UNIVERSITY OF ALBERTA MICROFUNGUS COLLECTION AND HERBARIUM (UAMH)

A Unit of the Devonian Botanic Garden, Faculty of Agriculture, Life and Environmental Sciences
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SUMMARY OF ACTIVITIES FOR 2011

Supporting fungal research for over 50 years

Staff, Volunteers

Professor Emeritus (Curator) - **L. Sigler**
Devonian Botanic Garden/UAMH, Fac. Agriculture, Life & Environmental Sciences
Medical Microbiology & Immunology, Fac. of Medicine
Adj. Prof. Biol. Sci.
Consultant in Mycology, PLNA/UAH Microbiology & Public Health
Assistant Curator (.5 FTE Non-academic, .5 FTE trust, NSERC) – **C. Gibas**
Technicians (trust): - **A. Anderson**; **V. Jajczay** (casual)
Volunteer- **M. Packer**

Affiliates
R. Currah, Professor Emeritus, Biological Sciences, Faculty of Science
M. Berbee, Professor, University of British Columbia, Vancouver
G. Hausner, Assistant Professor, University of Manitoba, Winnipeg

Cultures Received, Distributed and Accessioned

Cultures received for identification, deposit or in exchange (**Table 1**) **233**

Cultures distributed on request or in exchange (**Table 2**) **262**

Culture Collection and Herbarium Accessions

Accessions processed to Dec 31. ..... **284**

Total accessions **11630**

Information on Culture Accessions available through print and on-line CATALOGUES

Catalogue of the University of Alberta Microfungus Collection and Herbarium. [PDF]
http://www.uamh.devonian.ualberta.ca

Depository, Identification and Distribution Services

In 2011, 233 fungal isolates were received for deposit and 262 isolates were distributed for various purposes to scientists in universities, government and industry (**Tables 1 and 2**). Of the latter, 73 were distributed within U of A, 174 within Canada and the US, and 15 were sent internationally for various research purposes. Information on the use of UAMH strains in diverse research applications is provided in section *Publications citing UAMH cultures or assistance* (page 4 of this report).

Over the past two years, we have been cooperating with K. Vanderwolf, M. Sc. student from Univ of New Brunswick, who has done extensive surveying of living hibernating bats in New Brunswick caves for incidence of the white nose pathogen *Geomyces destructans*. *G. destructans* was detected for the first time in 2011 with bats showing significant morbidity and mortality and with confirmatory isolation of the fungus. In addition to 132 isolates deposited in 2010, another 68 isolates were received for deposit in 2011. These represented large numbers of *Geomyces* species other than *G. destructans* as well as numerous rare or uncommon fungi of scientific interest. We have verified or identified many of the isolates and we are now collaborating on several taxonomic projects.

Twenty two isolates of orchid mycorrhizal fungi were received from Dr. L.W. Zettler, Illinois College. His research focuses on conservation of threatened orchids and the symbiotic germination of orchid seed with host-specific and locally adapted mycorrhizal fungi. Isolates representing species of *Ceratorhiza* and *Epulorhiza* were obtained mainly from roots of the U.S. Federally threatened eastern prairie fringed orchid *Platanthera leucophaea*. Results of Dr. Zettler's work on symbiotic germinations identified specific UAMH cultures as ones promoting seed germination in vitro (Abstracts 17, 48). Over 175 orchid symbionts are accessioned at UAMH and most remain unclassified; in 2011, we supplied 50 isolates to Dr. R.S. Currah's student (Biol Sci) for molecular study.

Over 130 fungal associates of the mountain pine beetle representing six species of ophiostomatoid fungi (blue stain fungi) have been acquired from the mountain pine beetle genomics project involving scientists from the University of Alberta and the University of British Columbia (Abstracts 39 to 41). The most common pine pathogen is *Grosmannia clavigera*, for which the whole genome has recently been sequenced for isolate KW1407 = UAMH 11150 (Abstract 12). *Grosmannia clavigera* isolates from different species of beetle and pine have been found to represent two phylogenetic species based on genetic and ecological assessment (Abstract 3).

Isolates of a new mushroom species, *Coprinopsis neophlyctidospora*, were sent for deposit by Dr. K. Suzuki, Chiba University (Abstract 33) The fungus was detected during surveys for ammonia fungi in boreal forests during his sabbatical research in Alberta with Dr. R. Currah (Biol Sci.). Ammonia fungi are those in which growth is stimulated by addition of urea of other nitrogenous materials to forest soils. This mushroom fruits readily in culture.

Among isolates submitted by Dr. S.P. Abbott (Ph.D. U of A) was a slow growing, meristematic black fungus from an environmental source that we identified as *Pseudotaeniolina globosa* by ITS sequencing. This rare species is currently represented by only three other isolates worldwide. Another group of black slow growing fungi sent by Dr. J. Scott (Sporometrics, Inc.) represented additional isolates of the distillery warehouse staining fungus *Baudoinia compniacensis* for which the whole genome has recently been sequenced. In the case of both these fungi, growth on surfaces appears as sooty black deposits.

Six isolates of fungi associated with wood spalting (i.e. production of pigments and zone lines in wood) were deposited by Dr. S. Robinson (Fac Forestry, Univ of Toronto) (Abstracts 34 to 38). Among these were *Scytalidium cuboideum* (formerly known as *Arthrographis cuboidea*), several isolates of *Xylaria polymorpha* and *Trametes versicolor*. Although *Scytalidium cuboideum* is a species well represented in UAMH, these are the first isolates studied in these types of applications.

Although the focus of UAMH is primarily on fungi, we accepted an isolate of *Pseudomonas fluorescens* from Dr. J. Foght (Biol Sci U of A) because of the importance of this aromatic hydrocarbon degrading bacterium. Strain LP6a (=UAMH 11620), first isolated from petroleum-contaminated soil near Lodgepole AB in 1983, has since been extensively characterized by Dr. Foght's group and assessed for efficacy in bioremediation of oil spills. (Abstracts 1, 2).

Isolates sent for identification are determined by morphology and/or sequencing. Agencies sending isolates included: Microbiology and Public Health, Univ of Alberta Hospitals, Edmonton; Animal Health Centre, Toronto Zoo, Scarborough, Oakville Veterinary Emergency Hospital and Referral Group, Oakville, ON; Keystone Labs Inc., Edmonton, AB. We receive occasional samples of building materials for analysis of mold and provide advice regarding health risks of exposure to fungi.

Curatorial and Other Activities

- In 2011, a new website was launched under Sitecore [www.uamh.devonian.ualberta.ca]. The website offers users a new searchable Catalogue that improves the searching and displaying of strain data and the mechanism for ordering cultures. Assistance from ALES staff (G. Beaulieu, P. Ball) was helpful in developing the Catalogue. An objective is to have online catalogue illustrated with digital images.
- The UAMH database redevelopment project is nearing completion and migration to the new system is expected by mid 2012. The project involved a major rebuild of the storage tables and the front end application to allow viewing in multiple windows. A large amount of time has been spent in checking data integrity and in testing the application, analyzing and resolving problems. To avoid data corruption, it is critical to have the new database working properly before we migrate the data. The new application will improve procedures for data entry, updating, retrieval and for transferring data to the online catalogues. It will also allow for inclusion of hyperlinks to data located on other sites, e.g sequences or publications.
- With freezer space nearing capacity, a new cryofreezer was purchased with a grant from the U of A Support for the Advancement of Scholarship.
- We continue to employ sequencing of isolates on a more routine basis either to identify isolates involved in infection or to re-assess the identity of isolates that have accessioned for many years. These sequences are stored, together with reliable sequences from Genbank, in an in-house sequence database. We also supply DNA in place of, or in addition to, the supply of cultures.
- Editorial work (LS): Reviews Mycologia (1), Antonie van Leeuwenhoek (2), Journal of Clinical Microbiology (2)

In-house and Collaborative Research

Refereed Journal Articles Published

1. De Ravin SS, Challipalli M, Anderson V, Shea YR, Marciano B, Hilligoss D, Marquesen M, Decastro R, Liu YC, Sutton DA, Wickes BL, Kammeyer PL, Sigler L, Sullivan K, Kang EM, Malech HL, Holland SM, Zelazny AM. *Geosmithia argillacea*: An emerging cause of invasive mycosis in human chronic granulomatous disease. Clinical Infectious Diseases 2011; 52(6):e136-143.

   BACKGROUND: Chronic granulomatous disease (CGD) is an inherited disorder of the nicotinamide adenine dinucleotide phosphate oxidase that leads to defective production of microbicidal superoxide and other oxidative radicals, resulting in increased susceptibility to invasive infections, especially those due to fungi. METHODS: *Geosmithia argillacea* was identified from cultured isolates by genomic sequencing of the internal transcribed spacer region. Isolates previously identified as *Paecilomyces variotii*, a filamentous fungus closely resembling *G. argillacea*, were also examined. RESULTS: We identified *G. argillacea* as the cause of invasive mycosis in 7 CGD patients. In 5 cases, the fungus had been previously identified morphologically as *P. variotii*. All patients had pulmonary lesions; 1 had disseminated lesions following inhalational pneumonia. Infections involved the chest wall and contiguous ribs in 2 patients and disseminated to the brain in 1 patient. Four patients with pneumonia underwent surgical intervention. All patients responded poorly to medical treatment, and 3 died. CONCLUSIONS: We report the first cases of invasive mycosis caused by *G. argillacea* in CGD patients. *G. argillacea* infections in CGD are often refractory and severe with a high fatality rate. Surgical intervention has been effective in some cases. *G. argillacea* is a previously underappreciated and frequently misidentified pathogen in CGD that should be excluded when *P. variotii* is identified morphologically.

2. Morio F, Fraissinet F, Gastinne T, Pape PL, Delaunay J, Sigler L, Gibas CF, Miegeville M. Invasive *Myceliophthora thermophila* infection mimicking invasive aspergillosis in a neutropenic patient: a new cause of cross-reactivity with the *Aspergillus* galactomannan serum antigen assay. Medical Mycology 2011; 49(8):883-886.

   Myceliophthora thermophila is a thermophilic mould widely found in the environment but rarely responsible for human infections. We describe a case of invasive *Myceliophthora thermophila* infection mimicking invasive aspergillosis in a neutropenic patient with haematological malignancy. Cross-reactivity with *Aspergillus* galactomannan assay (GM) was demonstrated by repeated positive results and confirmed by cross-reaction between the fungal isolate and the GM assay. The patient was successfully treated with voriconazole. Potential GM cross-reactivity must be considered in future studies including patients categorized as having probable invasive aspergillosis using the GM as the only mycological criterion.

3. Johnson RSP, Sangster CR, Sigler L, Hambleton S, Paré JA. Deep fungal dermatitis caused by the *Chrysosporium* anamorph of *Nannizziopsis vriesii* in captive coastal bearded dragons (*Pogona barbata*). Australian Veterinary Journal 2011; 89(12): 515-519.

