be gene-rich, with many of the genes being predicted to have roles in pathogenicity. One chromosome end consists of the ~1.6 Mb ribosomal repeat array, which is interrupted by an insertion of a LTR retrotransposon approximately 11 kb from the telomere. Finally, sequence analysis of de novo telomeres that arose in culture have allowed us to explore mechanisms of telomere hypervariability, much of which appears to be promoted by the numerous transposable elements that frequent subtelomeric regions. These results suggest that localization of genes to chromosome ends may provide a source of genetic variation in this fungus, and thus contribute to pathogenic adaptation. contributed presentation

Richardson, Bryce A.^{1,2*}, McDonald, GERAL I.¹, Zambino, Paul J.¹, Klopfenstein, Ned B.¹ and Kim, Mee-Sook¹. ¹USDA Forest Service, Rocky Mtn. Research Station, Moscow ID, USA, ²Washington State University, Department of Plant Pathology, Pullman WA, USA. brichardson02@fs.fed.us. **First report of naturally occurring *Cronartium ribicola* infections on Scrophulariaceous hosts in North America.**

Cronartium infections were discovered on *Pedicularis racemosa*, *P. bracteosa*, *Castilleja miniata*, and *Ca. rhexifolia* in a mixed stand of whitebark and western white pine in northern Idaho. Most pines in this stand have white pine blister rust cankers caused by *Cronartium ribicola*. *Cronartium coleosporioides* (stalactiform rust) also occurs in the region. DNA sequencing of the rDNA internal transcribed spacer (ITS) was used to identify rust species from single telial columns. Based on 27 informative ITS sites that differentiate the two rust species, all five collections of *P. racemosa* infections were *C. ribicola*. For *Ca. miniata*, each rust species had infected a different single collection. One collection of *Ca. rhexifolia* and two collections of *P. bracteosa* were infected by *C. coleosporioides*. Subsequent artificial inoculations using aeciospores from whitebark pine cankers produced uredinia and telia on potted *Ca. miniata* and *P. racemosa*, and on leaf cuttings of *Ribes nigrum*. Telia of *Pedicularis*-infecting isolates grown on *R. nigrum* generated infections on western white pine seedlings, confirming the isolates' capacity to complete their lifecycle. Ongoing research aims to determine the distribution *C. ribicola* infections on Scrophulariaceous hosts, their role in the epidemiology of white pine blister rust, and genetic mechanisms involved in possible host switching. poster

Riquelme, Meritxell* and Bartnicki-García, Salomón. Department of Microbiology, Center for Scientific Research of Ensenada (CICESE), Km. 107 Ctra. Tijuana-Ensenada, Baja California, México. e@cicese.mx. **The role of the Spitzenkörper in hyphal growth and branching: the restless Spitzenkörper.**

Growing fungal hyphae exhibit at their apex a structure named the "Spitzenkörper" (Spk), whose composition and function has intrigued fungal biologists for decades. A dark phase structure by light microscopy, the Spk is a highly dynamic body composed of at least two parts: a conspicuous cluster of secretory vesicles and an inner core containing cytoskeletal components, ribosomes, and uncharacterized amorphous material. Our phase-contrast video-microscopy studies have confirmed qualitative and quantitatively earlier observations suggesting that the presence, position, and behavior of the Spk determine growth rate, growth direction, and morphology. Mutations and inhibitors affecting both the microtubular and the actin cytoskeleton destabilize the Spk with a major impact on hyphal growth and morphology. The hyphoid model for fungal morphogenesis attributes to the Spk the function of a vesicle supply center, and as such, the model can duplicate diverse hyphal morphogenetic processes. This model accounts for the fate of vesicles migrating from the Spk to the plasma membrane; it does not consider how vesicles arrive to the Spk. We are using molecular tools and high-resolution live imaging (fluorescence and phase contrast microscopy) to discern the actual paths of vesicle traffic from their synthesis sites to the plasma membrane in growing hyphae of *Neurospora crassa*. To fully understand Spk function we need to understand the mechanics and regulation of vesicle dynamics along the various steps in the secretory pathway: 1) vesicle formation at Golgi-like cisternae, 2) incoming vesicle migration via microtubules, 3) vesicle collection by the Spk, 4) outgoing vesicle migration from the Spk to the plasma membrane via actin microfilaments, and 5) exocytosis. symposium presentation

Rogers, Jack D.^{1*} and Ju, Yu-Ming². ¹Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA, ²Institute of Botany, Academia Sinica, Nankang, Taipei, 11529 Taiwan. rogers@wsu.edu. **The Xylariaceae of the Hawaiian Islands.**

Collections of xylariaceous fungi have been made on the major Hawaiian Islands, except Lanai. The holdings of the Bishop Museum have been studied. Many habitats and substrates have been examined at least once. In terms of species numbers collected (not frequency of collection) the following genera are noteworthy: *Hypoxyton* with 36 species (8 new to science and 5 probably endemic); *Xylaria* with 45 species (6 new to science and 3 probably endemic); *Biscogniauxia* with 5 species (1 new to science and 1 probably endemic); *Nemania* with 5 species (1 new to science and 1 probably endemic); and *Anthostomella* with ca. 9 species (1 new to science and 1 probably endemic), in part according to Lu & Hyde. Other genera frequently collected include *Daldinia* and

Kretzschmaria. Genus *Ascovirgaria* is new to science; its anamorph *Virgaria nigra* has a cosmopolitan distribution. Examples of problems being pursued include: does *Pisonia sandwicensis*, an endemic species, host the same leaf-inhabiting *Xylaria pisoniae* as the endemic *Pisonia brunoniana* (?); does *Acacia koa* host the same species as the introduced species, *A. mearnsii* (?). The origins of some of the xylariaceous fungi that have colonized the Islands will be discussed. A book dealing with the Xylariaceae of the Hawaiian Islands is contemplated. symposium presentation

Rogers, Jack D.¹ and *Ju, Yu-Ming². ¹Department of Plant Pathology, Washington State University, Pullman, Washington 99164-6430, USA, ²Institute of Botany, Academia Sinica, Nankang, Taipei 115, Taiwan. yumingju@gate.sinica.edu.tw **Xylaria species on termite nests.**

Xylaria arenicola, *X. brasiliensis*, *X. escharoidea*, *X. furcata*, *X. nigripes*, *X. piperiformis*, and *X. rhizomorpha* represent ancient names of fungi known to inhabit abandoned termite nests. We attempt to redescribe them and to reduce the confusion among them. *Xylaria tanganyikaensis* and *X. readeri*, species that might be associated with termite nests, are described. We describe a new variety, *X. furcata* var. *hirsuta*, and discuss an unnamed fungus that probably represents a new species. Photographs and a key are presented to facilitate the identification of these taxa. poster

Romaine, C. Peter. Department of Plant Pathology, The Pennsylvania State University, University Park, PA 16802, USA. cpr2@psu.edu. **Pharming in Mushrooms.**

The advent of a facile gene transfer method for the preeminent edible mushroom, *Agaricus bisporus*, has created new vistas for the genetic enhancement of this important crop, and now enables the exploration of this species as a biofactory for the production of high-value biopharmaceuticals (antibodies, enzymes, vaccines, etc.). While social concerns overshadowing the safety of genetically modified organisms are certain to impede the introduction of transgenic mushrooms grown for food, the use of transgenic strains in manufacturing biopharmaceuticals will likely find immediate public acceptance, for the end product (i.e., cheaper and safer drugs) would improve the quality of human life. Relative to other crops, the mushroom represents an intriguingly unique platform for the production of biopharmaceuticals, as an extraordinarily high biomass can be produced in a comparatively short time under high confinement and containment. Moreover, unlike therapeutic proteins derived from animal-based systems nowadays, mushroom-made protein drugs would not carry the risk of contamination by human pathogens, such as viruses and prions. symposium presentation

Romberg, Megan K.* and Davis, R. Michael. Dept. of Plant Pathology, UC Davis, Davis CA 95616, USA. mkromberg@ucdavis.edu. **Characterization of *Fusarium solani* f. sp. eumartii** on potato and tomato in California.

The causal agent of a wilt and stem-end rot recently seen in fields of seed potatoes in California was subsequently identified as *Fusarium solani* f. sp. *eumartii*. Four conserved DNA sequences (the ribosomal DNA intergenic transcribed spacer region, and the elongation factor 1-alpha, beta tubulin and alkaline phosphatase genes) of six isolates of this *F. solani* were compared to five isolates of *F. solani* from tomato fields with Foot Rot and found to be identical. *Lycopersicon* has apparently not previously been reported as a host for *F. solani* f. sp. *eumartii*. Comparison of the DNA sequences to other *Fusarium* spp. segregate this group of isolates into a separate monophyletic group. However, nit mutant pairings revealed that most of the tomato and potato isolates comprise separate VCG's, although one potato isolate paired with most of the tomato isolates. Cross inoculation experiments were used to determine the infectivity of isolates from different hosts on various solanaceous species. poster

Romberg, Megan K.* and Davis, R. Michael. Dept. of Plant Pathology, University of California, Davis, Davis CA 95616, USA. mkromberg@ucdavis.edu. **Characterization of California isolates of *Fusarium solani* f. sp. eumartii**.

The causal agent of a wilt and stem-end rot recently seen in fields of seed potatoes in California was subsequently identified as *Fusarium solani* f. sp. *eumartii*. Four conserved sequences (the ribosomal DNA intergenic transcribed spacer region, and the elongation factor 1-alpha, beta-tubulin, and phosphate permease genes) of six isolates of this *Fusarium solani* f. sp. *eumartii* were compared to five isolates of *F. solani* from tomato fields with Foot Rot and found to be identical. *Lycopersicon* sp. has apparently not previously been reported as a host for *F. solani* f. sp. *eumartii*. Comparison of the gene sequences to other *Fusarium solani* isolates segregate this group of isolates into a separate monophyletic group. However, pairings of nitrate-non utilizing mutants revealed that most of the tomato and potato isolates fall into separate VCG's, although one potato isolate paired with most of the tomato isolates. Cross inoculation experiments were used to determine the infectivity of isolates from different hosts on various solanaceous species. poster

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Sakai, Shunsuke^{1a}, Nishide, Tatsunori^{1b}, Munir, Erman², Baba, Kei'ichi¹, Inui, Hiroshi³, Nakano, Yoshihisa³, Hattori, Takefumi^{1*} and Mikio Shimada^{1c}. ¹Research Institute for Sustainable Humanosphere, Kyoto University, Uji, Kyoto 611-0011, Japan, ²University of North Sumatra, Jl. Bioteknologi No. 1 Kampus USU, Medan 20513, Indonesia., ³Department of Applied Biological Chemistry, University of Osaka Prefecture, Sakai, Osaka 599-8231, Japan. Present address: ^aDepartment of Microbiology, Graduate School of Medicine, Kyoto University, Kyoto 606-8501, Japan, ^bNisshin Foods Inc., Tokyo, Japan, ^cEnvironmental and Biotechnological Frontier Engineering, Fukui University of Technology. **Possible mechanism for oxalate biosynthesis involved in energy metabolism in wood-rotting basidiomycete *Fomitopsis palustris*.**

Oxalate biosynthesis in wood-destroying fungi, including *Fomitopsis palustris*, has been receiving much attention, because the acid is closely associated with wood decay processes and inactivation of copper-containing wood preservatives. Wood-rotting basidiomycete *F. palustris* acquires biochemical energy for growth by oxalate biosynthesis during glucose oxidation. Our biochemical study has proposed that oxalate biosynthesis is metabolically linked to both the short-cut TCA cycle and glyoxylate (GLOX) cycle. Isocitrate-lyase (ICL), together with malate synthase (MS) play a pivotal role in the metabolic system for the fungal vegetative growth. The purpose of this study is to elucidate subcellular localization of glyoxylate cycle enzymes of *F. palustris*. We have cloned full-length cDNA encoding ICL from the fungus. Peroxisomal targeting signal (PTS 1) found at its C-terminus suggests the localization of ICL in peroxisome. By immunoelectron microscopy with anti-*F. palustris* ICL antibody, ICL has been shown to be localized in peroxisome. Furthermore, subcellular fractionation of mycelial homogenate of *F. palustris* has shown peroxisomal localization of ICL and MS. However, oxaloacetate, one of the oxalate-producing enzymes, is cytosolic. The results strongly suggest that short-cut TCA cycle and GLOX cycle are localized in different organelles but cooperatively play a role in oxalate biosynthesis in *F. palustris*. poster

Sakuma, Daisuke. Osaka Museum of Natural History, Nagai-Park 1-23, Higashiumiyoshi-ku, Osaka 546-0034, Japan. sakuma@mus-nh.city.osaka.jp. **Gathering information for local myco-biota: current status of OSA mycological collection.**

OSA is the one of a local herbarium which has 3 curatorial staffs and 50yrs history, about 250,000 specimens for higher plants, and 50,000 for mosses. But for mycological collections, less than 1000 specimens are stored until 1990. Now we have improved the mycological collection for specimen number (about 6000) and also for quality of information. These are chiefly due to following 3 reasons. 1) Co-operations of local amateurs, such as Kansai Mycological Club. 2) Curatorial staff for mycology 3) "Digital Museum Project of Osaka City". These collections and informations would have importance for local biodiversity policies. But in reality, it is not a kind of well-balanced information and contains some problems. 1) Very poor for microfungi and Ascomycetes: due to limitation of curator's ability and lack of amateurs. 2) Limited accuracy of some taxonomic group, such as Cortinariaceae, Polyporeaceae. 3) Geographically limited information: amateurs are very active in some place but not for others. 4) Very limited old specimens: difficult to back date in early times. To overcome such limitations, some of the amateur reports can be utilized. These should be carefully assessed when in use, but it is informative though they can not be approved. We also compile such kinds of information. poster

Sasaki, Fumito*, Miyamoto, Toshizumi, Tamai, Yutaka and Yajima, Takashi. Laboratory of Forest Resource Biology, Graduate School of Agriculture, Hokkaido University, N9-W9, Kita-ku, Sapporo 060-8589, Japan. whomeet@for.agr.hokudai.ac.jp. **A *Cordyceps* parasitizing Scarabaeidae larvae.**

We collected *Cordyceps scarabaeicola*-like fungus in Hokkaido, which parasitized Scarabaeidae insects and had clavate yellowish stroma. However, they differed from *Cordyceps scarabaeicola* in morphologic generation of hosts, parasitized larvae rather than adults. The average length and width of ascostromata, perithecia, asci, and partspores were 28.8 mm long, 3.4 mm wide, 455.3 μ m, 231.8 μ m, 324.0 μ m, 3.1 μ m, 6.9 μ m, 1.2 μ m, respectively. Perithecia were semi immerse. Fungal strains were isolated from the ascostromata and partspores. The isolates formed conidia on the Sabouraud glucose medium. Conidium arrangement was sympodial and the conidia form was oval. Conidia were produced on elongations of flask shaped conidiogenous cells; accordingly anamorph of the isolates was considered a *Beauveria* sp. This *Cordyceps* fungus was compared with other *Cordyceps* spp. that have Scarabaeidae hosts and clavate stroma. *Cordyceps scarabaeicola* has shorter perithecia, asci, and partspores than the fungus, and conidium arrangement is different. *Cordyceps ravenelii* has wider, superficial perithecia, longer partspores, and a different conidium arrangement (phialidic). *Cordyceps coccidiocapitata* has long, immersed perithecia. While *C. bassiana* and *C. staphyliniadaecola*, they have a *Beauveria* anamorphic state, they differ from our fungus in having longer and immersed perithecia. We assume the fungus is *Cordyceps brongiartii*. poster

Sato, Hiroki. Kyushu Research Center, Forestry and Forest Products Research Institute, Kurokami, Kumamoto 860-0862, Japan. hirokis@ffpri.affrc.go.jp. **Ecology of *Cordyceps militaris*.**

In northeast Japan, fruiting abundance of *C. militaris* tracks population cycles of the moth *Syntypistis punctatella*. Moth population outbreaks occur every 8-11 years, and cause severe defoliation of *Fagus sp.* Moth eggs hatch in June and caterpillars feed on leaves through the summer. Caterpillars pupate in August and overwinter in forest litter. In outbreak years, moth densities reach 100-150 caterpillars/m² in the canopy and 40-50 pupae/m² in the A0 soil horizon. In the year after outbreaks, *C. militaris* infects over 90% of pupae and maximum infection rates occur in mid-August. I describe the phenology of *C. militaris* fruiting and the incidence of natural infections of pupae in the soil during 1992-1997, which includes the outbreak year 1993. Infection processes in the soil and above ground were also investigated. When lab-reared pupae were buried in forest litter, fungal infections occurred within 7-10 days. These individuals subsequently died within 40 days. To determine the potential for aerial infection, egg-masses on beech foliage were held in net enclosures and placed 2 m above the forest floor until they grew up to the last stadium larvae. They were then returned to the laboratory, incubated, and subsequently the less than 10% died from *C. militaris* infection. The role of *C. militaris* conidia and ascospores in the infection cycle of *S. punctatella* is discussed. symposium presentation

Schardl, Christopher*, Blankenship, Jimmy D., Spiering, Martin J., Faulkner, Jerome R., Hussaini, Syed Raziullah and Grossman, Robert B. University of Kentucky, 201F PSB, 1405 Veterans Drive, Lexington, KY 40546-0312. schardl@uky.edu. **Biosynthesis of loline alkaloids by bioprotective endophytes.**

Loline alkaloids, produced by several symbiotic *Neotyphodium* and *Epichloë* species, are potent, broad-spectrum insecticides, thus contributing to protection of host grasses. Lolines comprise a saturated pyrrolizidine ring structure with an amine at C1 and an oxygen bridge between C2 and C7. Lolines differ from each other in the presence or absence of methyl, formyl, acetyl, or other groups on the 1-amine. Precursors for the most common loline, N-formylloline, were identified. L-Proline (Pro) and L-homoserine (Hse), contribute the C and N atoms of the ring system, Hse also contributes the 1-amine, and the methyl and formyl carbons derive from C6 of L-methionine. A cluster of at least nine *lol* genes is involved in loline biosynthesis, and the predicted gene products include three (LoIC, LoID and LoIT) that use a pyridoxal phosphate cofactor, P450 (LoIP) and FAD (LoIF) monooxygenases, and two nonheme iron oxygenases (LoLE and LoLO). Functions of LoLA and LoLU are less apparent. LoLA is related to the allosteric domain, but not the active site, of fungal aspartyl kinase. LoLU has a putative Myb signature suggesting that it may be a transcription regulator. An RNAi experiment demonstrated that LoIC is involved in loline biosynthesis. Based on gene relationships and results from feeding positionally labeled precursors, a plausible route to the loline ring system is proposed. The first step, which may be catalyzed by LoIC, is a gamma-substitution linking Pro to the 2-aminobutyric acid moiety of Hse. A survey of the *lol* genes and loline alkaloid profiles associated with several endophyte species suggested that LoIP is involved in modifications of the 1-amine. A targeted knockout of the gene for LoIP demonstrated its role in converting N-methyllooline to N-formylloline. The current working hypothesis is that the nine known *lol* genes are sufficient for loline alkaloid biosynthesis. poster

Schmidt, Steve K.*, Schadt, Christopher W., Martin, Andrew P., Meyer, Allen F., Nemergut, Diana R. and Costello, Elizabeth K. Dept. of Ecology & Evolutionary Biology, University of Colorado, Boulder, CO 80309, USA. steve.schmidt@colorado.edu. **Seasonal dynamics and phylogenetic analysis of previously unknown fungal lineages in tundra soils.**

We will review our work exploring the seasonal dynamics and biogeography of previously unknown fungal lineages in tundra and forests in Colorado, Costa Rica and Peru. Phylogenetic of SSU and LSU rRNA clone libraries revealed a high diversity of novel fungi that constitute major new groups that are divergent at the subphylum and class levels in these soils. Even more surprisingly, our analyses show that unique fungal communities thrive under winter snow packs in Colorado. Fungal biomass actually reaches its annual peak under the late winter snow pack. An abundance of previously unknown, cold-tolerant, fungi beneath the snow substantially broadens our understanding of both the diversity and biogeochemical functioning of microorganisms in cold environments. symposium presentation.

Schoch, Conrad L.*, Spatafora, Joseph W. and the AFTOL consortium. Dept. Botany and Plant Pathology, Oregon State University, Corvallis, OR 97330, USA. schoch@science.oregonstate.edu. **Deep relationships in the non-lichenized Ascomycota.**

Previous research on supra-ordinal fungal phylogenies has relied heavily on the analysis of sequence data obtained from the nuclear ribosomal genes. Although a number of more focused studies used mitochondrial and protein coding genes, very few phylogenies have yet utilized a combination of all of these loci. The aim of this study is to improve the backbone phylogeny of the Ascomycota by intensive taxon sampling and inclusion of sequence data from multiple ribosomal and protein-coding loci. This research is a part of a collaborative effort involving five AFTOL research labs and numerous international collaborators. Se-

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quences were generated from three ribosomal loci (large nuclear subunit, small nuclear subunit, small mitochondrial subunit) and three protein-coding genes (RNA polymerase II largest and second largest subunits, translation elongation factor-1 alpha). Taxon sampling included representatives for all major Ascomycota classes with an emphasis on the filamentous fungi of the Pezizomycotina and non-lichenized lineages. Several comparative analyses utilizing parsimony and Bayesian methodologies were performed. The final data set includes more than 5000 molecular characters and more than 150 taxa. A total of 10 higher nodes, corresponding to classes, were recovered with strong support as measured by concurrent parsimony bootstrapping and Bayesian posterior probabilities. The inclusion of data from all genes in simultaneous analyses improved both the resolution of the phylogenies and overall nodal support as compared to analyses of individual loci. This study provides strong support for the majority of the Ascomycota classes as currently defined by Eriksson, but certain groups were not recovered as monophyletic (e.g. Leotiomycetes). The combination of protein and ribosomal data in simultaneous analyses provided increased resolution of class level clades, advancing the resolution of deep nodes in the Ascomycota phylogeny. As such, these results provide a more accurate phylogenetic foundation for comparative studies of the Ascomycota ranging from ecology to genomics. contributed presentation

Schoch, Conrad L.*, Spatafora, Joseph W. and the AFTOL consortium. Dept. Botany and Plant Pathology, Oregon State University, Corvallis, OR 97330, USA. schochc@science.oregonstate.edu. **Deep relationships in the non-lichenized Ascomycota - the poster**

See the Oral Presentation Abstract. poster

Scholler, Markus^{1*} and Boellmann, Joerg². ¹Staatliches Museum f. Naturkunde, Erbprinzenstr. 13, D-76133 Karlsruhe, Germany, ²Brandenburgische Technische Universität, Lehrstuhl für Bodenschutz und Rekultivierung, P. O Box 101344, D-03013 Cottbus, Germany. scholler@naturkundeka-bw.de. **Puccinia glechomatis and P. lagenophorae in North America: invasion patterns, life cycle and life strategies.**

Puccinia glechomatis and *P. lagenophorae* are taxonomically distinct autoecious rust species native to Eurasia and Australia which were recently introduced to the United States. Although their life cycle (microcyclic versus auto-demicyclic) and host range differ (monophagous on *Glechoma hederacea* s. l., Lamiaceae versus polyphagous on numerous Asteraceae) there are common characters with respect to their invasion pattern in North America. Both species have spread throughout the U.S. (not restricted to a certain geographical or climatical area), both species appeared first on the East Coast and the West Coast before establishing in Central U.S. and both species seem not to progress continuously but patchy. In order to explain these invasion patterns detailed lab, field and literature studies on the life cycle and life strategies of *P. glechomatis* and its host were carried out and compared with those of *P. lagenophorae*. Results indicate that the invasive capacity of rust fungi is supported by several factors, three of which are the production of several generations per year, a predominance of an asexual mode of reproduction, and ruderal host plants occurring in man-made habitats. symposium presentation

Seifert, Keith A.*, Hughes, Stanley J., Boulay, Hillary and Louis-Seize, Gerry. Biodiversity Theme (Mycology & Botany), Agriculture & Agri-Food Canada, 960 Carling Ave., Ottawa, Ontario K1A 0C6, Canada. seifertk@agr.gc.ca. **What should we call the jet fuel fungus?**

The jet fuel fungus, *Hormoconis resinae* (also widely known as *Cladosporium resinae*), grows in fuel contaminated with small amounts of water, and its growth can clog fuel lines and corrode metal parts. Consequently, fuel tanks in airports and on jets are carefully monitored for this fungus. Around the world, several private companies make their fortunes detecting and identifying this fungus using a variety of technologies. Unfortunately, when the anamorph genus *Hormoconis* was proposed (1973), an error was perpetuated that originated when the teleomorph *Amorphotheca resinae* was described (1969). Various nomenclatural options for stabilizing the name of the jet-fuel fungus will be discussed. Using morphological, cultural and molecular data, we will consider the taxonomy and phylogenetic relationships of several cladosporium-like fungi, including *A. resinae*, and the synnematous fungi *Sorocybe resinae* and *Pycnostysanus azalea*. The precise phylogenetic relationships of *A. resinae*, which sits alone in its own family *Amorphothecaceae*, are difficult to determine with certainty with existing data. contributed presentation

Setoguchi, Masanobu*, Yamada, Akiyoshi and Kuga, Yukari. Faculty of Agriculture, Shinshu University, Minami-minowa, Nagano 399-4598, Japan. akiyosh@gipmc.shinshu-u.ac.jp. **Fungal colonization occurs at the seed germination of achlorophyllous monotropoid plants, *Monotropa hypopithys* and *Monotropastrum humile*.**

Monotropaceae consists of achlorophyllous plants that develop monotropoid mycorrhizas in the root system of adult individuals. However, little is known about their fungal association at the seed germination and the early developmental stage. We buried seeds of *Monotropa hypopithys* and *Monotropastrum humile* in *Pinus densiflora* forests, where both the monotropoid plants are naturally dis-

tributed. Three to five months after the sowing, seed germination was observed, which was determined by the increase of seed size and the budding of root-like organ that possess vascular structure in the central. In addition, fungi epigeously colonized to most of such seeds, which often developed the fungal sheath as well as that of monotropoid mycorrhizas. In *M. humile*, cystidia were observed on the fungal sheath, and fungal penetration pegs were also observed in the epigeous cell of seed. In *M. hypopithys*, clamp connections were often observed on the hyphae of colonized mycelium. poster

Shefferson, Richard P.^{1*} and Taylor, D. Lee². ¹Forestry and Forest Products Research Institute, Tsukuba, Japan, ²Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, Alaska, USA. dormancy@gmail.com. **Lady-slipper orchid mycorrhizal associations reveal specificity suggestive of resource fragmentation and resource tracking.**

