UNIVERSITY OF ALBERTA MICROFUNGUS COLLECTION AND HERBARIUM (UAMH)

A Unit of the Devonian Botanic Garden, Faculty of Agriculture, Life and Environmental Sciences
Telephone 780-987-4811; Fax 780-987-4141; e-mail: lynne.sigler@ualberta.ca
http://www.devonian2.ualberta.ca/uamh/

SUMMARY OF ACTIVITIES FOR 2010

Celebrating 50 years of service to the scientific community

Staff, Volunteers

Professor (Curator) - **L. Sigler**
.66 FTE Devonian Botanic Garden/UAMH, Fac. Agriculture, Forestry & Home Economics
.33 FTE Medical Microbiology & Immunology, Fac. of Medicine
Consultant in Mycology, PLNA/UAH Microbiology & Public Health
Adj. Prof. Biol. Sci.
Assistant Curator (.5 FTE Non-academic, .5 FTE trust, NSERC) – **C. Gibas**
Technical or laboratory assistants (trust): - **A. Anderson**; **V. Jajczay** (casual)
Volunteer- **M. Packer**

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

Academic Teaching & Graduate Supervision

L. Sigler

- MMI 427 Fungi Affecting Human and Animal Health (full responsibility, fall session)
- BOT 306 Biology of the Fungi (1 lecture)

Graduate Supervisory Committees (Sigler)
M. Day, Biological Sciences, Supervisor, R. Currah; Ph.D. defense Sept. 17

Cultures Received, Distributed and Accessioned

Cultures received for identification, deposit or in exchange (**Table 1**) **267**

Cultures distributed on request or in exchange (**Table 2**)..... **245**

Culture Collection and Herbarium Accessions

Accessions processed to Dec 31. ..... **163**

Total accessions..... **11345**

Information on Accessions available through print and on-line CATALOGUES

Catalogue of the University of Alberta Microfungus Collection and Herbarium. [PDF]
http://www.devonian2.ualberta.ca/uamh/search

Identification, Advisory and Depository Services

In 2010, 267 fungal isolates were received for deposit or identification. Among these were 132 from hibernating bats in New Brunswick caves representing species of *Geomyces* and other unusual fungi of scientific interest sampled from the caves. We are cooperating with K. Vanderwolf, a M. Sc. student from New Brunswick University, who has surveyed hibernating bats in New Brunswick caves for incidence of the white nose pathogen *Geomyces destructans*. Among 71 *Geomyces*-like isolates received, none represented *G. destructans*.. Thirty isolates represent root endophyte fungi, all of which have been sequenced by Dr. G. Kernaghan as part of a study of endophytes from roots of white spruce, paper birch and balsam fir colonized with the mycorrhizal symbiont *Cenococcum geophilum*. We provided assistance in verifying the identity of some isolates and in helping to interpret some sequence data. Additional root associated isolates of *Meliniomyces* were sent by Dr. G. Grelet, formerly at the Macaulay Institute Aberdeen, Scotland. Another 33 isolates of the bark-beetle associated fungus *Grosmannia clavigera* were also received from the research group of C. Breuil at UBC. These isolates are part of a large-scale sequencing project.

Isolates sent for identification are determined by morphology and/or sequencing. Agencies sending isolates included: Microbiology and Public Health, Univ of Alberta Hospitals, Edmonton; Microbiology Service, Memorial Sloan Kettering Cancer Center, New York; Clinical Microbiology Lab., Stanford Univ Medical Center, Palo Alto, CA; Veterinary Diagnostic Laboratory, Univ of Florida, Gainsville; South Penrith Veterinary Clinic, Sydney, Australia; Adelaide Zoo, Adelaide, Australia. We also receive samples of building materials for analysis of mold and provide advice regarding health risks of exposure to fungi.

In 2010, 245 isolates were distributed for various purposes to scientists in universities, government and industry. Of these 182 were distributed within North America, 14 within the U of A, and 49 were sent internationally for various research purposes (see *Publications citing UAMH cultures or assistance*)..

Curatorial Activities

1. In 2010, the UAMH celebrated 50 years of service to the scientific community. The collection is recognized internationally as a Canadian fungal biorepository involved in education, conservation, distribution and research on living fungi of medical, scientific, industrial and heritage importance. Officially established by the University of Alberta in 1960 under the direction of J.W. Carmichael, the collection's origins began in 1933 with the development of the first diagnostic service in medical mycology at the Provincial Laboratory of Public Health. The 11,300 accessions belonging to more than 3200 species are the result of more than 70 years of medical, biodiversity and taxonomic research by other scientists and us. UAMH isolates are used in diverse research applications as documented below under "Publications Citing UAMH Cultures or Assistance."
2. A major project begun in 2009 and continuing through 2010 was redevelopment of the UAMH database. The database is essential to all aspects of collection work including selecting appropriate isolates for users, tracking inventories of preserved stocks, generating many types of reports, linking to digital images and sequences obtained by us. The project involved a major rebuild of the storage tables and the front end application to allow viewing in multiple windows. A considerable amount of time has been invested in testing the application, analyzing and resolving problems. This work proceeded slowly in part due to the complexities of the task and in part due to other work commitments of the programmer and me. The ability to update multiple records and other advances will streamline our work in the future, but it is critical to have the new application working properly before we migrate the data to the new system to avoid data corruption.

3. When complete, this application will improve entry, viewing and retrieval of data in different configurations, incorporate hyperlinks to data located on other sites, e.g sequences or publications; and offer greater flexibility for updating the online catalogue which is now obsolete. An objective is to have the online catalogue illustrated with digital images.
4. In summer of 2010, with assistance from ALES staff Genevieve Beaulieu and Patrick Ball and a summer student, we developed a new UAMH website under Sitecore. The design will be compatible with the Devonian Botanic Garden and other University webpages and the website will offer users new ways of searching and displaying information and of ordering cultures. The launch of the website is expected in early 2011.
5. 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. This year we obtained sequences from 150 isolates. These sequences are stored, together with reliable sequences from Genbank, in an in-house sequence database.

In-house and Collaborative Research

Refereed Journal Articles Published

1. Sigler L, Sutton DA, Gibas CFC, Summerbell RC, Noel RK, Iwen PC. *Phialosimplex*, a new anamorphic genus associated with infections in dogs and having phylogenetic affinity to the *Trichocomaceae*. Medical Mycology 2010; 48:335-345. (First publ. online 29 Sept 2009)

   Anamorphic members of the ascomycete family *Trichocomaceae* including *Aspergillus*, *Penicillium*, *Paecilomyces*, *Geosmithia* and *Sagenomella* have been reported from infections in canines. Six clinical isolates (five associated with infections in canines and one from a human source) demonstrated simple phialides producing conidia in long chains and were investigated for their potential relationship to *Sagenomella chlamydospora*, a known agent of canine disseminated mycosis. Phylogenetic analyses of internal transcribed spacer (ITS) and small subunit (SSU) region sequences revealed that all of the canine-associated isolates were distinct from Sagenomella species. The new anamorphic genus and species *Phialosimplex caninus* is described to accommodate the clinical isolates. *Sagenomella chlamydospora* and *Sagenomella sclerotialis* are transferred to the new genus as *Phialosimplex chlamydosporus* comb. nov. and *Phialosimplex sclerotialis* comb. nov.

