UNIVERSITY OF ALBERTA MICROFUNGUS COLLECTION AND HERBARIUM (UAMH)

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SUMMARY OF ACTIVITIES FOR 2012

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
Adjunct Professor in Biological Sciences
Consultant in Mycology, PLNA/UAH Microbiology & Public Health
Assistant Curator (.5 FTE Non-academic, .5 FTE trust, NSERC) – **C. Gibas**
Technicians (trust): **A. Anderson** (0.8 FTE to Dec 31; 0.2 FTE beginning Jan 1 2013); **V. Jajczay** (casual)
Volunteer- **M. Packer**

Affiliates [NSERC Major Resources Support coapplicants]
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**) **64**

Cultures distributed on request or in exchange (**Table 2**)..... **199**

Culture Collection and Herbarium Accessions

Accessions processed to Dec 31. ..... **42**

Total accessions..... **11672**

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

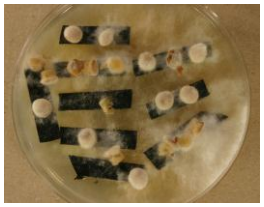
Catalogue of the University of Alberta Microfungus Collection and Herbarium. [PDF]
https://secure.devonian.ualberta.ca/uamh/searchcatalogue.php

Curatorial Activities

- In 2012, 64 fungal isolates were received for deposit or identification and 199 isolates were distributed for various research purposes to scientists in universities, government and industry (**Tables 1 and 2**). Of the latter, 20 were distributed within U of A, 146 within Canada and the US, and 33 were sent internationally. Over the past 5 years, the facility has supplied 1358 isolates to 200 users including 831 to external nonprofit institutions, 382 to industry and 145 to internal (U of A) users. During this period, 970 cultures were received from 100 users including 647 from North America, 113 from other countries and 210 from internal users.
- Current curatorial objectives are to authenticate older accessions, many of which have not been reexamined in recent years, to replenish preserved stocks and to sequence as many accessions as possible. Cryopreservation or freezing of cultures in liquid nitrogen (LN) is considered the optimum method for long-term storage of microorganisms. Although all new accessions are preserved in LN, approximately 1000 older accessions are still

stored in -20C freezers. In 2012, 175 accessions were regrown and represerved by cryopreservation and freeze-drying. The UAMH holds over 1000 ex-type cultures and in 2012 we regrew and represerved 88 of the oldest ones. We obtained sequences for 32 types that are not yet represented in Genbank and the sequences are currently being prepared for deposit. Another 125 sequences were obtained from isolates regrown for authentication projects. Sequences are stored, together with reliable sequences from Genbank, in an in-house sequence database used for identification and phylogenetic analyses.

- At UAMH, all nonsporulating fungi are stored by two or three methods. Cryopreservation is the method of choice but a number of variables can affect recovery including the fungal species , the cryoprotectant, the age of the culture and possible presence of staling compounds. Among the most difficult to preserve are some ecto- and orchid mycorrhizal fungi. Based on a report by Stielow JB et al (Mycologia 2012; 104:324-330) who described improved recovery when isolates were grown on charcoal filter paper, C. Gibas conducted trials on 7 ectomycorrhizal and 8 orchid mycorrhizal fungi that had previously failed to survive LN or gave very poor recovery in multiple preservation attempts. She achieved 70 to 100% recovery for all 7 ectomycorrhizal fungi. Although only 4/8 orchid fungi survived, recovery rate was good (100%). Results suggested that the method works better when the filter paper is well colonized. A repeat trial on 8 orchid fungi (4 original and 4 new) indicate that 7/8 were recovered successfully. The method is more labor intensive and time consuming than our usual method, but appears to be of value for preserving important orchid fungi. [see **North American Orchid Conservation Center** below].