Generalism in biotic interactions, measured at one level of study, often masks specialization at finer scales. Here, we examine mycorrhizal specificity of temperate terrestrial lady's slipper orchids (*Cypripedium* spp.) in northern California, USA, to assess if high mycorrhizal specificity at the fungal family level masks low specificity to fungi within the Tulasnellaceae, the primary family of *Cypripedium*-mycorrhizal fungi. First, we hypothesized that if *Cypripedium* species are highly specialized to fungi within family Tulasnellaceae, then sympatric *Cypripedium* populations will associate with divergent tulasnelloid symbionts, while allopatric populations may not. Second, we hypothesized that within-Tulasnellaceae specificity may correspond to host abundance, leading to greater specialization in areas with lower diversity of potential host fungal families. We observed no evidence of ecological divergence in mycorrhizal association in sympatric populations. However, we observed evidence that within-Tulasnellaceae specificity varied inversely with among-family specificity. We suggest that in areas where potential host families are less abundant, *Cypripedium* species must compensate for a lower chance of mycorrhizal colonization by widening the breadth of association with fungi within remaining host families. *Cypripedium* species appear to be resource-trackers, specializing on resources provided by a range of host fungi. This implies that *Cypripedium* rarity may indeed be due to mycorrhizal specialization. poster

Shi, Ainong and Mmbaga, Margaret T. Tennessee State University, Nursery Crop Research Center, 472 Cadillac Lane, McMinnville, TN 37110, USA. mmbaga@tnstate.edu. **Molecular identification of the powdery mildew pathogen of crape myrtle (*Lagerstroemia indica*) using internal transcribed spacers or rDNA.**

The fungus, *Erysiphe lagerstroemiae*, has been reported to be the causal agent of powdery mildew in crape myrtle in the United States since 1933. However, in 1979, the powdery mildew pathogen of crape myrtle in China, Japan and Australia was reported to be caused by *Uncinuliella australiana*. Certain features of the teliomorph of powdery mildew pathogens are used for identification. However, these structures are rarely observed on crape myrtle in Tennessee (USA). In this study, DNA analysis of the internal transcribed spacer (ITS) region of rDNA was used for the identification of the powdery mildew pathogen in crape myrtle. Polymorphic band of 666 bp amplified using primer pair ITS1/ITS4 and a band of 704 bp amplified using primer pair ITS1-F/ITS4 were obtained and sequenced. The sequence of the ITS region of 16 Tennessee isolates was identical to the sequence reported for *U. australiana* clearly showing that the Tennessee isolates were the same as those reported in Asia. For this work, ITS-specific primers were developed to provide pathogen diagnosis tool using the anamorphic stage which is prominent during spring and autumn. Four primer pairs and four double primer pairs were highly specific to the crape myrtle powdery mildew and did not amplify *E. pulchra* found on dogwoods or *Microspora syringae-japonicae* on the common lilac. Recently, the genus *Uncinuliella* has been changed to *Uncinula* and presently to *Erysiphe*. This study provides conclusive evidence that that *E. lagerstroemiae* and *U. australiana* are the same. Because of international nomenclature rules, the name *E. lagerstroemiae* take priority over *U. australiana*. Thus, *E. lagerstroemiae* (syn. *U. australiana*) reported in the USA is the causal agent of powdery mildew pathogen in crape myrtle in mid-Tennessee and in China, Japan and Australia. poster

Shirasaka, Norifumi. Laboratory of Food Microbiological Science and Biotechnology, Faculty of Agriculture, Kin-ki University, 3327-204, Nakamachi, Nara 631-8505, Japan. sirasaka@nara.kindai.ac.jp. **Effect of cyanocobalamin and p-toluic acid on the fatty acid composition of *Schizochytrium limacinum* SR21.**

DHA (22:6n-3), which is one of most abundant components of the brain's structural lipids, has attracted great interest recently owing to its specific function in the brain and retina. It was reported that *Schizochytrium limacinum* SR21 was potent producer of DHA and the suitable conditions for DHA production was reported. Although the conditions of production of DHA were well investigated, the metabolic specificities of PUFAs are still unclear. In this study, we searched the compounds which affected fatty acid composition of *Schizochytrium limacinum* SR21. The structural analysis of newly detected fatty acids in the case of inhibitor addition was described putative biosynthetic pathway of fatty acid in this

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strain was also discussed. The addition of *p*-toluic resulted in the decrease of DPA (22:5n-6) content and the increase of EPA (20:5n-3) content in a dose-dependent manner, and the occurrence of two additional peaks of fatty acids, which were 4,7,10,14-eicosatetraenoic acid (20:4n-7) and 4,7,10,14-docosatetraenoic acid (22:4n-9). The supplement of cyanocobalamin, which is active component of vitamin B12, decreased the content of pentadecanoic acid (C15:0) and heptadecanoic acid (C17:0). These results suggested that cyanocobalamin may upregulate the propionic acid metabolism by cobalamin dependent methylmalonyl-CoA mutase. poster

Shishido, Kazuo. Dept. of Life Science, Tokyo Institute of Technology, Yokohama 226-8501, Japan. kshishid@bio.titech.ac.jp. **Reuse of waste plant biomass and degradation of chlorinated aromatic compounds by using molecular-genetically improved basidiomycete fungal strains.**

Plant biomass (lignocellulose) is the most abundant renewable organic resource on earth and mainly composed of cellulose, hemicellulose (its major component is xylan), and lignin. To isolate ethanol-convertible cellulose from waste plant biomass, we molecular-genetically produced the *Coprinus cinereus* strains secreting a large amount of *Pleurotus ostreatus* lignin-degrading enzyme, manganese peroxidase (MnP) or *Bacillus subtilis* endo-xylanase. By using these strains, we succeeded in the isolation of approx. 30% of total cellulose from rice straw (a popular waste plant biomass) as non-precipitable forms. Lignin peroxidase (LiP) produced/secreted by white-rot basidiomycete fungi is known to degrade chlorinated dioxins. Rat cytochrome P450, CYP1A1 plays an important role in metabolism of chlorinated dioxins. So we molecular-genetically produced the *Cortolus hirsutus* strains producing a large amount of homologous (*C. hirsutus*) LiP or rat CYP1A1. The 2,7/2,8-dichlorodibenzo-*p*-dioxins were efficiently degraded by extracellular manner in the former strain and by intracellular manner in the latter strain. symposium presentation

Simpson, Nicholas B.*, Barbare, Holly, Walker, John F. and Jumpponen, Ari. Kansas State University, Division of Biology Fungal Ecology Research Group, 214 Ackert Hall, Manhattan, Kansas 66506, USA. Fungi@ksu.edu. **Homologous morphologies of ericoid mycorrhizas formed by six different fungal species suggests host control of mycorrhizal colonization.**

The morphology of ericoid mycorrhizas (ErM) show a high degree of uniformity across host species and fungal species. However, most ErM resynthesis systems rely upon fungal isolates from either the Helotiales or the Onygenales, i.e. the *Hymenoscyphus ericae* complex or *Oidiodendron* spp., respectively. Recent molecular studies suggest a high diversity among ErM-forming fungi. Due to limited culturability, much of this suggested diversity remains persistently unobservable in laboratory experiments. We isolated 550 fungal cultures from the roots of five arctic ericaceous plant species using four different media to maximize our ability to capture cultivable diversity of ErM fungi. Of the 550 cultures, six conspecific groups account for over 60% of the diversity. Of the six different groups, five belong to the Helotiales, but none matched with the *Hymenoscyphus ericae* complex. The remaining group belongs within the basidiomycetous Polyporales. Of notable absence were any fungi from within the Onygenales. All six species form intracellular coils typical to ErM in resynthesis systems with *Vaccinium uliginosum*. This evidence underscores the importance of host type when determining mycorrhizal structure. poster

Skinner, Samuel J.* and Currah, Randolph S. University of Alberta, CW 405 Biological Sciences Building, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada. samuels@ualberta.ca. **Metabolic and taxonomic data show differences between the fungal communities associated with different organs of nodulated and non-nodulated roots of woody host plants.**

Roots of the nitrogen-fixing plant, *Alnus incana*, and a comparable, related, and cohabitating non nitrogen-fixing plant *Betula papyrifera* were collected from several sites in central Alberta, Canada. Standardized homogenates prepared from surface-sterilized root-tips and nodules from these samples were streaked on selective media to obtain culturable fungal associates and pipetted into Biolog microtitre plates to obtain a crude estimation of substrate utilization profiles of the associated fungal communities. Preliminary analyses show that while the profiles of all sample types overlap, the diversity of these profiles is greater for the roots of either species than for the nodules. Preliminary community composition data support these findings: fungal communities associated with nodules showed less interpopulation variability and were more distinct taxonomically than those associated with the roots of either plant species. Such a narrow suite of fungi may be indicative of unusual physiological conditions in and around nodules. These preliminary observations also suggest a link between fungal community ecology and plant functional ecology. poster

Skinner, Samuel J.*, Currah, Randolph S. and Tsuneda, Aki. CW 405 Biological Sciences Building, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada. samuels@ualberta.ca. **Ascomatal morphogenesis in *Auxarthron conjugatum* (Onygenaceae).**

We used a combination of light and electron microscopy to examine stages of ascoma development in *Auxarthron conjugatum*, from homothallic initials to mature reticuloperidial cleistothecia. In contrast to a superficially similar reticu-

loperidial species in the Myxotrichaceae (cleistothecial Helotiales), prototunicate asci developed in short, branched chains which ramified through the peridial cavity rather than forming singly and on a distinct hymenial membrane. Catenate asci matured basipetally rather than synchronously and arose from single unbranched crossers. Results of a cytological examination of catenate asci suggested that following karyogamy in the penultimate cell, the zygote nucleus divides mitotically. One of the resulting nuclei remains in this ascus initial and undergoes meiotic and mitotic divisions prior to ascosporeogenesis while the other moves forward into the distal cell of the developing ascus chain. When immature, these incipient asci, each with an apparently diploid nucleus, were able to detach by septum schizolysis, i.e., as spores, and gave rise to colonies that produced ascospores lacking reticuloperidia. The significance of these teliospore-like asci in the life cycle of this species is unknown. Development of the characteristic punctate-reticulate ascospores involved structural modifications of a three-layered secondary spore wall. poster

Slot, Jason* and Hibbett, David S. Department of Biology, Clark University, 950 Main Street, Worcester, MA 01610, USA. jslot@clarku.edu. **Molecular evolution of *nrt2*, a nitrate transporter gene, with an emphasis on *Hebeloma* phylogeny.**

The ectomycorrhizal genus *Hebeloma* obtains nitrate from the soil through a transporter, NRT2, which is encoded in a cluster of nitrate assimilation genes. This study investigates the molecular phylogeny of the *nrt2* gene within *Hebeloma* and closely related genera. Approximately 20 new ITS and *nrt2* sequences generated in the Hibbett lab at Clark University are presented here. Preliminary investigations suggest that *nrt2* could improve phylogenetic resolution in *Hebeloma*, a notoriously problematic clade of Euagarics. Structural and functional changes in this protein could serve as molecular markers for the transitions some *Hebeloma* have made to environments of extreme nitrogen status. ITS phylogenies suggest that *Hebeloma* is nested in a greater clade largely made up of saprotrophic species. Comparisons of *nrt2* phylogeny among closely related saprotrophic genera could provide insight into the role of nitrogen nutrition in the transition to ectomycorrhizal habit. The impact of nitrogen pollution on fungal diversity is also considered. poster

Smith, Jane E. USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR 97331, USA. jsmith01@fs.fed.us. **Effects of thinning and prescribed fire on fine root biomass and the ectomycorrhizal fungal community in ponderosa pine forests.**

Decades of fire suppression have resulted in high fuel levels in dry forests in eastern Oregon. To alleviate the risk of stand replacing wildfire, forest managers are applying prescribed underburning and thinning treatments. Little knowledge exists about the impacts of these restoration treatments on the belowground ecosystem. Aboveground ecosystem recovery after disturbance is directly linked to the survival of ectomycorrhizal fungi (EMF) that reside mostly in the surface layers of soil. The response of EMF species richness, live fine root biomass, and duff levels to seasonal burning and to thinning and burning was investigated in ponderosa pine dominated stands in the Blue Mountains of Oregon. The belowground community composition and structure of EMF was characterized using molecular methods. Treatments significantly reducing duff depth negatively impacted EMF species richness and live fine root biomass. The EMF community consisted of a large number of infrequently detected species. The distribution of a few abundant species in a majority of the treatments both before and after treatment application demonstrates that some EMF species survive or rapidly reestablish after disturbance. Understanding how EMF respond to prescribed fire and thinning will assist forest managers in selecting fuel-reducing restoration treatments that maintain critical soil processes. contributed presentation

Smith, Matthew E.*, Douhan, Greg W. and Rizzo, David M. Department of Plant Pathology, University of California at Davis, Davis CA 95616, USA. msmith@ucdavis.edu. **Dismantling the disconnect between EM fruiting bodies and root tips – hypogeous, resupinate, and inconspicuous taxa are dominant and diverse on EM roots and as fruiting bodies in a xeric oak woodland.**

Many studies of EM communities report a pervasive disconnect between EM fungi found colonizing root tips and those encountered as fruiting bodies. However, few studies intensively sample both roots and fruiting bodies simultaneously. In particular, taxa that produce inconspicuous fruiting bodies (ie: hypogeous, resupinate, and diminutive groups) are rarely included in fruiting body surveys. We intensively sampled both EM roots (4 sampling times X 2 years, 9600 root tips) and fruiting bodies (approximately 45 sampling visits in 4 years) in a xeric, *Quercus*-dominated woodland in California. The main lineages encountered on EM roots were *Tomentella* spp., *Tuber* spp., *Inocybe* spp., *Cenococcum* spp., and representatives from several lineages within the *Pezizales* and *Sebacinales*. *Russulaceae* and Corticioid fungi were notably uncommon. Most of the dominant taxa encountered on EM roots produced fruiting bodies at the site; but these were mainly small, inconspicuous, and/or seasonally restricted. While some roots remain unmatched to fruiting bodies, we argue that reproductive structures of these taxa are cryptic rather than absent from this forest. The available data sug-

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gests that the purported disconnect between EM roots and fruiting bodies is heavily influenced by sampling bias in favor of macroscopic, epigeous taxa, rather than the absence of reproductive structures in other EM fungal groups. contributed presentation

Sogonov, Mikhail V. Dept. of Plant Biology and Pathology, Rutgers University, New Brunswick NJ 08901, USA. msogonov@nt.ars-grin.gov. **Software for morphological and molecular taxonomic studies of fungi.**

Despite the significant progress achieved in software for taxonomic research, biologists often need specific tools that have not been developed by professional programmers because of the limited number of potential users. In this case, biologists can create the software themselves using simpler tools, such as Microsoft Access databases. Microphotographs are the main source of documentation in taxonomic studies of microfungi. Furthermore, morphotaxonomists need to make numerous measurements of different structures such as ascospores, conidia, phialids etc. Microsoft Access does not directly provide tools to link images to database records or to automate measurements. There are special image database programs but they lack the convenience and flexibility of Access for specimen data management. I developed an Access database for storage and manipulation of information on the taxonomy of Ascomycetes specimens and the cultures. Using VBA, I developed a program that integrates image management with other specimen information. This program allows 1) browsing image files from an Access form, 2) measuring morphological structures with automatic placement of the measurements into the database. Additionally, the program provides statistical analysis of these measurements, management of information for DNA extractions, PCR and sequencing sets. poster

Sogonov, Mikhail V.^{1*}, Castlebury, Lisa A.², Rossman, Amy Y.² and White, James F. Jr.¹ ¹Dept. of Plant Biology and Pathology, Rutgers University, New Brunswick NJ 08901, USA, ²Systematic Botany and Mycology Laboratory, Beltsville MD 20705, USA. msogonov@nt.ars-grin.gov. **Towards monophyletic genera in Gnomoniaceae.**

Gnomoniaceae is a diarthraceous family, which includes agents of serious plant diseases such as dogwood, oak and sycamore anthracnoses. Existing generic concepts for the family are based on morphological characters such as presence or absence of stroma, position of the perithecial beak, septation of ascospores. After analyzing LSU and ITS sequence data for approximately 100 isolates of gnomoniaceous species, it is apparent that the largest and most common genera in the family, *Gnomonia*, *Apiognomon* and *Cryptodiaporthe* are polyphyletic. The relationship of the type species of the family, *Gnomonia gnomon*, to other presumed species of *Gnomonia* is clarified. The type species of the anamorphic genus *Discula* has been linked to a species complex including *Apiognomon errabunda* and the type of species, *A. veneta*. However *Discula* is also apparently polyphyletic and the relationship of the *A. veneta/A. errabunda* complex to other species of *Discula* is characterized. Most phylogenetic lineages in the Gnomoniaceae have some preferences for host families but no strict fungus/host relationships were observed. The results of this work demonstrate that new character systems are required for delineating genera in this biologically diverse and economically important group of fungi. symposium presentation

Sotome, Kozue^{1*}, Ota, Yuko², Hattori, Tsutomu² and Kakishima, Makoto¹. ¹Graduate School of Life & Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan, ²Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan. zag41183@ffpri.affrc.go.jp. **Phylogeny of Asiatic species of *Polyporus sensu lato*.**

The genus *Polyporus* contains morphologically various species, and is often divided into six infrageneric groups based on morphology: *Polyporus*, *Polyporellus*, *Favolus*, *Melanopus*, *Admirabilis*, and *Dendropolyporus*. To reveal the phylogenetic relationships within the genus *Polyporus* and between *Polyporus* and the allied genera, we performed the phylogenetic analysis using Asian isolates based on nuclear ribosomal large subunit DNA (LSU) and ATPase subunit 6 (*atp6*) regions. The phylogenetic trees based on LSU and *atp6* showed that the species of the group *Polyporellus* were included in a single clade, while the groups *Favolus* and *Melanopus* were divided into two and three clades, respectively. Four out of the seven clades detected by the LSU trees contained species belonging to single morphological groups. This suggests that some of the morphological groups reflect phylogenetic relationship. On the other hand, one clade consisted of the group *Polyporellus* and *Lentinus squarrosulus* while another a part of the group *Polyporus* and *Pseudofavolus cucullatus* suggesting that the genus *Polyporus* is not monophyletic. contributed presentation

Spatafora, Joseph W. and Sung, Gi-Ho. Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA. spatafj@science.oregonstate.edu. **Phylogenetics of Clavicipitalean fungi.**

Clavicipitalean fungi comprise a diverse assemblage of obligate symbionts of animals, plants, and other fungi. They exhibit a range of interactions from antagonistic to beneficial with the majority of species being pathogens of arthropods and classified in the genera *Cordyceps*, *Hypocrella*, and *Torrubiella*, and associated anamorphs. Here we present an overview of the phylogenetics of the Clavicipitaceae that highlights the evolution of arthropod pathogenicity, a re-eval-

uation of morphology and ecology, and the importance of the East Asian species in understanding the evolution of *Cordyceps*. Multigene phylogenetic studies revealed that *Cordyceps* is not monophyletic and that host affiliation is characterized by frequent host-jumps, often between distantly related taxa. *Cordyceps* species are found throughout the Clavicipitaceae, which consists of three major clades. Morphological characters that are most consistent with phylogeny include color and texture of stromata, presentation of perithecia, and anamorph morphology, although exceptions do exist. We also use this phylogeny to re-evaluate ecology and present hypotheses on the evolution of niche specialization (e.g., attacking hosts in litter vs. embedded in wood). Finally we discuss the phylogenetic connection between globally distributed taxa, especially anamorphs, and East Asian endemics. symposium presentation

Spiegel, Frederick W.*, Jones, N. and Shadwick, John D. Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. fspiegel@uark.edu. **Protostelid biota of the South Island of New Zealand.**

Protostelids are eumycetozoans which have simple sporocarps that develop from single amoeboid cells. Each sporocarp consists of a simple stalk that supports from one to a few spores, depending upon the species. As part of a global biodiversity inventory of eumycetozoans, collections of substrates were made from several different types of habitats on the South Island of New Zealand in March, 2004. Samples were brought to the lab and plated out in primary isolation plates and the species of protostelids present were identified based upon morphology. Species richness and abundance in South Island seems to be less than might be expected from data on other comparable geographic regions. Within the island, the protostelid biota east of the Southern Alps appears to be different from that to the west of this range. Some species, such as those of *Nematostelium* appear to be less common than might have been expected. Others, such as *Schizoplasmodiopsis vulgare* are more common than would have been expected. This protostelid biota is distinct from others that are well documented. contributed presentation

Spiegel, Fredrick W.*, Lindley-Settlemyre, Lora A., Swanson, A.R., Nelson, R.K., Edwards, Sally M. and Shadwick, John D. Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. fspiegel@uark.edu. **Uses for Auto-Montage for mycological illustration.**

Many mycological objects are three dimensional and are difficult to illustrate with conventional photography because of depth of focus problems. While careful drawings are an option to overcome this difficulty, not all researchers have access to a talented enough scientific illustrator. Scanning electron microscopy, while also useful, only allows one to illustrate surface features in monochrome. The development of digital imaging systems that can compile montages of through-focus series into a single in-focus image can overcome the depth of field limitations to produce images in true color. One such system, Auto-Montage by Syncroscopy, will be illustrated here. It can be adapted to work with cameras on copy stands, dissecting microscopes, and compound microscopes, allowing one to create montages from the macro range to oil immersion. The images produced can be used to illustrate research results, in text books, and in teaching. Examples of a number of mycological applications will be shown. poster

Stadler, Marc. Bayer Health Care AG, Pharma Division, Natural Products Research, Bayer Research Center Wuppertal, Bldg. 0452, P.O. Box 101709, D-42115 Wuppertal, Germany. marc.stadler@t-online.de **New CNS-active secondary metabolites from cultures of Basidiomycetes - an example for discovery and optimization of natural lead compounds.**

Basidiomycetes are playing a crucial role in our ongoing high throughput screening for novel leads from natural sources in various pharmaceutical indications, including diseases of the central nervous system (CNS). It is common sense that the biochemical mode of action of active principles of various toxic mushrooms (e.g., *Amanita muscaria* and particular *Clitocybe*, *Inocybe* and *Psilocybe* spp.) relates to their modulation of receptors in the CNS. In contrast, there are only a few reports in the literature that actually dealt with CNS-active metabolites from their cultures, despite it is well-established that the secondary metabolism of these organisms substantially differs in basidiocarps and vegetative mycelia. Hence, a screening library comprising extracts of basidiomycete cultures was designed: Strains were selected according to (chemo-)taxonomic criteria to attain a maximum chemical diversity. Their fermentation was optimized to ensure that the cultures were only harvested after the onset of metabolite production. Extracts were standardized to enrich "druggable" low-molecular medium-polar compounds. Automated bioassay-guided fractionation and extensive analytical dereplication were employed to increase the efficiency of the screening process. The active principles are produced in pilot scale by fermentation and provided for medicinal chemistry programs and extensive evaluation of their *in vitro* and *in vivo* activities. This workflow is exemplified by the discovery of agaricoglycerides, a novel class of analgesics from *Agaricus macrosporus* and other Agaricales (World Patent WO 03.055843), and by other CNS-active metabolites that were discovered concurrently. symposium presentation

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Stadler, Marc^{1*}, Hellwig, Veronica^{1,2}, Fournier, Jacques³, Radulović, Niko⁴, Asakawa, Yoshinori⁵, Hashimoto, Toshihiro⁵ and Quang, Dang Ngoc⁵. ¹BHC-PH-R&D EU-ET, P.O.Box 101709, D-42115 Wuppertal, Germany; ²Institut für Küstenforschung, D-21502 Geesthacht, Germany; ³Las Muros, F-09240 Rimont; ⁴Dept. Chemistry, Nis University, Serbia & Montenegro; ⁵Tokushima Bunri University, Faculty of Pharmaceutical Sciences, Tokushima, Japan. marc.stadler@t-online.de. **Pigment chemistry, HPLC profiles and taxonomy of Hypoxylon.**

The large xylariaceous genus *Hypoxylon* in the definition according to the monograph by Ju & Rogers (1996) comprises two sections (*Hypoxylon* and *Annulata*). Among other features, the presence of characteristic stromatal pigments in KOH in most *Hypoxylon* spp. was emphasized in this generic concept. Many of these pigments, such as hypomiltin, the cohaerins, rubiginosins, entonaemins, multiformins and saffafirins, have meanwhile been isolated and identified. Their chemical structures allow for conclusions as to their biogenetic origin, revealing that similar pigment colors may result from significantly different chemical matters. Some of the pigments were also studied for biological activities. The results, along with the fact that they are located in granules directly beneath the stromatal surface, suggest their natural role as a means of chemical defense. Using these metabolites as standards, a large HPLC-based chemotaxonomic study was carried out, revealing various chemotypes, which are basically in accordance with the taxonomic classification. For instance, species of sect. *Annulata* significantly differ in their metabolite profiles from those of sect. *Hypoxylon*, and many species groups show apparently consistent, specific HPLC profiles. The non-destructive HPLC-based methodology even worked well with various ancient type materials, relating them to recent conspecific records. The utility of this approach is demonstrated, and possible implications for classification of *Hypoxylon* are discussed. poster

Stamenova, Elena K.*, Coumes, Kendra M., Balakrishna, Kanthi, Chalkley, David B. and Catranis, Catharine M. Mycology Collection, American Type Culture Collection, Manassas, VA 20110, USA. ccatranis@atcc.org. **Application and resolution – another look at how to answer the customer's questions.**

Two case histories are described. The first case was directed at resolving the discrepancies between an isolate that was identified as morphologically identical to the type, *Zygosaccharomyces bisporus* when deposited but now proves to be a distinct species, *Z. bailii*. Sequencing results for ITS1/ITS2 region of nuclear rDNA of ATCC® 38993™, deposited as *Z. bisporus* showed 96 % identity to the *Z. bailii*. This was confirmed by presentation of a repetitive PCR "barcode" pattern matching that for the *Z. bailii* type strain, ATCC® 58445™. Results from substrate oxidation and assimilation tests (Biolog) also identified the problematic strain as *Z. bailii*. The second case study employed similar technologies to resolve discrepancies between the type, *Hortaea werneckii* ATCC® 36317™, and two strains deposited as morphologically identical to the type, ATCC® 58301™ and ATCC® 58951™. Sequencing of ITS1/ITS2 rDNA showed one of these strains, ATCC® 58301™ as distinct from the type, with 97% identity to *Exophiala spinifera*. This result was confirmed by alignment of repetitive PCR "barcodes" and the agreement of results of carbon source utilization tests using Biolog microplates. Incorporation of DNA-based analyses and microplate-based physiological screens proved critical to resolving questions of species identity. poster

Stefani, Franck, O.P.^{1*} and Berube, Jean, A.² ¹Centre de Recherche en Biologie Forestière, Université Laval, Sainte-Foy (QC), Canada, G1K 7P4, ²Natural Resources Canada, Canadian Forest Service, 1055 du Peps, Sainte-Foy, QC, G1V4C7, Canada. fstefani@cfl.forestry.ca. **Biodiversity of foliar endophytes in white spruce and their use to assess the impact of transgenic trees on non-target organisms.**