2. Sigler L, Gibas CF, Kokotovica B, Bertelsen MF. Disseminated mycoses in veiled chameleons (*Chamaeleo calyptratus*) caused by *Chamaeleomyces granulomatis*, a new fungus related to *Paecilomyces viridis*. J Clin Microbiol 2010; 48:3182-3192. First published online Jul 21.

   An outbreak of disseminated granulomatous disease occurred in a group of veiled chameleons (*Chamaeleo calyptratus*) in a zoo collection. An adult female and six offspring developed large granulomas in multiple organs and were euthanized. At necropsy, roughly spherical yellow-to-white nodules 1 to 3 mm in diameter were grossly visible in the liver and other organs. Histopathology revealed fungal elements that were spherical to ovoid in shape, fragments of slender to irregularly swollen hyphae, and occasional conidia produced on phialides. Fungal isolates were initially suspected on the basis of morphology results to represent *Paecilomyces viridis*, a species known only from one outbreak of fatal mycosis in carpet chameleons (*Furcifer lateralis*). Data obtained from morphological studies and from phylogenetic analyses of nuclear ribosomal rRNA (rDNA) sequence data revealed the Danish chameleon isolates to be a related undescribed anamorphic species within the family *Clavicipitaceae* that includes many insect pathogens. *Chamaeleomyces granulomatis* gen. et sp. nov. is given as the name for the newly described fungus, and *P. viridis* is transferred to the new genus as *Chamaeleomyces viridis* comb. nov. *Chamaeleomyces* species are distinguished by having basally swollen phialides tapering to a

narrow neck, conidia in fragile chains, and pale green to greenish-gray colonies. Both species are dimorphic, producing a transitory yeast stage characterized by ovoid-to-subglobose or subcylindrical yeast-like cells. *Chamaeleomyces* species appear to be rare but aggressive pathogens of chameleons.

3. Kang, HJ, Sigler L, Lee J, Gibas CFC, Yun SH, Lee YW. *Xylogone ganodermophthora* sp. nov., an ascomycetous pathogen causing yellow rot on cultivated mushroom *Ganoderma lucidum* in Korea. Mycologia 2010; 102:1167–1184.

   Yellow rot, caused by an ascomycetous fungus having a distinctive arthroconidial anamorph, is the most destructive disease of cultivated *Ganoderma lucidum* in Korea, but the identity of the yellow rot pathogen (YRP) remains uncertain. Isolates have been identified as *Xylogone sphaerospora* (with putative anamorph *Sporendonema purpurascens*) or as *Arthrographis cuboidea*. Therefore, we used morphological features, pathogenicity tests and phylogenetic analyses of DNA sequences from the nuclear ribosomal genes including partial small subunit and internal transcribed spacer regions, and from the gene encoding RNA polymerase second largest subunit to evaluate the relationship between YRP isolates and these species. The YRP isolates formed a distinct subgroup within a clade that included X. sphaerospora, A. cuboidea and *Scytalidium lignicola*, the type species of *Scytalidium*, but the disposition of the clade within the *Leotiomycetes* was uncertain. We describe *Xylogone ganodermophthora* sp. nov. and *Scytalidium ganodermophthorum* sp. nov. for the teleomorph and anamorph of YRP, respectively. *Arthrographis cuboidea* is reclassified as *Scytalidium cuboideum* comb. nov. and the anamorph of *X. sphaerospora* is named *Scytalidium sphaerosporum* sp. nov. In pathogenicity tests, only *X. ganodermophthora* caused disease development in *Ganoderma lucidum*. Amplified fragment length polymorphism analyses showed that *X. ganodermophthora* populations from diseased fruiting bodies or from oak wood in Korea consisted of two clonal groups.

4. Dewar C.L, Sigler L. Fungal arthritis of the knee caused by *Mycoleptodiscus indicus*. Clinical Rheumatology 2010; 29:1061-1065. First publ April 12. (online at (http://www.springerlink.com/openurl.asp?genre=article&id=doi:10.1007/s10067-010-1448-9.)

   Mycoleptodiscus indicus is a recognized plant pathogen which has very rarely been reported as a cause of human infection. It is a tropical or subtropical fungus which is difficult to culture and identify from clinical specimens. This is the first report of septic arthritis with this fungus in a healthy Canadian male. The fungal infection was contracted on a vacation in Costa Rica, probably through direct inoculation through injured skin. The fungus was isolated from synovial fluid and identification was confirmed by DNA sequencing. There has only been one previous case of septic arthritis of the knee and one skin infection reported with this fungus; both cases involved immunocompromised hosts. Both septic arthritis patients required joint surgery and lavage to eradicate the fungus, however, only the immunocompromised patient required antifungal medications. In the future, it is very likely that the number of patients identified with *M. indicus* infection will rise due to increasing awareness of this pathogen as well as increasing exposure. Many immunocompromised patients on anti-retroviral or biologic therapy are healthy enough to travel, thereby exposing themselves to exotic and infected plants which increase the risk of unusual fungal infections.

5. Dadone, LI, Klaphake E, Garner MM, Schwahn D, Sigler L, Trupkiewicz JG, Myers G, Barrie MT. Pituitary cystadenoma, enterolipidosis, and cutaneous mycosis in an Everglades ratsnake (*Elaphe obsoleta rossalleni*). J Zoo Wildl Med 2010; 41:538-541.

   An 11-yr-old captive-born male Everglades ratsnake (*Elaphe obsoleta rosalleni*) presented with

dysecdysis, hyperkeratosis, and inappetance. Two skin biopsies demonstrated a diffuse hyperkeratosis with both a bacterial and fungal epidermitis. *Fusarium oxysporum* was cultured from both biopsies and considered an opportunistic infection rather than a primary pathogen. Medical management was unsuccessful, and the snake was euthanized. Histologic findings included a pituitary cystadenoma arising from the pars intermedia, severe intestinal lipidosis, generalized epidermal hyperkeratosis, and lesions consistent with sepsis. It is hypothesized that endocrine derangements from the pituitary tumor may have caused the skin and intestinal lesions.

Papers Accepted or Submitted

6. De Ravin, S.S., Challipalli, M., Anderson, V., Shea, Y., Marciano, B., Hilligoss, D., Marquesen, M., DeCastro, R., Liu, Y-C., Sutton, D.A., Wickes, B.L., Kammeyer, P.L., Sigler, L., Sullivan, K., Kang, E.M., Malech, H.L., Holland, S.M., and Zelazny, A. *Geosmithia argillacea :* an emerging cause of invasive mycosis in human chronic granulomatous disease. Clin. Infect. Dis. (MS 62489R1 accepted 13-Dec-2010 for electronic edition).
7. Johnson, R.S.P., C.R. Sangster, L. Sigler, S. Hambleton and J A Paré. Deep fungal dermatitis caused by the *Chrysosporium* anamorph of *Nannizziopsis vriesii* in captive coastal bearded dragons (*Pogona barbata*). Australian Vet. J. (submitted Dec 13, 2010)
8. Morio, F., F. Fraissine, T. Gastinne, P. Le Pape, J. Delaunay, L. Sigler, C.F.C. Gibas, and M. Miegeville. Invasive *Myceliophthora thermophila* infection mimicking invasive aspergillosis in a neutropenic patient: a new cause of cross-reactivity with the *Aspergillus* galactomannan serum antigen assay (TMMY-0368-2010 23-Dec-2010)

Presentations, Abstracts

9. Invited speaker, "Fungal friends and foe – a primer on current issues" Labcon 2010, CSMLS National Congress of Medical Laboratory Science, Session C25, Edmonton May 30.