   Deep fungal dermatitis caused by the *Chrysosporium* anamorph of *Nannizziopsis vriesii* (CANV) was diagnosed in a group of coastal bearded dragons (*Pogona barbata*). The outbreak extended over a 6-month period, with four of six lizards from the same zoological outdoor enclosure succumbing to infection. A fifth case of dermatomycosis was identified in a pet lizard originally sourced from the wild. Diagnosis of infection with the CANV was based on similar clinical signs and histopathology in all animals and confirmed by culture and sequencing of the fungus from one animal. This is the first report of the CANV causing disease in a terrestrial reptile species in Australia and the first in the coastal bearded dragon.

4. Hall NH, Conley K, Berry C, Farina L, Sigler L, Wellehan JF Jr, Heard D. Computed tomography of granulomatous pneumonia in an American alligator (*Alligator mississippiensis*) associated with *Metarhizium anisopliae*. Journal of Zoo and Wildlife Medicine 2011; 42(4):700-708.

   An 18-yr-old, male, albino, American alligator (*Alligator mississippiensis*) was evaluated for decreased appetite and abnormal buoyancy. Computed tomography (CT) of the coelomic cavity showed multifocal mineral and soft tissue attenuating pulmonary masses consistent with pulmonary fungal granulomas. Additionally, multifocal areas of generalized, severe emphysema and pulmonary and pleural thickening were identified. The alligator was euthanized and necropsy revealed severe fungal pneumonia associated with oxalosis. *Metarhizium anisopliae* var. *anisopliae* was cultured from lung tissue and exhibited oxalate crystal formation in vitro. Crystals were identified as calcium oxalate monohydrate by X-ray powder defractometry. Fungal identification was based on morphology, including tissue sporulation, and DNA sequence analysis. This organism is typically thought of as an entomopathogen. Clinical signs of fungal pneumonia in nonavian reptiles are often inapparent until the disease is at an advanced stage, making antemortem diagnosis challenging. This case demonstrates the value of CT for pulmonary assessment and diagnosis of fungal pneumonia in the American alligator. Fungal infection with associated oxalosis should not be presumed to be aspergillosis.

5. Armstrong PF, Sigler L, Sutton DA, Grooters AM, Hitt M**.** Fungal myelitis caused by *Phialosimplex caninus* in an immunosuppressed dog. Medical Mycology 2011 Nov 28; Epub ahead of print.

   A bone marrow infection caused by Phialosimplex *caninus* was diagnosed in a seven-year-old female spayed Cocker Spaniel that was receiving prednisone for autoimmune hemolytic anemia. Histopathologic examination of a bone marrow core biopsy revealed clusters of oval to round yeast-like cells of varying shape and size and occasional irregular hyphae. Culture of a bone marrow aspirate sample yielded a mould initially suggestive of *Paecilomyces inflatus* or *Sagenomella* species but later determined to be *P. caninus*. The dog was treated with itraconazole and amphotericin B, and prednisone was continued at the lowest dose needed to control the hemolytic anemia. The patient died after 18 months of treatment. This is the first detailed clinical report of infection caused by *P. caninus*, a newly described fungus associated with disseminated disease in dogs.

Papers Accepted or Submitted

6. Koo S, Sutton DA, Yeh WW, Thompson EH, Sigler L, Shearer JF, Hofstra DH, Wickes BL, Marty FM. Invasive *Mycoleptodiscus* fungal cellulitis and myositis. Medical Mycology in press.

   We report progressive necrotizing fungal cellulitis and myositis in the leg of a patient with glioblastoma multiforme treated with temozolomide and corticosteroids. While the morphologic appearance of the isolate and its ability to grow at temperatures greater than 32°C were suggestive of *Mycoleptodiscus indicus*, some of its conidia were atypical for this species, with single septa and occasional lateral appendages, and the strain was divergent from *M. indicus* based on sequencing of two rDNA regions. This is the first case of *Mycoleptodiscus* invasive fungal disease in which the causative agent could not be resolved at the species level because of incongruence between morphological and molecular data.

7. Iwen PD, Schutte SK, Florescu DF, Hurst RK, Sigler L. Invasive *Scopulariopsis brevicaulis* infection in an immunocompromised patient and review of prior cases caused by *Scopulariopsis* and *Microascus* species. Medical Mycology (Subm 1-Dec-2011 TMMY-0286-2011)

   Scopulariopsis species and their *Microascus* teleomorphs are cosmopolitan fungi that are uncommonly associated with invasive disease. This report describes a fatal case of disseminated *Scopulariopsis brevicaulis* disease in a patient with diffuse large B cell lymphoma who underwent high-dose chemotherapy followed by a matched unrelated donor stem cell transplant. This case is compared with 32 prior cases of invasive *Scopulariopsis* (*Microascus*) infections reported in the literature. A focus of this report is on the diagnostic methods utilized to include histopathology and culture with both micromorphologic and genotypic methods used to confirm the species identification.

8. Sigler L. Comment on the paper by Kpodzo *et al*. *Medical Mycology* January 2012, Early Online**,** 110 (letter).

External Funding (Grants/Fees for Services)

NSERC Major Resources Support (continuing). The University of Alberta Microfungus Collection and Herbarium (UAMH). Sigler (PI), Currah, Hausner, Berbee (2008-2013) (Total $273,000)	54,600
NSERC Discovery (completed 2011). Systematics of Fungi in the Human Environment Sigler, L. 2006 to 2011 (Total $159,390)	31,878
SAS grant Cryopreservaton equipment for preserving fungi, University of Alberta, April 12, 2011	5,021
Income from all services (cultures distributed, preservation services, identifications, microbial assessments, consultation)	16,600

Publications Citing UAMH Cultures or Assistance

1. Abbasnezhad H, Foght JM, Gray MR. Adhesion to the hydrocarbon phase increases phenanthrene degradation by *Pseudomonas fluorescens* LP6a. Biodegradation. 2011; 22(3):485-96.

   Microbial adhesion is an important factor that can influence biodegradation of poorly water soluble hydrocarbons such as phenanthrene. This study examined how adhesion to an oil-water interface, as mediated by 1-dodecanol, enhanced phenanthrene biodegradation by Pseudomonas fluorescens LP6a. Phenanthrene was dissolved in heptamethylnonane and added to the aerobic aqueous growth medium to form a two phase mixture. 1-Dodecanol was non-toxic and furthermore could be biodegraded slowly by this strain. The alcohol promoted adhesion of the bacterial cells to the oil-water interface without significantly changing the interfacial or surface tension. Introducing 1-dodecanol at concentrations from 217 to 4,100 mg l(-1) increased phenanthrene biodegradation by about 30% after 120 h incubation. After 100 h incubation, cultures initially containing

120 or 160 mg l(-1) 1-dodecanol had mineralized >10% of the phenanthrene whereas those incubated without 1-dodecanol had mineralized only 4.5%. The production and accumulation of putative phenanthrene metabolites in the aqueous phase of cultures likewise increased in response to the addition of 1-dodecanol. The results suggest that enhanced adhesion of bacterial cells to the oil-water interface was the main factor responsible for enhanced biodegradation of phenanthrene to presumed polar metabolites and to CO(2). [UAMH 11620]

2. Abbasnezhad H, Gray M, Foght JM. Influence of adhesion on aerobic biodegradation and bioremediation of liquid hydrocarbons. Applied Microbiology and Biotechnology 2011; 92(4):653-75.

   Biodegradation of poorly water-soluble liquid hydrocarbons is often limited by low availability of the substrate to microbes. Adhesion of microorganisms to an oil-water interface can enhance this availability, whereas detaching cells from the interface can reduce the rate of biodegradation. The capability of microbes to adhere to the interface is not limited to hydrocarbon degraders, nor is it the only mechanism to enable rapid uptake of hydrocarbons, but it represents a common strategy. This review of the literature indicates that microbial adhesion can benefit growth on and biodegradation of very poorly water-soluble hydrocarbons such as n-alkanes and large polycyclic aromatic hydrocarbons dissolved in a non-aqueous phase. Adhesion is particularly important when the hydrocarbons are not emulsified, giving limited interfacial area between the two liquid phases. When mixed communities are involved in biodegradation, the ability of cells to adhere to the interface can enable selective growth and enhance bioremediation with time. The critical challenge in understanding the relationship between growth rate and biodegradation rate for adherent bacteria is to accurately measure and observe the population that resides at the interface of the hydrocarbon phase. [UAMH 11620]

3. Alamouti SM, Wang V, DiGuistini S, Six DL, Bohlmann J, Hamelin RC, Feau N, Breuil C. Gene genealogies reveal cryptic species and host preferences for the pine fungal pathogen *Grosmannia clavigera*. Molecular Ecology 2011; 20:2581–2602.

   Grosmannia clavigera is a fungal pathogen of pine forests in western North America and a symbiotic associate of two sister bark beetles: Dendroctonus ponderosae and *D. jeffreyi*. This fungus and its beetle associate *D. ponderosae* are expanding in large epidemics in western North America. Using the fungal genome sequence and gene annotations, we assessed whether fungal isolates from the two beetles inhabiting different species of pine in epidemic regions of western Canada and the USA, as well as in localized populations outside of the current epidemic, represent different genetic lineages. We characterized nucleotide variations in 67 genomic regions and selected 15 for the phylogenetic analysis. Using concordance of gene genealogies and distinct ecological characteristics, we identified two sibling phylogenetic species: *Gc* and Gs. Where the closely related *Pinus ponderosa* and *P. jeffreyi* are infested by localized populations of their respective beetles, *Gc* is present. In contrast, Gs is an exclusive associate of *D. ponderosae* mainly present on its primary host-tree *P. contorta*; however, in the current epidemic areas, it is also found in other pine species. These results suggest that the host-tree species and the beetle population dynamics may be important factors associated with the genetic divergence and diversity of fungal partners in the beetle-tree ecosystems. *Gc* represents the original *G. clavigera* holotype, and Gs should be described as a new species. [4585, 4818, 11150-11155, 11347, 11355-11378]

4. Balasingham S, Chalkias S, Balasingham A, Saul Z, Wickes BL, Sutton DA. A case of bovine valve endocarditis caused by *Engyodontium album*. Medical Mycology 2011; 49:430–434.

   We report the first case of *Engyodontium album* bioprosthetic valve endocarditis in a 44-year-old male with a history of juvenile rheumatoid arthritis. There is only one other report of *Engyodontium album* as a human pathogen. The present case supports the increased incidence of fungal endocarditis especially in patients receiving immunotherapy. [UAMH 11234]

5. Calvo-Polanco M, Zwiazek JJ. Role of osmotic stress in ion accumulation and physiological responses of mycorrhizal white spruce (*Picea glauca*) and jack pine *(Pinus banksiana*) to soil fluoride and NaCl. Acta Physiologiae Plantarum 2011; 33:1365–1373.