To investigate the foliar endophyte biodiversity of white spruce (*Picea glauca*) and establish a baseline for future comparative studies examining impacts of forestry practices, we sampled seven natural stands, four trees per site, one branch per tree and 10 needles per branch for a total of 280 needles. We performed PCR-RFLP analysis on the ITS region and analysed the DNA sequence by maximum of parsimony and Bayesian inference. In all 23 morphotypes were identified as 14 sequences groups and we demonstrated that morphological groups are poor indicators for estimating species diversity. This study is the first to establish a baseline of foliar endophyte biodiversity of white spruce and to provide species richness values for foliar endophytes. Seventy-five percent of all 141 isolates in this study have a high sequence homology with *Lophodermium piceae*, 10.96% with a *Mycosphaerella* sp., and 5.47% with a *Hypoxylon* sp. This data was used as a baseline to determine the impact of transgenic white spruce on non-target organisms. To do so we sampled transgenic *Bt CryIa(b)* white spruce needles in a single plantation. Eight foliar endophyte taxa were identified and their frequencies were statistically analysed. No statistical difference in endophytes incidence or distribution was observed between control white spruce needles (with no genetic construct) and seedlings with kanamycin constructs containing the reporter gene *gus* or containing the *Bt CryIa(b)* gene. We have not observed an impact of the genetic constructs on the population of foliar endophyte living inside white spruce needles. Similarly the endophytes found in transgenic tree needles were not different from those of natural stands except for the presence of two endophytes linked to the juvenile state of the plantation. contributed presentation

Stephenson, Steven L. and Shadwick, John D.* Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. slsteph@uark.edu. **Snowbank myxomycetes from alpine areas of southeastern Australia.**

One group of myxomycetes (plasmodial slime molds or myxogastrids) is restricted to the rather special and very limited microhabitat represented by melting snowbanks in alpine regions of the world. The species that occupy this microhabitat are usually referred to as "snowbank" or "nivicolous" myxomycetes. Most records of snowbank myxomycetes are from the Northern Hemisphere, and the species found in the mountains of Europe and the western United States are particularly well known. During the period of mid- to late October of 2004, snowbank-associated myxomycetes were collected from alpine areas of southeastern Australia. Most collections came from the high-elevation region around Mt. Kosciuszko (the highest peak on the continent at 2228 m) in the southern part of New South Wales, but additional series of collections were obtained from two other study sites (Mt. Buller and Mt. Hotham) in northern Victoria. Approximately 300 specimens were collected over a period of two weeks. These specimens appear to include a number of species not previously known to occur in Australia. In contrast to most other areas of the world where snowbank myxomycetes have been studied, species of *Diderma* were poorly represented among the collections from Australia. (Supported in part by a grant from the Australian Biological Resources Participatory Program.) poster

Stephenson, Steven L. Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA. slsteph@uark.edu. **Myxomycetes from the antarctic and subantarctic.**

Myxomycetes (also called myxogastrids or plasmodial slime molds) have been reported from a number of localities in the Antarctic and Subantarctic. These include the Antarctic Peninsula (64–65 degrees S), Signy Island (60 degrees S), South Georgia Island (54–55 degrees S), Macquarie Island (54 degrees S) and Campbell Island (52 degrees S). Among the myxomycetes reported are several examples (e.g., *Diderma niveum*, *Didymium dubium* and *Trichia alpina*) known from nivicolous (snowbank) habitats elsewhere in the world, but the majority of records are those of more widely distributed or apparently cosmopolitan species such as *Arcyria cinerea*, *Craterium leucocephalum* and *Trichia verrucosa*. Lignicolous species (e.g., *Comatricha nigra*) are uncommon and appear to be restricted largely to imported wood except for those islands in the Subantarctic (e.g., Campbell Island) where there are a few woody plants. In the absence of woody substrates, most fruitings occur in association with living bryophytes, on living and dead portions of low-growing herbaceous plants, and on exposed surfaces of peat deposits. Interestingly, four species of myxomycetes (*Diderma antarctica*, *Leptoderma megaspora*, *Oligonema dancoii* and *Trichia antarctica*) have been described from material collected on the Antarctic Peninsula. (Supported in part by two grants from the National Science Foundation.) symposium presentation

Stewart, Jane E.^{1*}, Kim, Mee-Sook¹, James, Robert L.², Dumroese, R. Kasten³ and Klopfenstein, Ned B.¹ ¹USDA Forest Service Rocky Mountain Research Station, 1221 S. Main St., Moscow, ID 83843, USA, ²USDA Forest Service Forest Health Protection, 3815 Schreiber Way, Coeur d'Alene, ID 83815, USA, ³USDA Forest Service Southern Research Station, 1221 S. Main St., Moscow, ID 83843, USA. janestewart@fs.fed.us. **Molecular characterization of pathogenic and nonpathogenic *Fusarium oxysporum* from a conifer nursery.**

Root disease caused by *Fusarium oxysporum* can cause severe losses in conifer nurseries. This fungus commonly occurs in container and bareroot nurseries on healthy and diseased seedlings, conifer seeds, and in soils. Though isolates of the fungus differ in virulence, studies show that pathogenicity and isolate morphology are not correlated. Forty-one isolates of *F. oxysporum* collected from a conifer nursery were selected for pathogenicity tests and molecular characterization. Amplified Fragment Length Polymorphism (AFLP) and DNA sequences (internal transcribed spacer + 5.8S rDNA, mitochondrial small subunit, and nuclear translation elongation factor 1 alpha) used to compare molecular characterization of the isolates. Each isolate had a unique AFLP genotype, and 30 markers were unique to highly pathogenic isolates. In all analyses, highly pathogenic isolates and non-pathogenic isolates separated into two clades with 100 % bootstrap and posterior probability support. Genetic analyses indicate molecular probes could be developed to differentiate pathogenic from non-pathogenic isolates of *F. oxysporum*. This research will help aid the development of molecular tools to enable nursery managers to implement timely and appropriate disease management practices. poster

Stewart, Julie¹, Roy, Bitty¹ and Mulder, Christa². ¹Center for Ecology and Evolution, University of Oregon, Eugene, OR, USA, ²Department of Biology and Wildlife, University of Alaska, Fairbanks, AK, USA. jlk650@hotmail.com. **The effect of abiotic conditions and plant origin on pathogen and herbivore attack rates in interior Alaska: Implications for pest responses to climate change.**

Global climate change may influence plant growth and community composition not only through changes in temperature and precipitation, but also by altering attack rates by pests. Pathogens and herbivores are generally predicted to

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increase with warming, but few studies have tested this prediction, especially for pathogens. Pests are expected to alter their ranges in response to climate change more quickly than plant species. Exposure to new species of herbivores and pathogens may lead to changes in attack rates, especially if plants are locally adapted to their pests. We performed a reciprocal transplant experiment in order to disentangle the effects of environment and plant genotype on attack rates. *Alnus crispa* seedlings originating from 9 sites that vary widely in abiotic conditions were planted at their site of origin and at all other sites. Damage surveys revealed that attack rates by pathogens and herbivores and the number of attacking species varied by destination (the site at which seedlings were planted) but not by origin or seedling genotype. This suggests that *A. crispa* is not locally adapted to its pests. Pathogen damage varied with site moisture, plant density, winter temperature, and snowmelt date. However, herbivore damage was not explained by any of these site characters, suggesting that climate change may have a larger impact on pathogens than herbivores. contributed presentation

Strongman, Doug B. Biology Department, Saint Mary's University, 923 Robie St., Halifax, Nova Scotia, Canada. doug.strongman@smu.ca. **Trichomyces from eastern Canada.**

Trichomyces are commensalistic fungi inhabiting the gut of a variety of arthropods, including freshwater, aquatic species. Immature stages of stoneflies, mayflies and dipterans living in streams house a diverse array of gut-fungi. The biodiversity of these fungi in certain areas of North America, South America and Europe has been documented but in other areas, such as Canada, there are few records of Trichomyces. I have collected more than 20 species of Trichomyces from aquatic insect hosts in eastern Canada including several apparently undescribed species. A summary of these findings will be presented highlighting the proposed new species. contributed presentation

Summerbell, Richard C.*, Starink-Willemsse, Mieke and van Iperen, Arien. CBS Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, the Netherlands. summerbell@cbs.knaw.nl. **What to do about complex and simplified morphologies in the *Acremonium* coenosis?**

The anamorph genus *Acremonium* has long been known to be highly morphologically simplified, and over 40 genera of nectrioid, cephalothecoid and chaetomioid fungi are known to have *Acremonium*-like states. A molecular phylogenetic study of the biodiversity of *Acremonium* species other than known members of the *Chaetomiaceae* was undertaken by our group. Ribosomal sequences including complete 18S, 28S D1/D2 region, and internal transcribed spacer (ITS) were utilized as appeared appropriate, combined with actin or beta tubulin regions to resolve closely interrelated groups. The biodiversity of species was extensive, and ITS sequences were alignable only within 20 or more small groups of related species. An emerging pattern showed that one or more recognized *Acremonium* species often associated phylogenetically with a more morphologically complex anamorphic fungus: e.g., *Acremonium strictum* associated with *Sarocladium* spp., *Acremonium crocicimigenum* with *Trichothecium*, *Acremonium cucurbitacearum* with *Plectosporium*. Cladistically orthodox nomenclature would see such species combined into the morphologically complex generic concepts, while the anti-cladistic typology still upheld, at least for anamorphs, by many fungal systematists would have the convenient visual concept of *Acremonium* as a broad and phylogenetically abstruse 'nomenclatural substratum' out of which named, complex apomorphs would emerge. The pros and cons of each approach are complex and require careful consideration. symposium presentation

Sunagawa, Masahide* and Magae, Yumi. Department of Applied Microbiology, Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan. masahide@ffpri.affrc.go.jp. **Isolation of genes differentially expressed during the fruit body development of *Pleurotus ostreatus* by differential display of RAPD.**

To analyze genes involved in fruit body development of *Pleurotus ostreatus*, mRNAs from three different developmental stages: i.e., vegetative mycelium, primordium, and mature fruit body, were isolated and reverse-transcribed to cDNAs. One hundred and twenty random PCR amplifications were performed with the cDNAs, which generated 382, 394, 393 cDNA fragments from each developmental stage. From these fragments, four cDNA clones specifically expressed in primordium or mature fruit body were detected. Sequence analysis and database searches revealed significant similarity with triacylglycerol lipase, cytochrome P450 sterol 14 α -demethylase and developmentally regulated genes of other fungi. Northern blot analyses confirmed that all of the four cDNAs were unexpressed in mycelium, thus stage-specific genes for fruit body formation of *P. ostreatus* were successfully isolated. poster

Sung, Gi-Ho and Spatafora, Joseph W. Dept. of Botany and Plant Pathology, Oregon State University, Corvallis OR 97331, USA. sungg@science.oregonstate.edu. **Phylogenetic classification of *Cordyceps* and clavicipitaceae fungi.**

Cordyceps is a large genus with over 400 species. It is the member of Clavicipitaceae based on its cylindrical ascus, thickened ascus apices, and filiform ascospores, which often disarticulate into partspores. *Cordyceps* is distinguished from other genera of the family by the combination of the production of well-de-

veloped stromata and its ecology as a pathogen of arthropods and truffles. Current subgeneric classifications emphasize presentation of perithecia and ascospore morphology. To test and refine the classifications of *Cordyceps*, we present phylogenetic analyses of a combined dataset of five genes. The results reject the monophyly of *Cordyceps* and Clavicipitaceae and support the existence of three clavicipitaceae clades, all of which include the members of *Cordyceps*. We revise *Cordyceps* and the Clavicipitaceae to reflect this phylogeny. The family Cordycipitaceae is proposed based on placement of the type, *C. militaris* and includes *Cordyceps* species that possess brightly colored fleshy stromata. The family Ophiocordycipitaceae is proposed based on *Ophiocordyceps* Petch; the majority of species in this clade produce darkly pigmented, tough to pliant stromata. A new genus *Metacordyceps* is proposed for *Cordyceps* species that are closely related to the grass symbionts of Clavicipitaceae s.s. Additional characters and relationships among the proposed taxa are discussed. poster

Suzaki, Kouichi^{1*}, Kanematsu, Satoko¹, Matsumoto, Naoyuki², Ito, Tsutae¹ and Yoshida, Kouji³. ¹Department of Apple Research, National Institute of Fruit Tree Science, Shimokuriyagawa, Morioka 020-0123, Japan, ²National Institute for Agro-Environmental Sciences, Kannondai, Tsukuba, Japan, ³Department of Plant Protection, National Institute of Fruit Tree Science, Tsukuba, Japan. kcsuzaki@affrc.go.jp.

Horizontal transmission of mycoviruses in violet root rot fungus *Helicobasidium mompa*.

To examine the potential of a method of mycovirus infection to violet root rot fungus *Helicobasidium mompa*, horizontal transmission of mycoviruses between isolates of this fungus was investigated. Isolate V70, which was dikaryotic and infected with partitivirus, was used as a mycovirus donor. When isolate V70 was paired on plate media with either of the mycelially incompatible isolates of *H. mompa*, the partitivirus was not transmitted into different recipients at all. However, monokaryotic strains, which were genetically same with isolate V70 and contained the partitivirus, permitted the transmission of the partitivirus into different recipients. Then, the transmissibility of another mycovirus, totivirus in the hypovirulent isolate V17 of *H. mompa*, was examined using the monokaryotic strains as vectors of the mycovirus. When the monokaryotic strains containing the totivirus were paired on plate media with the 12 recipients belonging to 11 mycelial compatibility groups (MCGs), the totivirus was transmitted into 7 of the 12 recipients (i.e., 7 of 11 MCGs). Based on these results, we concluded that monokaryotic strains could act as vectors to transmit mycoviruses into various isolates of *H. mompa*. *H. mompa* isolates that acquired the totivirus from monokaryotic strains were inoculated into apple saplings, and virulence of the inocula was attenuated by infection of the totivirus. poster

Suzuki, Akira. Department of Biology, Faculty of Education, Chiba University, 1-33, Yayoi-cho, Inage-ku, Chiba 263-8522, Japan. asmush@faculty.chiba-u.jp. **Physiological ecology of ammonia fungi - studies using artificial media and natural substrates.**

This address reviews research on the ecophysiology of ammonia fungi. We investigated vegetative and reproductive growth of ammonia fungi on artificial media and on natural substrates to estimate fungal activity in the field. We also conducted culture of two to five species of ammonia fungi together on natural substrates as well as multiple cultures of ammonia fungi on nutrient agar media, to record interactions between ammonia fungi. Our results indicate that the sequential colonization and fruiting of ammonia fungi in the field can be explained primarily by the preference or tolerance of a species to high concentrations of ammonium-N under neutral to alkaline conditions. Saprobic, basidiomycete, ammonia fungi are more strongly adapted to invade ammonium-N rich substrates under acidic to alkaline conditions than are other saprobic ammonia fungi and mycorrhizal ammonia fungi. The pattern of colonization by each ammonia fungus in the field appears to relate to interactions between ammonia fungi. Saprobic ammonia fungi are the principal agents of litter decomposition in ammonium-N rich substrates under neutral to alkaline conditions. Such decomposition is mainly of cellulose due to the cellulolytic enzymes of these fungi having neutral to alkaline pH optima. MSJ Presidential Address

Szabo, Les J. USDA ARS Cereal Disease Laboratory, University of Minnesota, St. Paul, MN 55108, USA. lszabo@umn.edu. **Deciphering species complexes and the evolutionary implications.**

Species complexes are common among the Uredinales, which often results in confusion regarding the biology of these fungi. Two examples that are currently being studied are the heteroecious, macrocyclic rust fungi *Puccinia andropogonis* and *P. coronata*. *P. andropogonis* has a narrow telial host range (prairie grasses *Andropogon gerardii* and *Schizachyrium scopari*) and a broad aecial host range that spans seven plant families. In contrast, *P. coronata* has a broad telial host range (*Aveneae*, *Poeae*, and *Triticodae*) and a narrow aecial host range of a single genus (*Rhamnus*). The nuclear ribosomal region including the complete ITS and 5' end of the LSU was analyzed for 34 samples of *P. andropogonis* and 48 samples of *P. coronata*. Phylogenetic analysis divided the *P. andropogonis* complex into eight well supported groups that were divided along telial and aecial lines. These results indicate that there were two evolutionary events, the first separation

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on the telial hosts followed by radiation onto different aecial hosts. Speciation follows taxonomic classification of aecial families. Analysis of DNA sequence data divided the *P. coronata* complex into seven well support groups. Results indicate that speciation in the *P. coronata* complex has occurred primarily through radiation onto different telial hosts. symposium presentation

Takabatake, Koji^{1*}, Sasaki, Hiroko² and Sugahara, Tatsuyuki². ¹Toyama Forestry and Forest Products Research Center, Yoshimine, Tateyamama-machi, Toyama, 930-1362, Japan, ²Seitoku University, 550 Iwase, Matsudo-shi, Chiba, 271-8555, Japan. takabata@fes.pref.toyama.jp. **Cultural waste from *G. frondosa* cultivation for use as a substrate in the sawdust-based cultivation of *Hericum erinaceum*.**

Sawdust-based cultivation of *Hericum erinaceum* has just begun, and cultivators are hoping for an increase in yield. Consumers want the strong bitterness in the fruiting bodies of *H. erinaceum* reduced. When the cultural waste from *Gri-fola frondosa* cultivation was used as a substrate in the sawdust-based cultivation of *H. erinaceum*, the yield was increased compared with the usual case in which Buna, *Fagus crenata*, hardwood sawdust was used. By treating the cultural waste from *G. frondosa* cultivation with aging, the yield was increased even more and the total content of free amino acids which cause the bitter taste in the fruiting bodies of *H. erinaceum* was decreased. The sense examination in the fruiting bodies cultivated on a substrate using the cultural waste from *G. frondosa* cultivation treated with aging confirmed that the strong bitter taste of fruiting bodies was reduced. From the results above, it becomes clear that the cultural waste from *G. frondosa* cultivation treated with aging is a very useful substrate for the sawdust-based cultivation of *H. erinaceum*. poster

Takada, Nao and Tsujiyama, Sho-ichi*. Graduate School of Agriculture, Kyoto Prefectural University, Simogamo-nakaragi-cho, Sakyo-ku, Kyoto 606-8522, Japan. s_tsuji@kpu.ac.jp. **Biodegradation of 2,4-dichlorophenoxy acetic acid (2,4-D) by litter-decomposing basidiomycetes in soil.**

Artificial chemical compounds leaked into environments are sometimes harmful to human, animals, plants and other organisms. White-rot fungi are the strongest degrader in forest ecosystem and have been expected for the bioremediation of the environmental pollutants. However, it is questioned whether white-rot fungi would degrade the environmental pollutants in soil system. We found that the litter-decomposing basidiomycetes have a high degradability of lignin to the same level of white-rot fungi. Then, we applied the litter-decomposing basidiomycetes to bioremediation of chlorinated phenols. Among 11 kinds of litter-decomposing basidiomycetes, *Calvatia craniiformis* and *Psathyrella velutina* decomposed 2,4-dichlorophenoxy acetic acid (2,4-D) in a liquid culture to the same level of a white-rot fungus *Trametes versicolor*. Next, degradation of 2,4-D in sterile soil culture was tested using *C. craniiformis* and *P. velutina*. After 6 months, amounts of residual 2,4-D in the *C. craniiformis* culture were 0.8%, while those in the *P. velutina* cultures were 67.5%. *C. craniiformis* has a potential for the bioremediation of polluted soils. poster

Takahashi, Yukiko^{1*}, Matsushita, Norihisa¹ and Harada, Yukio². ¹Graduate School of Agricultural and Life Sciences, The University of Tokyo, Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan, ²Faculty of Agriculture and Life Science, The Hirotsuki University, Bunkyo-cho 3, Hirotsuki, Aomori 036-8561, Japan. y_takah@fr.a.u-tokyo.ac.jp. **A cup fungus in the Sclerotiniaceae having *Mycopappus*-like anamorph, parasitic on leaves of deciduous *Quercus* spp.: a phylogenetic study.**

Quercus L. spp. are widely distributed in Japan, and are important woody plant species, which have been closely related with Japanese cultures and lives since early time. Frosty mildew is one of the leaf disease caused by *Mycopappus quercus* Y. Suto and M. Kawai on deciduous *Quercus* spp. Although this disease was first reported as a nursery disease, the fungus has infected not only young seedlings but also mature trees. It is considered that early defoliation caused by the infection of the fungus might have effects on the tree health. Recently, the teleomorph of the fungus was found as a cup fungus arising from sclerotial stroma, thus the fungus was thought to belong to the Sclerotiniaceae. However, no genus in the Sclerotiniaceae was known having such *Mycopappus*-like anamorph, so it has been taxonomically unknown. A phylogenetic analysis of rDNA-ITS region of the fungus showed that it belongs to the Sclerotiniaceae but was distant from other sclerotiniaceous species. The result supported that the fungus is distinct from any known genera in the Sclerotiniaceae. Meanwhile, the result of analysis of small subunit rDNA showed that the fungus was distance from other *Mycopappus* species, whose teleomorph is known as the Phaeosphaeriaceae, suggesting the necessity of nomenclatural revision for the anamorph. poster

Takamatsu, Susumu^{1*}, Matsuda, Sanae¹ and Havrylenko, Maria². ¹Faculty of Bioresources, Mie University, Tsu 514-8507, Japan, ²Centro Regional Universitario Baliloché, Universidad Nacional del Comahue, San Carlos de Bariloche, Argentina. takamatsu@bio.mie-u.ac.jp. **Origin, co-speciation and biogeography of the genus *Golovinomyces* (Ascomycota: Erysiphales).**

Golovinomyces is a major genus of the powdery mildew fungi (Erysiphaceae), which infects more than 2000 host species in herbaceous plants covering 53 plant families. Molecular phylogenetic analyses using rDNA se-

quences suggested that the primary host of the genus *Golovinomyces* is the family Asteraceae. *Golovinomyces* first diverged in accord with the phylogeny of their hosts, which occurred within the Asteraceae. Subsequently, multiple transitions to different hosts occurred from the tribe Lactuceae of the Asteraceae to other plant families. Integrated phylogenetic analysis of *Golovinomyces* collected in South America, the center of origin of the Asteraceae, suggested that *Golovinomyces* first acquired parasitism to the Asteraceae after migration of the family into the Northern Hemisphere and before the divergence of the tribe Cardueae. Based on the comparative phylogenetic analyses of *Golovinomyces* and their host tribes of the Asteraceae, we estimated nucleotide substitution rates of the rDNA ITS regions and the D1/D2 domains of the 28S rDNA. The substitution rate of the ITS region (0.01D = 3.97 myr) agrees well with those of a wide range of plants. The substitution rate of the 28S rDNA (0.01D = 15.4 myr) estimated that the first radiation within the Erysiphaceae occurred in the late Cretaceous, which is congruent with our previous calculation using molecular clock of the 18S rDNA. symposium presentation

Takizawa, Kayoko¹, Abliz, Paride², Motta, Cristina, S.³, Xi, Liyan⁴, Vidotto, Valerio⁵ and Fukushima, Kazutaka^{1*}. ¹Res. Ctr. for Pathogenic Fungi & Microbial Toxicoses, Chiba University, 1-8-1 Inohana, Chuo-ku, Chiba, Japan, ²Xinjiang Medical University, Urumqi, China, ³Federal University Pernambuco, Recife, Brazil, ⁴Sun Yat-Sen University, Guangzhou, China, ⁵University of Turin, Torino, Italy. kfuky@faculty.chiba-u.jp. **New strain subtypes of *Trichophyton tonsurans*, a causative agent of tinea capitis, based on the variable internal repeat region within the nontranscribed spacer of rDNA locus.**

An epidemiological survey revealed that *Trichophyton tonsurans* has become a significant etiological agent of tinea capitis in USA, Europe and also in Japan. This paper deals with the finding of 6 new strain subtypes based on the variable internal repeat (VIR) region within the nontranscribed spacer (NTS) in interstrain of *T. tonsurans*. The corresponding amplicons from the VIR and NTS (2.3-2.9 kb) regions were successfully amplified in all of 27 isolates obtained from 4 countries of Brazil (15), USA (2), China (9) and Italy (1). For all VIR amplicons, complete sequencing was performed. A. Gaedigk found 5 variants differing in size within the VIR comprised of several large repeats arranged in tandem in 92 *T. tonsurans* isolates in USA. We found 6 new strain subtypes (A, B1, B2, C2, W1 and W2), differed from the 5 subtypes above. The subtypes Ws were consisted of a complex of two VIR with different sizes. Interestingly, all isolates from China were verified to possess new strain subtypes differed from those of American isolates including 2 isolates tested here, and were discriminated into four subtypes furthermore. Of 15 Brazilian isolates, two new subtypes were found in 3 isolates, but other isolates possessed identical subtypes as any one of American's. The VIR analysis is considered as the most accurate method that can facilitate strain discrimination in population-based studies. poster

Tamai, Yutaka*, Fukuchi, Sata, Iijima, Saori, Yajima, Takashi and Miyamoto, Toshizumi. Dept. of Forest Science, Hokkaido University, Sapporo 060-8589, Japan. ytamai@for.agr.hokudai.ac.jp. **Mycorrhizae from Mount Esan volcano, Hokkaido Japan.**

Twenty-one higher plant species from the crater floor of Mount Esan volcano in Hokkaido Japan were investigated for mycorrhizal features. Most of the woody plant species observed were shrubs. Ericales dwarf shrubs mainly composed from *Empetrum nigrum-Ledum palustre* communities were dominant in this area. Ectomycorrhiza had been observed on none of the plant species. Arbuscular mycorrhizal colonization was observed on 12 species (*Sasa senanensis*, *Miscanthus sinensis*, *Poaceae* sp., *Carex* sp. *Heloniopsis orientalis*, *Polygonum sachalinensis*, *Hydrangea paniculata*, *Empetrum nigrum*, *Ilex sugenokii*, *Ledum palustre*, *Enkianthus campanulatus*, *Vaccinium vitis-idaea*). No mycorrhizae were found on *Polygonum weyrichii*. All of the Ericales species except for *Enkianthus campanulatus* formed ericoid mycorrhizae. Thirteen RFLP types of ericoid mycorrhizal fungi like strains were isolated from roots of *Ledum palustre*. ITS sequence of the 7 strains showed high homology with some ericoid mycorrhizal fungi (*Oidiodendron maius*, *Hymenoscyphus ericae*). poster

Tanaka, Chihiro* and Oda, Takashi. Lab. of Environ. Mycoscience, Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan. chihiro@remach.kais.kyoto-u.ac.jp. **Molecular phylogeny and biogeography of some *Amanita* species.**