Posters

10. Bertelsen M.F., L. Sigler, and B. Kokotovic. An "outbreak" of disseminated mycosis in veiled chameleons (*Chameleo calyptratus*). Proceedings of the international conference on diseases of zoo and wild animals. Madrid, May 2010, p. 160.
11. Linde, E.M., L. Sigler, S.H. Hinrichs, and P.C. Iwen. *Schizophyllum commune* as a cause of allergic fungal sinusitis in an immunocompetent patient: An argument for histopathologic and molecular techniques for diagnosis. American Society for Microbiology Annual Meetings San Diego May 23-27, 2010
12. Schutte, S.D., L. Sigler, D. Florescu, R. Noel-Hurst, and P.C. Iwen. Utilization of a molecular method for the identification of *Scopulariopsis brevicaulis* as a cause of disseminated hyalohyphomycosis. American Society of Clinical Pathology, Oct 27-31, San Francisco. [abstract published in Am. J. Clin. Pathol. 2010: 134:686 http://ajcp.ascpjournals.org/content/134/4/local/back-matter.pdf)

External Funding (Grants/Fees for Services)

NSERC. Major Resources Support (**continuing**). The University of Alberta Microfungus Collection and Herbarium (UAMH). (2008-2013) (Total $273,000)	54,600
NSERC Discovery (**continuing**). Systematics of Fungi in the Human Environment Sigler, L. 2006 to 2011 (Total $159,390)	31,878
Income from all services including cultures distributed, preservation services, identifications, microbial assessments, consultation	18,000

Other Activities

Editorial work (LS): Journal of Clinical Microbiology (5), Medical Mycology (2), Mycologia (2), New Phytologist (1).

Committees (LS):

- Member of the Mycology Network established in 2007 by the Canadian Public Health Laboratory, Public Health Agency of Canada to coordinate reference mycology services in Canada.

Publications Citing UAMH Cultures or Assistance

1. Bidochka M, Clark DC, Lewis MW, Keyhani NO. Could insect phagocytic avoidance by entomogenous fungi have evolved via selection against soil amoeboid predators? Microbiology 2010; 156: 2164-2171.

The entomopathogenic fungi *Metarhizium anisopliae* and *Beauveria bassiana* are ubiquitously distributed in soils. As insect pathogens they adhere to the insect cuticle and penetrate through to the insect haemocoel using a variety of cuticle-hydrolysing enzymes. Once in the insect haemocoel they are able to survive and replicate within, and/or evade, phagocytic haemocyte cells circulating in the haemolymph. The mechanism by which these soil fungi acquire virulence factors for insect infection and insect immune avoidance is unknown. We hypothesize that insect phagocytic cell avoidance in *M. anisopliae* and *B. bassiana* is the consequence of a survival strategy against soil-inhabiting predatory amoebae. Microscopic examination, phagocytosis assays and amoeba mortality assays showed that these insect pathogenic fungi are phagocytosed by the soil amoeba *Acanthamoeba castellanii* and can survive and grow within the amoeba, resulting in amoeba death. Mammalian fungal and bacterial pathogens, such as *Cryptococcus neoformans* and *Legionella pneumophila*, respectively, show a remarkable overlap between survival against soil amoebae and survival against human macrophages. The insect immune system, particularly phagocytic haemocytes, is analogous to the mammalian macrophage. Our data suggest that the ability of the fungal insect pathogens *M. anisopliae* and *B. bassiana* to survive insect phagocytic haemocytes may be a consequence of adaptations that have evolved in order to avoid predation by soil amoebae. [UAMH 6742, 10047]

2. Chaturvedi V, Springer DJ, Behr MJ, Ramani R, Li X, Peck MK, Ren P, Bopp DJ, Wood B, et al. Morphological and molecular characterizations of psychrophilic fungus *Geomyces destructans* from New York bats with white nose syndrome (WNS). PLoS One. 2010; 5(5): e10783. Publ. online 2010 May 24. doi: 10.1371

Massive die-offs of little brown bats (*Myotis lucifugus*) have been occurring since 2006 in hibernation sites around Albany, New York, and this problem has spread to other States in the Northeastern United States. White cottony fungal growth is seen on the snouts of affected animals, a prominent sign of White Nose Syndrome (WNS). A previous report described the involvement of the fungus *Geomyces destructans* in WNS, but an identical fungus was recently isolated in France from a bat that was evidently healthy. The fungus has been recovered sparsely despite plentiful availability of afflicted animals. [UAMH 603, 723, 733, 1062, 1088, 1568, 2583, 2586, 10473]

3. Chau HW, Goh YK, Si BC, Vujanovic V. Assessment of alcohol percentage test for fungal surface hydrophobicity measurement. Lett Appl Microbiol 2010;50:295–300.

Aim: To determine whether assessing the penetration of solutions with different concentrations of ethanol (alcohol percentage test: APT) on fungal surfaces is effective in characterization of hydrophobicity on fungal surfaces.
Methods and Results: APT and contact angle (CA) measurements were conducted on nine hydrophobic and two hydrophilic fungal strains from the phyla of *Ascomycota*, *Basidiomycota* and *Zygomycota*.

There was a strong positive correlation (R2 = 0·95) between the APT and CA measurements from eight of the nine hydrophobic stains (four pathogenic and mycotoxigenic Fusarium taxa, one melanosporaceous biotrophic taxon, *Alternaria sp*, *Penicillium aurantiogriseum* and *Cladosporium cladosporioides*). Hydrophilic control strains, *Mortierella hyalina* and *Laccaria laccata*, had CAs <90° and no measurable degree of hydrophobicity using the APT method.
Conclusions: The APT method was effective in measuring the degree of hydrophobicity and can be conducted on different zones of fungal growth.
Significance and Impact of the Study: Characterization of fungal surface hydrophobicity is important for understanding of its particular role and function in fungal morphogenesis and pathogenesis. APT is a simple method that can be utilized for fungal hydrophobicity measurements when CA cannot be measured because of obscured view from aerial mycelia growth. [UAMH 10033]

4. Davey ML. *Annellosporium nemorosum* gen. et sp. nov., an annellidic anamorph with phylogenetic affinities to the genus *Daldinia (Xylariales)*. Karstenia 50: 1–10.