- Information on the use of UAMH strains in diverse research applications is provided in section ***Publications citing UAMH cultures or assistance*** page 6 of this report. For example, further research on *Pseudomonas fluorescens* (UAMH 11620) by J. Foght (Biol Sci, U of A) and her colleagues has implications for the bioremediation and biocatalytic transformation of polycyclic aromatic hydrocarbons and for the selection of appropriate strains for bioremediation [Refs 7,8]. Dark septate fungal plant endophytes of the *Phialocephala fortinii* s.l.–*Acephala applanata* species complex (PAC) are common fungi in roots of plants of temperate regions worldwide but their biological and genetic diversity is still being explored. Publications by C.R. Grünig (Microsynth AG, Balgach, Switzerland) and colleagues examined the complete mitochondrial genome of *P. subalpina* [UAMH 11012] (Ref 15), evaluated microsatellite loci for their use in species diagnosis and population genetic studies [UAMH 11659] (Ref 29) and identified extracellular metabolites produced by *P. europaea* [UAMH 11659] having inhibitory activity against the plant pathogen *Phytophthora citricola* (Ref 39). Characteristics of biologically active metabolites produced by the plant pathogen *Leptosphaeria maculans*, and of toxins and antigenic proteins produced *Chaetomium globosum*, a common fungus in the built environment, have been evaluated by Canadian chemists MS Pedras (Univ Sask) (Refs 30-32) and JD Miller (Carleton Univ) (Ref 27, 33) and their colleagues. *Chlorociboria aeruginascens*, which naturally produces blue-green staining in wood, was evaluated under laboratory conditions to develop methods for enhancing its potential decorative and commercial use in wood spalting by S.C. Robinson and D Tudor (Univ Toronto) and colleagues (Ref 35). As well, sequences for the isolates were deposited in Genbank [UAMH 7614-7615, 11655-11656].

Collection Activities

North American Orchid Conservation Center Initiative (NAOCC)

In nature, orchids depend on mycorrhizal fungi for seed germination and to provide a source of energy. Approximately 250 species of native orchids occur in North America. Almost half of these species are under severe threat due to habitat destruction and many species are likely to become extirpated unless action is taken soon to conserve them and their fungal partners. In recognition of this problem, the Smithsonian Environmental Research Center (Edgewater, MD) and the United States Botanic Garden (Washington, DC), proposed to establish the North American Center for Conservation of Native Orchids (NAOCC). I attended the inaugural meeting held June 25-26, 2012 and provided data on the UAMH collection of orchid associated fungi.

Priorities for the NAOCC include establishing seed and fungal banks that represent the broad genetic diversity of both partners, developing improved strategies for orchid propagation, promoting habitat conservation and restoration through partnerships with landowners and societies, and creating a web-based education program. Preliminary funding for the NAOCC came from a Grand Challenges grant from the Smithsonian Institution and the United States Botanic Garden, but more funding is being sought to bring the NAOCC to fruition.

Collaborating organizations include the Smithsonian Environmental Research Center, the Smithsonian Gardens, the National Museum of Natural History, the National Zoological Park, the National Museum of the American Indian, the US Botanic Garden, Alaska Botanical Garden, Atlanta Botanical Garden, Chicago Botanic Garden, Desert Botanical Garden, Devonian Botanic Garden (represented by the **Microfungus Collection and Herbarium**), Illinois College, The Center for Plant Conservation, New England Wild Flower Society, The Nature Conservancy, Bureau of Land Management, Mt. Cuba Center Inc., Duke Farms. Partnerships with other agencies is envisaged.

Our role is to work on fungal banking to ensure conservation of the genetic diversity of orchid mycorrhizal fungi. The UAMH bank of orchid mycorrhizal fungi is an invaluable North American resource built up over many years of research work by R.S. Currah (University of Alberta) and his students, L.W. Zettler (Illinois College, Jacksonville, IL) and other scientists. The research of L.W. Zettler focuses on conservation of threatened orchids and the symbiotic germination of orchid seed with host -specific and locally adapted mycorrhizal fungi. Results of Dr. Zettler's work on symbiotic germinations have identified almost 70 UAMH isolates that promote seed germination in vitro. In 2011-12, 23 isolates received for deposit included *Ceratorhiza* (*Ceratobasidium*) and *Epulorhiza* (*Tulasnella*) species obtained mainly from roots of the U.S. Federally threatened eastern prairie fringed orchid *Platanthera leucophaea*.

Mycological Collections in the Federal System & FLIG Meeting

Priorities for this meeting were to bring together the curators of federal fungal collections to verify details regarding the contents of their collections, the current state of affairs, and to plan or recommend plans for housing, moving or merging collections and to track and map relocated collections to ensure that critical collections are not physically lost or misplaced. I was invited to participate as the only University-based collection, as the coordinators recognize the scientific and medical importance of the UAMH collection and are concerned about its current vulnerable state. The Federal Laboratory Interdepartmental Governance (FLIG) committee is co-chaired by the Canadian Food Inspection Agency and the Public Health Agency. Within their mandate is a Scientific Collections Working Group co-chaired by Agriculture and Agri-Food Canada and Environment Canada. The UAMH differs from all Canadian fungal collections in holding fungi of medical and veterinary importance and in making full accession data available online. No fungi are held by Public Health Agency of Canada National Microbiology Lab. The National Collection of Fungus Cultures (Eastern Cereal and Oilseed Research Centre, Agriculture Canada) is comparable in size but differs in scope (mainly agriculturally relevant fungi). Fungi are held in Canadian Forest Service (NRCan) collections but many collections are not being actively curated.