The molecular phylogeny and biogeography of two widely distributed *Amanita* species, *A. muscaria* and *A. pantherina*, were studied based on specimens from diverse localities. Analyses of both a partial sequence of the ITS region of nuclear rDNA and a partial sequence of the beta-tubulin gene were able to resolve biogeographic structure of each species. The results of our analyses revealed a greater divergence in nucleotide sequences of the partial beta-tubulin gene than the ITS region. Based on molecular phylogeny of the combination of nucleotide sequences from the ITS region and the partial beta-tubulin gene, *A. muscaria* could be separated into at least three groups (Eurasian, Eurasian sub-alpine, and North American), and *A. pantherina* could be separated into at least two groups (North American and Eurasian). For both *A. muscaria* and *A. panthe-*

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rina, the intracontinental relationships of both Eurasia and North America were closer than the relationships between eastern Asia and eastern North America. contributed presentation

Tanaka, Eiji^{1*} and Tanaka, Chihiro². ¹Graduate School of Environmental Science, The University of Shiga Prefecture, 2500 Hassaka-cho, Hikone, Shiga 522-8533, Japan, ²Graduate School of Agriculture, Kyoto University, Kitashirakawa Oiwake-cho, Sakyo-ku, Kyoto-shi 606-8502, Japan. age-t@mbx.kyoto-u.ac.jp. **Phylogenetic study of clavicipitaceous fungi using acetaldehyde dehydrogenase gene sequences.**

Clavicipitaceous fungi are biotrophs and their hosts include plants and insects. Various molecular phylogenetic studies have been performed, especially among the *Cordyceps* species (parasites of insects and other organisms) or among the grass biotrophic species. However, the relationship among the subfamilies in Clavicipitaceae has not been cleared. We have searched reasonable regions to examine the phylogeny among the subfamilies. We demonstrated that sequences of one of aldehyde dehydrogenase (ALDH) gene families were useful. The DNA sequences of the third exon of this gene were 889 bp long and no insertions/deletions were observed in any fungi used in this study. The phylogenetic tree indicated that the clavicipitaceous fungi were divided into two large groups with extremely high bootstrap support. One group included species of *Cordyceps* and *Ustilaginoides*. This suggests the necessity for reexamination of the teleomorph of *Ustilaginoides virens*, because its teleomorph has been classified as *Claviceps oryzae-sativae*. Another group included only grass biotrophic species. This group was further divided into three reasonable groups: species with neotyphodial anamorph (e.g. *Epichloe*), species with ephelidial anamorph (e.g. *Heteroepichloe*) and *Aciculosporium-Claviceps* species. This phylogenetic tree using ALDH gene clearly indicated the putative subfamily in Clavicipitaceae. poster

Tanaka, Isshin^{1*} and Kurogi, Shuichi². ¹Sankyo Co., Ltd., Lead Discovery Research Laboratories, 33 Miyukigaoka, Tsukuba city, Ibaraki 305-0847, Japan, ²Miyazaki Prefectural Museum of Nature and History, 2-4-4 Jingu, Miyazaki city, Miyazaki 880-0053, Japan. itanak@sankyo.co.jp. **A revision of *Physalacria orientalis* (Agaricales, Basidiomycota).**

Physalacria orientalis is an unusual basidiomycete in Japan, known only from its original description in 1951. A study of *P. orientalis* has shown the presence of several unreported or unconfirmed characters in this fungus. In this study, it has wider basidiospores than those in the original description, small openings at the lower portion of the capitulum and clamp connections. Based on the original description, plus the above-mentioned additional characters, *P. orientalis* is considered to be conspecific to *P. tropica*. *Physalacria tropica* has been reported only in tropical regions (Malaysia, Cameroon, Papua New Guinea). This is the first record of *P. tropica* in a temperate region. Phylogenetic analysis using partial sequences of the nuclear large subunit ribosomal rDNA shows that this fungus should be placed in the physalacria clade and close to *P. decaryi* collected in Japan. poster

Tanaka, Kazuaki*, Hatakeyama, Satoshi and Harada, Yukio. Faculty of Agriculture and Life Science, Hirosaki University, 3 Bunkyo-cho, Hirosaki, Aomori 036-8561, Japan. kt881122@yahoo.co.jp. ***Massarina*-like species on bamboos and their hyphomycetous anamorphs having chiroid conidia.**

Several pleosporalean fungi belonging to *Massarina* sensu lato were collected from bamboos. They produced hyphomycetes with chiroid conidia, such as *Tetraploa* and *Piricaudiopsis*. To date, the congeneric relation between *Massarina* and *Tetraploa* has been known only from one example (*M. tetraploa* = *T. aristata*), while the teleomorph of *Piricaudiopsis* has not been reported. Based on morphological features, the bamboo fungi can be separated into following four groups; 1) "Tetraploa": characterized by the small subglobose ascomata and the *Tetraploa* anamorph (sensu stricto); 2) "Triposphaeria": characterized by the depressed ascomata and the *Tetraploa*-like anamorph having three appendages; 3) "Multiploa": characterized by the large ascomata composed of thick ascomal wall and the *Tetraploa* (or *Piricauda*)-like anamorph having several appendages; 4) "Piricaudioploa": characterized by the large depressed ascomata with well developed rim-like ascomal wall and the *Piricaudiopsis* anamorph. The taxonomy of *Massarina* is currently quite controversial and many species including *M. tetraploa* have been transferred to the genus *Lophiostoma*. We consider, however, the *Massarina*-like fungi on bamboos do not belong neither to *Massarina* nor *Lophiostoma* owing to the differences found in ascomata and anamorphs, and the above four groups are regarded as different at generic level. poster

Tang, Alvin M.C., Jeewon, Rajesh and Hyde, Kevin D. Centre for Research in Fungal Diversity, Department of Ecology & Biodiversity, The University of Hong Kong, Pokfulam Road, Hong Kong SAR, China. alvtangmc@yahoo.com.hk **Molecular Evolution of Genes for Phylogenetic Analysis of the Class Sordariomycetes.**

It is increasingly common in molecular phylogenetics to use combination of several gene regions to determine evolutionary relationships among fungi. This not only resolves deep phylogenetic relationships, but also increases support values for branches. However, very little is known about the processes of molecular

evolution in fungal genes and how these factors affect their classification. This study aims to address these problems by elucidating the modes and rates of molecular evolution for 6 genes (actin, atp6, cox3, EF-1 alpha, RPBII, beta-tubulin) in taxa of the Sordariomycetes. The utility of these genes for determining evolutionary relationships will be tested at various taxonomic levels using single and combined data sets. The study will provide valuable information for the selection of alternative genes to nuclear ribosomal DNA and lead to a more thorough understanding of evolutionary processes in the Ascomycota and fungi in general. poster

Taylor, D. Lee^{1*}, Herriott, Ian¹, Geml, Jozsef¹, Marr, Tom¹, Long, James¹, Ruess, Roger¹, Laursen, Gary¹ and Nusbaum, Harris². ¹Institute of Arctic Biology, University of Alaska, Fairbanks, AK 99775, USA, ²Broad Institute - MIT, Cambridge, MA 02141, USA. lee.taylor@iab.alaska.edu. **Fungal basidiome and soil diversity under the Aurora Borealis.**

Fungi are critical but poorly characterized players in nutrient cycling in the boreal forest, which holds approximately one quarter of the Earth's labile carbon. We are characterizing fungal communities in representative boreal ecosystems, primarily within the Bonanza Creek LTER site. We extracted soil genomic DNAs from ~1500 cores, and are constructing clone libraries of amplicons spanning the fungal ITS and LSU. Preliminary LSU analysis of 206 black spruce litter layer clones revealed the following trends. 1) Mycorrhizal taxa were far more abundant than any other guild: 64% of the clones fell into mycorrhizal clades, while only 4% of the clones could be identified as saprophytes. 2) ECM fungi comprised 42% of all clones, ericoid 18% and e-strain 4%. 3) The resupinate ECM taxa *Piloderma* and *Amphinema*, which are noted for litter decay tendencies, comprised more than half the ECM clones. 4) Interesting taxa include members of the novel Clade 1 of Schadt *et al.* (2002) and a distinct clade allied with the Clavicipitaceae. We have developed ITS and LSU databases of GenBank sequences and a powerful FASTA searching method which are publicly available at <http://iab-devel.arcs.edu/metagenomics/>. We are adding sequences from thousands of Alaskan sporocarps to these databases. Phylogeographic analysis of several genera suggests that Alaska is a hot-spot of fungal genetic diversity. symposium presentation

Terashima, Yoshie. Haniya 1887-1, Sanbu-machi, Sanbu-gun, Chiba, 289-1223, Japan. y.trsh2@ma.pref.chiba.jp. **The effect of substrate composition on quantity, quality and nutritional value of Shiitake mushroom, *Lentinula edodes*, fruit bodies.**

It was found on *Lentinula edodes*, that adding thiamine (VB1) to substrate affected the VB1 content of fruit bodies, that varying the supplements affected the taste of fruit bodies, and that fat in supplements affected fruit body yield. 1) VB1 is a water-soluble trace element that regulates the decomposition of sugars in the human body. Fruit bodies obtained from substrates with 10 mg per kg VB1 contained three times more VB1 than those grown on substrate without. The addition of VB1 did not influence the major nutritional components, mycelial growth, or yield. 2) In addition to medicinal benefits, the dietary fiber of fruit bodies is important for human health, and consumer satisfaction is one of the key factors for promoting consumption. Seven sensors that included appearance, color, smell, taste and general satisfaction were compared in relation to six substrates containing various supplements. Fat-free rice and wheat bran (1:1) was considered to be optimal for the first flush, but there was no difference in the sensors among the substrates for the second and third flushes. 3) Compared to raw rice bran, the lack of oil in fat-free rice bran resulted in decreased mycelial biomass and affected yield negatively. With longer spawn runs, there was no significant difference in the yield. However, shorter runs using fat-free rice bran as a substrate resulted in lower yields. symposium presentation

Terashita, Takao. Laboratory of Food Microbiological Science and Biotechnology, Faculty of Agriculture, Kin-ki University, 3327-204, Nakamachi, Nara 631-8505, Japan. terasita@nara.kindai.ac.jp. **Characterization of beta-glucosidase from *Tricholoma matsutake* and its enzyme production.**

Tricholoma matsutake (S. Ito & Imai) Sing. are difficult to cultivate artificially without the host plant. This fungus grows so slowly on the artificial media (about 20mm/month) and has low capability to decompose polysaccharides. From the artificial cultivation of *T. matsutake*, starch hydrolyzing ability is very important because the fungus has not been known to use other polysaccharides except starch. We studied the amylase productions in this fungus. As a result, we showed that *T. matsutake* has alpha-amylase, alpha-glucosidase and beta-glucosidase in the still culture filtrate. These finding suggests some saprotrophic abilities of *T. matsutake*. The purified beta-glucosidase was most active at pH 5.0 and stable within the pH range of 5.0-8.0. The molecular mass was 168kDa by SDS-PAGE and readily hydrolyzed the beta-1,4 glucosidic bond of oligosaccharides such as cellobiose and cellotriose. Moreover, we investigated the relationship between the vegetative mycelial growth and beta-glucosidase productions using cellobiose, maltose, trehalose as the growth substrate. The mycelial growth was about half of glucose medium when the cellobiose was used as a growth substrate in case of Z-1 strain, but 2/3 ~ 4/5 in other two strains. On the other hand, beta-

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glucosidase activity was higher compared with alpha-glucosidase activity when using cellobiose as a growth substrate. Our finding suggests that *T. matsutake* are able to utilize oligosaccharides released from cellulose and its related compounds having beta-1,4 glucosidic bond in nature. poster

Tian, ChengMing^{1,2}, Liang, YingMei¹ and Kakishima, Makoto^{1*}. ¹Graduate School of Life and Environmental Sciences, University of Tsukuba, Ibaraki 305-8572, Japan, ²College of Natural Resources and Environment, Beijing Forestry University, Beijing 100083, China. cmtian@126.com. **Morphological and phylogenetic analysis of *Melampsora* species on poplars in Japan and China.**

Rust caused by *Melampsora* is one of the most important leaf diseases of poplars. About 12 species have been reported in China and Japan, and they were mainly separated based on their morphological characteristics of both uredinal and telial stages and host plants including alternate hosts. However, their taxonomic identity and phylogenetic relationships are still poorly defined. 457 specimens collected from various areas of China and Japan were used for morphological observations. The morphological characteristics of urediniospores and teliospores were examined with light and scanning electron microscopy. The specimens from 11 species of *Melampsora* could be classified into five groups based on their morphology. For molecular phylogenetic analysis 48 specimens were selected from the specimens used in morphological observations and constructed phylogenetic trees based on the sequences of the nuclear large subunit rDNA (D1/D2) and 5.8S rDNA and their internal transcribed spacers, ITS1 and ITS2 region. These specimens were separated into six clades. All specimens on *P. euphratica* were morphologically and phylogenetically included in the same group and identified as *M. pruinosae*, which was clearly separated from other species. The specimens of *M. larici-populina*, *M. allii-populina*, *M. abietis-populi* formed different groups each other in the morphological and phylogenetic analyses. Specimens of *M. laricis*, *M. populnea*, *M. acedioides*, *M. magnusiana* and *M. rostrupii* belonging to the same morphological group were clearly separated into two phylogenetic groups, namely the specimens of *M. laricis* and *M. populnea* and the specimens of *M. acedioides*, *M. magnusiana* and *M. rostrupii* formed different groups based on the both NJ trees from D1/D2 and ITS regions with high bootstrap support. poster

To-Anun, Chaiwat^{1*}, Divarangkoon, Rangsi¹, Fangfuk, Wanwisai¹, Wathana-worawit, W.¹ and Takamatsu, Susumu². ¹Dept. of Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiangmai 50200, Thailand, ²Faculty of Bioresources, Mie University, 1515 Kamihama, Tsu 514-8507, Japan. agppi006@chiangmai.ac.th. ***Brasiliomyces doisuthepensis* sp. nov. (Erysiphaceae) on *Polyalthia simiarum* (Polygonaceae) from Thailand.**

A powdery mildew fungus found on leaves of *Polyalthia simiarum* (Polygonaceae) collected at Doi Suthep (Doi Suthep-Pui National Park), Chiang Mai, Northern Thailand, is characterized as mycelium hypophyllous, persistent, forming irregular white patches. Appressoria well-developed, lobed, single or occasionally opposite in pairs. Conidiophores and conidia were not found. Ascospores scattered to gregarious, ca. 62.1 µm; peridium thin, one layered, yellowish to light brown, with few basal appendages (2-5, sometimes lacking). Ascus containing 2 asci, sessile or short-stalked, thin walled, ca. 41.4 x 37.2 µm, 6-8 spored. Ascospores ellipsoid-ovoid, olivaceous to pale greenish due to oil drops, ca. 19.7 x 10.8 µm. This fungus agrees well with the general characteristics of the genus *Brasiliomyces*, and is proved to be a new species and described as *B. doisuthepensis* sp. nov. with light and SEM micrographs. Differences in known *Brasiliomyces* species are discussed, and a key to species of this genus is provided. poster

Tokiwa, Toshiyuki^{1*} and Okuda, Toru². ¹NMG Co., Ltd., 2-8-33 Wakamatsu, Fuchu, Tokyo 183-0005, Japan, ²Tamagawa University Research Institute, 6-1-1 Tamagawa-Gakuen, Machida, Tokyo 194-8610, Japan. t.tokiwa@n-m-g.co.jp. **Japanese species of *Hypomyces* and their anamorphs VI.**

Three interesting *Hypomyces* species are herewith reported from Japan. *Hypomyces* state of *Cladobotryum apiculatum* (Tubaki) W. Gams & Hooz. Subiculum on the substrate pale yellow to pastel yellow and KOH(-); ascospores fusiform, 2-celled, (25.5-)29.5-32(-36) x 6.5-7(-9) micrometer; anamorph *Cladobotryum apiculatum*. The teleomorph grew on the plant debris on the ground probably after the fruiting bodies of host agaric with *Cladobotryum* anamorph were completely decomposed. *C. apiculatum* is known in Japan, but its teleomorph has not yet been reported. Collected in Chiba, Japan. *Hypomyces transformans* Peck. Subiculum on the substrates vivid yellow, KOH(-); ascospores fusiform, aseptate, (21-)35-37(-41) x 6.5-8(-11) micrometer; anamorph *Sepedonium* sp. According to Rogerson & Samuels, this species has been recorded on the fruiting bodies of *Suillus bovinus* in North America, as our specimen was. New to Japan. Collected in Yamanashi, Japan. *Hypomyces chlorinigenus* Rogerson & Samuels. Subiculum on the substrates yellowish brown to brown and KOH(-); ascospores fusiform, 2-celled and (5.5-)11.5-13(-15) x 3-3.5(-4) micrometer; anamorph *Sepedonium chlorinum*. The anamorph and the corresponding teleomorph have once been reported from Japan. A new antibacterial antibiotic was purified from the culture filtrate of this fungus. Distributed in various parts of eastern Japan including Yamanashi, Japan. poster

Tokuda, Sawako^{1*}, Ota, Yuko² and Hattori, Tsutomu². ¹Hokkaido Forestry Research Institute, Higashiyama, Koshunai-cho, Bibai, Hokkaido 079-0198, Japan, ²Forestry and Forest Products Research Institute, P.O. Box 16, Norin Kenkyu Danchi, Tsukuba, Ibaraki 305-8687, Japan. yuota@ffpri.affrc.go.jp. **Spatial distribution of *Heterobasidion annosum* clones in a Todo fir stand.**

Heterobasidion annosum sensu lato is a serious pathogen of coniferous trees throughout the boreal and temperate regions of the Northern hemisphere. Recently, Tokuda *et al.* (2003) reported that *H. annosum* s.l. causes decay in *Abies sachalinensis* (Todo fir) in Hokkaido Japan, and, via phylogenetic analysis of the ITS region, appears closely related to European S and F groups. To reveal the spatial distribution of *Heterobasidion annosum* clones, a 80 X 60 m plot was established in a clear-cut area of a 68-yr-old Todo fir plantation at Urahoro, Hokkaido. All stumps in the plot were mapped, then decay fungi were isolated from each stump. All isolates of *Spiniger* spp., the anamorphic stage of *Heterobasidion* spp., were selected, then clone analyses were made by somatic incompatibility tests and molecular analysis (RAPD). Twelve clones in total were detected within the plot. The number of trees infected by a single clone varied from 1 to 9. The largest clone occupied an area of up to 14 X 39 m. RAPD analyses indicated that neighboring clones were genetically more related than those apart in many cases. We suggest that this fungus spreads by multiple inoculations of basidiospores in addition to mycelial outgrowth through root contacts. contributed presentation

Tokumasu, Seiji. Sugadaira Montane Research Center, University of Tsukuba, 1278-294 Osa, Sanada-machi, Chiisagata-gun, Nagano 386-2201, Japan. tokumasu@sugadaira.tsukuba.ac.jp. **Ecology of microfungi inhabiting pine leaf litter.**

Fungal successions associated with the decay of pine needles on the ground progress slowly under various climates, which is suited for the study on the relation of a fungal species to environment: the geographic range of a species, its niche within a community and its competition for available resource with other species. To study the geographic distributions of saprotrophic microfungi inhabiting pine leaf litter, I began from a detailed description of a mycofloral succession on fallen needles in the O horizon of a pine forest. The influence of seasonal change on the succession occurring on the needles was clarified directly by field experiments. The species composition involved in the succession varied according to the needles fallen at different seasons. It appeared that temperatures at the surface of the O horizon were a cardinal factor contributing to these phenomena. The geographical distribution of saprotrophic microfungi in pine forests of Japan have been studied based on the data of over 280 fungal communities of pine leaf litter collected over diverse climatic conditions. Centers and boundaries of distribution of equivalent species populations were scattered along the temperature gradient, similar to plants. This means that the climatic factors can explain the distribution patterns of microfungi inhabiting decaying pine needles for a long period in Japan. MSJ Award Lecture

Toledo-Hernandez, Carlos^{1*}, Sabat, Alberto and Bayman, Paul. Departamento de Biología, Universidad de Puerto Rico - Río Piedras, P.O. Box 23360, San Juan PR 00931, USA. donq65@hotmail.com. **Multiple *Aspergillus* species associated with sea fan aspergillosis.**

Among the coral disease recently reported from the Caribbean, aspergillosis is perhaps the best studied. Aspergillosis in sea fans (*Gorgonia ventalina* and *G. flabellum*) was reported to be caused by *Aspergillus sydowii*. However, we believe that aspergillosis may be caused by other fungi as well. Here we report for the first time other species of *Aspergillus* and *Penicillium* isolated from healthy and diseased sea fan tissues. Fungi were isolated from healthy and diseased *Gorgonia ventalina* colonies in Puerto Rico. Of 129 colonies sampled in this study, 40% showed signs of aspergillosis. *Aspergillus* was isolated from 24% of diseased colonies and 4% of healthy colonies. The most common species isolated were *A. niger*, *A. terreus*, and *A. flavus*. *Aspergillus sydowii* was not found in any tissue sample, in marked contrast to previous studies. These data suggest that other species of *Aspergillus* might also cause aspergillosis. *Aspergillus* species may be part of the commensal flora of sea fans, becoming opportunistic pathogens under conditions of stress. contributed presentation

Trest, Marie T. and Gargas, Andrea^{1*}. Dept. of Botany, University of Wisconsin - Madison, Madison, WI 53706, USA. mttrest@wisc.edu. **Phenotypic characters used for species delimitation in the lichenized genera *Everniastrum* and *Cetrariastrum*.**

Species of the lichen genera *Everniastrum* and *Cetrariastrum* are delimited by morphological characters, reproductive structures, and secondary chemical compounds. Inhabiting higher elevation sites across tropical regions, as well as extending into some temperate areas, species exhibit distributional differences - either widespread or narrow. Here we assess how these characters and the distribution of species correlate with phylogeny by sequencing the ITS region for multiple individuals of species of both genera to estimate their phylogenetic relationships. Species of *Cetrariastrum* are sister to a group of species of *Everniastrum* while the remaining species of *Everniastrum* form a well-supported sister group 'core *Everniastrum*'. Asexual reproductive structures have arisen multiple times within *Everniastrum*, and species concepts will need to be adjusted especially

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with respect to chemistry and geography. The secondary chemical compounds of core *Everniastrum* are not good predictors of relatedness within the clade; however, the presence of secondary chemical compounds is helpful in recognizing the *Everniastrum*+*Cetrariastrum* clade and the core *Everniastrum* clade. In order to reflect monophyletic groups, both genus and species concepts will require some revision. poster

Tsuchiya, Yuki^{1*}, Uchida, Masaki², Koizumi, Hiroshi³ and Okuda, Toru¹. ¹Tamagawa University Research Institute, 6-1-1 Tamagawa-Gakuen, Machida, Tokyo 194-8610, Japan, ²National Institute for Polar Research, 1-9-10 Kaga, Itabashi, Tokyo 173-8515, Japan, ³Gifu University River Basin Research Center, 1-1 Yanagido, Gifu 501-1193, Japan. tsuchy@lab.tamagawa.ac.jp. **Fungi decomposing leaf litter under the snow.**

Although microorganisms decompose leaf litter even under the deep snow, mycoflora is still unknown under such an environment in the cool temperate forest. We thus investigated saprophytic fungi grown under the snow. In January 2004, 15 samples of leaf-litter of *Quercus crispula* and *Betula ermanii* were collected under the deep snow in Gifu Pref., Japan (36N, 137E; 1420 m a.s.l.). Ten pieces in 7 mm in diam. were punched out from each leaf sample and treated with surface washing and/or sterilization. The chips were placed onto a water agar medium containing chloramphenicol and incubated at 2C for two months. Hyphae grown from the chips were transferred onto LCA medium and the isolates were examined under the microscope. The isolates recognized were *Cylindrocarpus destructans*, *Epicoccum nigrum*, *Fusarium* sp., *Mortierella* spp., *Mucor* spp., *Penicillium* sp., *Phoma* spp., *Varicosporium elodeae*. However, 194 isolates (82%) did not sporulate. To clarify their taxonomic positions, the ITS region including 5.8S rDNA of these sterile strains were sequenced. According to the homology search, 99 strains (51% of the sterile isolates) were close to the Helotiales fungi reported from the mycorrhizal roots. We thus isolated fungi from the roots under the snow and compared the ITS region. The mycoflora and their infection to the roots under the snow will be discussed. poster

Tsui, Clement K.M.* and Berbee, Mary L. Department of Botany, The University of British Columbia, #3529-6270 University Blvd., Vancouver, B.C. V6T 1Z4, Canada. clement@mail.botany.ubc.ca. **Evolutionary origins and phylogenetic relationships of helicosporous fungi inferred from ribosomal DNA sequences.**

We have been investigating the evolutionary origins and phylogenetic relationships among helicosporous fungi in the asexual genera *Helicoma*, *Helicomycetes*, *Helicosporium*, *Helicodendron*, and *Helicoon*, and in the sexual genus *Tubeufia* (Tubeufiaceae, Dothideomycetes, Ascomycota). We initially generated SSU and partial LSU rDNA sequences from thirty-nine fungal cultures. These and related sequences from GenBank were analysed using parsimony, likelihood and Bayesian analysis. Results showed that helicosporous species arose convergently from six lineages of fungi in the Ascomycota. The Tubeufiaceae s. str. formed a strongly-supported monophyletic lineage comprising most species from *Helicoma*, *Helicomycetes* and *Helicosporium*. However, within the Tubeufiaceae, none of the asexual genera were monophyletic. In spite of their distinctive, barrel-shaped spores, *Helicoon* species were polyphyletic and had evolved in different ascomycete orders. *Helicodendron* appeared to be polyphyletic although most representatives originated from Leotiomycetes. We speculate that some of the convergent spore forms may represent adaptation to dispersal in aquatic environments. The relationships among *Helicoma*, *Helicomycetes* and *Helicosporium* within Tubeufiaceae s. str. were further inferred from phylogenetic analysis of ITS sequences from forty-five taxa. *Helicoma sensu stricto* and *Helicosporium sensu stricto* are recognised but *Helicomycetes* is doubtful. Traditional generic characters, such as whether conidiophores were conspicuous or reduced, the thickness of the conidial filament, and whether or not conidia were hygroscopic were more useful for species delimitation than for predicting higher level relationships. contributed presentation

Tsujiyama, Sho-ichi¹ and Tsujiyama, Komako^{2*}. ¹Graduate School of Agriculture, Kyoto Prefectural University, Simogamo-nakaragi-cho, Sakyo-ku, Kyoto 606-8522, Japan, ²Kinoko Seminar, Sakyo-ku, Kyoto 606-8163, Japan. pony_kom@za.cyberhome.ne.jp. **The increasing occurrence of *Echinochaete ruficeps* at Mt. Yoshida in Kyoto City.**