During a survey of fungi occurring in soil from swift fox dens in a zoo enclosure in Alberta, Canada, a free-living xylariaceous mitosporic fungus was repeatedly isolated and is herein described as *Annellosporium nemorosum* gen. et sp. nov. The fungus is characterized by mononematous, dichotomously branched conidiophores with termini bearing groups of 1–3 cylindric, smooth to minutely roughened, enteroblastic, percurrently proliferating, annellated conidiogenous cells that produce sub-globose to obovate conidia with attenuated, flattened basal ends. Phylogenetic analysis of the ?-tubulin region indicates *A. nemorosum* has strong phylogenetic affinities to the teleomorphic genus *Daldinia* (Xylariaceae, Xylariales), and is included in a clade with those *Daldinia* species known to produce *Nodulisporium*-like anamorphs with enteroblastic conidiogenesis, rather than the holoblastic conidiogenesis typical of true *Nodulisporium* species. A teleomorphic state was not observed, but is expected to be *Daldinia loculata*-like, given the close affiliation between this species and *A. nemorosum* that was revealed by phylogenetic analyses of the internal transcribed spacer (ITS) region of rDNA. [UAMH 11227 holotype]

5. DiGuistini S, Liao NY, Platt D, Robertson G, Seidel M, Chan SK, Docking TR, Birol I, Holt RA, Hirst M, Mardis E, Marra MA, Hamelin RC, Bohlmann J, Breuil C, Jones SJ. De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. Genome Biol 2009; 10(9):R 94. Epub 2009 Sep 11.

Sequencing-by-synthesis technologies can reduce the cost of generating de novo genome assemblies. We report a method for assembling draft genome sequences of eukaryotic organisms that integrates sequence information from different sources, and demonstrate its effectiveness by assembling an approximately 32.5 Mb draft genome sequence for the forest pathogen Grosmannia clavigera, an ascomycete fungus. We also developed a method for assessing draft assemblies using Illumina paired end read data and demonstrate how we are using it to guide future sequence finishing. Our results demonstrate that eukaryotic genome sequences can be accurately assembled by combining Illumina, 454 and Sanger sequence data. [UAMH 11150 = SLKW1407]

6. DeGuistini S, Ralph SG, Lim YW, Holt R, Jones S, Bohlmann J, Breuil C. Generation and annotation of lodgepole pine and oleoresin-induced expressed sequences from the blue-stain fungus Ophiostoma clavigerum, a mountain pine beetle-associated pathogen. FEMS Microbiol Lett 2007; 267:151-158.

Ophiostoma clavigerum is a destructive pathogen of lodgepole pine (*Pinus contorta*) forests in western North America. It is therefore a relevant system for a genomics analysis of fungi vectored by bark beetles. To begin characterizing molecular interactions between the pathogen and its conifer host, we created an expressed sequence tag (EST) collection for *O. clavigerum*. Lodgepole pine sawdust and oleoresin media were selected to stimulate gene expression that would be specific

to this host interaction. Over 6500 cDNA clones, derived from four normalized cDNA libraries, were single-pass sequenced from the 3' end. After quality screening, we identified 5975 high-quality reads with an average PHRED 20 of greater than 750 bp. Clustering and assembly of this high-quality EST set resulted in the identification of 2620 unique putative transcripts. BLASTX analysis revealed that only 67% of these unique transcripts could be matched to known or predicted protein sequences in public databases. Functional classification of these sequences provided initial insights into the transcriptome of *O. clavigerum*. Of particular interest, our ESTs represent an extensive collection of cytochrome P450 s, ATP-binding-cassette-type transporters and genes involved in 1,8-dihydroxynaphthalene-melanin biosynthesis. These results are discussed in the context of detoxification of conifer oleoresins and fungal pathogenesis.

7. Foos KM, May NL, Beach DL, Pomper M, Sheehan KB, Ruch DG. Phylogeny of Pilobolaceae. Mycologia 2011; 103:36-44. Epub 2010 Aug 31.

The three genera traditionally classified as *Pilobolaceae* have been identified on the basis of morphological characteristics. In the absence of distinctive morphological differences, phylogenetic techniques have proven to be superior for developing phylogenies. Molecular techniques have been used primarily for studies of higher fungi; there are few investigations of the Zygomycota using genetic sequences for classification. DNA sequences coding for three regions of rRNA were used to investigate phylogenetic relationships of the three genera traditionally considered within the Pilobolaceae. Evidence indicates that *Pilaira* should be removed from the Pilobolaceae and the family redescribed. Sporangiospore size is the morphological characteristic that most closely correlates with rDNA clades of phylogenetic trees. This study demonstrates that traditional morphological characteristics alone are not adequate to differentiate species of *Pilobolus*. [UAMH 7297, 7298, 3070, 1312].

8. Grelet GA, Meharg AA, Duff EI, Anderson IC, Alexander IJ.Small genetic differences between ericoid mycorrhizal fungi affect nitrogen uptake by Vaccinium. New Phytol. 2009;181(3):708-18. Epub 2008 Nov 13

Ericoid mycorrhizal fungi have been shown to differ in their pattern of nitrogen (N) use in pure culture. Here, we investigate whether this functional variation is maintained in symbiosis using three ascomycetes from a clade not previously shown to include ericoid mycorrhizal taxa. Vaccinium macrocarpon and Vaccinium vitis-idaea were inoculated with three fungal strains known to form coils in Vaccinium roots, which differed in their patterns of N use in liquid culture. (15)N was used to trace the uptake of -N, -N and glutamine-N into shoots. (15)N transfer differed among the three fungal strains, including two that had identical internal transcribed spacer (ITS) sequences, and was quantitatively related to fungal growth in liquid culture at low carbon availability. These results demonstrate that functional differences among closely related ericoid mycorrhizal fungi are maintained in symbiosis with their hosts, and suggest that N transfer to plant shoots in ericoid mycorrhizas is under fungal control. [UAMH 11281, 11282, 11285]

9. Hesse-Orce U, DiGuistini S, Keeling CI, Wang Y, Li M, Henderson H, Docking TR, Liao NY, Robertson G, Holt RA, Jones SJM, Bohlmann J, Breuil C. Gene discovery for the bark beetle-vectored fungal tree pathogen *Grosmannia clavigera*. BMC Genomics 2010; 11:536-547.

Background: *Grosmannia clavigera* is a bark beetle-vectored fungal pathogen of pines that causes wood discoloration and may kill trees by disrupting nutrient and water transport. Trees respond to attacks from beetles and associated fungi by releasing terpenoid and phenolic defense compounds. It is unclear which genes are important for G. clavigera's ability to overcome antifungal pine terpenoids and phenolics.
Results: We constructed seven cDNA libraries from eight *G. clavigera* isolates grown under various culture conditions, and Sanger sequenced the 5' and 3' ends of 25,000 cDNA clones, resulting in

44,288 high quality ESTs. The assembled dataset of unique transcripts (unigenes) consists of 6,265 contigs and 2,459 singletons that mapped to 6,467 locations on the *G. clavigera* reference genome, representing ~70% of the predicted *G. clavigera* genes. Although only 54% of the unigenes matched characterized proteins at the NCBI database, this dataset extensively covers major metabolic pathways, cellular processes, and genes necessary for response to environmental stimuli and genetic information processing. Furthermore, we identified genes expressed in spores prior to germination, and genes involved in response to treatment with lodgepole pine phloem extract (LPPE).
Conclusions: We provide a comprehensively annotated EST dataset for *G. clavigera* that represents a rich resource for gene characterization in this and other ophiostomatoid fungi. Genes expressed in response to LPPE treatment are indicative of fungal oxidative stress response. We identified two clusters of potentially functionally related genes responsive to LPPE treatment. Furthermore, we report a simple method for identifying contig misassemblies in de novo assembled EST collections caused by gene overlap on the genome. [UAMH 11150-11155]

10. Houbraken J, Verweij PE, Rijs AJMM, Borman AM, Samson RA. Identification of *Paecilomyces variotii* in clinical samples and settings. J Clin Microbiol 2010; 48(8):2754-61.