Impact of the Moratorium on the NSERC Major Resources Support Program (MRS)

The NSERC Major Resources Support program has been crucial in providing operational support for nationally and internationally recognized Canadian facilities and resources. The moratorium on funding for the MRS due to federal budget cuts was announced on April 19, 2012. This decision placed 39 scientific facilities, including critical field stations and biological repositories like UAMH, in jeopardy since there is no other funding stream dedicated to the operation of nationally and internationally unique resources. Although many universities in Canada house herbaria and biological collections, there are very few that maintain collections of living organisms. Historically, four of these have received partial support from NSERC MRS (and predecessor programs MFA, Infrastructure).

The UAMH has been funded since 1990 by MRS and prior similar programs with a lifetime value of $947,301. The central support provided by MRS allowed for the maintenance of the facility in a state of readiness, for the training and retention of HQ personnel to sustain the service activities, and for obtaining additional funds through fees. NSERC funds pay 0.5 FTE salary of the technologist (Assistant Curator) and some operational expenses. The remaining 0.5 FTE salary has been paid by the Devonian Botanic Garden since 1989. The loss of the program means that resources built up over many years could be lost or be made inaccessible due to loss of personnel required to maintain living material. The approximate current value of its unique assets is estimated at $500,000 to $1.25 million based on 10,000 living organisms x the user fee of $50 per culture for nonprofit or $125 per culture for industry. Equipment and capital assets exceed $700,000.

31 March 31 2013 – NSERC funding for the UAMH will end leaving an immediate shortfall to cover 0.5 FTE salary and operational support.

18 December 2012 – Provided data on UAMH concerns to a NSERC questionnaire entitled "Analysis of Issues Associated with the NSERC MRS Program" (J. Halliwell coordinator).

29 August 28 2012 – A survey by Kennedy Stewart (Burnaby–Douglas), NDP Critic for Science & Technology, entitled "Pennywise, Pound Foolish" outlined the significant impacts of the loss of NSERC Major Resources Support (MRS) Program for research facilities and programs across Canada. Mr. Stewart noted that "The decision to eliminate the MRS program was made without any consultation and represents how our country's long-standing commitment to basic science is being undermined …"
http://kennedystewart.ndp.ca/sites/default/files/kennedystewart.ndp.ca/field_attached_files/mrs_program_moratorium_impact_report_0.pdf

3 May 2012 – A letter of concern was endorsed by 47 senior scientists from affected facilities and resource centres across Canada addressed to the Honourable Christian Paradis, Minister of Industry, NSERC Council and others.

External Funding (Grants/Fees for Services)

NSERC Major Resources Support (continuing to Mar 31, 2013). The University of Alberta Microfungus Collection and Herbarium (UAMH). Sigler (PI), Currah, Hausner, Berbee (2008-2013) (Total $273,000)	54,600
SAS grant Equipment. Refrigerated incubator for fungal culture.	$5,000
Income from all services (cultures distributed, preservation services, identifications, microbial assessments, consultation)	16,000

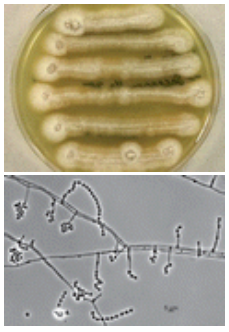
Other Activities (Sigler)

- 27 January – Guest lecture "Conidial Development in Fungi Imperfecti" for Botany 306 Biology of the Fungi.
- March – submitted NSERC MRS Form 181 but in April a moratorium was placed on the program.
- 25 – 26 June – invited speaker NAOCC, Smithsonian Environmental Research Center, Edgewater, MD. See section above **Collection Activities**
- 17 September – Invited talk "Fungal Friends and Foe -- conserving fungal diversity at the Devonian Botanic Garden's Microfungus Collection" for Canadian Federation of University Women, Edmonton Chapter.
- 17 October – Invited talk "Making sense of mold" for Occupational Physicians of Edmonton Third Wednesday Club. Partipants included 22 physicians from Medical Officer of Health, Edmonton zone, Workman's compensation, and U of A Dept of Medicine Community and Occupational Medicine Program.
- 3 December – Invited speaker at a meeting on federal collections "Mycological collections in the federal system & FLIG", Ottawa. See section above **Collection Activities**
- Book review on Pictorial Atlas of Soil and Seed Fungi, CRC Press, published in The Quarterly Review of Biology 87(3): 270, 2012
- Review Med Mycol (1)

In-house and Collaborative Research

Refereed Journal Articles Published

1. Armstrong P, Sigler L, Sutton D, Grooters A, Hitt M. Fungal myelitis caused by *Phialosimplex caninus* in an immunosuppressed dog. Med Mycol. 2012; 50:509–512.