   To examine the mechanisms of earlier reported alleviation of fluoride injury in ectomycorrhizal plants by NaCl, jack pine (*Pinus banksiana*) and white spruce (*Picea glauca*) seedlings were subjected to 1 mM and 5 mM KF in the presence of either 60 mM NaCl or 10% polyethylene glycol 3350 (PEG) for 2 weeks. Before the treatments, seedlings had either been inoculated with the ectomycorrhizal fungus *Suillus tomentosus* or remained non-inoculated. The inoculation with *S. tomentosus* reduced Na uptake by shoots and roots of jack pine seedling and by roots of white spruce that were treated with 60 mM NaCl. Mycorrhizal associations also drastically decreased fluoride uptake by jack pine seedlings, but did not affect shoot fluoride concentrations in white spruce. When NaCl was replaced by PEG in the 5 mM KF treatment solution, shoot fluoride concentrations were reduced by more than twofold without corresponding reductions in transpiration rates in mycorrhizal and non-mycorrhizal white spruce seedlings. When fluoride was present in the treatment solution, Na concentrations were lower in shoots and roots of both jack pine and white spruce mycorrhizal and non-mycorrhizal

seedlings. The results suggest that *Suillus tomentosus* may help alleviate the effects of soil fluoride and salinity in jack pine and that fluoride uptake in white spruce is sensitive to osmotic stress. [UAMH 5506]

6. Chaturvedi S, Rudd RJ, Davis A, Victor TR, Li X, Appler KA, Rajkumar SS, Chaturvedi V. Rapid real-time PCR assay for culture and tissue identification of *Geomyces destructans*: the etiologic agent of bat geomycosis (white nose syndrome). Mycopathologia 2011; 172:247–256.

   Geomyces destructans is the etiologic agent of bat geomycosis, commonly referred to as white nose syndrome (WNS). This infection has caused severe morbidity and mortality in little brown bats (*Myotis lucifugus*) and has also spread to other bat species with significant decline in the populations. Currently, *G. destructans* infection is identified by culture, ITS–PCR, and histopathology. We hypothesized that a real-time PCR assay would considerably improve detection of G. destructans in bats. The 100 bp sequence of the Alpha-L-Rhamnosidase gene was validated as a target for real-time PCR. The assay sensitivity was determined from serial dilution of DNA extracted from *G. destructans* conidia (5×10^{-1}–5×10^{7}), and the specificity was tested using DNA from 30 closely and distantly related fungi and 5 common bacterial pathogens. The real-time PCR assay was highly sensitive with detection limit of two *G. destructans* conidia per reaction at 40 PCR cycles. The assay was also highly specific as none of the other fungal or bacterial DNA cross-reacted in the real-time PCR assay. One hundred and forty-seven bat tissue samples, suspected of infection with *G. destructans*, were used to compare the real-time PCR assay to other methods employed for the detection of *G. destructans*. Real-time PCR was highly sensitive with 80 of 147 (55%) samples testing positive for *G. destructans* DNA. In comparison, histopathology examination revealed 64/147 (44%) positive samples. The internal transcribed spacer (ITS)–PCR yielded positive amplicon for *G. destructans* from 37 tissue samples (25%). The least sensitive assay was the fungal culture with only 17 tissue samples (12%) yielding *G. destructans* in culture. The data suggested that the real-time PCR assay is highly promising for rapid, sensitive, and specific identification of *G. destructans*. Further trials and inter-laboratory comparisons of this novel assay are recommended to improve the diagnosis of bat geomycosis. [20 UAMH strains of *Geomyces* species, *Pseudogymnoascus* species and other]

7. Cheema MS, Christians JK. Virulence in an insect model differs between mating types in *Aspergillus fumigatus*. Medical Mycology 2011; 49:202–207.

   Aspergillus fumigatus is an opportunistic fungal pathogen that has recently been found to undergo sexual reproduction. Previous work suggested that invasiveness differs between mating types, and in the present study we tested whether virulence differs between mating types in an in vivo model, i.e., larvae of the wax moth *Galleria mellonella*. We measured virulence of 20 *A. fumigatus* isolates; three MAT1-1 isolates of environmental origin, five MAT1-1 isolates of clinical origin, seven MAT1-2 isolates of environmental origin and five MAT1-2 isolates of clinical origin. For each isolate, we measured virulence in six replicates and for each replicate, conidia were grown, harvested, and counted independently, and 2,500 colony forming units were injected into each of 10 *G. mellonella* larvae. Virulence differed between mating types, with lower survival in larvae injected with MAT1-1 isolates. Virulence also differed between clinical and environmental isolates, but surprisingly larvae injected with environmental isolates had lower survival. Identification of the mechanisms underlying variation in virulence may identify novel targets for the treatment of *Aspergillus* infections. [UAMH 3109, 3762, 3906, 4052, 4299, 4338, 6948, 7676, 9309, 10100]

8. Day MJ, Currah RS. In vitro degradation of the moss *Hylocomium splendens* by three pleosporalean fungi. Canadian Journal of Microbiology 2011; 57:382-391.

   Three darkly pigmented species of conidial fungi of the family *Pleosporaceae* isolated from plants colonizing the Saskatchewan Glacier forefield were examined for potential roles in the degradation of moss gametophytes. *Curvularia inaequalis* and *Ulocladium atrum* isolated from bryophytes *Ditrichum flexicaule* and *Tortella tortuosa*, respectively, and *Chalastospora gossypii* from *Saxifraga oppositifolia* were inoculated onto autoclaved gametophytes of the moss *Hylocomium splendens*. All three species of fungi caused mass losses of the moss gametophytes. In vitro enzymatic tests revealed that all three fungi degraded cellulose, while none degraded insoluble polyphenols. When this material was examined by scanning electron microscopy, it was evident that the fungi had eroded the outer wall layer of the moss leaf cells to some extent but not the inner layer containing more lignin-like compounds. Once the outer wall layer was removed, the cells easily disarticulated. It is proposed that accumulations of these phenolics-rich leaf fragments subsequently ameliorate the rooting environment for vascular plants and have the potential to support the growth of basidiomycetes and other fungi, potentially mycorrhizal with pioneer vascular plants. [UAMH 11179, 11180, 11181]

9. Day MJ, Currah RS. Role of selected dark septate endophyte species and other hyphomycetes as saprobes on moss gametophytes. Botany 2011; 89:349-359.

   Dark septate endophytes (DSEs) live asymptomatically in the roots of vascular plants, are common in arctic and alpine areas, and are thought to play a quasimycorrhizal role. It is not known, however, whether they precede or arrive with their hosts. Previously reported enzymatic abilities of *Phialocephala fortinii* suggest that DSEs can live on organic debris in the soil, but there is little direct or experimental evidence for this. *Phialocephala fortinii*, *Leptodontidium orchidicola*, *Cadophora melinii*, *Cadophora luteo-olivacea*, and *Lecythophora sp.* were

inoculated onto autoclaved *Hylocomium splendens* gametophytes and incubated for 3 months to determine if they degrade this organic material based on observations made using light and scanning electron microscopy. All fungi were able to colonize the bryophyte tissue to some extent. *Lecythophora sp.* and *L. orchidicola* penetrated cells by forming bore holes. *Cadophora luteo-olivacea* and *P. fortinii* were also observed inside cells, but bore holes through bryophyte cell walls were not observed. *Cadophora melinii* sporulated and grew abundantly on the surface of gametophytes but did not appear to penetrate cell walls. *Phialocephala fortinii* and *L. orchidicola* formed sclerotia in the gametophytes similar to those formed in roots. These results suggest that DSE fungi can persist and produce propagules, i.e., sclerotia and conidia, in the absence of host roots. These observations support the hypothesis that DSE fungi are able to precede their hosts during primary succession events. [UAMH 5422, 11228, 11229]

10. Day M, Hall JC, Currah RS. Phialide arrangement and character evolution in the helotialean anamorph genera *Cadophora* and *Phialocephala*. Mycologia. Epub Nov 2011; doi: 10.3852/11-059.

    The dematiaceous hyphomycete genera *Cadophora* and *Phialocephala* are anamorphs associated with mollisoid inoperculate discomycetes (*Helotiales*) and are delineated based on the complexity of the phialide arrangement, with members of *Cadophora* producing solitary phialides and species of *Phialocephala* producing complex heads of multiple phialides. A third, phylogenetically related taxon, *Leptodontidium orchidicola*, produces mostly indehiscent conidia that may represent non-functional phialides. Morphological characteristics of both sexual and asexual states of these and other fungi in a focal group of helotialean taxa were re-examined, in light of relationships shown by molecular phylogenetic analyses of rDNA ITS sequences, to determine the evolutionary significance of phialide arrangement. The focal species of *Phialocephala* formed a monophyletic clade while five of six species of *Cadophora*, including the type, were in a separate clade along with *L. orchidicola*. *C. finlandica* was placed in a third clade with species of *Meliniomyces* and *Rhizoscyphus*. We hypothesized that the ancestral state for species in *Cadophora* and *Phialocephala* is the production of sclerotium-like heads of multiple phialides, which has been retained in most species assignable to *Phialocephala*. A reduction to solitary phialides occurred in the lineage leading to the clade containing most of the *Cadophora* species. Two possible reductions to non-functional phialides were identified: one in the *Meliniomyces-C. finlandica-Chloridium paucisporum* clade and another in the *L. orchidicola* and Mollisia "rhizophila"clade. A reversion to increased phialide complexity may have occurred in the clade containing *C. finlandica* and *Ch. paucisporum*. Our data and analyses also show a previously unrecognized relationship between teleomorph and anamorph morphology, in that *Mollisia* species with smaller asci would be expected to have *Phialocephala* states, while those with larger asci would be expected to have *Cadophora* states. Based on morphology and phylogenetic placement, *L. orchidicola* and *C. hiberna* are transferred to *Cadophora* and *Phialocephala* respectively. [UAMH 1221, 5422]

11. Desjardins CA, Champion MD, Holder JW, Muszewska A, Goldberg J, Bailão AM, Brigido MM, Ferreira MES, Garcia AM, Grynberg M, Gujja S, Heiman DI, Henn MR, Kodira CD, León-Narváez H, Longo LVG, Ma L, Malavazi I, Matsuo AL, Morais FV, Pereira M, Rodríguez-Brito S, Sakthikumar S, Salem-Izacc SM, Sykes SM, Teixeira MM, et al. Comparative genomic analysis of human fungal pathogens causing Paracoccidioidomycosis. PLoS Genetics. Epub October 2011 doi:10.1371/journal.pgen.1002345.