Echinochaete ruficeps (Berk. & Br.) Ryvarden (Japanese name, sabihachinosutake) is a tropical white-rot fungus. There are few reports about its distribution and ecology in Japan. We found the occurrence of *E. ruficeps* and observed that the number of its fruit bodies increased in these 5 years while we researched the mushroom flora at Mt. Yoshida in Kyoto City. Mt. Yoshida is a hill which is located on the residential area and belongs to the temperate zone. The vegetation at the area are mainly Fagaceae (*Quercus*, *Cyclobalanopsis*), and others, such as Theaceae (*Cleyera*, *Eurya*), Cupressaceae (*Chamaecyparis*), Aquifoliaceae (*Ilex*), Aceraceae (*Acer*). In the area, we examine the relationship between the numbers of fruit bodies and the meteorology. As the result, the temperature of winter season became warmer in these decades. So we presume that the increase of *E. ruficeps* occurrence relates to the rise of temperature accompanied with urban heat island because *E. ruficeps* could survive in warmer winter. We will investigate the distribution, habitat and occurrence season of *E. ruficeps* in Japan and overseas. poster

Tsukihara, Takahisa*, Honda, Yoichi, Watanabe, Takahito and Watanabe, Takashi. Gokasho, Uji, Kyoto, Japan 611-0011. tsukihara@rish.kyoto-u.ac.jp. **Homologous expression of versatile peroxidase, MnP2, in *Pleurotus ostreatus*.**

Pleurotus ostreatus is a white-rot fungus known as an efficient degrader of lignin and various organo-pollutants. One of the major *P. ostreatus* MnP isozymes, MnP2 has versatile functions: it can oxidize not only Mn2+ to Mn3+ but also non-phenolic compounds and high-molecular weight compounds which are not oxidized by other 'classical' MnPs directly. To establish a homologous expression system for MnP2, a recombinant plasmid containing the coding sequence of *mnp2* under the control of *sd11* expression signals was constructed and introduced in wild-type *P. ostreatus*. We isolated 32 transformants containing the recombinant *mnp2* sequence. In a screening experiment, 13 transformants showed elevated decolorizing activity for Poly R-478 in the absence of Mn2+. On a synthetic liquid medium, significant MnP activity was produced by one of the recombinants, TM2-10, while no detectable MnP activity was observed for wild-type control. In TM2-10, transcripts from the recombinant *mnp2* were observed by an RT-PCR experiment. Moreover, an anion-exchange chromatography analysis with a Mono-Q column showed secretion of MnP2 by the recombinant. On the other hand, for wild-type strain, neither transcript nor MnP2 enzyme were detected in the similar experiments. From these results, it was demonstrated that a successful expression of the recombinant *mnp2* was carried out in the transformant. poster

Tsurumi, Yasuhisa. Fermentation Research Labs., Astellas Pharma Inc., 5-2-3, Tokodai, Tsukuba, Ibaraki 300-2698, Japan. yasuhisa.tsurumi@jp.astellas.com. **How can mycologists contribute in the invention of commercial products?**

Most important and first step to discover drug seeds from microbial metabolites is an isolation of microorganisms producing useful compounds from natural resources. An antifungal products Micafungin (FUNGARD®/MYCAMINE®) was synthesized as a derivative of lipopeptides which were purified from fungal culture broth. The producing strain F-11899 was isolated from a forest soil, using dilution plate and ultraviolet (UV) radiation method. UV radiation treatment is effective to selective isolation of dematiaceous fungi, because dark pigment contained in their cell protect against DNA damage induced by high energy. Strain F-11899 had hyaline conidia and dark hyphae; the former was sensitive while the later was resistant against UV ray. It didn't form reproductive structures on many kinds of agar media, so we induced their conidial structure using the autoclaved leaf put on Miura's LCA or its modified medium. As a result of identification, the strain belonged to the coelomycete fungus *Coleophoma empetri* (Rostrup) Petrak. On the basis of this taxonomic knowledge, we collected new isolates related to *Coleophoma empetri* from living/decayed leaves using dilution plate and UV radiation method. Then we succeeded the discovery of similar but new antifungals from other strains of *Coleophoma* spp. I will discuss about the role of mycologists on natural products research. symposium presentation

Twieg, Brendan D.¹, Durall, Daniel M. and Simard, Suzanne W.² ¹University of British Columbia, Okanagan, 3333 University Way, Kelowna, BC, V1V 1V7, Canada, ²University of British Columbia, Vancouver, 2424 Main Mall, Vancouver, BC, V6T 1Z4, Canada. dmdurall@ouc.bc.ca. **Below-ground ectomycorrhizal community succession of Douglas-fir and paper birch in stands initiated by clearcutting and wildfire.**

Studies on below-ground succession of ectomycorrhizal communities after forest stand initiation are few, and those conducted thus far have not utilized molecular techniques for identification of fungal species. We examined ectomycorrhizal communities on Douglas-fir (*Pseudotsuga menziesii*) and paper birch (*Betula papyrifera*) roots in a chronosequence of stands initiated by clearcut or wildfire. Median stand ages of four replicates for each of the four age classes studied were: 5, 25, 60, and 100 years. We used thorough morphological examination of ectomycorrhizal root tips and subsequent sequencing of their fungal ITS regions to identify the fungal community. Species richness of ectomycorrhizal fungi in 5 year-old burned and clearcut stands was lower than in the older age classes for both host trees, but the magnitude of this difference was greater for Douglas-fir. The Douglas-fir ectomycorrhizal community also had low species richness in the 25 year-old burned stands, being dominated, like the 5 year-old stands, by *Rhizoglyphus* spp. Similarity between the five year-old and older stands was higher in birch ectomycorrhizal communities than those of Douglas-fir. Perhaps this is because new birch stems sprout directly from parent stumps after being cut or burned whereas Douglas-fir do not. All stands besides 5 year-old stands and 25 year-old burned stands had a high portion of their ectomycorrhizal communities composed of fungal species common to both host trees, ranging between 25-40% of each host's total community. Fungal species shared by both hosts included *Piloderma fallax*, *Cenococcum geophilum*, a *Hysterangium* sp., and *Lactarius scrobiculatus*, as well as species in the genera *Russula*, *Tomentella*, and *Hebeloma*. All of these taxa, with the exception of *Cenococcum*, were far more prevalent in stands greater than 5 years of age. poster

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Upadhyay, Srijana, Long, Melissa and Shaw, Brian D.* Program for the Biology of Filamentous Fungi, Department of Plant Pathology and Microbiology, Texas A&M University, College Station, Texas 77803, USA. bdshaw@tamu.edu. **Protein glycosylation is essential for maintenance of hyphal growth in *Aspergillus nidulans*.**

Two temperature sensitive developmental mutants of *A. nidulans* have been isolated and characterized. The *swoM1* mutant extends a primary germ tube that quickly loses polarity and swells to a uniform cell of approximately 20 micrometer diameter, while the *swoN1* mutant is roughly wild type, with the exception of numerous periodic swellings along the hyphae that give rise to multiple germ tubes leading to a hyper-branched appearance. The *swoM1* mutant is fully complemented by a gene encoding a homolog of a phosphoglucose isomerase. This enzyme interconverts glucose-6-phosphate and fructose-6-phosphate. The *swoN1* mutant is fully restored to wild type growth when transformed with a gene encoding a GDP-mannose pyrophosphorylase. This enzyme synthesizes GDP-mannose from GTP and mannose-1-phosphate. These two enzymes are both upstream of production of Dol-P-Mannose and thus are important for protein glycosylation. Previous work with the *swoA* mutant defective in a protein mannosyl transferase also implicated mannoprotein synthesis in cell morphogenesis (Shaw and Mooney, 2002). We hypothesize that a mannosylated protein(s) is critical for proper cell wall assembly that leads to maintenance of polar growth. symposium presentation

van der Merwe, Marlien M.^{1*}, Maier, Wolfgang, Burdon, Jeremy J.², Thrall, Peter H.², Ericson, Lars³ and Walker, John.² ¹CSIRO Plant Industry, Canberra, Australia, ²FABI, University of Pretoria, Pretoria, South Africa, ³University of Umea, Umea, Sweden. marlien.vandermerwe@csiro.au. **Phylogenetic relationships within the family Pucciniaceae with emphasis on *Puccinia* and *Uromyces*.**

The family Pucciniaceae is by far the most speciose family in the Uredinales. Within this family species numbers per genus vary dramatically among the genera with *Puccinia* and *Uromyces* having between 3000 and 4000 and over 600 described species respectively with less than 8 species in most of the other genera. Thus species diversity within the family can be attributed almost exclusively to *Puccinia* and *Uromyces*. As with most rusts morphological characters do not always shed light on evolutionary relationships among the species within this family. The aim of our study is to get a deeper understanding of the evolutionary relationships among the species within this family by integrating DNA sequence data with what is known regarding host plant specificity and morphological characters. Here we use the results from two separate studies to discuss phylogenetic patterns found mainly within *Puccinia* and *Uromyces*. Sequence data from three genes, the nuc lsu rDNA, beta-tub 1 and EF 1-alpha, was generated. As has been hinted at before neither *Uromyces* nor *Puccinia* were supported as monophyletic genera with the molecular data. However all three data sets supported the division of the sampled taxa into two clades. The host plant specificities of the telial stage seem to mirror the evolutionary split of these two clades. symposium presentation

Van der Nest, Magrieta A.¹, Slippers, Bernard², Wingfield, Brenda D.^{1*} and Wingfield, Michael J.¹. ¹Dept. of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa, ²Dept. of Forest Mycology and Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden. brenda.wingfield@fabi.up.ac.za. **Vegetative incompatibility in *Amylostereum areolatum*.**

The wood wasp, *Sirex noctilio* and its fungal symbiont, *Amylostereum areolatum*, seriously threaten pine plantations in the southern hemisphere. The genetic diversity of *A. areolatum*, as expressed in vegetative incompatibility (VC) groups, is limited. This is most pronounced in areas where the fungus is introduced, but also in some native environments. To explore the potential impact of the introduction of new VC groups into Southern Hemisphere countries and to promote our understanding of VC in this fungus, we are investigating the genetics of vegetative incompatibility in *A. areolatum*. Basidiomata were collected from native European locations and single basidiospore cultures were made. These monokaryons were subjected to mating-type compatibility tests, where sexual compatibility was reflected in the formation of clamp connections. Sexually compatible monokaryons from one parent sporocarp were paired to produce sibling dikaryons. Sib-related dikaryons were also generated by pairing monokaryons from the first parent with those of a second, unrelated parent. The results of the sexual compatibility tests confirmed that *A. areolatum* has a typical tetrapolar mating system. VC interactions were either compatible, weakly incompatible or strongly incompatible. Approximately 25% of the interactions among the sib-related dikaryons were compatible, which indicates that a minimum of two hetloci control VC in *A. areolatum*. Such low numbers of VC loci are also present in other basidiomycetes (e.g. *Armilaria ostoyae*, *Phellinus weirii* and *Heterobasidium annosum*). Our findings also suggest that VC tests may result in an underestimation of the true genetic diversity as compatible isolates may differ genetically. poster

Van Wyk, Marelize*, Roux, Jolanda, Barnes, Irene, Wingfield, Brenda D. and Wingfield, Michael J. Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa. marelize.vanwyk@fabi.up.ac.za. ***Ceratocystis tribiliformis* prov. nom. a new**

species from Sumatra, Indonesia.

Two recently described *Ceratocystis* spp. (*C. bhutanensis* and *C. moniliformis*) are morphologically almost indistinguishable from *C. moniliformis*. This similarity in morphology has led us to consider previous suggestions that *C. moniliformis* could represent a species complex. The aim of this study was to consider the phylogenetic relationships between isolates identified as *C. moniliformis* from various hosts and origins, based on comparisons of DNA sequences for three gene regions. Results showed that most of the isolates of *C. moniliformis* used in this study represent a well-resolved monophyletic group. However, a collection of isolates initially identified as *C. moniliformis*, from *Pinus merkusii* in Sumatra resided in a distinct clade. These isolates can also be distinguished from *C. moniliformis* based on minor morphological features and the fungus is being described as *Ceratocystis tribiliformis* prov. nom. Recognition of this new species adds credence to the view that *C. moniliformis* includes many cryptic species and we expect that more will be identified in the future. poster

Vellinga, Else C.* and Bruns, Thomas D. Department of Plant and Microbial Biology, University of California, Berkeley, Berkeley CA 94720-3102, USA. vellinga@berkeley.edu. **Lepiotaceous fungi in California - diversity and phylogenetics.**

California is recognized as a biodiversity hotspot and lepiotaceous fungi (Agaricaceae) bear this out. Stands of endemic *Sequoia sempervirens* and *Cupressus macrocarpa* harbor an exceptional variety of this group, notably 26 species in one small cypress grove south of San Francisco. Inventories during the last six years in the northern coastal part of the state have revealed approx. 70 species, of which about a third are endemic, and at least 20 are new to science. The species are distinguished by morphological and molecular characters; ITS and EF1alpha have proven especially useful. Phylogenies of the family Agaricaceae as a whole with representatives from all over the world have been constructed using a variety of loci and several analytical methods. The *Leucoagaricus/Leucocoprinus* clade, which contains many species that fruit with the first rains at the end of the long dry summer, is the most diverse with around 40 species. The *Lepiota* clade, with approx. 25 species, has its peak fruiting later when temperatures are lower. This reflects a universal biogeographic pattern, in which species in the *Leucoagaricus/Leucocoprinus* clade occur at lower latitudes and altitudes than *Lepiota* species. In addition, the few *Chlorophyllum* species in California are cosmopolitan cultivation followers, whereas the genus *Macrolepiota* occupies natural habitats but occurs very rarely. poster

Vilgalys, Rytas J.^{1*}, Moncalvo, Jean-Marc², Parrent, Jerri L.¹, O'Brien, Heath¹, Richter, Daniel D.¹ and Jackson, Jason L.¹ ¹Dept. of Biology and Nicholas School of the Environment and Earth and Ocean Sciences, Duke University, Durham, NC 27708, USA, ²Royal Ontario Museum, and Department of Botany, University of Toronto, Toronto, Canada. fungi@duke.edu. **Probing fungal diversity using sequence libraries: lessons from the Duke Forest Mycological Observatory (DFMO).**

This talk will summarize results from recent culture-independent studies of fungal diversity in southeastern USA Piedmont forests based in the Duke Forest (Durham, NC) and the Calhoun Experimental Forest (Sumter National Forest, SC). Analysis of ribosomal DNA sequences from soil clone-libraries reveals a diverse community of eukaryotic microorganisms dominated by fungi, and also including protistan, chlorophyte and metazoan lineages. Phylogenetic analysis of ITS sequences from basidiome surveys and environmental sources, combined with data available in public databases, permits the identification to the species level for many common saprobic and mycorrhizal groups (*Russula*, *Suillus*, *Mycena*, *Gymnopus* and others). As a taxonomic reference database, the DFMO sequence collection used to study how fungal communities respond to global change. Examples include study of community shifts in response to CO₂ enrichment (FACE study), and community response to long-term land-use histories with different recovery histories (Calhoun Forest). The development of DFMO protocols also identified a number of technical problems (chimeric sequences, PCR-bias, etc.); these will be discussed. Development of new screening technologies, including RT-PCR and the use of taxon-specific primers will also be discussed. symposium presentation

Voth, Peter D.^{1*}, Lockhart, Ben² and May, Georgiana³. ¹Plant Biological Sciences Graduate Group, ²Dept. of Plant Pathology, and ³Dept. of Ecology, Evolution, and Behavior; University of Minnesota, St. Paul, MN, USA. voth0016@umn.edu. **Population dynamics of a fungal virus across the Americas.**

Fungal viruses appear to be ubiquitous throughout Fungi, often persisting with no detriment to the host. All mycoviruses have no extracellular stage and are transmitted only through cytoplasmic fusion of host cells. Symbiotic interactions strongly affect the evolutionary trajectory of each other and are important in structuring communities. One such symbiosis is that of *Ustilago maydis*, *Ustilago maydis* Virus H1 (UMV-H1), and *Zea mays*. *Ustilago maydis*, commonly known as corn smut, causes infections on vegetative and reproductive tissues of corn. UMV-H1 is vertically transmitted during mating of *U. maydis* individuals and, thus, the population dynamics of *U. maydis* can affect the population structure of

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UMV- H1. In this work, I investigate the population dynamics of a dsRNA virus (UMV- H1) with *U. maydis* to determine the phylogeography of UMV- H1 throughout the Americas. I have collected sequence data from regions of two genes in the viral genome. Infection frequency, genetic diversity, and recombination frequency have indicated that Mexico is the ancestral population. The demographics of UMV-H1 in South America will be discussed. poster

Walker, John F.*, Johnson, Loretta C., Simpson, Nicholas B., Trowbridge, Justin and Jumpponen, Ari*. Division of Biology, Kansas State University, Manhattan, KS 66506, USA. jfw@ksu.edu. **Arctic ericoid plants depend on a unique assemblage of fungi for uptake of organic N.**

We investigated the diversity and function of fungi isolated from five arctic ericoid tundra plant species. The predominant fungi were *Phialocephala* sp. (195 isolates), *Pezicula* sp. (72), *Irpex* sp. (12), cf. *Leptodontidium* sp. (12), two *Hymenoscyphus* spp. (10), *Lachnum* sp. (6), and *Mollisia* sp. (3) based on molecular characterization of ~350 cultures obtained from surface sterilized roots. These fungi all formed intracellular coils in roots in resynthesis tests with *Ericales*. Most types were referred to the Helotiales, ascomycetes typically forming ericoid mycorrhizae. However, several of the isolated genera have not previously been reported from ericoid hosts, and *Hymenoscyphus ericae* was not detected. To test the function of the root/soil fungi, we assessed uptake of ¹⁵N by an ericoid plant *Vaccinium vitis-idaea* in intact sections of tundra: organic N uptake was 40% lower when fungal activity was inhibited by fungicides, while uptake of inorganic N was unaffected. The ability of the dominant fungal types to provide ericoid plants with a variety of organic N sources is being investigated currently in petri plate resynthesis systems. poster

Wang, Qi*¹, Li, Yu¹ and Kakishima, Makoto². ¹College of Chinese Medicinal Materials, Jilin Agricultural University, Changchun 130118, P. R. China, ²Graduate School of Life and Environment Sciences, University of Tsukuba, Ibaraki 305-8572, Japan. qwang2003@hotmail.com. **Observation of plasmodia and cysts of Trichiales (Myxomycetes).**

Alexopoulos (1960) reported three basic types of plasmodia: protoplasmodium (Echinosteliales) (Pr), aphanoplasmodium (Stemonitales) (Ap) and phaneroplasmodium (Physarales) (Ph). However, plasmodia of Trichiales were not characterized well though they were known as intermediate type between Ap and Ph. Therefore, in order to clarify their characteristics, plasmodia and cysts of 8 species of *Perichaena*, *Arcyria*, *Metatrachia*, *Hemitrachia* and *Trichia* were cultured in the laboratory by corn-meal agar with *E. coli* JA-01 or oat meal agar media, and observed with a stereoscope and a light microscope. Plasmodia of Trichiales obtained in this study are divided into 2 groups. Group I is small, not fun-shaped, veined and similar to the type Ap (*T. decipiens*, *T. fovoginea*). Group II is big, fun-shaped, and the front margin of fun is thick, dense and similar to the type Ph (*P. depressa*, *A. pomiformis*, *A. denudata*, *H. calyculata*, *H. clavata* *M. vesparium*). When plasmodia lost water and dried, they gradually become dense and divide into many small blocks (cysts). These cysts are bigger than those of Stemonitales, sometimes visible, globose, nearly globose, angular or irregular, composed of 1-7 small cells and sometimes covered by the same membrane. The wall of cyst is thick and dark when it is observed by transmission light. [Supported by National Natural Science Foundation of China (No. 30270008).] poster

Wang, C.J.K.¹ and Zhou, Shuang^{2*}. ¹Faculty of Environmental and Forest Biology, State University of New York College of Environmental Science and Forestry (SUNY-ESF), Syracuse, NY 13210, USA, ²Faculty of Construction Management and Wood Products Engineering, SUNY-ESF, Syracuse, NY 13210, USA. szhou@sy.edu. **Synanamorphs of *Pseudaegerita corticalis*.**

The hyphomycete *Pseudaegerita corticalis* (Peck) J.L. Crane & Schohn, collected in Wales, 1979 has both phialidic and sympodial conidiogenesis. Type and authentic specimens and/or cultures of *Oidium corticale* Peck, *Pseudaegerita corticalis*, *P. matsushimae* Abdullah & Webster, and *P. viridis* (Bayl.Ell.) Abdullah & Webster were studied. A re-interpretation of the conidiogenous structures of *P. corticalis* is presented that is based on the results of light microscopy, scanning electron microscopy, DNA sequences of the ITS regions of specimens or cultures. poster

Wang, Guangyi* and Li, Quanzi. University of Hawai'i at Manoa, 1680 East-West Road, POST 109, Honolulu, Hawai'i 96822, USA. guangyi@hawaii.edu. **Diversity of marine fungi associated with marine sponges in Hawai'i.**

Marine fungi play significant roles in nutrient regeneration cycles in the marine environment and impact coral reef ecosystems as decomposers, pathogens, parasites, and symbionts. In the center of the Pacific Ocean, the Hawaiian Islands offer different unique micro-ecological niches for diverse marine fungi and other marine organisms. However, the diversity of marine fungi in Hawai'i has barely been explored. In our efforts to study microbial diversity in the Hawaiian marine ecosystems, we found marine sponges harbored morphologically and phylogenetically diverse filamentous fungi and were different among various sponge species. Some of isolates were not described species. Phylogenetic analyses of fungal isolates from two sponge species *Haliclona caerulea* and *Gelliodes fibrosa* revealed a high diversity of fungal phylotypes. Fungi from *H. caerulea* failed into two phyla, Ascomycota and Basidiomycota. On the phylogenetic tree, the iso-

lates of ascomycetes are clustered in 7 major clades (xylariales, mycosphaerellales, hypocreales, eurotiales, diaportheales, pleosporales, and an unknown order). One isolate stood alone as an unclassified basidiomycetes fungus. On the other hand, fungi associated with *G. fibrosa* were less diverse than those in *H. caerulea*. All the isolates belonged to the phylum Ascomycota and were clustered in only 5 major clades (eurotiales, mycosphaerellales, hypocreales, pleosporales, and an unidentified order). Several fungal species (e.g. *Myrothecium cinctum*) were present in both species. Investigation of the specificity and symbiosis of marine fungi with the two sponges are in progress. poster

Wang, Guangyi* and Li, Quanzi. University of Hawai'i at Manoa, 1680 East-West Road, POST 109, Honolulu, HI 96822, USA. guangyi@hawaii.edu. **Diversity of marine fungi associated with marine algae in Hawai'i.**

The symbiotic co-existence between fungi and algae is very well established. However, the diversity of marine fungi associated with algae and their co-evolution relationship are still poorly understood. Investigation of the diversity of marine fungi associated with marine algae can be crucial to understand the significances and impacts of marine algal invasions and biocomplexity in marine ecosystems. In our efforts to understand the microbial diversity in Hawaiian marine ecosystems, we isolated marine fungi from several algae collected on several Hawaiian Islands. The fungal isolates from algae displayed diverse morphologies and phlotypes. Comparison of the diversity of fungi associated with a specific algal species at different locations or different algal species at the same location revealed interesting results. This study greatly improves our understanding of the specificity of fungi associated with marine algae and spatial variation of fungal diversity associated with marine algae in Hawai'i. poster

Wang, Wei*, Gibas, Connie and Currah, Randolph S. Dept. of Biological Sciences, University of Alberta, Edmonton AB T6G 2E9, Canada. ww1@ualberta.ca. **New reports of *Cryptosporiopsis* species from the roots of *Populus tremuloides* in western Canada.**

Species of *Cryptosporiopsis* are usually considered pathogens of woody plants but a few species occur as apparently harmless endophytes in roots. Recently we obtained 83 isolates of species of this genus from apparently healthy roots of *P. tremuloides* in central Alberta. Ten isolates were identified as *C. ericacea* Sigler, a species recently described from the roots of ericaceous plants. Our cultures of this species produced phialides on simple conidiophores borne in sporodochial tufts and produced aseptate, cylindrical, slightly curved, macro and microconidia. Identifications were confirmed using 5.8S nuclear rDNA and ITS1, 2. In contrast to the original description, our isolates indicate that this species is not confined to the Ericaceae. Two isolates of *C. radicicola*, a species described originally from the roots of oak in Europe, were identified using morphological features and confirmed using DNA sequence comparisons. Sequencing results also support recognizing both species as anamorphs of the genus *Pezicula*. poster

Wang, Zheng, Binder, Manfred and Hibbett, David S. Department of Biology, Clark University, 950 Main Street, Worcester, MA 01610, USA. zwang@clarku.edu. **Characterizing *atp6* in multilocus phylogenetics of polyporoid homobasidiomycetes.**

Phylogenetic relationships of polyporoid homobasidiomycetes have been difficult to resolve using ribosomal RNA genes. We are investigating the phylogenetic utility of *atp6* (coding for the subunit 6 of ATPase in mitochondria) in polyporoid homobasidiomycetes. Touch-down PCR using four primers (*atp6*-1, -2, -3 and *atp6*-4) is useful for amplifying partial *atp6* genes. Nucleotide sequences coding for this *atp6* region have been generated from 43 polypores and many representatives of other major clades in the homobasidiomycetes. The resolution using *atp6* gene to infer phylogenetic relationships within homobasidiomycetes at higher fungal taxonomic level and within polyporoid classes is being evaluated. Each of the 3 codon positions are being investigated for A-T bias, saturation, phylogenetic information level, and substitution frequency. Phylogenetic analyses are applied using amino acid sequences and nucleotide sequences of *atp6*, separately and combined with a dataset of 4 rDNA regions and partial *atp2* genes using parsimony, likelihood and Bayesian methods. poster

Wang, Zheng*¹, Binder, Manfred¹, Hibbett, David S.¹, Schoch, Conrad L.² and Spatafora, Joseph W.² ¹Department of Biology, Clark University, 950 Main Street, Worcester, MA 01610, USA, ²Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331, USA. zwang@clarku.edu. **Phylogenetic relationships of the Helotiales inferred from 3 rDNA regions.**

The Helotiales is probably the largest and the most diverse group of non-lichen forming ascomycetes, which includes 13 families and 395 genera (92 with uncertain positions). The helotialean fungi inhabit diverse ecosystems and utilize a broad range of nutritional sources and form saprobic, parasitic, and symbiotic associations with plants and other fungi. High ecological and morphological diversity make this group of fungi one of the most problematic group in terms of classification. Sequences from 3 rDNA regions (18s, 28s and 5.8s, total 2025 bp) have been generated from 41 species in major groups of the Helotiales in Hibbett lab at Clark University. Combined with data generated from Spatafora lab at Ore-