A bone marrow infection caused by *Phialosimplex caninus* was diagnosed in a sevenyear-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. [UAMH 10337]

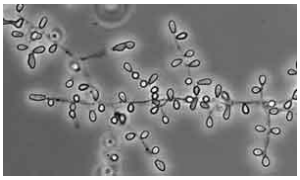
2. Koo S, Sutton DA, Yeh WW, Thompson EH, Sigler L, Shearer JF, Hofstra DE, Wickes BL, Marty FM. Invasive *Mycoleptodiscus* fungal cellulitis and myositis. Med Mycol. 2012; 50:740-745.

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 the conidia were atypical for this species in that they had single septa and occasional lateral appendages. Furthermore, the isolate was different from *M. indicus* based on the sequencing analysis 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 inconsistencies between morphological and molecular data. [UAMH 11158]

3. Iwen PC, Schutte SD, Florescu DF, Noel-Hurst RK, Sigler L. Invasive *Scopulariopsis brevicaulis* infection in an immunocompromised patient and review of prior cases caused by *Scopulariopsis* and *Microascus* species. Med Mycol. 2012; 50:561-569.

Scopulariopsis species and their *Microascus* teleomorphs are cosmopolitan fungi that are uncommonly associated with invasive disease. This report describes a case of fatal 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 proven invasive *Scopulariopsis* (*Microascus*) infections reported in the literature. A focus of this report is the diagnostic methods utilized which included histopathology and culture with both micromorphologic and genotypic procedures employed to confirm the species identification. [UAMH 10915]

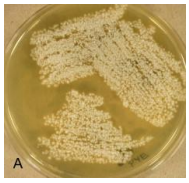
4. Toplon DE, Terrell SP, Sigler L, Jacobson ER. Dermatitis and cellulitis in leopard geckos (*Eublepharis macularius*) caused by the *Chrysosporium* anamorph of *Nannizziopsis vriesii.* Vet Pathol. Epub Nov 2012; doi: 10.1177/0300985812465324.

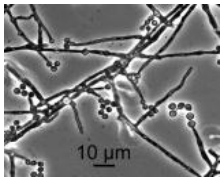


An epizootic of ulcerative to nodular ventral dermatitis was observed in a large breeding colony of 8-month to 5-year-old leopard geckos (*Eublepharis macularius*) of both sexes. Two representative mature male geckos were euthanized for diagnostic necropsy. The *Chrysosporium* anamorph of *Nannizziopsis vriesii* (CANV) was isolated from the skin lesions, and identification was confirmed by sequencing of the internal transcribed spacer region of the rRNA gene. Histopathology revealed multifocal to coalescing dermal and subcutaneous heterophilic granulomas that contained septate fungal hyphae. There was also multifocal epidermal hyperplasia with hyperkeratosis, and similar hyphae were present within the stratum corneum, occasionally with terminal chains of arthroconidia consistent with the CANV. In one case, there was focal extension of granulomatous inflammation into the underlying masseter muscle. This is the first report of dermatitis and cellulitis due to the CANV in leopard geckos. [UAMH 11231, 11232]

Papers In Press or In Review

5. Sigler L, Hanselman B, Ruotsalo K, Tsui KG, Richardson S. Cytological, microbiological and therapeutic aspects of systemic infection in a dog caused by the fungus *Phialosimplex caninus.* Medical Mycology Case Reports. Available online 11 January 2013 http://dx.doi.org/10.1016/j.mmcr.2012.12.007





A seven-year-old immunocompetent dog presenting with lymphadenopathy, mesenteric masses and splenic nodules was diagnosed with *Phialosimplex caninus* infection. Cytology of a mesenteric mass aspirate demonstrated few intact cells but numerous variably sized fungal cells and rare hyphal fragments. The identity of the cultured fungus was confirmed by DNA sequencing. Itraconazole therapy improved clinical signs, but the fungus was reisolated at follow-up. *P. caninus* systemic infection should be suspected in dogs presenting with lymphadenopathy and splenomegaly. [UAMH 11502, 11532]