    Paracoccidioides is a fungal pathogen and the cause of paracoccidioidomycosis, a health-threatening human systemic mycosis endemic to Latin America. Infection by *Paracoccidioides*, a dimorphic fungus in the order Onygenales, is coupled with a thermally regulated transition from a soil-dwelling filamentous form to a yeast-like pathogenic form. To better understand the genetic basis of growth and pathogenicity in *Paracoccidioides*, we sequenced the genomes of two strains of *Paracoccidioides brasiliensis* (Pb03 and Pb18) and one strain of *Paracoccidioides lutzii* (Pb01). These genomes range in size from 29.1 Mb to 32.9 Mb and encode 7,610 to 8,130 genes. To enable genetic studies, we mapped 94% of the *P. brasiliensis* Pb18 assembly onto five chromosomes. We characterized gene family content across Onygenales and related fungi, and within *Paracoccidioides* we found expansions of the fungal-specific kinase family FunK1. Additionally, the Onygenales have lost many genes involved in carbohydrate metabolism and fewer genes involved in protein metabolism, resulting in a higher ratio of proteases to carbohydrate active enzymes in the Onygenales than their relatives. To determine if gene content correlated with growth on different substrates, we screened the non-pathogenic onygenale *Uncinocarpus reesii*, which has orthologs for 91% of *Paracoccidioides* metabolic genes, for growth on 190 carbon sources. U. reesii showed growth on a limited range of carbohydrates, primarily basic plant sugars and cell wall components; this suggests that Onygenales, including dimorphic fungi, can degrade cellulosic plant material in the soil. In addition, *U. reesii* grew on gelatin and a wide range of dipeptides and amino acids, indicating a preference for proteinaceous growth substrates over carbohydrates, which may enable these fungi to also degrade animal biomass. These capabilities for degrading plant and animal substrates suggest a duality in lifestyle that could enable pathogenic species of Onygenales to transfer from soil to animal hosts. [UAMH 3881]

12. Diguistini S, Wang Y, Liao NY, Taylor G, Tanguay P, Feau N, Henrissat B, Chan SK, Hesse-Orce U, Alamouti SM, Tsui CK, Docking RT, Levasseur A, Haridas S, Robertson G, Birol I, Holt RA, Marra MA, Hamelin RC, Hirst M, Jones SJ, Bohlmann J, Breuil C. Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont

Grosmannia clavigera, a lodgepole pine pathogen. Proceedings on the National Academy of Sciences of the United States of America. 2011; 108:2504-2509.

In western North America, the current outbreak of the mountain pine beetle (MPB) and its microbial associates has destroyed wide areas of lodgepole pine forest, including more than 16 million hectares in British Columbia. Grosmannia clavigera (Gc), a critical component of the outbreak, is a symbiont of the MPB and a pathogen of pine trees. To better understand the interactions between Gc, MPB, and lodgepole pine hosts, we sequenced the ~30-Mb Gc genome and assembled it into 18 supercontigs. We predict 8,314 protein-coding genes, and support the gene models with proteome, expressed sequence tag, and RNA-seq data. We establish that Gc is heterothallic, and report evidence for repeat-induced point mutation. We report insights, from genome and transcriptome analyses, into how Gc tolerates conifer-defense chemicals, including oleoresin terpenoids, as they colonize a host tree. RNAseq data indicate that terpenoids induce a substantial antimicrobial stress in Gc, and suggest that the fungus may detoxify these chemicals by using them as a carbon source. Terpenoid treatment strongly activated a ~100-kb region of the Gc genome that contains a set of genes that may be important for detoxification of these host-defense chemicals. This work is a major step toward understanding the biological interactions between the tripartite MPB/fungus/forest system. [kw1407 NCBI genome = UAMH 11150 = SLKW 1407, 11151-11156]

13. Hafez M, Hausner G. The highly variable mitochondrial small-subunit ribosomal RNA gene of *Ophiostoma minus*. Fungal Biol. 2011; 115:1122-1137. Epub 2011 Jul 23.

    Mitochondrial genomes in the true fungi are highly variable both in size and organization. Most of this size variation is due to the presence of introns and intron-encoded open reading frames (ORFs). The objectives for this work were to examine the mitochondrial small-subunit ribosomal RNA (rns) gene of strains of Ophiostoma minus for the presence of introns and to characterize such introns and their encoded ORFs. DNA sequence analysis showed that among different strains of O. minus various rns gene exon/intron configurations can be observed. Based on comparative sequence analysis and RNA secondary structure modeling group I introns with LAGLIDADG ORFs were uncovered at positions mS569 and mS1224 and group II introns were present at positions mS379 and mS952. The mS379 group II intron encoded a fragmented reverse transcriptase (RT)-like ORF and the mS952 group II intron encoded a LAGLIDADG-type ORF. Examples of intron ORF degeneration due to frameshift mutations were observed. The mS379 group II intron is the first mitochondrial group II intron to have an ORF inserted within domain II, typically RT-like ORFs are inserted in domain IV. The evolutionary dynamics of the intron-encoded ORFs have also been examined. [UAMH 5035, 9594, 9775, 9805, 10159

14. Hafez M, Iranpour M, Mullineux ST, Sethuraman J, Wosnitza KM, Lehn P, Kroeker J, Loewen PC, Reid J, Hausner G. Identification of group I introns within the SSU rDNA gene in species of *Ceratocystiopsis* and related taxa. Fungal Biol 2012;116:98-111. Epub 2011 Nov 2.

    During a recent phylogenetic study, group I introns were noted that interrupt the nuclear small subunit ribosomal RNA (SSU rDNA) gene in species of Ceratocystiopsis. Group I introns were found to be inserted at the following rDNA positions: S943, S989, and S1199. The introns have been characterized and phylogenetic analysis of the host gene and the corresponding intron data suggest that for S943 vertical transfer and frequent loss appear to be the most parsimonious explanation for the distribution of nuclear SSU rDNA introns among species of Ceratocystiopsis. The SSU rDNA data do suggest that a recent proposal of segregating the genus Ophiostoma sensu lato into Ophiostoma sensu stricto, Grosmannia, and Ceratocystiopsis has some merit but may need further amendments, as the SSU rDNA suggests that Ophiostoma s. str. may now represent a para-phyletic grouping. [UAMH 7004, 9552, 9581, 9594, 9650, 9761, 9774, 9788, 9797, 9800, 9802, 9813, 11218]

15. Heslop OD, Nyi Nyi M, Abbott SP, Rainford LE, Castle DM, Coard KCM. Disseminated trichosporonosis in a burn patient: meningitis and cerebral abscess due to *Trichosporon asahii*. Journal of Clinical Microbiology 2011; 49(12):4405-4408.

    A 44- year-old diabetic female presented to hospital in Jamaica with thermal burns. *Trichosporon asahii* was isolated from facial wounds, sputum and meningeal swab. Dissemination of the fungus was demonstrated in stained histological sections of the meninges and a brain abscess at autopsy. Pure growth of the fungus from patient samples submitted and an environmental isolate obtained from a wash basin in the hospital supported the diagnosis. [UAMH 11582, 11583, 11584]

16. Hospenthal DR, Chung KK, Lairet K, Thompson EH, Guarro J, Renz EM, Sutton DA. *Saksenaea erythrospora* infection following combat trauma. Journal of Clinical Microbiology. 2011; 49:3707–3709.

    Saksenaea erythrospora is a newly described species of the order Mucorales which has not previously been reported as a cause of human infection. We report a fatal case of *S. erythrospora* invasive burn wound infection in a 26-year-old male injured during combat operations in Iraq. [UAMH 11526]

17. Keel BG, Zettler LW, Kaplin BA. Seed germination of *Habenaria repens* (*Orchidaceae*) in situ beyond its range, and its potential for assisted migration imposed by climate change. Castanea. 2011; 76:43-54. (online under http://www.bioone.org/doi/full/10.2179/09-054.1)

All orchids require free-living, mycorrhizal fungi to complete their life cycles in nature and consequently, orchid conservation must take into account both organisms. In light of climate change now underway, orchids and other plants must be capable of migrating to higher latitudes, either on their own or with human intervention (=assisted migration). In this paper, we describe the symbiotic germination of a common terrestrial orchid, *Habenaria repens*, in situ using seeds from a southern ecotype (Florida) placed at latitudes at and above the species' current natural range. To recover fungi in situ, 500 nylon packets containing 25,000–50,000 seeds were buried at 5 field sites within the Atlantic coastal plain in North Carolina, Maryland, and Virginia. After ca. 5 months, a total of 10 leafless seedlings (protocorms) were recovered from two North Carolina sites, one harboring an extant *H. repens* population, the other an extirpated population. These protocorms yielded mycorrhizal fungi assignable to the anamorphic genus *Epulorhiza*. The physiological significance of each isolate was confirmed after *H. repens* seeds germinated in vitro following fungal inoculation (=symbiotic germination). This study demonstrates that seeds of *H. repens* from a southern ecotype (Florida) are indeed capable of germinating at higher latitudes where fungi already persist. Consequently, the mycotrophic demands of orchids like *H. repens* might be met by assisted migration involving seed release alone. [UAMH 10749 to 10754]

18. Kernaghan G, Patriquin G. Host associations between fungal root endophytes and boreal trees. Microbial Ecology. 2011; 62:460-473.

    Fungal root endophytes colonize root tissue concomitantly with mycorrhizal fungi, but their identities and host preferences are largely unknown. We cultured fungal endophytes from surface-sterilized *Cenococcum geophilum* ectomycorrhizae of *Betula papyrifera*, *Abies balsamea*, and *Picea glauca* from two boreal sites in eastern Canada. Isolates were initially grouped on the basis of cultural morphology and then identified by internal transcribed spacer ribosomal DNA sequencing or by PCR restriction fragment length polymorphism. Phylogenetic analysis of the sequence data revealed 31 distinct phylotypes among the isolates, comprising mainly members of the ascomycete families Helotiaceae, Dermateaceae, Myxotrichaceae, and Hyaloscyphaceae, although other fungi were also isolated. Multivariate analyses indicate a clear separation among the endophyte communities colonizing each host tree species. Some phylotypes were evenly distributed across the roots of all three host species, some were found preferentially on particular hosts, and others were isolated from single hosts only. The results indicate that fungal root endophytes of boreal trees are not randomly distributed, but instead form relatively distinct assemblages on different host tree species. [UAMH 11124-11133, 11165-11175, 11194-11205, 11207, 11220-11224 UAMH 11124–11133, 11165–11175]

19. Kimura M, Yaguchi T, Sutton DA, Fothergill AW, Thompson EH, Wickes BL. Disseminated human conidiobolomycosis due to *Conidiobolus lamprauges*. Journal of Clinical Microbiology. 2011; 49:752-756.

    We describe a disseminated fungal infection by *Conidiobolus lamprauges* in a patient with malignant lymphoma. Histopathology and mycological studies were performed, along with molecular analyses. This is the first record of this species causing human disease and the fifth reported disseminated infection by a *Conidiobolus sp.* in humans. [UAMH 11219]

20. Kovács L, Virágh M, Takó M, Papp T, Vágvölgyi C, Galgóczy L. Isolation and characterization of *Neosartorya fischeri* antifungal protein (NFAP). Peptides. 2011; 32:1724-1731.