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gon State University and downloaded from GenBank, a dataset of 3 rDNA regions from 88 taxa including 5 orders and 17 families in the Leotiomycetes is available. Analyses using equally weighted Parsimony and Bayesian approaches under GTR and GTR+I+R models have been applied. Relationships between the Helotiales and Geoglossaceae, Rhytismatales, Erysiphales and Cyttariales and within the Helotiales have been investigated. This work provides a framework for future phylogenetic study and classification of the Helotiales and the Leotiomycetes. poster

Watanabe, Kyoko* and Kurihara, Masayuki. Dept. of Agriculture, Tamagawa University, Machida, Tokyo 194-8610, Japan. wkyoko@agr.tamagawa.ac.jp. **Endophytes coexisting in leaves of Japanese andromeda and their infection manner.**

All foliage supports phylloplane fungi and most of them, if not all, contain symptomless endophytic fungi. We monitored the frequency of endophyte within green leaves of Japanese andromeda over two full seasons (2000, 2001). Of the many fungi isolated as endophyte, *Guignardia mangiferae* (anamorph = *Phyllosticta*), *Colletotrichum gloeosporioides* and *Pestalotiopsis neglecta* were the most consistent and numerous, although their numbers were different in each sampling day. To determine the distribution of endophyte within leaves, each leaf was cut into 60 to 141 pieces, about 9 mm²/piece, depending on leaf size. Each piece was numbered to confirm its original position on a leaf when plated out. These species coexisted in a leaf, and their distribution within leaves was random. The frequencies increased as leaves aged and/or senesced, although the species isolated were same. Seeds were picked out from surface sterilised fruits, and were plated out for isolation of these endophytes. They were also examined by PCR for detection. But the above species were not found by either method. Results indicate that dispersal of these endophytes is horizontal. poster

Weraduwage, Sarathi¹* and Moncalvo, Jean-Marc^{1,2}. ¹Department of Botany, University of Toronto, Canada, ²Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, Toronto, Canada. sarathi.weraduwage@utoronto.ca. **Biogeographic relationships of *Amanita* from Thailand.**

At least 23 species of *Amanita* are known from Thailand but many more species probably exist in the country. Thailand encompasses a high diversity of forest ecosystems, ranging from exclusively tropical (dipterocarp-dominated, evergreen or deciduous) in the lowlands to subtropical (oak and conifer-dominated) in the highlands. Are highland taxa related to taxa found in the tropical lowland areas, or are they more closely related to taxa from other temperate areas of the world? We sequenced ITS for several Thai *Amanitas*, and examined their phylogenetic relationships to species from other regions of the world. We found a high level of relationships between collections from Thailand, China, and Japan, with no evidence for a clear disjunction between tropical and subtropical collections. A very high level of ITS sequence variation was found among species of the *A. caesarea/hemibapha* complex, suggesting that many cryptic species may exist in this group. poster

White, Merlin M.* and Lichtwardt, Robert W. Department of Ecology and Evolutionary Biology, The University of Kansas, Lawrence, KS 66045-7534, USA. trichos@ku.edu. **Phylogeny of insect-associated gut fungi with emphasis on the Harpellales.**

Worldwide, obligately symbiotic gut fungi, Harpellales (Trichomycetes), may be found living in various aquatic arthropods (more commonly in larval insects, although one genus is associated with isopods). Current efforts in our lab include two fronts 1) to continue to discover new taxa of gut fungi and 2) to build a molecular based phylogeny that incorporates new and interesting taxa for a more complete understanding of the evolutionary relationships of this unique group of Zygomycota. Evolutionary relationships have been difficult to infer because of the paucity of morphological characters and unculturability of most of the 38 genera of Harpellales. We report here current phylogenetic analyses that incorporate newly discovered harpellid taxa, some isolated in culture while most were obtained from guts (mixed genomic template) to generate rDNA sequences to infer the phylogeny of the Harpellales using cladistic analyses. We highlight the genus *Orphella* and its affinity to the Kickxellales (Zygomycetes) and expand the phylogeny of the otherwise monophyletic Harpellales. Polyphyly of the largest genera, *Smittium* and *Stachylina*, is masked morphologically by convergent and limited characters. We consider this to be a comparative, molecular snapshot of the taxonomy and systematics of the gut fungi, which will ultimately lead to revisions in their classification. symposium presentation

Wicklow, Donald T.¹*, Roth, Shoshana², Deyrup, Stephen T.² and Gloer, James B. ¹USDA, ARS, National Center for Agricultural Utilization Research, Peoria IL, USA, ²Department of Chemistry, University of Iowa, Iowa City IA, USA. wicklodi@ncaur.usda.gov. **A protective endophyte of maize: *Acremonium zeae* antibiotics inhibitory to *Aspergillus flavus* and *Fusarium verticillioides*.**

The maize endophyte *Acremonium zeae* is antagonistic to kernel rotting and mycotoxin producing fungi *Aspergillus flavus* and *Fusarium verticillioides* in cultural tests for antagonism and interferes with *A. flavus* infection and aflatoxin contamination of preharvest maize kernels. Chemical studies of an organic extract from maize kernel fermentations of *A. zeae* NRRL 13540, which displayed sig-

nificant antifungal activity against *A. flavus* and *F. verticillioides*, revealed that the metabolites accounting for this activity were two newly reported antibiotics pyrrocidines A and B. Pyrrocidines were detected in fermentation extracts for twelve NRRL cultures of *A. zeae* isolated from maize kernels harvested in the USA. Pyrrocidine B was detected by LCMSMS in whole symptomatic maize kernels removed at harvest from ears of a commercial hybrid that were maize-inoculated in the milk stage with *A. zeae*. In an evaluation of cultural antagonism between 13 isolates of *A. zeae* in pairings with *A. flavus* and *F. verticillioides*, *A. zeae* NRRL 6415 and NRRL 34556 produced the strongest reaction, inhibiting both organisms at a distance while continuing to grow through the resulting clear zone at an unchanged rate. The potential significance of pyrrocidines in *A. zeae* interactions with fungal or bacterial pathogens of maize is considered. This is the first report of natural products from *Acremonium zeae*. poster

Wilson, Andrew W.* and Hibbett, David S. Clark University Biology, 950 Main St., Worcester, MA 01610, USA. anwilson@clarku.edu. **Toward a phylogeny of the Sclerodermatineae with emphasis on the taxonomic position of *Calostoma*.**

The suborder Sclerodermatineae is a diverse group of gasteroid basidiomycetes that form a monophyletic group within the Boletales. This group is represented by a number of morphologically distinct genera, including *Scleroderma*, *Calostoma*, *Astraeus*, and *Gyroporus*, among others. The gasteroid genus *Calostoma* represents a unique fruiting structure, with its gelatinized tissues and wide variety of spore morphologies. Previous phylogenetic studies position *Calostoma* alongside genera such as *Gyroporus* (non-gasteroid) and *Astraeus* (earth-star like). Only two species of *Calostoma* from North America, out of the nearly 28 spp. worldwide, have ever been used for phylogenetic analysis. The primary goal of this study is to create a comprehensive phylogeny of the Sclerodermatineae and define *Calostoma*'s position within the suborder. This study will sample 40 Sclerodermatineae species, including 8 *Calostoma* species, from which six genetic loci identified in the Assembling the Fungal Tree of Life (AFTOL) project will be collected. A preliminary analysis utilizing all six AFTOL loci from a subset of 12 Sclerodermatineae taxa is being conducted now. The preliminary analysis will help determine which loci are most appropriate for sequencing in all 40 taxa. This presentation will outline the results of this preliminary analysis and the implications for future study of the Sclerodermatineae. poster

Winder, Richard S.* and Ka, Kang-Hyeon. Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, 506 W. Burnside Rd., Victoria, B.C. V8Z1M5 CANADA. **Fungal indicators of disturbance and productivity in forests of Vancouver Island.**

Fungi are potentially useful indicators of sustainable forest growth, particularly where regulators must evaluate the safety of pest control or other forest management practices. At the Pacific Forestry Centre, we are searching for microbial indicators of forest soil health, including fungi. Field studies were conducted at two Levels of Growing Stock (LOGS) sites on Vancouver island, each containing replicated plots with various levels of applied thinning. One site (Shawnigan Lake, B.C.) is relatively unproductive, while the other site (Sayward, B.C.) is relatively productive. During the autumn and spring of 2004-2005, mushrooms from 45 genera and 102 species were observed at Shawnigan Lake, while 46 genera and 109 species were observed at Sayward. In the Sayward plots, some fungi such as *Cantharellus formosus*, and *Lactarius rubrilacteus* fruited only in the control plots, while others such as *Armillaria spinipina* only fruited in the thinned plots. At Shawnigan Lake, fungi including *Cortinarius cinnamomeus* and *Pluteus cervinus* fruited only control plots, while *Hypoholoma capnoides* only fruited in the thinned plots. Soil DNA amplified by PCR with primers targeting fungal ITS regions has been subjected to DGGE (Denaturing Gradient Gel Electrophoresis). DGGE has produced electrophoretic bands unique to control or clear-cut stands; these bands are currently being sequenced. By continuing to accumulate information in thinned stands and other sites, we hope to eventually separate the signal of background effects, such as site productivity, tree removal, or tree retention, from other disturbances or impacts. poster

Winder, Richard S.* and Keefer, Michael E. Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, 506 W. Burnside Rd., Victoria, B.C. V8Z1M5 Canada **Cultural, ecological, and socioeconomic studies of *Morchella elata* (Black morel) in British Columbia.**

Morels are a well-known non-timber forest product (NTFP) in burned forests of the Pacific Northwest. This study characterized 1) the cultural growth of *Morchella elata* collected in 2003 on Vancouver Island, 2) the ecology of *M. elata* in vast burned areas of the East Kootenay region during 2004, and 3) the socioeconomic status of morel pickers in the E. Kootenay. Sucrose, mannose, and lactose were optimal substrates, but some isolates grew poorly in some composite media. Growth was best in a composite medium containing 1:1 sucrose:mannose. Faster growth correlated with the length of the parental pileus, and ascocarps that initially produced dormant or abortive colonies produced thriving colonies after storage at 20°C for 96 wk. In liquid cultures adjusted with KOH, growth was optimal at pH 7.0, and was relatively sensitive to more acidic or al-

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kaline pH. In the E. Kootenay region, fires produced an average of 760 ascocarps / ha, while areas devastated by mountain pine beetle produced ca. 120 ascocarps / ha. Production was highest in areas where 50-60% of the duff layer was consumed. Overall commercial production from the area was ca. 122 metric tons, one third of it dried. Although morel habitat was very heterogeneous, preliminary measurements indicated a tendency of ascocarps to associate with members of the Rosaceae (e.g. *Spirea betulifolia*) and other plants such as *Erythronium grandiflorum*. During 2004, 27 morel pickers were surveyed at buying stations near the burns. Pickers earned \$ 90 - \$ 7,500 (CDN), averaging \$175/day. Half of the pickers had not picked the previous year, but half also reported harvesting other NTFPs. poster

Wingfield, Brenda D.^{1*}, Coetzee, Martin¹, Maphosa, Lance¹, Mwenje, Eddie² and Wingfield, Michael J.¹. ¹Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa, ²Dept. Applied Biology, National University of Science and Technology, Bulawayo, Zimbabwe. Brenda.Wingfield@fabi.up.ac.za. **African *Armillaria* species: increasingly better understood.**

Modern DNA-based techniques have made identification of *Armillaria* species considerably less subjective. However, linking DNA sequences or RFLP profiles to species described based on morphology is possible only if appropriate herbarium material is available. In the case of many isolates obtained from a wide variety of African countries, the available herbarium material does not lend itself to DNA analysis. In addition, morphological descriptions of *Armillaria* basidiocarps are often incomplete or ambiguous. This has resulted in confusion as to the number of *Armillaria* spp. occurring in Africa. A question that is particularly contentious concerns the relationship between *A. heimii* and *A. fuscipes*. We present an overview of the *Armillaria* spp. found in Africa and examine the DNA evidence (sequence, RFLPs and AFLPs) for the different species. We show that *A. mellea* is present in Africa but that it most likely entered the continent a number of times via the activities of humans. We further suggest that *A. heimii* and *A. fuscipes* represent the same taxon but that a number of other undescribed *Armillaria* spp. also occur in Africa. contributed presentation

Winsett, Katherine E.* Rajguru, Satyendra, Silberman, Jeffrey and Stephenson, Steven L. Dept. of Biological Sciences, University of Arkansas, Fayetteville, AR 72701 USA. kwinset@uark.edu. **Genetic variation in local and widespread populations of myxomycetes.**

Myxomycetes (also called plasmodial slime molds or myxogastriids) are eukaryotic protists whose classification is based almost entirely on the morphology of the fruiting body and spores. Many of the described species appear to be cosmopolitan, but the level of genetic variation within local populations and the extent of gene flow between geographically widespread populations of the same morphospecies are not yet understood. The data for this project were obtained from specimens of *Didymium squamulosum* collected from localities on several continents, and the variation revealed by a preliminary study of the DNA sequence data suggests a more complex situation than might be anticipated from a consideration of observable morphological differences. These molecular data and previously published studies of reproductive compatibility suggest that there is an appreciable degree of genetic distinction among geographically separated specimens that would be classified as the same morphological species. It remains to be seen if many of the myxomycetes regarded as cosmopolitan are, instead, complexes of cryptic species. (Supported in part by two grants from the National Science Foundation.) contributed presentation

Winter, Melanie D.* and Volk, Thomas J. Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601, USA. winter.mela@students.uwlax.edu. **"Rediscovery" of C.W. Hesseltine's PhD thesis on the Mucorales (Zygomycota).**

Although Dr. C.W. Hesseltine is probably best known for his work in food and industrial mycology, his 1950 doctoral thesis, "A revision of the Mucorales based especially upon a study of the representatives of this order in Wisconsin", was a far-reaching, 568 page, 2-volume study. Besides a history of their ever-changing classification, Hesseltine also proposed possible evolutionary relationships between the genera that are now being substantiated through modern genetic methods. However, the most striking accomplishments in this work are the extensive identification keys. Keys distinguishing the families Choanephoraceae, Cunninghamellaceae, Mortierellaceae, Pilobolaceae, and Thamnidaceae are included. Even more impressive are the keys to 30 genera including *Absidia*, *Choanephora*, *Circinella*, *Cunninghamella*, *Mortierella*, *Mucor*, *Mycorhiza*, *Phycomyces*, *Pilobolus*, *Rhizopus*, *Spiellus*, *Szygites*, *Thamnidium*, and *Zygorhynchus*. These keys are exceptional because the primary characteristics they use are from the asexual state. This makes them much more practical, since most species, especially heterothallic species, will not form zygospores under typical laboratory conditions. Despite the scale of his work, many mycologists remain unaware of it. Through this presentation, hopefully more will become aware of and appreciate Hesseltine's impressive and exhaustive study. poster

Wong, Valerie. Department of Plant & Microbial Biology, 321 Koshland Hall, University of California, Berkeley, CA 94720-3102, USA. vwong@uclink.berkeley.edu. **Seduction of mycorrhizal fungi: characterizing an epiparasitic model for plant-fungal networks.**

Plant-fungal mycorrhizal networks are ubiquitous in terrestrial ecosystems and influence ecosystem structure. These extremely complex networks involve a unique degree of connectivity among a multitude of organisms. Individual plants typically host many mycorrhizal fungi, and each fungus colonizes a number of plants. Epiparasitic plants are non-photosynthetic and obtain all of their fixed carbon from surrounding photosynthetic plants through a shared mycorrhizal fungus. In doing so, epiparasites reverse the normal direction of net carbon flow in mycorrhizal interactions and apparently cheat one of the most widespread mutualisms in terrestrial ecosystems. Epiparasitic interactions represent extremes in a continuum of plant-fungal interactions within mycorrhizal symbioses. I propose to investigate the molecular basis of these interactions between mycorrhizal fungi and epiparasitic plants. My approach will involve constructing a genomic shotgun microarray for *Rhizopogon salebrosus* (section *Amyloporogon*). Using genomic clones will avoid the high copy and developmental stage biases often found in cDNA arrays. This microarray will be the first of its kind for mycorrhizal fungi and will serve as an important and versatile tool for further studies. I will use it to characterize the transcriptional changes in *R. salebrosus* as it establishes mycorrhizae with the epiparasitic plant *Pterospora andromedea* through the following stages of seed germination: pre-contact, cracked seed coat, swollen seed, and radicle formation. This will greatly expand our understanding of not only myco-heterotrophic interactions but also inform our understanding of epiparasitic mycorrhizal interactions. poster

Wong, Yiu-Kwong*, Lee, Pui-Nin, Gong, Jun, Yu, Stephen and Chiu, Siu-Wai. Environmental Science Programme, and Dept. of Biology, The Chinese University of Hong Kong, Hong Kong SAR, China. SWChiu@cuhk.edu.hk. **Production of citrinin-free statin-containing *Monascus* biomass and novel water-soluble *Monascus* pigments with anti-cancer effects by submerged fermentation.**

Monascus purpurus-fermented rice is a traditional Chinese medicine for improving blood circulation and invigorating digestion. The lipophilic *Monascus* pigments with strong antioxidation capacity can be applied as food colorants and preservative substitute. Yet during fermentation, *Monascus* often produces citrinin, a nephrotoxin, heptatoxin and carcinogen. By formulating a cultivation medium and manipulating the fermentation condition, a citrinin-free fermentation protocol was developed. The *Monascus* biomass generated was rich in minerals, proteins and dietary fiber, and bore red color and strong cheese-flavor. It also contained the beneficial lovastatin, GABA and squalene and other terpenes. *Monascus* also secreted a novel highly water-soluble red pigment which showed higher stabilities than the reported *Monascus* pigments. Both novel *Monascus* products were non-toxic, and possessed anti-proliferation property against liver and prostate cancer cells via induction of apoptosis. poster

Woolfolk, Sandra W.*, Baird, Richard E. and Goodman, Daisy M. Department of Entomology and Plant Pathology, Mississippi State University, MS 39762, USA. woolfolk@entomology.msstate.edu. **Fungi associated with fire ants and mounds in Mississippi: an effort to discover potential biological control agent(s).**

Fire ant is one of the major pests throughout southeastern of the United States. This aggressive pest is difficult to control and has caused problems in agricultural settings as well as human and animals. Area-wide control efforts are currently being conducted in the midsouth area. As a part of the control efforts, in Mississippi we are conducting a study to determine fungi present in hybrid/black imported and red imported fire ant mounds. Once identified, many of the isolates, particularly those which were shown to be pathogens for other insects, will be tested for their potential as biological control agents. Fungi were isolated from four counties inhabited by hybrid/black imported fire ants and three counties inhabited by red imported fire ants in Mississippi. Identification using standard mycological references showed the following taxa were associated with the fire ants and mounds: *Cytospora*, *F. graminearum*, *Fusarium sambusinum*, *Gloeosporium*, *Macrophoma*, *Mucor*, *Nigrospora sphaerica*, *Paecilomyces*, *Penicillium*, *Phoma*, *Pythium*, *Rhinoctadiella*, *Rhizopus*, *Spiegelia*, *Trichoderma*, and *Tuberularia*. Identification is currently in progress and confirmation of identification will be conducted for each representative isolate using molecular technique. poster

Woolfolk, Sandra W.^{1*}, Cohen, Allen C.² and Inglis, G. Douglas³. ¹Department of Entomology and Plant Pathology, Mississippi State University, MS 39762, USA, ²Insect Diet and Rearing Institute, P.O. Box 65708, Tucson, AZ 85728, USA, ³Agriculture and Agri-Food Canada, Lethbridge AB T1J 4B1, Canada. woolfolk@entomology.msstate.edu. **Morphology of the alimentary canal of *Chrysoperla rufilabris* adults: Do those yeasts play roles in nutritional provision to lacewings?**

An internal morphology study of the alimentary canal of *Chrysoperla rufilabris* adults in relation to yeast symbionts was conducted utilizing scanning and

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transmission electron, and epifluorescence microscopy. The alimentary canal adults possessed a large diverticulum at the posterior end of the foregut. Although yeast cells were distributed throughout the gut, large numbers of yeasts were observed to accumulate within the diverticulum. Large tracheal trunks were attached to the lateral side of the diverticulum suggesting a high demand for gas exchange within this organ. However, the diverticulum was lined with cuticle, and the underlying tissues indicated that minimal absorption occurs within this gut region. This suggests that the high potential for gas exchange in the diverticulum is primarily to support yeast metabolic activity. Observation with fluorescence particles indicated that the foregut and/or diverticulum do not possess an absolute mechanism for retaining particles based on size. The presence of large numbers of yeast cells in between hairs of proventriculus suggests that the proventriculus may play a role in retention of yeast cells. The midgut possessed typical absorptive structures. Since evidence indicated no or minimal absorption of nutrients within the diverticulum, nutrients provided by the yeasts must be transferred to the midgut where absorption occurs. poster

Woolley, Lance P.* and Henkel, Terry W. Department of Biological Sciences, Humboldt State University, Arcata, California 95521, USA. tw5@humboldt.edu. **The role of the heart rot fungus *Phellinus robustus* in shoot turnover and long-term development of the multi-stemmed, tropical monodominant tree *Dicymbe corymbosa* (Caesalpinaceae).**

Preliminary investigations examined the role of the heart rot fungus *Phellinus robustus* (Karst.) Bourd. & Galz. in the structural development of the multi-stemmed, monodominant tree *Dicymbe corymbosa* Spruce ex Benth. in the Pakaraima Mountains of Guyana. *Dicymbe corymbosa* persistently produced reiterated shoots resulting in large individual trees with multiple stems of various size classes. Turnover of canopy shoots may be driven by *Phellinus* heart rot, which occurred in nearly 100% of fallen shoots. Canopy shoot turnover and subsequent reiteration may allow for prolonged survival of mature *D. corymbosa* individuals, promoting continual canopy coverage and a clumped distribution. By circumventing gap-phase dynamics, successive reiteration may reduce the ability of other species to establish and maintain themselves in monodominant stands. The reiterative capacity of *D. corymbosa* may be an evolutionarily-derived response to the high incidence of *Phellinus* heart rot. poster

Worrall, James J.¹*, Johnston, Barry C.² and Adams, Gerard C.³ ¹USDA Forest Service, Rocky Mountain Region, Forest Health Management, Gunnison CO 81230, USA, ²USDA Forest Service, Grand Mesa, Uncompahgre and Gunnison National Forests, Gunnison, CO 81230, USA, ³Department of Plant Biology, Michigan State University, East Lansing, MI 48824, USA. jworrall@fs.fed.us. **Dieback and mortality of *Alnus* in the southern Rocky Mountains.**

Poor condition of thineaf alder (*Alnus incana* ssp. *tenuifolia*) has been noted in the Southern Rocky Mtns. in recent years. To quantify the extent and severity, and gather data that may suggest a cause, we surveyed watersheds that had alder and were at least partly in Colorado. Of 6,503 standing stems (≥ 3 cm DBH) inspected, 34% were live and healthy, 29% live with dieback, and 37% were dead. Alder condition was unrelated to geographic area, elevation, distance to stream, and distance to road. Alder clumps with the most dieback and mortality also had low numbers of sprouts. Transects with full sun exposure had significantly poorer alder condition than transects in full shade. Cytospora canker appears to be consistently associated with dieback and mortality. Isolates clustered into a distinct clade in phylogenetic analysis based on ITS-rDNA sequence. *Cytospora* isolates from other studies of alder were unrelated. Morphological and phylogenetic studies helped differentiate the *Cytospora* state from similar species; preliminary results indicate the pathogen is *Valsa melanodiscus*. This disease is usually associated with plant stress. Other potential causes are climate dynamics, bark beetles, wood borers, alder phytoplasma, and alder *Phytophthora* (though preliminary isolations were negative and symptoms are not consistent). poster

Wu, Mei-Lee¹ and Yu-Zhi Su². ¹Graduate School of Environmental Education, Taipei Municipal Teachers' College, ²Institute of Life Science, National Kaohsiung Normal University, Taiwan. wuml@mail1.tmtc.edu.tw. **Discomycetes from Tengjih and Shaping, Taiwan.**

Most of the saprophytic discomycetes were reported recently from northern Taiwan. Therefore southern mountain areas of Taiwan including Tengjih and Shaping had been selected for investigating the flora of discomycetes since September, 2004. Total 317 samples including 9 terricolous, 10 foliicolous, 73 pteridicolous, 129 lignicolous, 40 grassicolous as well as 23 samples from gymnosperms and 33 from bamboos had been collected. Twenty-one species from 10 genera, 8 families and 4 orders were identified. Among the above 21 species *Lachnum brasiliense*, *Lachnum oncospermatium* and *Lachnum sclerotii* were abundant in the warm season while *Clavisdiscium acuum* and *Lachnum abnormis* were abundant in the cold season. However, *Lachnum controversum*, *Lachnum pteridophyllum*, *Lachnum lanariceps* and *Baeomyces absolutus* were dominant either from cold or warm months. *Clavisdiscium acuum*, *Lachnum blechnophilum* and *Lachnum lanariceps* were reported for the first time in Taiwan from this study. Besides photographs of macroscopic and microscopic morphologies of the newly reported species, the ecological distribution of the species collected from the above two areas will be also discussed in detail. poster

Yaguchi, Takashi¹*, Horie, Yoshikazu², Tanaka, Reiko¹, Matsuzawa, Tetsuhiro¹ and Nishimura, Kazuko¹. ¹Res. Ctr. for Pathogenic Fungi and Microbial Toxicoses, Chiba Univ., 1-8-1 Inohana, Chuo-ku, Chiba 260-8673, Japan, ²Natural History Museum and Inst., Chiba, 123 Yoshio, Katsuura, Chiba 299-5242, Japan. t-yaguchi@faculty.chiba-u.jp. **Classification of pathogenic *Aspergillus* Section *Fumigati*.**

About 300 strains identified as *A. fumigatus* and related species by morphology and preserved at Chiba Univ. were reexamined. First, those strains were genotyped based on electric flow patterns by RAPD analysis. About 95% of strains had a typical RAPD pattern and strains with atypical patterns were selected. Analyses of the sequences on beta-tubulin gene, the hydrophobin gene and the ITS region of some strains of *A. fumigatus* with a typical RAPD pattern, all strains with atypical patterns and related species were performed. Then, the correlation between molecular phylogeny and micromorphology of conidia by SEM was examined. As a result, the strains with a typical RAPD pattern clustered together in a clade and had globose conidia with lobate-reticulate ornamentations. The strains with atypical ones were divided into two groups distant from the clade of strains with a typical one, and had conidia with microtuberculate ornamentations. They were distinguished from a typical *A. fumigatus* on molecular phylogeny and micromorphology. poster