6. Malejczyk K, Sigler L, Gibas CFC, Smith SS. Invasive sino-orbital mycosis in an aplastic anemia patient caused by *Neosartorya laciniosa.* J Clin Microbiol. (JCM02919-12R1 subm 31-Oct-2012)

We report the first case of *Neosartorya laciniosa* invasive sinusitis involving the orbit in an immunocompromised male with aplastic anemia. Treatment included surgical debridement with enucleation of the eye, combination voriconazole and micafungin therapy followed by voriconazole alone. The fungus was identified using sequencing of beta-tubulin and calmodulin gene regions. [UAMH 11627 isolated from patient at UA Hospitals]

Publications Citing UAMH Cultures or Assistance

7. Adebusuyi AA, Foght JM. The EmhABC efflux pump in *Pseudomonas fluorescens* LP6a is involved in naphthalene tolerance but not efflux. Appl Microbiol Biotechnol. Epub Sep 2012; doi 10.1007/ s00253-012-4373-9.

The EmhABC efflux pump in *Pseudomonas fluorescens* LP6a effluxes polycyclic aromatic hydrocarbons (PAHs) such as phenanthrene and anthracene but not naphthalene. We previously showed that the presence of EmhABC decreased the efficiency of phenanthrene biodegradation. In this study, we determined whether *P. fluorescens* LP6a tolerance to naphthalene is a function of the EmhABC efflux pump and how its presence affects the efficiency of naphthalene biodegradation. Growth, membrane fatty acid (FA) composition, and cell morphology showed that 5-mmolL−1 naphthalene is inhibitory to *P. fluorescens* LP6a strains. The deleterious effect of naphthalene is suppressed in the presence of EmhABC, which suggests that, although naphthalene is not effluxed by EmhABC, this efflux pump is involved in tolerance of naphthalene toxicity. LP6a mutants lacking the EmhB efflux pump were unable to convert cis-unsaturated FAs to cyclopropane FAs, indicating that naphthalene interferes with the formation of cyclopropane FAs and supporting the proposal that EmhABC is involved in FA turnover in *P. fluorescens* LP6a strains. The EmhABC efflux pump increases the efficiency of naphthalene metabolism in strain LP6a, which may make naphthalene efflux unnecessary. Thus, the activity of hydrocarbon efflux pumps may be an important factor to consider when selecting bacterial strains for bioremediation or biocatalysis of PAHs. [UAMH 11620]

8. Adebusuyi AA, Smith AY, Gray MR, Foght JM. The EmhABC efflux pump decreases the efficiency of phenanthrene biodegradation by *Pseudomonas fluorescens* strain LP6a. Appl Microbiol Biotechnol. 2012; 95:757–766.

Pseudomonas fluorescens strain LP6a, designated here as strain WEN (wild-type PAH catabolism, efflux positive), utilizes the polycyclic aromatic hydrocarbon phenanthrene as a carbon source but also extrudes it into the extracellular medium using the efflux pump EmhABC. Because phenanthrene is considered a nontoxic carbon source for *P. fluorescens* WEP, its energy-dependent efflux seems counter-productive. We hypothesized that the efflux of phenanthrene would decrease the efficiency of its biodegradation. Indeed, an emhB disruptant strain, wild-type PAH catabolism, efflux negative (WEN), biodegraded 44% more phenanthrene than its parent strain WEP during a 6-day incubation. To determine whether efflux affected the degree of oxidation of phenanthrene, we quantified the conversion of ^{14}C-phenanthrene to radiolabeled polar metabolites and $^{14}CO_2$. The emhB$^-$ WEN strain produced approximately twice as much $^{14}CO_2$ and radiolabeled water-soluble metabolites as the WEP strain. In contrast, the mineralization of ^{14}C-glucose, which is not a known EmhB efflux substrate, was equivalent in both strains. An early open-ring metabolite of phenanthrene, trans-4-(1-hydroxynaphth-2-yl)-2-oxo-3-butenoic acid, also was found to be a substrate of the EmhABC pump and accumulated in the supernatant of WEP but not WEN cultures. The analogous open-ring metabolite of dibenzothiophene, a heterocyclic analog of phenanthrene, was extruded by EmhABC plus a putative alternative efflux pump, whereas the end product 3-hydroxy-2-formylbenzothiophene was not actively extruded from either WEP or WEN cells. These results indicate that the active efflux of phenanthrene and its early metabolite(s) decreases the efficiency of phenanthrene degradation by the WEP strain. This activity has implications for the bioremediation and biocatalytic transformation of polycyclic aromatic hydrocarbons and heterocycles. [UAMH 11620]

9. Adeleke RA , Cloete TE, Bertrand A, Khasa DP. Iron ore weathering potentials of ectomycorrhizal plants. Mycorrhiza. Epub Feb 2012; doi 10.1007/s00572-012-0431-5.