    A novel 6.6 kDa antifungal peptide (NFAP) from the culture supernatant of the mold, *Neosartorya fischeri* (anamorf: *Aspergillus fischerianus*), and its encoding gene were isolated in this study. NFAP is a small, basic and cysteine-rich protein consisting of 57 amino acid residues. It shows 37.9–50% homology to similar proteins described in literature from *Aspergillus clavatus*, *Aspergillus giganteus*, *Aspergillus niger,* and *Penicillium chrysogenum*. The in silico presumed tertiary structure of NFAP, e.g. the presence of five antiparallel β-sheet connected with filaments, and stabilized by three disulfide bridges, is very similar to those of the defensin-like molecules. NFAP exhibited growth inhibitory action against filamentous fungi in a dose-dependent manner, and maintained high antifungal activity within broad pH and temperature ranges. Furthermore, it exhibited relevant resistance to proteolysis. All these characteristics make NFAP a promising candidate for further in vitro and in vivo investigations aiming at the development of new antifungal compounds. [UAMH 7955 T longibrachiatum]

21. Kpodzo DS, Calderwood MS, Ruchelsman DE, Abramson JS, Piris A, Winograd JM, Kotton CN. Primary subcutaneous *Alternaria alternata* infection of the hand in an immunocompromised host. Medical Mycology 2011; 49:543–547.

    We describe a case of a progressive subcutaneous *Alternaria alternata* infection in the hand of a patient with chronic lymphocytic leukemia (CLL). The diagnosis was based upon the examination of tissue biopsy and isolation of the etiologic agent in culture. The identity of the isolate was determined by phenotypic characteristics and by sequencing the ITS and D1/D2 regions of the rDNA. Despite combination therapy with voriconazole and micafungin, the lesion continued to progress. Posaconazole therapy, along with surgical excision of the infected tissue, resulted in the eradication of infection. The limitations of the clinical management of invasive *Alternaria* infections are discussed. [UAMH 11333]

22. Lawhon SD, Sutton DA, Halbert ND, Watkins JP. Intra-articular Infection by *Scedosporium prolificans* in a horse. Journal of Equine Veterinary Science. 2011; 31:696-699.

Two months following the surgical repair of an acute, open, comminuted, and articular fracture of the left olecranon, a 15-year-old American Saddlebred gelding presented with nonweight-bearing lameness. A fungus cultured from the cubital joint was identified as *Scedosporium prolificans* by sequencing of the D2 large subunit ribosomal DNA region and subsequently confirmed by phenotypic methods. Therapy with systemic fluconazole, terbinafine and intra-articular voriconazole was attempted, but was unsuccessful. [UAMH 11331]

23. Madden AA, Stchigel AM, Guarro J, Sutton DA, Starks PT. *Mucor nidicola* sp. nov., a novel fungal species isolated from an invasive paper wasp nest. International Journal of Systematic and Evolutionary Microbiology. Epub September 19, 2011 doi: 10.1099/ijs.0.033050-0.

    Mucor nidicola sp. nov. is a novel mucoralean fungus isolated from a nest of the invasive paper wasp, *Polistes dominulus*. Phylogenetic analysis based on the internal transcribed spacers (ITS) and 5.8S rRNA gene sequences, along with physiological tests, revealed that this is a species within the genus *Mucor*. The new species also includes a representative that had previously been characterized as part of the *M. hiemalis* complex. Unlike the type strain of *M. hiemalis*, these two strains can grow at 37 °C and sporulate at 35 °C. Here we present a partial resolution of the *M. hiemalis* species complex and identify the novel species *Mucor nidicola*. [UAMH 11442]

24. Miller SA, Roth-Johnson L, Kania SA, Bemis DA. Isolation and sequence-based identification of *Oxyporus corticola* from a dog with generalized lymphadenopathy. Journal of Veterinary Diagnostic Investigation. Epub December 6, 2011

    The present case report describes isolation of the fungus *Oxyporus corticola* from multiple lymphocutaneous tissues of a Beagle dog. Until recently, this fungus had not been reported in the human or veterinary medical literature as a cause of animal disease. A single previous report also involved infection in a German Shepherd dog, a breed with reported increased susceptibility to disseminated fungal infection and dysfunctional immune response. Isolates were non-sporulating and required molecular identification methods for prompt differenttiation from other fungal pathogens. Risk factors for infection with *O. corticola* are unknown. [UAMH 11535]

25. Miossec C, Morio F, Lepoivre T, Le Pape P, Garcia-Hermoso D, Gay-Andrieu F, Haloun A, Treilhaud M, Leclair F, Miegeville M. Fatal invasive infection with fungemia due to *Microascus cirrosus* after heart and lung transplantation in a patient with cystic fibrosis. Journal of Clinical Microbiology. 2011; 49:2743-2747.

    Scopulariopsis species are rarely but increasingly recognized as opportunistic pathogens in immunocompromised patients. We report on a patient suffering from cystic fibrosis who developed disseminated fungal infection due to a rare *Scopulariopsis* species, *Microascus cirrosus*, after heart and lung transplantation. Despite antifungal combination therapy with voriconazole and caspofungin, the patient died 4 weeks after transplantation. Diagnostic difficulties and optimal management of disseminated *Scopulariopsis*/ *Microascus* infections are discussed. [UAMH 11523]

26. Morio F, Horeau-Langlard D, Gay-Andrieu F, Talarmin JP, Haloun A, Treilhaud M, Despins P, Jossic F, Nourry L, Danner-Boucher I, Pattier S, Bouchara JP, Le Pape P, Miegeville M. Disseminated *Scedosporium*/ *Pseudallescheria* infection after double-lung transplantation in patients with cystic fibrosis. Journal of Clinical Microbiology. 2010; 48:1978-1982.

    We report a case of disseminated *Scedosporium/Pseudallescheria* infection due to *Pseudallescheria boydii* sensu stricto after lung transplantation in a patient with cystic fibrosis. Dissemination occurred under voriconazole. Despite surgery and combination therapy with voriconazole, caspofungin, and terbinafine, the patient died 8 months after transplantation. Previously reported cases are reviewed. [UAMH 11524]

27. Mullineux S, Willows K, Hausner G. Evolutionary dynamics of the mS952 intron: A novel mitochondrial group II intron encoding a LAGLIDADG homing endonuclease gene. Journal of Molecular Evolution. 2011; 72:433–449.

    Examination of the mitochondrial small subunit ribosomal RNA (rns) gene of five species of the fungal genus *Leptographium* revealed that the gene has been invaded at least once at position 952 by a group II intron encoding a LAGLIDADG homing endonuclease gene. Phylogenetic analyses of the intron and homing endonuclease sequences indicated that each element in *Leptographium* species forms a single clade and is closely related to the group II intron/homing endonuclease gene composite element previously reported at position 952 of the mitochondrial rns gene of *Cordyceps* species and of *Cryphonectria parasitica*. The results of an intron survey of the mt rns gene of *Leptographium* species superimposed onto the phylogenetic analysis of the host organisms suggest that the composite element was transmitted vertically in *Leptographium lundbergii*. However, its stochastic distribution among strains of *L. wingfieldii*, *L. terebrantis*, and *L. truncatum* suggests that it has been horizontally transmitted by lateral gene transfer among these species, although the random presence of the intron may reflect multiple random loss events. A model is proposed describing the initial invasion of the group II intron in the rns gene of *L. lundbergii* by a LAGLIDADG homing endonuclease gene and subsequent evolution of this gene to recognize a novel DNA target site, which may now promote the mobility of the intron and homing endonuclease gene as a composite element. [UAMH 9724, 9690, 9722]

28. Najafzadeh MJ, Vicente VA, Sun J, Meis JF, de Hoog GS. *Fonsecaea multimorphosa* sp. nov, a new species of Chaetothyriales isolated from a feline cerebral abscess. Fungal Biol. 2011;115:1066-1076.

A novel fungal species is described originating from the left occipital lobe of the cerebrum of an 18-month-old spayed female cat in Australia. Neurological disorder of the animal became apparent by circling movements and uncoordinated behaviour. Sequencing of the SSU rRNA gene reveals this strain as belonging to the genus *Fonsecaea* in Chaetothyriales. This order includes many black yeasts and relatives known as etiologic agents of disease in humans and animals, including several neurotropic species. Novelty of the species was corroborated by morphology and by multilocus sequencing of the ribosomal internal transcribed spacers (ITS) and partial sequences of the β-tubulin (BT2) and translation elongation factor (TEF1) genes. The strain is very similar to several strains recovered by a selective isolation technique from the natural environment in Brazil. [UAMH 7249 = CBS 980.96 Type]

29. Peart PC, McCook KP, Russell FA, Reynolds WF, Reese PB. Hydroxylation of steroids by *Fusarium oxysporum*, *Exophiala jeanselmei* and *Ceratocystis paradoxa*. Steroids. 2011; 76:1317-1330.

    The potential of *Fusarium oxysporum* var. *cubense* UAMH 9013 to perform steroid biotransformations was reinvestigated using single phase and pulse feed conditions. The following natural steroids served as substrates: dehydroepiandrosterone (1), pregnenolone (2), testosterone (3), progesterone (4), cortisone (5), prednisone (6), estrone (7) and sarsasapogenin (8). The results showed the possible presence of C-7 and C-15 hydroxylase enzymes. This hypothesis was explored using three synthetic androstanes: androstane-3,17-dione (9), androsta-4,6-diene-3,17-dione (10) and 3α,5α-cycloandrost-6-en-17-one (11). These fermentations of non-natural steroids showed that C-7 hydroxylation was as a result of that position being allylic. The evidence also pointed towards the presence of a C-15 hydroxylase enzyme. The eleven steroids were also fed to *Exophiala jeanselmei* var. *lecanii-corni* UAMH 8783. The results showed that the fungus appears to have very active 5α and 14α-hydroxylase enzymes, and is also capable of carrying out allylic oxidations. *Ceratocystis paradoxa* UAMH 8784 was grown in the presence of the above-mentioned steroids. The results showed that monooxygenases which effect allylic hydroxylation and Baeyer–Villiger rearrangement were active. However, redox reactions predominated. [UAMH 8783, 8784, 9013]

30. Perdomo H, Sutton DA, García D, Fothergill AW, Gené J, Cano J, Summerbell RC, Rinaldi MG, Guarro J. Molecular and phenotypic characterization of *Phialemonium* and *Lecythophora* isolates from clinical samples. Journal of Clinical Microbiology. 2011; 49:1209-1216.

    Several members of the fungal genera *Phialemonium* and *Lecythophora* are occasional agents of severe human and animal infections. These species are difficult to identify, and relatively little is known about their frequency in the clinical setting. The objective of this study was to characterize morphologically and molecularly, based on the analysis of LSU rDNA sequences, a set of 68 clinical isolates, presumed to belong to these genera. A total of 59 isolates were determined as *Phialemonium* species (32) or a related *Cephalotheca* species (6), and 20 isolates were determined as *Lecythophora* species or a related *Coniochaeta* species (1). Nine isolates identified as *Acremonium sp.* or *Phaeoacremonium sp.* were excluded for further study. The most common species were *Phialemonium obovatum* and *Phialemonium curvatum*, followed by *Lecythophora hoffmannii*, *Cephalotheca foveolata* and *Lecythophora mutabilis*. [UAMH 10952]

31. Quiroz-Castañeda RE, Martínez-Anaya C, Cuervo-Soto LI, Segovia L, Folch-Mallol JL. Loosenin, a novel protein with cellulose-disrupting activity from *Bjerkandera adusta*. Microbial Cell Factories 2011, 10:8-16.