Paecilomyces variotii is a commonly occurring species in air and food, but is also associated with many types of human infections, and is among the emerging causative agents of opportunistic mycoses in immunocompromised hosts. *Paecilomyces* can cause hyalohyphomycosis and two species, *Paecilomyces lilacinus* and *P. variotii*, are the most frequently encountered organisms. In this study, a set of thirty-four clinical isolates, morphologically identified as *P. variotii* or *P. lilacinus*, were formally identified by sequencing the intergenic transcribed spacer regions (ITS1, 2 including 5.8S rDNA) and a part of the ß-tubulin gene. Three isolates were identified as *P. lilacinus*, and five of the presumptive *P. variotii* isolates did not belong to the genus *Paecilomyces*, but were identified as *Talaromyces eburneus* (anamorph: *Geosmithia argillacea*) or *Hamigera avellanea* (anamorph: *Merimbla ingelheimense*). Applying the most recent taxonomy, we found that the clinical *P. variotii* isolates could be identified as *P. variotii* sensu stricto (14 strains), *P. formosus* (11 strains) and *P. dactylethromorphus* (1 strain). These data indicate that *P. formosus* occurs in clinical samples as commonly as *P. variotii*. Susceptibility tests showed that the antifungal susceptibility profiles of *P. variotii*, *P. formosus* and *P. dactylethromorphus* are similar and all tested strains were susceptible *in vitro* to amphotericin B. *P. lilanicus, T. eburneus* and *H. avellanea* had different susceptibility profiles and flucytosine and voriconazole were the least active of the antifungal drugs tested against these species. Our results indicate that correct species identification is important to help to guide appropriate antifungal therapy.

11. Kimura M, Yaguchi T, Sutton DA, Fothergill AW, Thompson EH, Wickes BL. Disseminated human conidiobolomycosis due to *Conidiobolus lamprauges*. J Clin Microbiol. Epub 8 Dec 2010, doi:10.1128/JCM.01484-10.

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]

12. Khadempour L, Alamouti SM, Hamelin R, Bohlmann J, Breuil C. Target-specific PCR primers can detect and differentiate ophiostomatoid fungi from microbial communities associated with the mountain pine beetle *Dendroctonus ponderosae*. Fungal Biology 2010; 114:825-833.

The aim of this study was to develop DNA probes that could identify the major fungal species associated with mountain pine beetles (MPB). The beetles are closely associated with fungal species that include ophiostomatoid fungi that can be difficult to differentiate morphologically. The most

frequently isolated associates are the pine pathogens *Grosmannia clavigera* and *Leptographium longiclavatum*, the less pathogenic *Ophiostoma montium*, and an undescribed *Ceratocystiopsis* species (Cop. sp.). Because growing, isolating and extracting DNA from fungi vectored by MPB can be time and labour intensive, we designed three rDNA primer sets that specifically amplify short rDNA amplicons from *O. montium*, Cop. sp. and the pine Leptographium clade. We also designed two primer sets on a gene of unknown function that can differentiate *G. clavigera* and *L. longiclavatum*. We tested the primers on 76 fungal isolates that included MPB associates. The primers reliably identified their targets from DNA obtained from pure fungal cultures, pulverized beetles, beetle galleries, and tree phloem inoculated with *G. clavigera*. The primers will facilitate large-scale work on the ecology of the MPB-fungal-lodgepole pine ecosystem, as well as phytosanitary/quarantine sample screening. [11150, 11153, 11155, 10946, 10947, 9551]

13. Lee SH, Calvo-Polanco M, Chung GC, Zwiazek JJ. Role of aquaporins in root water transport of ectomycorrhizal jack pine (*Pinus banksiana*) seedlings exposed to NaCl and fluoride. Plant, Cell & Environment 2010; 33:769–780.

Effects of ectomycorrhizal (ECM) fungus *Suillus tomentosus* on water transport properties were studied in jack pine (*Pinus banksiana*) seedlings. The hydraulic conductivity of root cortical cells (Lpc) and of the whole root system (Lpr) in ECM plants was higher by twofold to fourfold compared with the non-ECM seedlings. HgCl2 had a greater inhibitory effect on Lpc in ECM compared with non-ECM seedlings, suggesting that the mercury-sensitive, aquaporin (AQP)-mediated water transport was largely responsible for the differences in Lpc between the two groups of plants. Lpc was rapidly and drastically reduced by the 50 mm NaCl treatment. However, in ECM plants, the initial decline in Lpc was followed by a quick recovery to the pre-treatment level, while the reduction of Lpc in non-ECM seedlings progressed over time. Treatments with fluoride reduced Lpc by about twofold in non-ECM seedlings and caused smaller reductions of Lpc in ECM plants. When either 2 mm KF or 2 mm NaF were added to the 50 mm NaCl treatment solution, the inhibitory effect of NaCl on Lpc was rapidly reversed in both groups of plants. The results suggest that AQP-mediated water transport may be linked to the enhancement of salt stress resistance reported for ECM plants. [UAMH 5506]

14. Lievens B, van Kerckhove S, Justé A, Cammue BPA, Honnay O, Jacquemyn H. From extensive clone libraries to comprehensive DNA arrays for the efficient and simultaneous detection and identification of orchid mycorrhizal fungi. Journal of Microbiological Methods 2010; 80: 76-85.

A DNA array was developed from extensive clone library sequence data sets for the assessment of dominant members of mycorrhizal fungi that associate with terrestrial orchid species. As a-proof-of-concept, the array was developed for the basidiomycetous mycorrhizal partners from three closely related perennial *Orchis* species, including *Orchis anthropophora*, *O. militaris* and *O. purpurea*. Based on internal transcribed spacer regions, oligonucleotides were developed for seven operational taxonomic units (OTUs; defined as groups of sequences sharing at least 97% sequence similarity), corresponding to members of the *Tulasnellaceae* family. In order to cover a broader spectrum of tulasnelloid fungi, oligonucleotides were as well developed for two subsets of closely related OTUs. The array was evaluated using multiple primer pairs. In addition, hybridization results were validated by recovery and sequencing of the hybridized amplicons as well as by hybridizing reference DNA samples. Considering the unlimited expansion possibilities of DNA arrays to include specific detector oligonucleotides for other and more microorganisms, the method described here has the major advantage that it provides a powerful, rapid and cost-effective way for the simultaneous detection and identification of a wide range of orchid mycorrhizae. The design, development and advantages of the array are discussed in relation to its potential for future research in mycorrhizal ecology. [7782, 7783, 7784, 6095, 6096, 6097, 6098, 5163, 5425.]