Plants in association with soil microorganisms play an important role in mineral weathering. Studies have shown that plants in symbiosis with ectomycorrhizal (ECM) fungi have the potential to increase the uptake of mineral-derived nutrients. However, it is usually difficult to study many of the different factors that influence ectomycorrhizal weathering in a single experiment. In the present study, we carried out a pot experiment where *Pinus patula* seedlings were grown with or without ECM fungi in the presence of iron ore minerals. The ECM fungi used included *Pisolithus tinctorius*, *Paxillus involutus*, *Laccaria bicolor* and *Suillus tomentosus*. After 24 weeks,

harvesting of the plants was carried out. The concentration of organic acids released into the soil, as well as potassium and phosphorus released from the iron ore were measured. The results suggest that different roles of ectomycorrhizal fungi in mineral weathering such as nutrient absorption and transfer, improving the health of plants and ensuring nutrient circulation in the ecosystem, are species specific, and both mycorrhizal roots and non-mycorrhizal roots can participate in the weathering process of iron ore minerals. [UAMH 6252, UAMH 8232]

10. Burrough E, Deitz K, Kinyon J, Andreasen C, Frana T, Sutton D, Thompson E, Fu J, Wickese B, Hostetter J. Disseminated aspergillosis in a dog due to *Aspergillus alabamensis*. Medical Mycology Case Reports 2012; 1:1-4.

Disseminated aspergillosis is uncommon in dogs and often associated with *Aspergillus terreus*. A case of disseminated disease in an English springer spaniel is reported from which *Aspergillus alabamensis* was recovered by culture and identified by molecular means suggesting a potential role for this agent as a primary pathogen of dogs. [UAMH 11632]

11. Cariello PF, Wickes BL, Sutton DA, Castlebury LA, Levitz SM, Finberg RW, Thompson EH, Daly JS. *Phomopsis bougainvilleicola* Pre-patellar Bursitis in a Renal Transplant Recipient. J Clin Microbiol. Epub Nov 2012; doi:10.1128/JCM.02674-12.

Pre-patellar bursitis is typically a monomicrobial bacterial infection. Rarely is a fungal cause identified. We describe a 61 year-old man who had received a renal transplant 21 months prior to presentation whose synovial fluid and surgical specimens grew *Phomopsis bougainvilleicola*, a pycnidial coelomycete. [UAMH 11634]

12. Day MJ, Hall JC, Currah RS. Phialide arrangement and character evolution in the helotialean anamorph genera *Cadophora* and *Phialocephala*. Mycologia. 2012; 104:371-81.

The dematiaceous hyphomycete genera *Cadophora* and *Phialocephala* are anamorphs associated with mollisioid 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 might 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 respectively to *Cadophora* and *Phialocephala*. [UAMH 1221, 5422]

13. Dela Cruz WP, Calvano TP, Griffith ME, White CE, Kim SH, Sutton DA, Thompson EH, Fu J, Wickes BL, Guarro J, Hospenthal DR. Invasive *Apophysomyces variabilis* infection in a burn patient. J Clin Microbiol 2012;50:2814-7

Apophysomyces variabilis is an emerging fungal pathogen that can cause significant infection in immunocompetent patients. We report a case of *A. variabilis* invasive wound infection in a 21-year-old male after a self-inflicted burn injury. [UAMH 11571]

14. Doyon JB, Sutton DA, Theodore P, Dhillon G, Jones KD, Thompson EH, Fu J, Wickes BL, Koehler JE, Schwartz BS. *Rasamsonia argillacea* pulmonary and aortic graft infection in an immune competent patient. J Clin Microbiol. Epub Dec 2012; doi: 10.1128/JCM.02884-12.

Rasamsonia argillacea (formerly known as *Geosmithia argillacea*) is a fungus recently recognized as a pathogen of immunocompromised patients. Here we report the first case of *Rasamsonia* infection in an immunocompetent host presenting as a pulmonary and aortic graft infection. Its morphological similarity to nonpathogenic *Penicillium* species delayed the diagnosis and initiation of appropriate treatment. [UAMH 11662, 11663]

15. Duo A, Bruggmann R, Zoller S, Bernt M, Grünig CR. Mitochondrial genome evolution in species belonging to the *Phialocephala fortinii* s.l. - *Acephala applanata* species complex. BMC Genomics. 2012; 13:166 doi:10.1186/1471-2164-13-166.