    Background: Expansins and expansin-like proteins loosen cellulose microfibrils, possibly through the rupture of intramolecular hydrogen bonds. Together with the use of lignocellulolytic enzymes, these proteins are potential molecular tools to treat plant biomass to improve saccharification yields. Results: Here we describe a new type of expansin-related fungal protein that we have called loosenin. Its corresponding gene, loos1, from the basidiomycete *Bjerkandera adusta*, was cloned and heterologously expressed in *Saccharomyces cerevisiae*. LOOS1 is distantly related to plant expansins through the shared presence of a DPBB domain, however domain II found in plant expansins is absent. LOOS1 binds tightly to cellulose and chitin, and we demonstrate that cotton fibers become susceptible to the action of a commercial cellulase following treatment with LOOS1. Natural fibers of *Agave tequilana* also become susceptible to hydrolysis by cellulases after loosenin treatment. Conclusions: LOOS1 is a new type of protein with disrupting activity on cellulose. LOOS1 binds polysaccharides, and given its enhancing properties on the action of hydrolytic enzymes, LOOS1 represents a potential additive in the production of fermentable sugars from lignocellulose. [UAMH 8258]

32. Rank C, Nielsen KF, Larsen TO, Varga J, Samson RA, Frisvad JC. Distribution of sterigmatocystin in filamentous fungi. Fungal Biology. 2011; 115:406-420.

    During the last 50 y, the carcinogenic mycotoxin sterigmatocystin (ST) has been reported in several phylogenetically and phenotypically different genera: *Aschersonia*, *Aspergillus*, *Bipolaris*, *Botryotrichum*, *Chaetomium*, *Emericella*, *Eurotium*, *Farrowia*, *Fusarium*, *Humicola*, *Moelleriella*, *Monocillium* and *Podospora*. We have reexamined all available strains of the original producers, in addition to ex type and further strains of each species reported to produce ST and the biosynthetically derived aflatoxins. We also screened strains of all available species in *Penicillium* and *Aspergillus* for ST and aflatoxin. Six new ST producing fungi were discovered: *Aspergillus asperescens*, *Aspergillus aureolatus*, *Aspergillus eburneocremeus*, *Aspergillus protuberus*, *Aspergillus*

tardus, and *Penicillium inflatum* and one new aflatoxin producer: *Aspergillus togoensis* (=*Stilbothamnium togoense*). ST was confirmed in 23 *Emericella*, four *Aspergillus*, five *Chaetomium*, one *Botryotrichum* and one *Humicola* species grown on a selection of secondary metabolite inducing media, and using multiple detection methods: HPLC–UV/Vis DAD, – HRMS and – MS/MS. The immediate precursor for aflatoxin, O-methylsterigmatocystin was found in *Chaetomium cellulolyticum*, *Chaetomium longicolleum*, *Chaetomium malaysiense* and *Chaetomium virescens*, but aflatoxin was not detected from any *Chaetomium* species. In all 55 species, representing more than 11 clades throughout the Pezizomycotina, can be reliably claimed to be ST producers and 13 of these can also produce aflatoxins. It is not known yet whether the ST/aflatoxin pathway has been developed independently 11 times, or is the result of partial horizontal gene transfer. [UAMH 4515, 4810, 7645, 8230]

33. Raut JK, Suzuki A, Fukiharu T, Shimizu K, Kawamoto S, Tanaka C. *Coprinopsis neophlyctidospora* sp. nov., a new ammonia fungus from boreal forests in Canada. Mycotaxon 2011; 115:227-238.

    Coprinopsis neophlyctidospora sp. nov. (Basidiomycota, Agaricales), collected in urea treated soil of boreal forests from Canada is described and illustrated. Its micromorphological features, phylogenetic analysis, and mating test delineate this taxon as a new species. In addition, its ecological characters also indicate it is a new ammonia fungus. [UAMH 11230 T, 11404 to 11407]

34. Robinson SC, Laks PE. Wood species and culture age affect zone line production of *Xylaria polymorpha*. The Open Mycology Journal 2010; 4:18-21.

    Three pure cultures of *Xylaria polymorpha* were isolated from fruiting bodies at yearly intervals over two years and maintained on 2% malt agar plates at room temperature. Immediately after isolation of the third culture, the cultures were inoculated onto sugar maple (*Acer saccharum)*, aspen (*Populus tremuloides)*, birch (*Betula alleghaniensis),* and basswood (*Tilia americana*) 14 mm cubes and incubated for 10 weeks in jars containing vermiculite. More zone lines were produced on aspen and sugar maple than on yellow birch or basswood. Increasing culture age generally caused a decrease in zone line production; however the effect was only statistically significant in sugar maple. The results indicate that aspen is preferable for zone line production with *X. polymorpha*, as both external and internal zone lines occur on this wood species, and zone line production remains high despite the age of the culture. [accessioned as UAMH 111518 – 11520]

35. Robinson SC, Tudor D, Cooper PA. Feasibility of using red pigment producing fungi to stain wood for decorative applications. Canadian Journal of Forest Research 2011; 41:1722-1728.

    This research investigated the use of red pigment producing fungi in controlled inoculation into woody substrates for decorative applications. Two *Fusarium* species isolated from red-stained wood and two strains of *Arthrographis cuboidea* capable of producing red stain in culture were inoculated onto sugar maple (*Acer saccharum Marsh*.), incubated for 6–14 weeks, and evaluated for their ability to produce a high-saturation, penetrating stain. Both *Fusarium* species failed to produce significant pigmentation either externally or internally. Both strains of *A. cuboidea* produced high amounts of surface and penetrating red stain within a moderate incubation period (over 80% of the wood samples stained by 10 weeks of incubation) but were capable of doing so only under sterile or semisterile conditions. Production of red stain did not differ between *A. cuboidea* isolates except at 6 and 8 weeks where isolate ELS-1 had significantly higher internal red stain. It was also found that an increase in incubation time for *A. cuboidea* past 8 weeks led to increasing amounts of blue pigment on external wood surfaces. The findings indicate that *A. cuboidea* is suitable for production of red pigmentation on decorative wood applications only if utilized under sterile or semisterile conditions and incubation is halted before blue pigment begins to form. [UAMH 4802, 7066, 11517 as ELS-1]

36. Robinson SC, Tudor D, Cooper PA. Wood preference of spalting fungi in urban hardwood species. International Biodeterioration & Biodegradation 2011; 65:1145-1149.

    Five fungal species representing the three major spalting categories were inoculated onto wood of five different urban tree species with low to moderate economic value. Sugar maple (*Acer saccharum*) was also inoculated to serve as a control. Test samples were evaluated both internally and externally for spalting. The tested fungi had significant preferences for different wood species, and the preferences appeared to be related to sucrose availability. Specifically, zone line producing fungi preferred American elm (*Ulmus americana*), while *Arthrographis cuboidea* (pink stain) preferred tree-of-heaven (*Ailanthus altissima*). Wood species preference was also significant by decay class, with decay fungi preferring American elm, silver maple (*Acer saccharinium*), and horse chestnut (*Aesculus hippocastanum*). Staining fungi showed a preference for tree-of-heaven, while both decay classes readily colonized sugar maple and Norway maple (*Acer platanoides*). [Accessioned as UAMH 11517, 11520, 11521]

37. Robinson SC, Tudor D, Cooper PA. Promoting fungal pigment formation in wood by utilizing a modified decay jar method. Wood Science and Technology. Epub 17 January 2011.

    The role of test block placement within a modified decay jar system for promotion of fungal pigments was investigated. Beech and sugar maple blocks were inoculated with common pigment producing fungi and

incubated for 10 weeks. Blocks were placed either below the vermiculite or resting on its surface; no feeder strips were utilized. Amount of pigmentation differed with block placement with *Arthrographis cuboidea* (on sugar maple and beech) and *Xylaria polymorpha* (only on sugar maple) producing more pigment when placed on the surface of the vermiculite. The differences in pigmentation, however, were not necessarily due to moisture content differences within test blocks, as moisture content did not vary significantly by block placement with *A. cuboidea*. Results indicate that placement of wood above vermiculite may increase pigmentation; however, reasons for the increase appear to differ among fungi. [UAMH 4802, UAMH 11517 to 11520]

38. Robinson SC, Tudor D, Cooper PA. Utilizing pigment-producing fungi to add commercial value to American beech (*Fagus grandifolia*). Applied Microbiology and Biotechnology 2011; Sep 20 Epub ahead of print.

    American beech (*Fagus grandifolia*) is an abundant, underutilized tree in certain areas of North America, and methods to increase its market value are of considerable interest. This research utilized pigment-producing fungi to induce color in beech to potentially establish its use as a decorative wood. Wood samples were inoculated with *Trametes versicolor, Xylaria polymorpha, Inonotus hispidus*, and *Arthrographis cuboidea* to induce fungal pigmentation. Black pigmentation (*T. versicolor, X. polymorpha, I. hispidus*) was sporadic, occurred primarily on the surfaces of the heartwood, but not internally. Pink pigmentation (*A. cuboidea*) occurred throughout all of the tested beech samples, but was difficult to see in the heartwood due to the darker color of the wood. To increase the visibility of the pink stain, beech blocks were pretreated with *T. versi-color* for 4 weeks before being inoculated with *A. cuboidea*. This method significantly increased the saturation of the pink stain on both beech heartwood and sapwood, creating coloration similar to that found on sugar maple. This value-adding process should be particularly effective for small-scale wood pigmentation, and should help establish a market for this currently underutilized wood species. [Accessioned as 11517, 11520, 11521]

39. Roe AD, James PMA, Rice AV, Cooke JEK, Sperling FAH. Spatial community structure of mountain pine beetle fungal symbionts across a latitudinal gradient. Microbial Ecology. 2011; 62:347-360.