15. Martinez-Ortiz J, Flores R, Vazquez-Duhalt R. Molecular design of laccase cathode for direct electron transfer in a biofuel cell. Biosensors and Bioelectronics Epub 15 Nov 2010

In order to improve the direct electron transfer in enzymatic biofuel cells, a rational design of a laccase electrode is presented. Graphite electrodes were functionalized with 4-[2-aminoethyl] benzoic acid hydrochloride (AEBA). The benzoic acid moiety of AEBA interacts with the laccase T1 site as ligand with an association constant (K_A) of 6.6×10^{-6} M. The rational of this work was to orientate the covalent coupling of laccase molecule with the electrode surface through the T1 site and thus induce the direct electron transfer between the T1 site and the graphite electrode surface. Direct electron transfer of laccase was successfully achieved, and the semi-enzymatic fuel cell Zn-AEBA laccase showed a current density of 2977 μA cm^{-2} and a power density of 1190 μW cm^{-2} at 0.41 V. The molecular oriented laccase cathode showed 37% higher power density and 43% higher current density than randomly bound laccase cathode. Chronoaperometric measurements of the Zn-AEBA fuel cell showed functionality on 6 h. Thus, the orientation of the enzyme molecules improves the electron transfer and optimizes enzyme-based fuel cells efficiency. [UAMH 8260]

16. Metry CA, Hoien-Dalen PS, Maddox CW, Thompson EH, Sutton DA, Romanelli AM, Wickes BL, MacNeill AL. Subcutaneous *Mycoleptodiscus indicus* infection in an immunosuppressed dog. J Clin Microbiol. Epub 2 Jun 2010, doi:10.1128/JCM.02368-09.

An 8-year-old dog presented with several dermal excoriations. Lesion cytology revealed pyogranulomatous inflammation with branching, septate hyphae. A mould identified as *Mycoleptodiscus indicus* by morphology and sequencing was cultured from fine needle aspirates. This is the first report of a *Mycoleptodiscus* species as an etiologic agent in a dog. [UAMH 11157].

17. Pedras MSC, Hossain S, Snitynsky RB. Detoxification of cruciferous phytoalexins in *Botrytis cinerea*: Spontaneous dimerization of a camalexin metabolite. Phytochemistry Epub 20 December 2010 doi:10.1016/j.physletb.2003.10.071.

Phytopathogenic fungi are able to overcome plant chemical defenses through detoxification reactions that are enzyme mediated. As a result of such detoxifications, the plant is quickly depleted of its most important antifungal metabolites and can succumb to pathogen attack. Understanding and predicting such detoxification pathways utilized by phytopathogenic fungi could lead to approaches to control plant pathogens. Towards this end, the inhibitory activities and metabolism of the cruciferous phytoalexins camalexin, brassinin, cyclobrassinin, and brassilexin by the phytopathogenic fungus *Botrytis cinerea* Pers. (teleomorph: *Botryotinia fuckeliana*) was investigated. Brassilexin was the most antifungal of the phytoalexins, followed by camalexin, cyclobrassinin and brassinin. Although *B. cinerea* is a species phylogenetically related to the phytopathogenic fungus *Sclerotinia sclerotiorum* (Lib) de Bary, contrary to *S. sclerotiorum*, detoxification of strongly antifungal phytoalexins occurred via either oxidative degradation or hydrolysis but not through glucosylation, suggesting that glucosyl transferases are not involved. A strongly antifungal bisindolylthiadiazole that *B. cinerea* could not detoxify was discovered, which resulted from spontaneous oxidative dimerization of 3-indolethiocarboxamide, a camalexin detoxification product. [UAMH 1784, UAMH 1809].

18. Peterson SW, Jurjevic Z, Bills GF, Stchigel AM, Guarro J, Vega FE. Genus *Hamigera*, six new species and multilocus DNA sequence based phylogeny. Mycologia 2010; 102:847–864.

Genus *Hamigera* was erected for *Talaromyces* species that make asci singly instead of in chains. Initially it contained two species, *H. avellanea* and *H. striata*. We describe six new species in the genus, *H. fusca*, *H. inflata*, *H. insecticola*, *H. pallida*, *H. paravellanea* and *H. terricola. Merimbla*

ingelheimensis is a distinct anamorphic species in the *Hamigera* clade. None of our DNA sequence data (*BT2*, calmodulin, ITS, lsu rDNA, *RPB2*, *Tsr1* and *Mcm7*) supported the placement of *H. striata* in the same clade as *H. avellanea*, thus we accepted *Talaromyces striatus*. In addition to *Hamigera* species we examined the phylogenetic disposition of *Warcupiella spinulosa*, *Penicillium megasporum*, *Penicillium arenicola* and *Merimbla humicoloides*. Despite nominal similarity of some of these species to *Merimbla*, none of these species are part of the *Hamigera* clade and *M. humicoloides* is placed in *Penicillium* to have a monophyletic genus *Hamigera*.. [UAMH 2878, UAMH 4054]

19. Quiroz-Castañeda RE, Pérez-Mejía N, Martínez-Anaya C, Acosta-Urdapilleta L, Folch-Mallol J. Evaluation of different lignocellulosic substrates for the production of cellulases and xylanases by the basidiomycete fungi *Bjerkandera adusta* and *Pycnoporus sanguineus*. Biodegredation Epub 11 Oct 2010, DOI 10.1007/s10532-010-9428-y.

Agricultural waste products are potential resources for the production of a number of industrial compounds, including biofuels. Basidiomycete fungi display a battery of hydrolytic enzymes with prospective use in lignocellulosic biomass transformation, however little work has been done regarding the characterization of such activities. Growth in several lignocellulosic substrates (oak and cedar sawdust, rice husk, corn stubble, wheat straw and Jatropha seed husk) and the production of cellulases and xylanases by two basidiomycete fungi: *Bjerkandera adusta* and *Pycnoporus sanguineus* were analyzed. Growth for *P. sanguineus* was best in rice husk while corn stubble supported the highest growth rate for *B. adusta*. Among the substrates tested, cedar sawdust produced the highest cellulolytic activities in both fungal species, followed by oak sawdust and wheat straw. Xylanolytic activity was best in oak and cedar sawdust for both species. We found no correlation between growth and enzyme production. Zymogram analysis of xylanases and cellulases showed that growth in different substrates produced particular combinations of protein bands with hydrolytic activity. [UAMH 8258].

20. Reid J, Hausner G. The epitypification of *Ophiostoma minutum*, now *Ceratocystiopsis minuta*. Mycotaxon 2010;113:463-474.

Siemaszko's (1939) illustrations and figure legends for *Ophiostoma minutum* are designated herein as the lectotype for *Ceratocystiopsis minuta*, and a strain UAMH 11218 [= WIN(M) 1532, = R. Jankowiak 705] isolated from perithecia in galleries of *Ips typographus* in stems of *Picea abies*, from Biebrzanski National Park (Polish: Biebrzański Park Narodowy), Werklye Protection Range, grown and dried on wood chips, is then designated as the epitype and deposited in UAMH. This specimen will serve as a reference in future studies on species of *Ceratocystiopsis* that use modern morphological, chemotaxonomic, and molecular approaches. Morphological details are also presented for the epitype material. [UAMH 11218 epitype, 11217]

21. Reid J, Iranpour M, Rudski SM. Loewen PC, Hausner G. A new conifer-inhabiting species of *Ceratocystis* from Norway. Botany 2010; 88: 971–983

A new species, *Ceratocystis norvegica* J. Reid & Hausner sp. nov., is described from Norway. Based on morphological criteria and analyses of rDNA internal transcribed spacer and small subunit rDNA sequences, strains collected from galleries of the bark beetle *Ips typographus* on *Picea abies* (L.) H. Karst, were shown to be distinct both from members of the *Ceratocystis coerulescens* complex and from other species described previously from conifers. *Ceratocystis norvegica* has the following defining characteristics: convergent ostiolar hyphae; a sharply defined temperature optimum at 20 8C; an apparent lack of a conidial state; and ascospores that on germination produce either self-fertile or self-sterile strains. [UAMH 9778 holotype, 11187 – 11193]

22. Sharma N, Rahman MH, Liang Y, Kav NNV. Cytokinin inhibits the growth of *Leptosphaeria maculans* and *Alternaria brassicae*. Canad J Plant Pathol 2010; 32: 306 – 314.