Background: Mitochondrial (mt) markers are successfully applied in evolutionary biology and systematics because mt genomes often evolve faster than the nuclear genomes. In addition, they allow robust phylogenetic analysis based on conserved proteins of the oxidative phosphorylation system. In the present study we sequenced and annotated the complete mt genome of *P. subalpina*, a member of the *Phialocephala fortinii* s.l. – *Acephala applanata* species complex (PAC). PAC belongs to the Helotiales, which is one of the most diverse groups of ascomycetes including more than 2,000 species. The gene order was compared to deduce the mt genome evolution in the Pezizomycotina. Genetic variation in coding and intergenic regions of the mtDNA was studied for PAC to assess the usefulness of mt DNA for species diagnosis. Results: The mt genome of *P. subalpina* is 43,742 bp long and codes for 14 mt genes associated with the oxidative phosphorylation. In addition, a GIY-YIG endonuclease, the ribosomal protein S3 (*Rps3*) and a putative N-acetyl-transferase were recognized. A complete set of tRNA genes as well as the large and small rRNA genes but no introns were found. All protein-coding genes were confirmed by EST sequences. The gene order in *P. subalpina* deviated from the gene order in *Sclerotinia sclerotiorum*, the only other helotialean species with a fully sequenced and annotated mt genome. Gene order analysis within Pezizomycotina suggests that the evolution of gene orders is mostly driven by transpositions. Furthermore, sequence diversity in coding and non-coding mtDNA regions in seven additional PAC species was pronounced and allowed for unequivocal species diagnosis in PAC. Conclusions: The combination of non-interrupted ORFs and EST sequences resulted in a high quality annotation of the mt genome of *P. subalpina,* which can be used as a reference for the annotation of other mt genomes in the Helotiales. In addition, our analyses show that mtDNA loci will be the marker of choice for future analysis of PAC communities. [UAMH 11012, 11659]

16. el Feghaly RE, Sutton DA, Thompson EH, Fu J, Wickes BL, Al-Zubeidi D, Storch GA, Burnham CD. *Graphium basitruncatum* fungemia in an immunosuppressed child post stem-cell transplantation. Medical Mycology Case Reports. 2012; 1:35–8.

Graphium basitruncatum is genetically and morphologically distinct from other *Graphium* and *Scedosporium* species, and has been reported only once previously as a cause of human disease. We report a case of *Graphium basitruncatum* fungemia in a two year old child with dyskeratosis congenita who underwent stem cell transplantation two months prior to infection. [UAMH 10611, 11332]

17. Fairs A, Agbetile J, Bourne M, Hargadon B, Monteiro WR, Morley JP, Edwards RE, Wardlaw AJ, Pashley CH. Isolation of *Aspergillus fumigatus* from sputum is associated with elevated airborne levels in homes of patients with asthma. Indoor Air. Epub Nov 2012; doi: 10.1111/ina.12020.

Indoor bioaerosols, such as mold spores, have been associated with respiratory symptoms in patients with asthma; however, dose-response relationships and guidelines on acceptable levels are lacking. Furthermore, a causal link between mold exposure and respiratory infections or asthma remains to be established. The aim of this study was to determine indoor concentrations of *Aspergillus fumigatus* and a subset of clinically relevant fungi in homes of people with asthma, in relation to markers of airways colonization and sensitization. Air and dust samples were collected from the living room of 58 properties. Fungal concentrations were quantified using mold-specific quantitative PCR and compared with traditional microscopic analysis of air samples. Isolation of *A. fumigatus* from sputum was associated with higher airborne concentrations of the fungus in patient homes (P = 0.04), and a similar trend was shown with *Aspergillus*/*Penicillium*-type concentrations analyzed by microscopy (P = 0.058). No association was found between airborne levels of *A. fumigatus* and sensitization to this fungus, or dustborne levels of *A. fumigatus* and either isolation from sputum or sensitization. The results of this study suggest that the home environment should be considered as a potential source of fungal exposure and elevated home levels may predispose people with asthma to airways colonization. [UAMH 7863 as internal reference]

18. Galgoczy L, Viragh M, Kovacs L, Toth B, Papp T, Vagvolgyi C. Antifungal peptides homologous to the *Penicillium chrysogenum* antifungal protein (PAF) are widespread among *Fusaria*. Peptides. Epub Nov 2012; doi: 10.1016/j.peptides.2012.10.016.