Yamaguchi, Kaoru*, Nakagiri, Akira, Okane, Izumi and Ito, Tadayoshi. Biological Resource Center (NBRC), Department of Biotechnology, NITE, 2-5-8, Kazusakamatari, Kisarazu, Chiba, 292-0818, Japan. yamaguchi-kaoru@nite.go.jp. **Phylogenetic analysis of aero-aquatic fungi, *Diplocladiella* and *Candelabrum*, based on rDNA sequences.**

Based on the sequences of 18S rDNA and D1/D2 region of 28S rDNA, we analyzed phylogeny of the two genera of aero-aquatic fungi, *Diplocladiella* and *Candelabrum*, which have been frequently isolated from Japan. The results suggested that *Diplocladiella* is an anamorph with affinity to Loculoascomycetes and that two new species, which are distinguishable in morphology from other known species, are included in our isolates. Phylogenetic trees showed *Candelabrum* species are separated into two groups in Ascomycota. One group including the type species, *C. spinulosum* clustered within Helotiales and the other group with *C. brochiatum* nested in Pyrenomyces clade. The polyphyly of the genus may be reflected in the difference of the morphology of conidia, especially their shape and mode of branching. Molecular and morphological data also suggested a new species of *Candelabrum* is included in our isolates. poster

Yamaguchi, Yuichi*, Masuma, Rokuro, Uchida, Ryuji, Tomoda, Hiroshi and Omura, Satoshi. Kitasato Institute for Life Sciences, Kitasato University and Kitasato Institute, 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan. ymagu@lisci.kitasato-u.ac.jp. **Fungal strain FKI-1778, a producer of new antibiotics sesquicillins, isolated from mangrove mud.**

In the course of our search for new antibiotics from subtropical microorganisms, fungal strain FKI-1778, isolated from mangrove mud, was found to produce four new antibiotics, sesquicillins B to E together with known sesquicillin. The structures of sesquicillins were elucidated by spectroscopic studies including various NMR experiments. All sesquicillins have a common pyrano-diterpene skeleton. New sesquicillins B to E showed insecticidal activity against *Artemina salina* (brine shrimps) and caused the S phase arrest in Jurkat cells. On agar media the producing fungus showed white conidiomata, that had frill-like decoration of conidia, so the strain FKI-1778 was considered to belong to the genus *Albophoma*. Only one species *A. yamanashiensis* Kobayashi, Masuma, Omura et Watanabe for the genus was reported. Furthermore, their morphological characteristics, sequencing data of the internal transcribed spacer region (ITS region) and metabolite profile by LC/UV were compared. Strain FKI-1778 were 95-350 mm (av. 170 mm, n=30) in conidiomatal length, 1.5-2.2 mm (av. 2.0 mm, n=30) in conidial length, 50-70 mm frill-like structure length. *Albophoma yamanashiensis* FO-2546 were 125-360 mm (av. 215 mm, n=30) in conidiomatal length, 2.0-3.0 mm (av. 2.4 mm, n=30) in conidial length, 150-250 mm frill-like structure length. Strain FKI-1778 could be particularly distinguished from *A. yamanashiensis* by its frill-like structure. Comparison of the ITS 1 and 2, total length 321 bp excluding gaps showed that the sequence similarity between them was 92.5% with 24 bp differences. Sequence analysis of rDNA ITS 1 and 2 supported their distinction in morphological analyses. Furthermore, the metabolites of strain FKI-1778 and *A. yamanashiensis* FO-2546 were compared by LC/UV analysis. Sesquicillin, sesquicillin B, C, D and E were detected in the culture broth of FKI-1778, while they were not detected in the culture broth of *A. yamanashiensis*. The whole chromatographic profiles by LC/UV were also different. Taken together, it was concluded that strain FKI-1778 differs from *A. yamanashiensis*, proposing that the strain FKI-1778 is a new species. poster

Yamaguchi, Yuichi, Masuma, Rokuro*, Kim, Yong-Pil, Uchida, Ryuji, Tomoda, Hiroshi and Omura, Satoshi. Kitasato Institute for Life Sciences, Kitasato University and Kitasato Institute, 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan. masuma@lisci.kitasato-u.ac.jp. **Taxonomy and secondary metabolites of *Pseudobotrytis* sp. FKA-25 from Yakushima Island.**

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We have studied various fungi as a screening source for useful bioactive compounds. Fungal strain FKA-25, isolated from forest soil collected in Yakushima Island, Kagoshima Prefecture, Japan, was assigned to genus *Pseudobotrytis* based on its morphological characteristics. Conidiophores were erect, swollen at the end of the tip, and gave rise to umbellate conidigenous cells that were in an expanded denticulate portion at the end and formed ellipsoidal to clavate conidia in sympodial succession. Identification as *Pseudobotrytis terrestris* was made on the basis of the character of 1-septate conidium. Though *Pseudobotrytis terrestris* distributed widely in nature, its isolation has been rarely reported in Japan. Furthermore, no secondary metabolites have been reported from the genus *Pseudobotrytis*. The culture broth of strain FKA-25 was analyzed, leading to isolation of four secondary metabolites A to D. From the structure elucidation, metabolites B to D were identified as FK-17-p2a, lunatinin, and 3,4-dihydro-3,4,8-trihydroxy-1(2H)-naphthalenone, respectively. Metabolite A was found to be a new compound designated Sespandole possessing a unique indole-sesquiterpene skeleton. Sespandole showed inhibitory activity against lipid droplet accumulation in macrophages. poster

Yamaoka, Naoto* and Matsumoto, Isao. Lab. of Plant Pathology, Ehime University, Matsuyama 790-8566, Japan. yamaoka@agr.ehime-u.ac.jp. **The role of primary germ tube for the life cycle of *Blumeria graminis*.**

The conidia of *Blumeria graminis* f. sp. *hordei* (Bgh), following contact with the host surface, first form a short germ tube, called the primary germ tube (PGT), and then second, an elongating germ tube emerges. It differentiates into the appressorial germ tube (AGT), and then the AGT elongates and swells. It forms a hooked, appressorial lobe that penetrates the epidermal cell wall of the host. In a series of infections, the positive role of PGT for morphogenesis of the fungus is unclear except for the possibility reported by Carver and Ingerson that the growth of a long germ tube, with the potential to differentiate an appressorium, seems to be dependent on the perception of a suitable host surface through contact with the PGT. Therefore, the aim of the present studies is to further clarify the role of PGT for morphogenesis of the fungus. When the conidia of Bgh were inoculated onto the coleoptile surface whose cuticle was removed with cellulose acetate, the emergence of the AGT was delayed. This delay was related with the length of PGT, that is, on the cuticleless coleoptile surface, the PGT tended to continue elongating without stopping. If there were gaps on the coleoptile surface such as a cell border, the PGT stopped elongating there and after that AGT emerged. Therefore, it is necessary for the trigger of AGT emergence to stop the PGT elongation. poster

Yamaoka, Yuichi^{1*}, Masuya, Hayato², Chung, Wen-Hsin¹, Goto, Hideaki³, To-Anun, Chairat⁴ and Tokumasa, Seiji¹. ¹Life and Environmental Sciences, Univ. of Tsukuba, Tsukuba 305-8572, Japan, ²Forestry and Forest Products Research Institute (FFPRI), Tsukuba 305-8687, Japan, ³Kyusyu Branch of FFPRI, Kumamoto 860-0862, Japan, ⁴Department of Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiangmai 50200, Thailand. yamaoka@sakura.cc.tsukuba.ac.jp. **Ophiostoma species with *Leptographium anamorph* isolated from pines invaded by bark beetles in Thailand and Japan.**

During survey of ophiostomatoid fungi associated with bark beetles invading pines, *Leptographium yunnanense* was isolated from *Pinus kesiya* in Thailand and *Pinus densiflora* in Japan. Teleomorph state was obtained from a cross between isolates of the fungus. Ascocarps are black, globose to subglobose, 206-349 X 206-357 µm in diam lacking neck. Ascospores are hyaline, 1-celled surrounded by hyaline sheaths, appearing cucullate in side view, 5.6-7.2 X 2.8-4.0 µm, quadrangular in face view, triradiate in end view. We consider the present fungus as a new species. poster

Yamashita, Satoshi^{1,2*} and Hijii, Naoki¹. ¹Laboratory of Forest Protection, Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya 464-8601, Japan, ²Present Address: Research Institute for Humanity and Nature (RIHN), 335 Takashima-cho, Kamigyo-ku, Kyoto 602-0878, Japan. satsosy@chikyu.ac.jp. **Loss of lamellae does not significantly reduce *Collybia* sp. spore count.**

To examine the effects of loss of lamellae on the number of spores discharged, we collected 28 fruiting bodies of *Collybia* sp. such as *C. dryophila* in a Japanese red pine forest and estimated the daily discharge from each fruiting body. We divided the fruiting bodies into four groups according to the extent of loss of lamellae and the developmental stage: sound at early stage ($n = 11$); sound at late stage ($n = 8$); damaged at early stage ($n = 5$); and damaged at late stage ($n = 4$). We found a heavy loss of lamellae on four fruiting bodies, which lost more than 2/3 of the lamellae on the pileus in orthogonal projection area. The daily discharge of spores from each of the sound and damaged fruiting bodies ranged from 31 250 to 95 317 500. The result of ANCOVA showed that neither the developmental stage nor the loss of lamellae significantly affected the number of spores discharged. We suggest that under natural conditions, loss of lamellae has little effect on the number of discharged spores of *Collybia* sp., probably because of insect feeding. poster

Yamato, Masahide. Biological Environment Institute, Kanso Technos Co., Ltd., 8-4 Ujimatafuri, Uji, Kyoto 611-0021, Japan. yamato_masahide@kanso.co.jp. **Morphology and ecology of arbuscular and orchid mycorrhizas.**

Arbuscular mycorrhiza (AM) is morphologically divided into two types, *Arum* and *Paris* type. The *Arum* type was dominantly found in herbaceous plants in a vacant land and seedlings of pioneer woody plants in an oil palm plantation, whereas the *Paris* type was dominant in understory plants in deciduous broadleaved forests. These results suggest that the *Arum* type could be advantageous to the fast-growing plants, while the *Paris* type is advantageous to slow growers in shaded condition. The hyphal coils of mycorrhizal fungi, which are similar to those of *Paris* type AM, are also formed in orchid mycorrhiza (OM). It was first shown in this study that *Coprinus* and *Psathyrella* in Coprinaceae form OM in an achlorophyllous orchid, *Epipogium roseum*. Most of the coiled hyphae of the mycorrhizal fungi in *E. roseum* were found to be degenerated. In OM, it is well known that nutrients including carbon compounds are transferred from mycorrhizal fungi to orchids. Mycorrhizal fungus of an achlorophyllous plant *Sciaphila tosaensis* forming *Paris*-type AM was revealed to be *Glomus* sp. by fungal isolation and molecular analysis. The degeneration of coiled hyphae was found in this mycorrhiza, which was similar to that of OM. The intact and/or the degenerated coiled hyphae of the *Paris*-type AM in *S. tosaensis* were assumed to have the function to transfer the carbon compounds from AM fungi to the plant. **MSJ Research Encouragement Award Lecture.**

Yoshida, Kouta^{1*}, Yamada, Akiyoshi¹, Murata, Hitoshi² and Kobayashi, Hisayasu³. ¹Faculty of Agriculture, Shinshu University, Minami-minowa, Nagano 399-4598, Japan, ²Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan, ³Ibaraki Prefectural Forestry Center, Naka-machi, Ibaraki 311-0122, Japan. akiyosh@gipmc.shinshu-u.ac.jp. **Mycorrhiza synthesis between *Tricholoma matsutake* and Pinaceae plants.**

Tricholoma matsutake, one of the most commercially important edible ectomycorrhizal mushrooms in the world, has been established the technique for in vitro mycorrhization with the Japanese red pine, *Pinus densiflora*. Although several other Pinaceae species have been reported their mycorrhization with *T. matsutake* in vitro, another combination is desired from the viewpoint of suitable tree species for transplantation at the local scale. In vitro mycorrhiza syntheses were conducted between *T. matsutake* and three Pinaceae plants, i.e. *Pinus koraiensis*, *Pinus parviflora*, and *Picea abies*. Five months after cultivation of the seedlings with *T. matsutake* mycelium, fine roots were observed under the microscope. All three combinations showed ectomycorrhizal features, i.e. fungal sheath and Hartig net structure at the root cortex. poster

Yoshimi, Akira^{1*}, Shimizu, Kiminori², Kojima, Kaihei^{3,4}, Takano, Yoshitaka³, Kawamoto, Susumu² and Tanaka, Chihiro¹. ¹Laboratory of Environmental Mycology, Graduate School of Agriculture, Kyoto University, Kyoto, 606-8502, Japan, ²Research Center for Pathogenic Fungi and Microbial Toxicoses, Chiba University, Chiba, 260-8673, Japan, ³Laboratory of Plant Pathology, Graduate School of Agriculture, Kyoto University, Kyoto, 606-8502, Japan, ⁴Present address: Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, NC 27710, USA. akira@remach.kais.kyoto-u.ac.jp. **Functional comparison of the group III histidine kinases in ascomycetous and basidiomycetous fungi.**

In many filamentous fungi including a model ascomycetous fungus *Neurospora crassa* and a maize pathogenic ascomycete *Cochliobolus heterostrophus*, the mutations of the group III histidine kinase (HK-III) genes resulted in resistance to dicarboximide- and phenylpyrrole-fungicides and also in increased osmosensitivity. In this presentation, we analyzed structure and function of *CnNIK1* encoding an HK-III from *Cryptococcus neoformans*, a human pathogenic basidiomycetous yeast, to ask whether the the HK-III in basidiomycete is involved in drug resistance and other features. The results revealed that *CnNIK1* is also responsible for the phenylpyrrole sensitivity but not in osmo-resistance, suggesting that the HK-IIIs function similarly in terms of drug resistance in both ascomycete and basidiomycete, but not in case of osmo-tolerance. It has been shown that exposure to the phenylpyrrole led to improper activation of HOG1-type MAPKs in ascomycetous plant pathogens *C. heterostrophus* and *Colletotrichum lagenarium*. We analyzed the phosphorylation pattern of HOG1-type MAPKs of *C. heterostrophus*, *C. neoformans* and *N. crassa* to elucidate the relationship between HK-IIIs and the MAPKs in fungi in general. The results indicated that HK-IIIs positively regulate the activation of HOG1-type MAPKs in all fungi tested, suggesting that this signaling pathway is broadly conserved in the fungal kingdom. poster

Yuan, G. F., Chu, W. S., Chen, C. C., Liaw, L. L., Chen, Y. P., Huang, L. N., Liua, T. D. and Liao, C. C. Food Industry Research and Development Institute, P.O. Box 246, Hsinchu, Taiwan, R.O.C. gfy@firdi.org.tw. **Functional genomics study of *Monascus* spp.**

Monascus can produce various secondary metabolites useful as food additives and/or pharmaceuticals. A *Monascus* strain, BCRC 38072, isolated from red rice can produce monacolin K, a cholesterol serum synthesis inhibitor. The genome

Continued on following page

MSA ABSTRACTS

sequence of *Monascus* sp. BCRC 38072 was obtained by whole-genome shotgun of a variety of clone types at 11-fold sequence coverage. The Arachne package was used to assemble the genome sequence. A total of 673,853 highly qualified reads were input into the assembly program. The resulting draft consists of 709 contigs, larger than 2 kb in length, with the total length of 26.8 Mb. Seventeen major supercontigs were assembled covering 94.8% of the whole assembly length and 422 ungrouped contigs were assembled in the rest 5.2%. The N50 lengths of supercontig and contig are 2.5 Mb and 224 Kb, respectively. With the aid of 13 known BAC and fosmid contigs, the draft was aligned to 99.1% of the known contigs sequences. A total of 6,855 unigenes were generated from 41,453 EST reads. Positions of 8,840 introns with an average size of 79 bp were identified on the draft and the GT-AG rule was conserved in most exon-intron boundary. More than 1,000 genes are considered as novel since no significant hit was found in public databases. A proteomic analysis of a pigment producing strain, along with its albino mutant, has been performed to investigate proteins related to pigment production. A total of 117 protein spots with significantly differential expression were obtained. These protein spots were identified by tandem mass spectrometry and Mascot search system. An online *Monascus* spp. proteome database has been constructed by integrating 2-DE experimental data and mass spectrometric identification data. This proteomic analysis shall provide useful information for further analysis of secondary metabolites production in *Monascus* spp. Polyketide (PK) synthesis genes and their products are the focus of *Monascus* functional genomic studies. Series of PK related gene transformants were generated in *Monascus* spp. Besides the conventional PEG-mediated transformation and electroporation, *Agrobacterium*-mediated gene transfer system adapted from plant systems was established and successfully used in *Monascus* spp. with high efficiency. The monacolin k gene cluster of *Monascus* sp. BCRC 38072 was cloned and examined in detail. Individual genes of the gene cluster were transformed and expressed in *E. coli*. The transformants with portion of the nine genes of the cluster produce a polyketide-like product. symposium presentation

Zhang, Ning^{1*}, Geiser, David M.² and Smart, Christine D.¹ ¹Dept. of Plant Pathology, NYSAES, Cornell University, Geneva, NY 14456, USA, ²Dept. of Plant Pathology, Penn State University, University Park, PA 16802, USA. nz35@cornell.edu. **Molecular detection of *Fusarium solani* species complex using microarray.**

Members of *Fusarium solani* species complex (FSSC) are pathogens of a number of plants, ubiquitous saprophytes in soil, and opportunistic human pathogens. Morphologically similar, molecular phylogenetic studies revealed that there are more than 40 distinct lineages (phylogenetic species) in FSSC. In this study, we designed oligonucleotides from internal transcribed spacer of the ribosomal RNA genes of 21 FSSC isolates in order to rapidly and accurately detect them from the field samples. Our hybridization results showed that the sensitivity and specificity of the array signals are dependent on the length and melting temperature of the oligomers. The 70-mers usually are able to discriminate three nucleotide mismatches, while the 20-mers with melting temperatures of 53 C-56 C are able to discriminate a single nucleotide mismatch with the target DNA. Our optimized array is able to distinguish FSSC down to species level and even infraspecies level for certain groups. poster

Zhou, Shuang* and Anagnost, Susan E. Faculty of Construction Management and Wood Products Engineering, State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13210, USA. szhou@syr.edu. **Morphological and molecular studies of basidiomycetes isolated from utility poles and air samples.**

The identities of cultures of basidiomycetes are important to the population study of fungi in wood products and indoor air from "sick" buildings, two growing fields of interest. Yet, the difficulties of observing diagnostic microscopic cultural characters make identification prolonged and slow. With molecular biology techniques, morphology and phylogeny of seventy basidiomycete cultures isolat-

ed from utility poles and air samples in the city of Syracuse, NY were studied. Their ITS rDNA sequences were obtained using universal primers ITS4 and ITS5; phylogeny analysis was conducted using PAUP; cultural morphologies were observed using phase contrast illumination after phloxine staining. In our study, both morphology and molecular methods showed their strengths and limitations in identifying fungi. To use them complementarily was essential to my study. The basidiomycetes isolated from indoor air samples are wood-decay basidiomycetes, such as *Trametes versicolor*, *Peniophora nudal/cinerea*, *Stereum sanguinolentum*. The comparison of isolation numbers from indoor and outdoor air samples indicated a possible past water damage and on-going decaying of wood structures of the houses. Cultural characters and phylogeny of several representative genera will be presented. poster

Zitomer, Nickolas C.^{1*}, Geiser, David M.¹, Archibald, D. D.², Ward, T. J.³, O'Donnell, Kerry³, Jones, A. D.⁴, Jimenez-Gasco, M. M.¹ and Kuldau, Gretchen A.¹ ¹Department of Plant Pathology, ²Department of Crop and Soil Sciences, ³Department of Chemistry, The Pennsylvania State University, University Park PA, USA, ⁴Microbial Genomics and Bioprocessing Research Unit, National Center for Agricultural Utilization Research, USDA, Peoria, IL 61604-3999, USA. ncz103@psu.edu. **HPLC-MS analysis of type-A trichothecene-producing fusaria for correspondence between toxin profiles and molecular phylogenetic groups.**

Trichothecenes are mycotoxins produced by many *Fusarium* species. *Fusarium* trichothecenes are generally divided into two categories, type A, which lack oxygen at the C-8 position and include T-2 toxin and diacetoxyscirpenol, and type B, which include nivalenol and deoxynivalenol. Phylogenetic relationships of trichothecene-producing fusaria (TPF) were inferred based on DNA sequences from seven gene regions, EF1- α translation elongation factor, phosphate permease, 28S rDNA, Tri101, Tri4, Tri5, and B-tubulin, determined in isolates comprising the known species diversity of TPF. The TPF was found to represent a monophyletic group. Gene genealogies independently supported the existence of four major clades within the TPF, one of which represented a species complex that includes the major type B trichothecene producers *Gibberella zeae* and its relatives. Across all four clades, at least thirty species lineages were identified based on genealogical concordance. The production of five type A and five type B trichothecenes was analyzed using high performance liquid chromatography and atmospheric pressure chemical ionization mass spectrometry (HPLC/APCI-MS) in rice cultures of isolates representing the phylogenetic breadth of TPF. The production of type B trichothecenes was found to be widespread, occurring in species across the TPF, including species known only to be type A producers. contributed presentation

Zuccaro, Alga^{1*} and Mitchell, Julian, I.² ¹Institut für Mikrobiologie, Technische Universität Braunschweig, Spielmannstr. 7, D-38106 Braunschweig, Germany, ²University of Portsmouth, School of Biological Sciences, King Henry Building, Portsmouth PO1 2DY, England. a.zuccaro@tu-bs.de. **Development and application of real-time PCR approach for detection and quantification of the marine fungus *Acremonium fuci* beta tubulin sequences from its algal host.**

A TaqMan real time quantitative PCR assay targeting the intron 3 of the beta tubulin gene was developed to monitor the colonization rate of the saprophytic marine fungus *Acremonium fuci* in algal host tissues. Twenty-one healthy-looking and six decaying *Fucus serratus* independent tissue samples of ten grams each were analysed. The results were concordant with those obtained using a conventional nested PCR amplification of 28S rDNA fungal sequences from algal tissue and DGGE analysis, as well as with the recovery rate of *A. fuci* isolates after culturing. The real time procedure showed a higher abundance of the fungus in the dead compared to the living tissues of the alga, suggesting a latency of the fungus in healthy tissues. This apparent latency may represent an adaptive strategy of the saprobe for rapid colonization of the decaying material. contributed presentation

MYCOLOGICAL NEWS

A Simple Blue Staining Technique for Arbuscular Mycorrhizal and Other Root-Inhabiting Fungi

Vierheilig *et al.* (1998) published a method for staining the fungal symbiont in arbuscular mycorrhizae in which they used ink and vinegar to reduce the use of dangerous and noxious chemicals such as Trypan blue. Besides having obvious health and safety advantages, the method is useful for circumstances where access to chemicals is restricted or difficult, as in field studies, work in which young students are involved, or use by amateur mycologists or gardeners who might wish to examine organisms in roots.

One disadvantage of the ink and vinegar method is that acetic acid is somewhat unpleasant to use because of its odor. Consequently, another safe method of acidifying the roots with a less odorous compound was sought. Using very dilute HCl gave good results (see Figure). If, hydrochloric acid is not available, other weak acids can be used. Trials with Tonic Water (SUGAR-FREE!) (pH measured at 3.7) worked perfectly, resulting in an even less hazardous method. However, in a laboratory setting, HCl is easy to obtain, and at the dilution suggested, relatively safe. Probably virtually any acidic liquid will suffice for the acidification process.

In the original recipe, Vierheilig *et al.* used various inks, and found them to have different efficacies. One product not mentioned, but which gives excellent results (see Figure), is Parker Quink with SOLV-X®, a proprietary solvent that appears to assist with the staining. This has been found to be available in several different countries, including Mexico, the UK, and Belgium. Whichever ink is chosen, ensure it is permanent. For example, Quink also comes in a Royal Blue Washable version, which should not be used.

Reagents

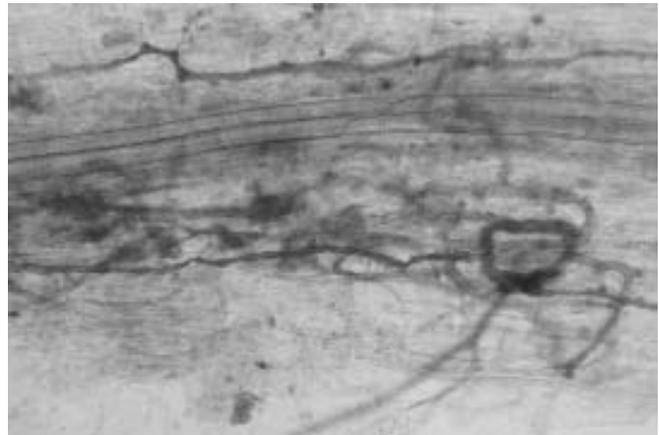
For initial clearing of alkali-soluble pigments, 1 M KOH solution is used. If, for example, in the field, potassium hydroxide cannot be obtained, a proprietary caustic drain cleaner (these mainly consist of sodium hydroxide) can be diluted and used instead, but the result is not as good because the roots do not soften as much as with KOH.

For roots that retain some pigment after alkali-clearing, an aqueous solution of 10 % household bleach (resulting in approximately 0.25 % sodium hypochlorite solution) works very well. Other bleaching agents, such as hydrogen peroxide can be used.

The ink can be made up in 1 % HCl (or other acid) at 1:50 v/v, or it can be added with a dropper directly to the roots after they are placed in the acidifying reagent.

The Protocol

1. Wash the roots with tapwater to remove soil particles and select those for staining.



An arbuscular mycorrhiza between *Plantago lanceolata* and an un-named Chinese fungus stained with acidified Quink. An entry point with a hyphal coil and a colonization unit with abundant arbuscules is revealed. The mycorrhiza was provided by courtesy of Yuan Yuan Ling (China) and Mauritz Vestberg (Finland).

2. On a hotplate or gas burner, bring the roots to the boil in the alkaline solution, and immediately remove the heat source (take extreme care and wear suitable safety goggles). It is also possible to use a microwave oven by placing the roots in about a 2-cm depth of reagent, starting the microwave on full power, and when boiling point is observed, immediately switching off. Alternatively, very hot (near-boiling) alkali solution can be added, or the roots can be heated in the alkali solution at about 60-80 C for 1 hour. If the roots are not heavily pigmented, they can just be left in cold KOH for 24 hours with quite a good result.
3. Remove heat and leave to stand for a time up to 24 hours (minimum, for fine roots with very little pigmentation, 2 hours). It seems to do little harm to leave most roots for a few days, although some of the finest roots will disintegrate. It is necessary to experiment with the system for the particular plant species being stained.
4. Rinse briefly in tapwater to remove excess alkali.
5. If the roots are still dark and opaque because of pigmentation (as in many woody perennials), they can be bleached whilst observing them under a dissecting microscope until the stele just becomes visible. The bleaching should be for the shortest possible time, as excessive bleaching reduces the staining efficacy. Transmitted

Continued on following page

MYCOLOGICAL NEWS

light helps with observations in this process, though it is not essential.