    Symbiont redundancy in obligate insect–fungal systems is thought to buffer the insect host against symbiont loss and to extend the environmental conditions under which the insect can persist. The mountain pine beetle is associated with at least three well-known and putatively obligate ophiostomatoid fungal symbionts that vary in their environmental tolerances. To better understand the spatial variation in beetle–fungal symbiotic associations, we examined the community composition of ophiostomatoid fungi associated with the mountain pine beetle as a function of latitude and elevation. The region investigated represents the leading edge of a recent outbreak of mountain pine beetle in western Canada. Using regression and principal components analysis, we identified significant spatial patterns in fungal species abundances that indicate symmetrical replacement between two of the three fungi along a latitudinal gradient and little variation in response to elevation. We also identified significant variation in the prevalence of pair-wise species combinations that occur within beetle galleries. Frequencies of pair-wise combinations were significantly different from what was expected given overall species abundances. These results suggest that complex processes of competitive exclusion and coexistence help determine fungal community composition and that the consequences of these processes vary spatially. The presence of three fungal symbionts in different proportions and combinations across a wide range of environmental conditions may help explain the success of mountain pine beetle attacks across a broad geographic range. [UAMH 10965-10970, 11000-11007, 11013-11020, 11035-11084, 11105-11119, 11134-11149]

40. Roe AD, Rice AV, Bromilow SE, Cooke JEK, Sperling FAH. Multilocus species identification and fungal DNA barcoding: insights from blue stain fungal symbionts of the mountain pine beetle. Molecular Ecology Resources. 2010; 10:946-959.

    There is strong community-wide interest in applying molecular techniques to fungal species delimitation and identification, but selection of a standardized region or regions of the genome has not been finalized. A single marker, the ribosomal DNA internal transcribed spacer region, has frequently been suggested as the standard for fungi. We used a group of closely related blue stain fungi associated with the mountain pine beetle (*Dendroctonus ponderosae* Hopkins) to examine the success of such single-locus species identification, comparing the internal transcribed spacer with four other nuclear markers. We demonstrate that single loci varied in their utility for identifying the six fungal species examined, while use of multiple loci was consistently successful. In a literature survey of 21 similar studies, individual loci were also highly variable in their ability to provide consistent species identifications and were less successful than multilocus diagnostics. Accurate species identification is the essence of any molecular diagnostic system, and this consideration should be central to locus selection. Moreover, our study and the literature survey demonstrate the value of using closely related species as the proving ground for developing a molecular identification system. We advocate use of a multilocus barcode approach that is similar to the practice employed by the plant barcode community, rather than reliance on a single locus. [UAMH 10965-10970; 11000-11020, 11139-11149]

41. Roe AD, Rice AV, Coltman DW, Cooke JEK, Sperling FAH. Comparative phylogeography, genetic differentiation, and contrasting reproductive modes in three fungal symbionts of a multipartite bark beetle symbiosis. Molecular Ecology. 2011; 20:584-600.

Multipartite symbioses are complex symbiotic relationships involving multiple interacting partners. These types of partnerships provide excellent opportunities in which to apply a comparative approach to identify common historical patterns of population differentiation and species-specific life history traits. Using three symbiotic blue stain fungal species (Ophiostomatacea) associated with outbreaking populations of the mountain pine beetle (*Dendroctonus ponderosae* Hopkins) in western Canada, we applied phylogenetic, population genetic, and demographic approaches to clarify phylogeographic patterns among the three fungal species. Broadly, the three species showed significant population differentiation, forming northern and southern populations, despite dramatic differences in haplotype diversity. Finer scale structuring and population demographic patterns were less consistent, showing some interspecific incongruence. By contrasting these species simultaneously, we were able to identify differences in recombination rate and ecological traits that can explain the observed patterns of incongruence among the fungal species. By applying a comparative approach to partners of a multipartite symbiosis we were able to distinguish congruent population structuring and species-specific differences that help us to understand the complexity and evolution of this symbiotic system. [UAMH 11013-11020, 11035-11044, 11055-11084, 11105-11118]

42. Siemens JA, Calvo-Polanco M, Zwiazek JJ. *Hebeloma crustuliniforme* facilitates ammonium and nitrate assimilation in trembling aspen (*Populus tremuloides*) seedlings. Tree Physiology. Epub 6 Sept 2011

    This study examined the role of ectomycorrhizal associations in nitrogen assimilation of *Populus tremuloides* seedlings. Seedlings were inoculated with *Hebeloma crustuliniforme* and compared with non-inoculated plants. Nitrogen-metabolizing enzymatic properties were also determined in *H. crustuliniforme* grown in sterile culture. The seedlings and fungal cultures were subjected to nitrogen treatments (including NO3−, NH4+ and a combination of NO3−+NH4+) for 2 months to examine the effects on growth, nitrogen-assimilating enzyme activities and xylem sap concentrations of NH4+ and NO3−. Seedlings were also provided for 3 days with 15N-labeled NH4+ and NO3−, and leaf and root 15N content relative to total nitrogen was measured. Both NO3− and NH4+ were effective in supporting seedling growth when either form was provided separately. When NO3− and NH4+ were provided together, seedling growth decreased while enzymatic assimilation of NH4+ increased. Additionally, nitrogen assimilation in inoculated seedlings was less affected by the form of nitrogen compared with non-inoculated plants. Fungal ability to enzymatically respond to and assimilate NH4+ combined with aspen's enzymatic responsiveness to NO3− was likely the reason for efficient assimilation of both nitrogen forms by mycorrhizal plants. [UAMH 5247]

43. Siemens JA, Zwiazek JJ. *Hebeloma crustuliniforme* modifies root hydraulic responses of trembling aspen (*Populus tremuloides*) seedlings to changes in external pH. Plant and Soil. 2011; 345:247-256.

    The main objective of the study was to compare the effects of short-duration pH treatments on root hydraulic properties in trembling aspen (*Populus tremuloides*) seedlings that were either inoculated with the ectomycorrhizal fungus *Hebeloma crustuliniforme* or remained non-inoculated (control). Inoculated and non-inoculated plants were exposed in solution culture to the root zone pH ranging from 4 to 9 and their root hydraulic conductivity was examined using the hydrostatic method and after subjecting the plants to treatments with 100 µM HgCl2 (aquaporin blocker) and 0.02% trisodium 3-hydroxy-5,8,10-pyrenetrisulfonic acid (apoplastic transport tracer). In a separate experiment, pure cultures of *H. crustuliniforme* were also grown on a slid medium with the pH ranging from 4 to 9 to determine their pH growth optimum and changes in medium pH over time in the presence and absence of 8 mM NH4NO3. When grown in pure culture, *H. crustuliniforme* demonstrated maximum growth at pH 7–8 and was capable of modifying the pH of its growth media, especially in the presence of NH4NO3. The plants that were inoculated with *H. crustuliniforme* had a maximum root hydraulic conductivity at pH 7. At this pH, root hydraulic conductivity was significantly higher compared with non-inoculated plants and showed greater sensitivity of root water transport to pH changes relative to non-inoculated seedlings. Relative apoplastic flux was largely unaffected by pH in inoculated seedlings. Fungal inoculation modified the response of root hydraulic conductivity to pH. The increased root hydraulic conductivity in inoculated seedlings was likely due to an increase in aquaporin-mediated cell-to-cell water transport, particularly at the higher pH. A possible role of fungal aquaporins in the root hydraulic conductivity responses of mycorrhizzal plants should be examined. [UAMH 5247]

44. Tsuneda A, Davey ML, Currah RS. A new endoconidial black meristematic genus, *Atramixtia*, associated with declining white spruce and phylogenetically allied to a lineage of dothidealean conifer pathogens. Botany. 2011; 89: 323–336.

    An endoconidial, black meristematic taxon *Atramixtia arboricola* gen. et. sp. nov. (Dothideales) from the black subicula found on twigs of declining white spruce, *Picea glauca* (Moench) Voss, in Alberta is described. It is morphologically distinguishable from other endoconidial taxa by the conidioma composed of clumps of endoconidial conidiogenous cells, scattered meristematically dividing cells, dematiaceous hyphae, abundant brown, granular matrix materials, and sometimes plant tissue. Endoconidia also occur in conidiogenous cellular clumps that are not organized into a conidioma but develop directly from stromatic cells on the bark. In culture, it forms similar endoconidial conidiomata and also a mycelial, blastic synanamorph that superficially resembles *Hormonema*. *Atramixtia arboricola* is a member of the Dothideales and shows phylogenetic affinities to a clade of conifer-stem and -needle pathogens, including *Sydowia* and *Delphinella*, although no teleomorph was found

either on the natural substrate or in culture. It has not been determined whether *A. arboricola* is pathogenic to its host, but the occurrence of abundant intracellular hyphae in the host periderm suggests that the fungus is at least parasitic. [UAMH 11211 Type, 11212, 11213, 11008, 10297, 10298, 9731]

45. Tsuneda A, Davey ML, Tsuneda I, Hudgins A, Currah RS. *Endophoma*, a new didymellaceous endoconidial genus from bat-cave soil. Mycologia 2011; 103:1146–1155.

    A new endoconidial taxon, *Endophoma elongata* gen. et sp. nov., isolated from bat-cave soil, is reported from Alberta, Canada. It is morphologically unique in producing two forms of unilocular, endoconidial conidiomata (i.e. a superficially *Phoma*-like spherical, often ostiolate form and a cylindrical, non-ostiolate, often setose cleistopycnidial form). Locules of both forms are pseudoparenchymatous, filled with hyaline, thin-walled, endoconidial conidiogenous cells. Endoconidia are hyaline and unicellular. One- or two-celled chlamydospores are abundant in culture. Phylogenetic analysis of the LSU, ITS and β-tubulin regions indicates *Endophoma* is a member of the Didymellaceae and remote from all other endoconidial genera. Endoconidiogenesis has not been reported previously within the Didymellaceae, and *Endophoma* represents the first report of a coelomycetous, endoconidial genus in the Pleosporales. [UAMH 11216 Type]

46. Untereiner WA, Gueidan C, Orr M, Diederich P. The phylogenetic position of the lichenicolous ascomycete *Capronia peltigerae*. Fungal Diversity. 2011; 49:225-23.

    The genus *Capronia* includes a number of lichenicolous (lichen-inhabiting) species, none of which have previously been characterized in vitro or considered in molecular phylogenetic studies. We cultured *Capronia peltigerae* from *Peltigera rufescens* and report here the growth of this species on a variety of media and its phylogenetic position based on the analyses of nuclear ribosomal RNA, mitochondrial ribosomal RNA, and RNA polymerase II (RPB1) gene sequences. This species differs from the majority of *Capronia* studied in axenic culture in lacking a conidial anamorph. Phylogenetic analyses position *C. peltigerae* outside the Herpotrichiellaceae within a robustly supported basal lineage of the Chaetothyriales composed primarily of melanized, rock-inhabiting anamorphic fungi. Our results demonstrate that *Capronia*, as circumscribed, is polyphyletic, but they do not resolve the relationship of *C. peltigerae* with members of the Chaetothyriaceae. [UAMH 11090, 11091]

47. Wang, W. Conidiomatal ultrastructure and cultural characteristics of root-inhabiting species of *Cryptosporiopsis*. Mycology: An International Journal on Fungal Biology. 2011; 2:237-247.