Blackleg and blackspot are economically important diseases of canola caused by *Leptosphaeria maculans* and *Alternaria brassicae*, respectively, and can lead to significant crop losses. In this study, we investigated the effects of cytokinins on the symptoms caused by these two pathogens. We observed that cytokinin, especially 6-benzyl amino purine, was able to significantly reduce disease symptoms and mycelial growth within plant tissues. This cytokinin was also able to inhibit the *in vitro* growth of both fungi. Other cytokinins such as kinetin or adenine hemisulfate were unable to inhibit fungal growth *in vitro*, suggesting that the presence of a benzene ring structure is required for the inhibitory effects observed. Our findings are discussed within the context of plant-pathogen interactions. [UAMH 7476]

23. Stevenson LG, Drake SK, Shea YR, Zelazny AM, Murray PR. Evaluation of matrix-assisted laser desorption ionization-time of flight mass spectrometry for identification of clinically important yeast species. J Clin Microbiol 2010; 48:3482-3486.

We evaluated the use of matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) for the rapid identification of yeast species. Using Bruker Daltonics MALDI BioTyper software, we created a spectral database library with m/z ratios of 2,000 to 20,000 Da for 109 type and reference strains of yeast (44 species in 8 genera). The database was tested for accuracy by use of 194 clinical isolates (23 species in 6 genera). A total of 192 (99.0%) of the clinical isolates were identified accurately by MALDI-TOF MS. The MALDI-TOF MS-based method was found to be reproducible and accurate, with low consumable costs and minimal preparation time. [UAMH 563, 635, 672, 4260, 4261, 7654, 7655, 7656, 7658, 7663, 7664, 7670, 7671, 10278].

24. Tsui CL, Wang B, Khadempour L, Alamouti SM, Bohlmann J, Murray BW, Hamelin RC. Rapid identification and detection of pine pathogenic fungi associated with mountain pine beetles by padlock probes. J. Microbial Methods 2010; 83(1):36-33. Epub 2010 Jul. 25.

Fifteen million hectares of pine forests in western Canada have been attacked by the mountain pine beetle (*Dendroctonus ponderosae*; MPB), leading to devastating economic losses. *Grosmannia clavigera* and *Leptographium longiclavatum*, are two fungi intimately associated with the beetles, and are crucial components of the epidemic. To detect and discriminate these two closely related pathogens, we utilized a method based on ligase-mediated nucleotide discrimination with padlock probe technology, and signal amplification by hyperbranched rolling circle amplification (HRCA). Two padlock probes were designed to target species-specific single nucleotide polymorphisms (SNPs) located at the inter-generic spacer 2 region and large subunit of the rRNA respectively, which allows discrimination between the two species. Thirty-four strains of *G. clavigera* and twenty-five strains of *L. longiclavatum* representing a broad geographic origin were tested with this assay. The HRCA results were largely in agreement with the conventional identification based on morphology or DNA-based methods. Both probes can also efficiently distinguish the two MPB-associated fungi from other fungi in the MPB, as well as other related fungi in the order Ophiostomatales. We also tested this diagnostic method for the direct detection of these fungi from the DNA of MPB. A nested PCR approach was used to enrich amplicons for signal detection. The results confirmed the presence of these two fungi in MPB. Thus, the padlock probe assay coupled with HRCA is a rapid, sensitive and reproducible method for the identification and detection of these ophiostomatoid fungi. [UAMH 4585, 4876, 9722, 11150, 10622, 10623]

25. Tsuneda A, Hambleton S, Currah RS. *Endoconidioma populi* from aspen and alder: phylogeny, and variations in cleistopycnidial morphology and their ecological implications. Botany 2010; 88:675–684.

Cleistopycnidial ontogeny and sequences of nuclear internal transcribed spacers (ITS) and large subunits (LSU) were compared for five strains of *Endoconidioma populi* Tsuneda et al.: three from trembling aspen and two from alder. The cleistopycnidia of two of the aspen strains, including the type strain, were subglobose to flask-shaped (mostly 35–100 µm × 30–60 µm), and consisted solely of meristematic cells with thick cell walls that were heavily impregnated with melanin granules. Peridial cells were not visibly differentiated from locular cells and were also capable of forming endoconidia. Endoconidia were released from one to several sites of the cleistopycnidium by the dissolution of peridial cell wall. The alder strains shared these characteristics, except that their cleistopycnidia released both endoconidia and conidiogenous cells. Unlike those four strains, cleistopycnidia of the third aspen strain were cylindrical, often exceeding 500 µm in length, branched, and possessed a peridium of textura angularis that developed from short, determinate hyphae. Conidiogenous cells contained abundant lipid bodies that were not mobilized until the onset of endoconidiogenesis. The peridium at the basal area was prone to breakage by external forces, indicating that the individual cleistopycnidium, as a whole, functions as a dispersal unit. A small number of ITS nucleotide differences among strains corresponded to their observed morphological differences and host association. Phylogenetic analyses suggested a close relationship of *E. populi* with *Hormonema carpetanum* Bills, Peláez & Ruibal, and *Coniozyma leucospermi* (Crous & Denman) Crous. [UAMH; 10902, 10903, 10297, 10298, 10299.]