6. Acidify the roots with 1 % HCL or other acid. The acidification can be seen to work, because the roots lighten in color immediately. Move the roots to acidified ink or add ink by dropper directly to the acidified roots.

The roots can be examined microscopically after about 30 minutes, though staining generally improves over a longer period. It is best to leave them at least 4 hours, or preferably overnight. They can be kept in acidified glycerol + ink indefinitely. Destaining for a period of a few hours in acidified glycerol is recommended, resulting in improved clarity and contrast, but if one is in a hurry, the stained root fragments can be transferred immediately to a suitable mountant on microscope slides for observation. Polyvinyl alcohol lacto-glyc-

erol (PVLG) (Omar, Boland & Heather 1979) produces a semi-permanent mount (these last many years), or acidified glycerol can be used if there is no need for longer term preservation of specimens.

This method reduces even more the use of unpleasant chemicals when compared with the ink and vinegar technique. Nevertheless, all health and safety recommendations and regulations must be followed when using acids, dilute or otherwise, or hot alkaline solutions.

References: Omar, M. B., Bolland, L. & Heather, W. A. (1979). *Bulletin of the British Mycological Society* **13**, 31-32.; Vierheilig, H., Coughlan, A.P., Wyss, U. & Piché, Y. (1998). *Applied Environmental Microbiology* **64**, 5004-5007.

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Joan Bennett Elected to the National Academy of Sciences

Joan W. Bennett, Professor of Cell and Molecular Biology at Tulane University, was elected to the National Academy of Sciences in May. Election to the National Academy, which serves as a national advisory group on matters of science, engineering and medicine, is one of the highest honors bestowed across the sciences. Dr. Bennett will be only the second current Academy member in the Society, along with T.N. Taylor from the University of Kansas.

Dr. Bennett is broadly known for her contributions in research, teaching and service. Her election to the National Academy recognizes her seminal contributions in the areas of fungal production of secondary metabolites and industrial microbiology. She is an active instructor with responsibilities for many courses, and her excellence in teaching and advising is recognized through numerous awards. Her record of service, to Tulane and to professional societies, is staggering.

Dr. Bennett has co-edited five books, and served in an editorial capacity on twelve different journals and book series. MSA members may be best acquainted with Dr. Bennett from her service as Editor-in-Chief of MYCOLOGIA



Bennett

from 2002-2004, a period of major changes in the journal, including an ownership transition from the New York Botanical Garden to the MSA, on-line publishing, and most significantly, the conversion from an all-paper to an all-electronic submission, review and publication system. Dr. Bennett oversaw all of this turmoil with aplomb, and with all of those changes now safely in place, it's hard to imagine how it was managed in such a short time period.

We cannot claim Dr. Bennett as ours alone, however. Among other positions in the American Society for Microbiology,

she served as its President, and throughout her career has been instrumental in representing fungi in the broad realm of microbiology, particularly on an international level. She counts among the very small number of fungal biologists with membership in the National Academy, and she is certain to be a strong and effective advocate for mycology. So, it is both with pleasure and pride that we congratulate Joan on her election to the National Academy.

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MYCOLOGICAL NEWS

Introductory Mycology – Laboratory Review – MycoAlbum CD

A year or so ago I decided it was time I put together a Family Photo Album CD so I could pass along the images of this and earlier generations of my family to my children and their children and so on down the ages! So! I searched around the web for what I thought was the best software of the day and persuaded my family to buy me a program called FlipAlbum as a Christmas gift. Armed with this software, I started the family album with obsessive vigour.

I hadn't been long into the project when it dawned on me that the program was not only much better than I had anticipated but was even better suited to fungi than to people and you don't get any complaints about the quality of the scans. This being true, I put the family album on hold, transferred my efforts from Man (*sensu lato!*) to Moulds and started a CD ALBUM on fungi. As the saying goes 'a wise man learns from other peoples mistakes - a fool from his own'. Unfortunately this simple truth has never impressed itself on my senses. So I played the 'fool' for a year or more and, as with many of my other projects, if I knew as much at the beginning as I did at the end, I could have done it in a fraction of the time. Apart from the learning curve, I kept changing my mind about what I wanted to include and the album just grew and grew and GREW. This naturally added considerably to my headaches. Indeed, it took me so long to complete the project that, a few months ago, the company came out with an update of the software even before I had mastered the original version. Isn't that the way of it?

To cut to the merry chase, I have nearly completed my album. The less than dazzling title is 'Introductory Mycology - Laboratory Review'. It's an A - Z visual treatment of most of the fungi covered in laboratory sessions of a classical course in introductory mycology (am I a generation too late?). All the illustrations are accompanied by short, simple, straightforward, explanatory annotations (a student's delight). Hopefully the album will be useful not only to budding mycology students but also as comparatively painless review material for graduate students in Plant Pathology, Microbiology and also for many other biology professionals whose lack of appreciation or understanding of the massive impact of fungi on the real world never ceases to surprise me.

FlipAlbum has a lot of excellent features. Indeed too many to comfortably consider here. I'll stick them on my website soon for anyone with a compelling interest in dull reading (www.uoguelph.ca/~gbarron). The bottom line is that FlipAlbum is a powerful program for presenting visual information. For anyone who wants to make a family album or make their personal mycology course into an album this software is hard to beat. Want to put out an E-book on mushrooms of Gorky Park with projected sales of ten - this is the way to go.

I did have a lot of problems initially with the album but the upgrade solved many of these. Some difficulties still remain but I'm working on these as I write. Those who have seen my album have been pleasantly surprised. Indeed a few have expressed awe and wonder (e.g. my wife). There are over **900** images on the CD (diagrams, photomicrographs, SEMs, macrophotographs etc.). The MycoAlbum CD has twice as many images as the APS CD on 'Fundamentals of Fungi' and, all going well, will sell for about 25% of the price even less for grad students. There are a few poor shots but most are pretty good, and a few are exceptional (I'm modest too!). The quality of the images and file sizes are several times that of web pictures and those at full screen size on a 17" LCD monitor are impressive. The idea of the CD is to put it out in the lab and let the students browse through it as they need using bookmarks preselected by the instructor for that particular lab. This way they can see a good 'reality' image of what they are looking for in their own mounts.

For your delight and edification I have persuaded Don Hemmes to showcase the MycoAlbum CD during the poster sessions at the Hilo meetings. There will be Ten Copies of the CD available for auction. Unfortunately, much as I would wish it, I will be unable to attend the Hilo meeting personally. Those who know me will understand my deep sense of regret on this issue. But who knows? If I can make a few dollars out of this stuff I might see you all in Montreal! At least if I can figure out a way to market this thing and I'm not tied up with the Family Album.

George Barron
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MYCOLOGIST'S BOOKSHELF

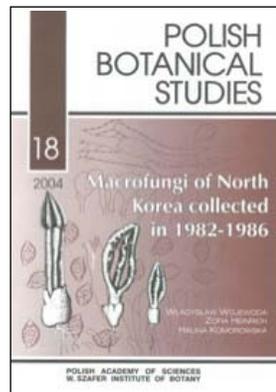
This issue of Inoculum contains one book review. Books received since May are listed followed by books received earlier. If you look on-line for the latest Inoculum, you will see the new books for review months before the hardcopy comes in the mail. When you review a book, then you may keep it! All requests for books to review should be sent to Dr. Amy Rossman at arossman@nt.ars-grin.gov.

Macrofungi of North Korea Collected in 1982-1986

Macrofungi of North Korea Collected in 1982-1986. W. Wojewoda, Z. Heinrich, & H. Komorowska. 2004. Polish Botanical Studies 18: 1-289. IB Publisher Polish Academy of Sciences, W. Szafer Institute of Botany, Lubica 46, PL-312-512, Kraków, Poland, email: ed-office@ib-pan.krakow.pl. Price: € 50.00 plus postage.

This volume includes 431 species of fungi, primarily Basidiomycota plus 13 species of Ascomycota, based on materials collected during five expeditions to North Korea in 1982-1986. Of these, 259 species are reported for the first time from North Korea (Democratic People's Republic of Korea). For each species, the information contains short descriptions of macro- and microscopic features, sites and substrata, accepted names and synonyms with basionym, and references concerning taxonomy and geographical distribution, especially in Asia. Microscopic elements of some species are illustrated in 152 figures of fine line drawings. Specimens were collected at 65 sites, especially in representative mountains of North Korea: Kumgang-san Mts, mountains near Kaesong city, Myohyang-san Mts., Paekdu-san Mts., Ryongak-san Mt., Suian-san Mts and Taesong-san Mts. The characteristics of North Korean mycobiota are given in details.

North Korea occupies 55% of the land area of the Korean peninsula and is divided from China to the north by the



Amnok-gang (Amur) and Tuman-gang (Tumen) Rivers, and from a slight sliver of Russia to the extreme northeast by the Tuman-gang. A military wire fence marks the border with South Korea. The climate is similar to that in South Korea, but the winters are colder and drier. There are four distinct seasons with summer monsoon rains. Annual rainfall in the lowlands averages (600) 800-1000 mm, and in the mountains 1000-1500 mm. The vegetation season in the northern part of the country lasts 5-6 months in the lowlands and 4-5 months in the mountains. North Korea has a diverse range of plants, with climatic regions that include zones of alpine mountains, coniferous forests, mixed forests, and deciduous forests, thus providing ideal environments for mycofloral studies.

The fungi of North Korea have been little studied and the mycobiota and fungal diversity are unknown outside of the country. This volume is the first account on North Korean fungi published in English, except for some short articles by mycologists from the Institute of Botany of the Polish Academy of Sciences in Krakow published in 1990-1992. Previous North Korean mycological papers were published only in Korean and are practically inaccessible to foreign students. This book is a valuable guide and excellent reference to the studies of North Korean fungi that should be of great interest to mycologists working in Asian regions who want to understand the mycoflora of this little-discovered country.

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MYCOLOGIST'S BOOKSHELF

Books Received May – June 2005

- **Antifungal Agents: Methods and Protocols. Methods in Molecular Medicine 118.** 2005. E.J. Ernst & P.D. Rogers. The Humana Press, 999 Riverview Drive, Suite 208, Totowa, New Jersey 07512, USA, email: humana@humanapr.com, ISBN 1-58829-277-0. 198 p. Price: \$99.50. *Requested from publisher.*
- **Common Mushrooms of the Talamanca Mountain, Costa Rica.** 2005. R.E. Halling & G.M. Mueller. *Memoirs of the New York Botanical Garden* 90: 1-195. The New York Botanical Garden, 200th St. & Kazimiroff Blvd., Bronx, New York 10458-5126 USA, <http://www.nybg.org/bcsi/spub>, ISBN 0-89327-460-7. Price: \$19.95. *Review needed.*
- **Flora Agaricina Neerlandica. Volume 6.** 2005. M.E. Noordeloos, Th. W. Kuyper, & E.C. Vellinga. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, USA, email: orders@crcpress.com. ISBN 9-0541-0496-1, 310 p. Price: \$59.95. *Requested from publisher.*
- **The Fungal Community: Its Organization and Role in the Ecosystem. Third Edition.** 2005. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, USA, email: orders@crcpress.com. ISBN 0-8247-2355-4, c. 936 p. Price: \$139.95. *Requested from publisher.*
- **Fungi: Experimental Methods in Biology.** 2005. R. Maheshwari. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, USA, email: orders@crcpress.com. ISBN 1-57444-468-9. ca. 350 p. Price: \$149.95. *Requested from publisher.*
- **Handbook of Industrial Mycology.** 2005. Z. An. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, USA, email: orders@crcpress.com. ISBN 0-8247-5655-X, 784 p. Price: \$169.95. *Requested from publisher.*
- **Isolation and Characterization of Melanized, Slow-growing Fungi from Semi-arid Rock Surfaces of Central Spain and Mallorca.** 2004. C. Ruibal Villaseñor, Tesis Doctoral, Universidad Autonoma de Madrid, Facultad de Ciencias, Departamento de Biología Molecular. For further information, contact G. Bills, email: Gerald_Bills@Merck.com.
- **Macrofungi of North Korea Collected in 1982-1986.** 2004. W. Wojewoda, Z. Heinrich, & H. Komorowska. *Polish Bot. Stud.* 18: 1-289. IB Publisher Polish Academy of Sciences. W. Szafer Institute of Botany, Lubica 46, PL-312-512, Kraków, Poland, email: ed-of-fice@ib-pan.krakow.pl. Price: €50.00 plus postage. *Reviewed in this issue.*
- **Mushrooms: Cultivation, Nutritional Value, Medicinal Effect, and Environmental Impact, second Edition.** 2004. S.-T. Chang & P.G. Miles. CRC Press, 6000 Broken Sound Parkway, NW, Suite 300, Boca Raton, FL 33487, USA, email: orders@crcpress.com. ISBN 0-8493-1043-1. 480 p. Price: \$159.95. *Requested from publisher.*
- **Röhrlinge und Blätterpilze in Europa.** 2005. E. Horak. Elsevier GmbH, Spectrum Akademischer Verlag, Verlagsbereich Biologie, Chemie und Geowissenschaften, Dr. Ulrich G. Moltmann, Slevogtstr. 3-5, 69126 Heidelberg, Germany, email: info@s-f-g.com. Price: €40.00 plus postage. *Review needed.*

Mycological Society of America – Gift Membership Form

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

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

MYCOLOGIST'S BOOKSHELF

Previously Listed Books

- **Biodiversity of Fungi: Inventory and Monitoring Methods.** 2004. GS Mueller, GF Bills, & MS Foster (eds). Elsevier Academic Press, Burlington, MA, www.elsevier.com, ISBN 0-12-509551-1, 777 pp. Price: \$99.95. *Requested from publisher.*
- **CBS Centenary: 100 Years of Fungal Biodiversity and Ecology.** 2004. PC Crous, RA Samson, W Gams, RC Summerbell, T Boekhout, G. Sybren de Hoog, JA Stalpers (eds). Studies in Mycology 50(1&2): 1-580. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands, www.cbs.knaw.nl. Price: € 100.00. *Review needed.*
- **Cultivation and Diseases of Proteaceae: *Leucadendron*, *Leucospermum* and *Protea*.** 2004. PW Crous, S Denman, JE Taylor, L Swart, & ME Palm. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands, www.cbs.knaw.nl/publications/index.htm 227 pp. Price: € 60.00. *Review needed.*
- **Cytology and Plectology of the Hymenomyces.** 2004. H Cléménçon. Bibliotheca Mycologica vol. 199. J. Cramer. www.schweizerbart.de 488 pp. Price: €96.00. *Reviewed in Jan-Feb 2005.*
- **Dothideales Dictiosporicos/Dictyosporic Dothideales.** 2004. J Checa. Flora Mycological Iberica vol. 6. J. Cramer, Stuttgart, Germany, www.schweizerbart.de, 162 pp. Price: €58.00. *Reviewed in Jan-Feb 2005.*
- **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. *Reviewed in Mar-Apr 2005.*
- **Environmental Microbiology, A Laboratory Manual. Second Edition.** 2004. IL Pepper, CP Gerba. Elsevier Inc, Amsterdam, The Netherlands, <http://books.elsevier.com>, ISBN 0-12-550656-2, 232 pp. Price: \$39.95. *Reviewed in Mar-Apr 2005.*
- **Fire Blight. The Foundation of Phytobacteriology.** 2003. CS Griffith, TB Sutton & PD Peterson (eds). APS Press, 3340 Pilot Knob Road, St. Paul, MN 55121, aps@scisoc.org, 144 pp. Price: \$55.00. *Reviewed in Mar-Apr 2005.*
- **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 Disease Resistance in Plants: Biochemistry, Molecular Biology, and Genetic Engineering.** 2004. ZK Punja (ed). Food Products Press, New York, www.HaworthPress.com/store/product.asp?sku=5093, ISBN 1-56022-961-6, 266 pp. Price \$39.95 softbound, \$59.95 hardbound. *Review in progress.*
- **Fungi of New Zealand. Nga Harore o Aotearoa. Vol. 1. Introduction to Fungi of New Zealand.** 2004. E.H.C. McKenzie (ed.). Fungal Diversity Press, Centre for Research in Fungal Diversity, The University of Hong Kong, China, www.hku.hk/ecology/mycology/FDP.html, ISBN 962-86765-5, 168 pp. Price: \$60.00. *Review in progress.*
- **Insect-Fungal Associations: Ecology and Evolution.** 2005. FE Vega, M Blackwell (eds). Oxford University, Oxford, United Kingdom, www.oup.com/us, ISBN 0-19-516652-3, 333 pp. Price: \$49.50 (hardbound). *Review in progress.*
- **Introduction of Biodeterioration, 2nd Edition.** 2004. D Allsopp, K Seal & C. Gaylarde. Cambridge University Press, New York, NY, uk.cambridge.org/, 237 pp. Price: \$75.00 hardback, \$34.99 paperback. *Review in progress.*
- **Introduction to Food and Airborne Fungi. Seventh Edition.** 2004. RA Samson, ES Hoekstra & JC Frisvad. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands, www.cbs.knaw.nl/publications/index.htm, 389 pp. Price: €50.00. *Requested from publisher.*
- **Invasive Species: Vectors and Management Strategies.** 2003. GM Ruiz & JT Carlton (eds). Island Press 76381 Commercial Street, P.O. Box 7, Covelo, CA 95428, www.islandpress.org, 518 pp. Price: \$40.00 paperbound, \$75.00 hardbound. *Review in progress.*
- **Laboulbeniales, II. *Acompsomyces-Ilyomyces*.** 2003. S Santamaria, Flora Mycologica Iberica vol. 5. J. Cramer, Stuttgart, Germany, www.schweizerbart.de, 344 pp. Price: €78.00. *Reviewed in Mar-Apr 2005.*
- **List of Plant Diseases in Korea, Fourth Edition.** 2004. W-D Cho, H-D Shin (editors-in-chief), The Korean Society of Plant Pathology, Seoul, Korea, email: s3213@korea.com, ISBN 89-88154-37-1, 779 pp. Price: unknown. Data available on-line at <<http://nt.ars-grin.gov/fungal-databases/fungushost/fungushostframe.cfm>>.
- **Los Hongos de El Edén, Quintana Roo. Introducción a la Microbiota Tropical de México.** 2003. G Guzmán. Instituto de Ecología, Departamento de Publicaciones, Xalapa, Veracruz, México, vallejos@ecologia.edu.mx, 319 pp plus 140 color plates. Price: \$30.00. *Reviewed in Jan-Feb 2005.*
- **Microbe-vector Interactions in Vector-borne Diseases.** 2004. SH Gillespie, GL Smith & A Osbourn. Cambridge University Press, New York, NY 1011-4211, 383 pp. Price: \$125.00 hardbound. *Reviewed in Mar-Apr 2005.*
- ***Mycosphaerella* and its Anamorphs: 1. Names Published in *Cercospora* and *Passalora*.** 2003. PW Crous & U Braun. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands, www.cbs.knaw.nl/publications/index.htm, 571 pp. Price: € 75.00. *Review needed.*
- ***Phoma* Identification Manual. Differentiation of Specific and Infra-specific Taxa in Culture.** 2004. GH Boerema, J deGruyter, ME Noordeloos, MEC Hamers. CABI Publishing, Oxfordshire, United Kingdom, www.cabi-publishing.org, 448 pp. incl. one color plate. Price: \$140.00. *Review needed.*
- **Die Pilzflora des Ulmer Raumes.** (translated: The Fungus Flora of the Ulm area/Southern Germany). 2004. M Enderle. Süddeutsche Verlagsgesellschaft Ulm, Germany, www.suedvlg.de, 521 pp incl. numerous color illustrations. Price: €24.50. *Review needed.*
- ***Penicillium* subgenus *Penicillium*: new taxonomic schemes, mycotoxins, and other extralites.** 2004. RA Samson & JC Frisvad. Studies in Mycology 49: 1-257. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands, www.cbs.knaw.nl/publications/index.htm, 257 pp. Price: €50.00. *Reviewed Mar-Apr 2005.*
- **A Preliminary Monograph of *Lentinellus* (Russulales).** 2004. RH Petersen & KW Hughes. Bibliotheca Mycologica 198: 1-268. www.schweizerbart.de/pubs/series/bibliotheca-mycologica-59.html. Price: € 80.00. *Review needed.*
- **Revision of the Genus *Amphisphaeria*.** 2004. YZ Wang, A Aptroot, KD Hyde. Fungal Diversity Press, Centre for Research in Fungal Diversity, The University of Hong Kong, China, www.hku.hk/ecology/mycology/FDP.html, ISBN 962-86765-5, 168 pp. Price: \$60.00. *Review needed.*
- ***Sporidesmium*, *Endophragmiella* and related genera from China.** 2005. W Wu & W Zhuang. Fungal Diversity Press, Centre for Research in Fungal Diversity, The University of Hong Kong, China, www.hku.hk/ecology/mycology/FDP.html, ISBN 962-86765-5, 168 pp. Price: \$60.00. *Review needed.*

MYCOLOGICAL CLASSIFIEDS

Mushroom Ecotour in Northern Thailand

Are you interested in looking for mushrooms in northern Thailand? We are currently trying to organize a mushroom-oriented "ecotour" in northern Thailand, outside of Chiang Mai. The tour will include a variety of things to be determined by participants later, but will revolve around collecting in the mountainous areas near Chiang Mai. Lectures, cultivation workshops, cooking demonstrations, field identification and microscope work will also be components of the tour.

The tour will be all-inclusive, including transport, food, accommodations, use of laboratory equipment and guided collecting trips with a native English speaker (Dr. Edward

Grand). Dr. Edward Grand is a recent graduate from the University of Tennessee, where he studied *Lentinus*, *Panus* and other Basidiomycetes with Dr. Ronald Petersen. The Centre also houses several students working with Basidiomycetes as well as frequent visiting researchers.

For more information about the Centre or the tour, please email Dr. Edward Grand at edwardgrand@yahoo.com or visit our website at: www.mushroomresearchcentre.net

Please note that biological material cannot be taken outside of Thailand without the permission and/or collaboration of a Thai university or institution.

Postdoctoral Fellowships Available at Duke University

The Institute for Genome Sciences & Policy's Center for Evolutionary Genomics at Duke University is pleased to announce the continuation of its Post-doctoral Fellowships in Evolutionary Genomics and Molecular Evolution. This Fellowship provides an annual salary of \$37,000 plus benefits and \$11,000 in research funds per year for a two-year period. The program allows Fellows to pursue research in the laboratory of a sponsoring faculty member affiliated with the Institute for Genome Sciences & Policy. Two Fellowships will be awarded this year.

We invite innovative proposals from scientists of any nationality to carry out research at Duke University for a two-year appointment, beginning in the fall of 2005. We are particularly interested in proposals that address mechanisms of molecular evolution, comparative genomics, and the evolution of development. Although proposals focused exclusively on building phylogenies will not be considered, the appli-

cation of phylogenetic approaches to analyzing the evolution of genes and genomes is certainly appropriate. Faculty sponsors can be located within any department or school at Duke University; the only stipulation is that the project fall within the areas of research listed above.

Please send curriculum vitae, a three-page research proposal, a one-page summary of past research, and two letters of recommendation to: Evolutionary Genomics, c/o Greg Wray, Department of Biology, Box 90338, Duke University, Durham, NC 27708-0338, USA. Applications received by 1 June 2005 will be guaranteed full consideration. Duke University is an Equal Opportunity/Affirmative Action Employer. Female and minority candidates are especially encouraged to apply.

Questions can be directed to Greg Wray by email (gwwray@duke.edu). For information about the IGSP Center for Evolutionary Genomics and genomics at Duke University, visit www.genome.duke.edu.

Doctoral Student Funding Available

Research support is available for graduate study in the biodiversity of pyrenomycetes beginning January 1, 2006 at the Illinois Natural History Survey. This project is part of an inventory of the wood-inhabiting pyrenomycetes of the Great Smoky Mountains National Park and emphasizes training in: 1) the diverse methods of traditional collections-based research, 2) the development and management of digital information tools, and 3) the application of molecular sequencing techniques and phylogenetic analyses. The project will include research on the systematics, biogeography, and ecology of temperate pyrenomycetes and will contain a large field-work component. Desirable qualifications includes experience in fungal systematics and DNA sequencing techniques. Support includes a full RA stipend (\$20,000 per year) and tuition waiver for 3 years including summers. The successful candidate will join a group using multidisciplinary approaches in systematic research. The Illinois Natural History Survey is affiliated with the University of Illinois Urbana-Champaign (UIUC) and is located on the south end of campus.

Students should apply to the Department of Plant Biology at UIUC (www.life.uiuc.edu/plantbio/). For more information, please contact Andrew Miller [amiller@inhs.uiuc.edu; (217) 244-0439] at the Illinois Natural History Survey, Center for Biodiversity, 607 East Peabody Drive, Champaign, IL 61820.

Mold Testing and Identification Services

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MYCOLOGY ON-LINE

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

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

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

Corticoid Nomenclatural Database (56-2)
phyloinformatics.org

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

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

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

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

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

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

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

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

The Myconet Classification of the Ascomycota
www.umu.se/myconet/Myconet.html

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)

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

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

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

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

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.

2005 (July 23-28)

Joint Meeting of the Three Divisions (Bacteriology and Applied Microbiology, Mycology, and Virology) of the International Union of Microbiological Societies

San Francisco, CA, United States

Carol Shearer, Chair,

US National Committee for IUMS

www.IUMS2005.org

IUMS@asmusa.orgor (to submit a poster)

2005 (July 23-28)

IX International Congress on Mycology

San Francisco, California

www.iums2005.org/iums.asp

2005 (July 30 - August 5)

2005 MSA Annual Meeting

University of Hawaii in Hilo

Hilo, Hawaii

2005 (August 1-5)

The Congress will be a joint Meeting with the XXXVIII Brazilian Phytopathological Congress and commemoration of 30 YEARS of Plant Pathology at the University of Brasilia

Brasilia, Brazil

J.C. Dianese, President

Latin Am. Mycological Association

alm@unb.br

2005 (August 1-5)

V Latin American Mycological Congress / XXXVIII Brazilian Commemorating Phytopathological Congress. Thirty Years of Graduate Teaching in Plant Pathology at the Universidade de Brasilia. Hotel Nacional

Brasília, DF, Brasil

Jose Carmine Dianese, President

www.alm.org.br, www.sbfito.com.br,

www.newvisonbsb.com.br

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

Change of Address

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

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

inoculum

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