    The conidiomatal differences among six root-inhabiting *Cryptosporiopsis* species were studied at an ultrastructural level and a dichotomous key was then provided. *Cryptosporiopsis brunnea* is delimited by its conidiomata having a distinct sterile excipular covering tissue without adhesive amorphous material and smooth to pitted macroconidia. *Cryptosporiopsis radicicola* produces only excipular covering conidioma-like tissue with adhesive amorphous material and setae. Synnematous conidiomata with abundant macroconidia dominate the colony of *C. ericae*. *Cryptosporiopsis rhizophila* is different in its globose to subglobose conidio-mata, consisting of loosely aggregated vegetative hyphae developing macroconidial conidiophores. *Cryptos-poriopsis grisea*, being the only teleomorph-connected species, differs from the others in its distinct columnar surface structures composed of entangling hyphae and rising well above the aerial mycelium, and unique platform-like hymenium consisting of tightly packed hyphal stroma interspersed with macroconidial conidio-phores and localized microconidia conidiophores. *Cryptosporiopsis melanigena* is distinguished by the produc-tion of abundant chlamydospores that secede schizolytically. [UAMH 9445, 10106, 10729-10731, 10860, 10864, 10920]

48. Zettler LW, Piskin KA. Mycorrhizal fungi from protocorms, seedlings and mature plants of the eastern prairie fringed orchid, *Platanthera leucophaea* (Nutt.) Lindley: A comprehensive list to augment conservation. The American Midland Naturalist. 2011; 166:29-39.

    The Federally threatened Eastern Prairie Fringed Orchid, *Platanthera leucophaea* (Nutt.) Lindley (Orchidaceae), has experienced long-term decline largely due to habitat loss and degradation. Although this species has been propagated from seed in the laboratory, achieving seedling survival ex vitro has been problematic, forcing conservationists to sow seeds directly into field sites in an attempt to generate seedlings. Given that the mycorrhizal fungi needed for germination in situ have sporadic distributions, sowing seeds of this threatened species indiscriminately is not a preferable option. Thus, locating fungal “hotspots” using seed baits, and amending soil with fungi may have practical merit. In anticipation of the latter possibility, we provide a comprehensive list of the 75 mycorrhizal fungi isolated from *P. leucophaea* protocorms, seedlings and mature plants during the past 10 y from sites in Illinois and Michigan, including newly acquired strains from five additional sites in Illinois. Collectively, 66 of the 75 isolates (88%) were assignable to the anamorphic form-genus *Ceratorhiza*, including all of the fungi recovered from the five additional sites. This further supports the hypothesis that *P. leucophaea* relies primarily on *Ceratorhiza* to fulfill its initial and long-term mycotrophic needs. Although *Ceratorhiza* appears to be an ubiquitous associate of *P. leucophaea*, it should not be assumed that specific strains of this genus are equally widespread. Thus, we advocate that the fungi used in conservation should be limited to strains acquired from the same or nearby populations. [UAMH 9610, 9611, 10217-10220, 10457, 10498-10500, 10974-10990, 11011]

Table 1. Cultures Received in 2011

	Person or industry or culture collection and address	Purpose	Total
1.	Andersen B, Mycology Group, BioCentrum-DTU, Technical Univ of Denmark, Lyngby, Denmark	D/ID	4
2.	Bemis D, Comparative Medicine, Univ of Tennessee College of Veterinary Medicine, Knoxville, TN	D	2
3.	Canadian Collection of Fungal Cultures (CCFC / DAOM) (Babcock C), Agriculture & Agri-Food Canada, Ottawa, ON	EX	2
4.	Centraalbureau voor Schimmelcultures (Merkx T), Utrecht, Netherlands	EX	1
5.	Long T (Dutton C, Barker I, Mihailovic D), Animal Health Centre, Toronto Zoo, Scarborough, ON	ID	1
6.	Foght J, Biological Sciences, Univ of Alberta, Edmonton, AB	D	1
7.	Hanselman B, Oakville Veterinary Emergency Hospital and Referral Group, Oakville, ON	ID	1
8.	Keystone Labs Inc. (Kozak S, MacDonald J), Edmonton, AB	ID	25
9.	Madden A (Stark P), Biology Dept., Tufts Univ, Medford, MA	D	1
10.	Morio F, Laboratory of Parasitology & Medical Mycology, Nantes Univ Hospital, Nantes, France	D	5
11.	Natural Link Mold Lab Inc. (Abbott SP), Reno, NV	D/ID	12
12.	Rennie R (Jansen B, Woods J), Mycology, Microbiology and Public Health, Univ of Alberta Hospitals, Edmonton, AB	ID	8
13.	Richardson S (Tsui G, Witkowski M), Mycology, Central Public Health Laboratory, Ontario Agency for Health Protection and Promotion, Toronto, ON	D	1
14.	Robinson S, Faculty of Forestry, Univ of Toronto, Toronto, ON	D	6
15.	Sporometrics Inc. (Scott J, Maharaj A, Wong B), Toronto, ON	D	26
16.	Sutton DA, Fungus Testing Lab., Dept of Pathology, Univ of Texas Health Science Center, San Antonio, TX	D	3
17.	Suzuki A, Dept of Science Education, Chiba Univ, Chiba, Japan	D	5
18.	Untereiner W, Dept of Biology, Brandon Univ, Brandon, MB	D/ID	37
19.	Vanderwolf K, Dept of Zoology, New Brunswick Museum & Univ New Brunswick, St. John, NB	D/ID	68
20.	Vederas J (Thuss J), Dept of Chemistry, Univ of Alberta, Edmonton, AB	D	1
21.	Zettler L, Dept of Biology, Illinois College, Jacksonville, IL	D	22
22.	Zhang S (Lee R), Mycology Laboratory, Johns Hopkins Hospital, Johns Hopkins Univ, Baltimore, MD	D	1

Cultures received from:

Internal (Univ Alberta/UA Hospitals)	10
North America	208
International	15
Total cultures received	**233**

Codes: **D**= Deposit; **EX**= Exchange; **ID**= Identification

Table 2. Cultures Distributed in 2011

	Person or industry or culture collection and address	Purpose	Total
1.	Amano Enzyme Inc. (Tada S), Gifu, Japan	BD	1
2.	Bassi A (Turnbull T), Chemical & Biochemical Engineering, Univ of Western Ontario, London, ON	BD	1
3.	Bayne E (Cameron E), Biological Sciences, Univ of Alberta, Edmonton, AB	ME	1
4.	Bio-Chem Consulting Services Ltd. (Sheppard M), Analytical Services Division, Calgary, AB	QC	5
5.	Bressler D (Espinosa I), Agriculture, Food & Nutrional Sciences, Univ of Alberta, Edmonton, AB	RG	5
6.	Centraalbureau voor Schimmelcultures (Crous P), Utrecht, Netherlands	EX	1
7.	Chen S, Molecular & Cellular Biology, Ohio Univ, Athens, OH	EX/MS	1
8.	Currah RS (Cardinal-McTeague W), Biological Sciences, Univ of Alberta, Edmonton, AB	MS/MR	48
9.	Gentox Laboratories Inc. (Choo S, Th'ng J), Markham, ON	RD	2
10.	Hambleton S, Biodiversity (Mycology and Botany), Agriculture & Agri-Food Canada, Ottawa, ON	CR/MS	61
11.	Harvey R, Salish Sea Mycological Society, Salt Spring Island, BC	B	1
12.	Hsiang T, School of Environmental Sciences, Univ of Guelph, Guelph, ON	TE/MS	6
13.	Khasa D (Beaulieu M), Centre de Recherche en Biologie, Univ Laval, Quebec, QC	MR	7
14.	Kurtzman C, Microbial Properties Research, USDA-Agricultural Research Services, Peoria, IL	CR/MS	8
15.	Lilleskov E, Northern Research Station, United States Forest Service, Houghton, MI	MR	6
16.	Luminex Molecular Diagnostics (Mohr S, Pitsikas P), Early Product Development, Toronto, ON	RD/DN	14
17.	Massey C, Pathobiology, Canadian Cooperative Wildlife Health Centre, Ontario Veterinary College, University of Guelph	MS	1
18.	Moore M, Biological Sciences, Simon Fraser Univ, Burnaby, BC	P	3
19.	Pedras S (Surtees C), Chemistry Dept, Univ of Saskatchewan, Saskatoon, SK	PP/M	3
20.	Rajchenberg M, Area Proteccion Forestal, Centro de Investigacion y Extension Forestal Andino Patagonia (CIEFAP), Esquel, Argentina	T	2
21.	Read Sir D (Johnson I), Dept of Animal and Plant Science, Univ of Sheffield, Sheffield, UK	MR	3
22.	Rennie R (Jansen B), Mycology, Microbiology and Public Health, Univ of Alberta Hospitals, Edmonton, AB	ST	2
23.	Rittenour B, Allergy and Clinical Immunology, National Institute of Occupation Safety and Health (NIOSH), Morgantown, WV	MS	8
24.	Robinson S (Cooper P), Faculty of Forestry, Univ of Toronto, Toronto, ON	BD	7
25.	Schroers H, Agricultural Institute of Slovenia, Ljubljana, Slovenia	CR/MS	6
26.	Seifert K, Biodiversity (Mycology and Botany), Agriculture & Agri-Food Canada, Ottawa, ON	MS	12
27.	Sporometrics Inc. (Guardiola Y, Hollis E), Toronto, ON	PT	9
28.	Strelkov S (Dunfield K, Strelkov I), Agriculture, Food & Nutritional Sciences, Univ of Alberta, Edmonton, AB	MT/PP	15

Table 2. Cultures Distributed in 2011 (cont.)

	Person or industry or culture collection and address	Purpose	Total
29.	Sutton JC (Wing L), School of Environmental Sciences, Univ of Guelph, Guelph, ON	B	4
30.	Tanguay P, Laurentian Forestry Centre, Canadian Forestry Service, Sainte-Foy, QC	PP	6
31.	Untereiner W, Dept of Biology, Brandon Univ, Brandon, MB	MS	5
32.	Vederas J (Thuss J, Agnew R), Dept of Chemistry, Univ of Alberta, Edmonton, AB	PS(5)/M	2
33.	Wingfield M (Marincowitz S), Forestry / Agricultural Biotechnology Institute, Univ of Pretoria, Hatfield, Republic of South Africa	MS	3
34.	ZeptoMetrix Corporation (Trabold P), Bacteriology Dept, Buffalo, NY	RD	2
35.	Zettler L, Biology Dept, Illinois College, Jacksonville, IL	MR	1

Cultures distributed to:

Internal (Univ Alberta/UA Hospitals)	73
North America	174
International	15
Total cultures distributed	**262**

Codes: **B** – Biocontrol; **BD** – Biodegredation/ Bioremediation; **CR** – Collaborative Research; **DN**- DNA; **EX** – Exchange; **M** – Metabolites; **ME –** Microbial Ecology; **MR** – Mycorrhizae; **MS** - Molecular Systematics; **P** – Pathogenicity; **PP** – Plant Pathology; **PS** – Preservation Service; **PT** – Proficiency Testing; **QC** – Quality Control; **RD** – Reference Diagnostics; **RG** – Research General; **ST** - Susceptibility Testing; **T** – Taxonomy; **TE** - Teaching