Table 1. Cultures Received in 2010

	Person or industry or culture collection and address	Purpose	Total
1.	Babcock, C., Canadian Collection of Fungal Cultures, Ottawa, ON	EX	2
2.	Breuil, C., Univ. of British Columbia, Vancouver, BC	D	33
3.	Centraalbureau voor Schimmelcultures, (Snippe-Claus, F.), Utrecht, Netherlands	EX	4
4.	Conley, K. (Schuman Rose, C.), Veterinary Diagnostic Labs., Univ. of Florida, Gainesville, FL	ID	1
5.	Currah, R. (Day, M., Tsuneda, A.), Dept. of Biological Sciences, Univ. of Alberta, Edmonton, AB	D	9
6.	Fukiharu, T., Natural History Museum & Institute, Chiba, Japan	D	1
7.	Grelet, G. (Smart, C.), The Macaulay Institute, Aberdeen, Scotland	D	21
8.	Jacobson, E. (Williams, S.), Veterinary College, Univ of Florida, Gainesville, FL	ID	2
9.	Jansen, B. (Rennie, R.), Mycology, Microbiology and Public Health, Univ. of Alberta Hospitals, Edmonton, AB	ID	2
10.	Johnson, R. (Humphreys, K.), South Penrith Veterinary Clinic, Taronga Zoo, Mosman, Sydney, Australia	ID	2
11.	Kappagoda, S. (Banaei, N.), Clinical Microbiology Lab., Stanford Univ. Medical Center, Palo Alto, CA	ID	1
12.	Kernaghan, G., Mount Saint Vincent Univ., Halifax, NS	D/ID	30
13.	Kiehn, T., Microbiology Service, Memorial Sloan Kettering Cancer Center, New York, NY	ID	1
14.	McLelland, D., Adelaide Zoo, Adelaide, Australia	ID	1
15.	Peterson, S.W. (Cardamone, J.; Swezey, J.;), Agicultural Research Service Culture Collection, Peoria, IL	ID	1
16.	Reid, J. (Hausner, G.), Univ. of Manitoba, Winnipeg, MB	D	13
17.	Sutton, D. (O'Dowd, M.E.), Fungus Testing Lab., Dept of Pathology, Univ of Texas Health Science Center, San Antonio, TX	D	11
18.	Vanderwolf, K. (Malloch, D.), Zoology, New Brunswick Museum, St. John, & Univ. New Brunswick, Fredericton, NB	D/ID	132

Cultures received from:

1. Internal (Univ Alberta/UA Hospitals)	**11**
2. North America	**227**
3. International	**29**

Total cultures received **267**

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

Table 2. Cultures Distributed in 2010

	Person or industry or culture collection and address	Purpose	Total
1.	Assured Biotechnology Corporation, (Pope, L.), Oak Ridge, TN	IAQ	1
2.	BD-Diagnostics (White, V.), Diagnostic Systems, Sparks, MD	RD	15
3.	Bidochka, M. (Cywinska, A.), Dept of Biological Sciences, Brock Univ, St. Catharines, ON	RG	17
4.	Bio-Chem Consulting Services Ltd. (Sheppard, M.), Analytical Services Division, Calgary, AB	RD	6
5.	Canadian Collection of Fungal Cultures (Babcock, C.), Ottawa, ON	EX	2
6.	Centraalbureau voor Schimmelcultures (Verkley, G.J.M. , Houbraken, J., Crous, P.), Utrecht, Netherlands	EX	9
7.	Chen, S., Molecular and Cellular Biology Program, Dept of Biological Sciences, Ohio Univ, Athens, OH	MS	3
8.	Currah, R. (Day, M., Tsuneda, A.), Dept of Biological Sciences, Univ of Alberta, Edmonton, AB	T	4
9.	Danisco Sweeteners Oy (Gros, H.), Kantvik, Finland	RD	2
10.	Dlusskaya, E., Environmental Engineering, Univ of Alberta, Edmonton, AB	BD	2
11.	Fonseca, A., Portuguese Yeast Culture Collection, Capus da Caparica, Caparica, Portugal	EX	1
12.	Frisvad, J., Dept. of Systems Biology, Center for Microbial Biotechnology, Technical Univ. of Denmark, Lyngby, Denmark	M	3
13.	GAP EnviroMicrobial Services Ltd, (Couture, T.), London, ON	RD	1
14.	Gentox Labs, (Choo, S.), Markham, ON	RD	1
15.	Hambleton, S., Biodiversity (Mycology and Botany), Agriculture & Agri-Food Canada, Ottawa, ON	CR	51
16.	Harris, H., Biology, Concordia Univ College of Alberta, Edmonton, AB	TE	1
17.	Hausner, G., Dept of Microbiology, Univ of Manitoba, Winnipeg, MB	T	5
18.	Jeya, M., Dept of Chemical & Bioengineering, Konkuk Univ, Seoul, South Korea	RG	1
19.	Kernaghan, G., Biology Dept, Mount Saint Vincent Univ, Halifax, NS	ST	2
20.	Kubicek-Pejic, A., Chemical Biology, Chemical Genomics Center of the Max Planck Society, Dortmund, Germany	RG	1
21.	Lamarche, J., Laurentian Forestry Centre, Canadian Forest Service, Quebec, QC	P	4
22.	Luminex Molecular Diagnostics, (Mohr, S.), Toronto, ON	RD	1
23.	Malek, L., Biology, Lakehead Univ, Thunder Bay, ON	BD	1
24.	Nargang, F., Dept of Biological Sciences, Univ of Alberta, Edmonton, AB	FG	1
25.	Ochoa, R.P. (Goldaranzena, A.), Dept of Plant Protection and Production, Basque Institute of Research and Agricultural Development, Vitoria-Gasteiz, Spain	B	5
26.	Oros Monton, J.I., Veterinary Faculty, Univ of Las Palmas de Gran Canaria, Arucas, Spain	ST	3
27.	Pedras, S., Chemistry Dept, Univ of Saskatchewan, Saskatoon, SK	M	8
28.	Peterson, S., Bacterial Foodborne Pathogens and Mycology, National Center for Agricultural Utilization Research, US Dept of Agriculture, Peoria, IL	CR	26
29.	Pickard, M., Dept of Biological Sciences, Univ of Alberta, Edmonton, AB	EZ	6

30.	Reese, P., Dept of Chemistry, The Univ of West Indies, Mona, Jamaica, West Indies	M	16
31.	Romer Labs Division Holdings GmbH, (Labuda, R.), Tulln, Austria	RD	1
32.	Sporometrics Inc. (Saleh, M.), Toronto, ON	RD	8
33.	Taylor, J.W. (Whiston, E.), Plant and Microbial Biology, Univ of California, Berkeley, CA	MS	6
34.	Thomson, E.. (Dennis, J.), Dept of Biological Sciences, Univ of Alberta, Edmonton, AB	ST	1
35.	Tsui, C. (Breuil, C.), Dept of Forest Science, Univ of British Columbia, Vancouver, BC	MS	18
36.	Tudor, D. (Cooper, P.), Faculty of Forestry, Univ of Toronto, Toronto, ON	BD	1
37.	Venkateswerlu, G. (Narayana, J.V.), Dept of Biotechnology, Joginpally B R Engineering College, Andrapradesh, India	RG	1
38.	Vohnik, M., Dept of Mycorrhizal Symbioses, Institute of Botany, Academy Science, Pruhonice, Czech Republic	MR	3
39.	Wieder, K. (Harris, M.), Dept of Biology, Villanova Univ, Villanova, PA	BD	4
40.	Zalar, P., Dept of Biology, Biotechnical Faculty, Univ of Ljubljana, Ljubljana, Slovenia	M	3

Cultures distributed to:

1. Internal (Univ Alberta/UA Hospitals)	**14**
2. North America	**182**
3. International	**49**
Total cultures distributed	**245**

Codes: **B** – Biocontrol; **BD** – Biodegradation/ Bioremediation; **CR** – Collaborative Research; **EX** – Exchange; **EZ** – Enzymes; **FG** – Fungal Genetics; **IAQ** - Indoor Air Quality; **M** – Metabolites;**MR** – Mycorrhizae; **MS** - Molecular Systematics; **P** – Pathogenicity; **PP** – Plant Pathology; **RD** – Research Diagnostics; **RG** – Research General; **ST** - Susceptibility Testing; **T** – Taxonomy; **TE** - Teaching