Putative antifungal peptide encoding genes containing *Penicillium chrysogenum* antifungal protein (PAF) characteristic amino acid motifs were identified in 15 *Fusarium* isolates, representing 10 species. Based on the predicted sequences of mature peptides, discrepancy in one, two or three amino acids was observed between them. Phylogenetic investigations revealed that they show high amino acid sequence similarity to PAF and they belong to the group of fungal derived antifungal peptides with PAF-cluster. Ten from the 15 partially purified <10kDa peptide fraction of *Fusarium* ferment broths showed antifungal activity. The presence of approximately

6.3kDa molecular weight peptides was detected in all of the antifungally active ferment broths, and this peptide was isolated and purified from *Fusarium polyphilaidicum*. The minimal inhibitiory concentrations of *F. polyphilaidicum* antifungal protein (FPAP) were determined against different filamentous fungi, yeasts and bacteria. Filamentous fungal species were the most susceptible to FPAF, but some yeasts were also slightly sensitive. [UAMH 7955]

19. Ghasemian E, Naghoni A, Tabaraie B, Tabaraie T. In vitro susceptibility of filamentous fungi to copper nanoparticles assessed by rapid XTT colorimetry and agar dilution method. J Med Microbiol. 2012; 22:322-8.

Objective: Metal nanoparticles and their uses in various aspects have recently drawn a great deal of attention. One of the major applications is that it can be used as an antimicrobial agent. They can be considered in approaches targeted to decrease the harms caused by microorganisms, specifically fungi, threatening the medical and industrial areas. The aim of this study was to investigate the antifungal activity of synthesized copper nanoparticles (CuNPs) against four filamentous fungi including *Alternaria alternata*, *Aspergillus flavus*, *Fusarium solani*, and *Penicillium chrysogenum*. Material and methods: Zerovalent copper nanoparticles of mean size 8 nm were synthesized by inert gas condensation (IGC) method. The antifungal activity of these synthesized copper nanoparticles was measured against selected fungi by using two different techniques including agar dilution method and XTT reduction assay. Results: The minimal inhibitory concentrations (MICs) for copper nanoparticles by agar dilution method were less or equal to 40 mg/L for *P. chrysogenum*, less or equal to 60 mg/L for *A. alternata*, less or equal to 60 mg/L for *F. solani*, and less or equal to 80 mg/L for *A. flavus*. And also MICs obtained by XTT reduction assay ranged from 40 to 80 mg/L. Conclusion: Our data demonstrated that the copper nanoparticles inhibited fungal growth, but the fungal sensitivity to copper nanoparticles varies depending on the fungal species. Therefore, it is advisable that the minimal inhibitory concentrations (MICs) be examined before using these compounds. It is hoped that, in future, copper nanoparticles could replace some antifungal agents, making them applicable to many different medical devices and antimicrobial control system. [UAMH 3317]

20. Girard M, Viens P, Ramirez AA, Brzezinski R, Buelna G, Heitz M. Simultaneous treatment of methane and swine slurry by biofiltration. J Chem Technol Biotechnol. 2012; 87:697-704.

BACKGROUND: The piggery industry is important both worldwide and in Canada, but localized production of large quantities of swine slurry causes severe environmental problems such as aquatic pollution and greenhouse gas emissions. The main objective of this study was to determine whether it is possible to simultaneously treat methane (CH4) and swine slurry using an inorganic biofilter. RESULTS: A novel biofilter was designed to overcome the inhibition of CH4 biodegradation by swine slurry. The CH4 elimination capacity increased with the inlet load and a maximum value of 18.8 ± 1.0 g m−3 h−1 was obtained at an inlet load of 46.7 ± 0.9 g m−3 h−1 and a CH4 concentration of 3.3 g m−3. Four pure strains of fungi were used in an attempt to improve the removal of CH4, but no significant effect was observed. Between 0.35 and 3.4 g m−3, the CH4 concentration had no effect on swine slurry treatment with removal efficiencies of 67 ± 10% for organic carbon and 70 ± 7% for ammonium. The influence of the slurry supply was analyzed and the best results were obtained with a supply method of six doses of 50 mL per day. CONCLUSION: Even though the results were lower than those obtained for the biofiltration of CH4 alone, this study demonstrated the feasibility of treating CH4 and swine slurry with the same biofilter using a novel design. [UAMH 4521, 7369, 10067]

21. Gordon RA, Sutton DA, Thompson EH, Shrikanth V, Verkley GJ, Stielow JB, Mays R, Oleske D, Morrison LK, Lapolla WJ, Galfione S, Tyring S, Samathanam CA, Fu J, Wickes BL, Mulanovich V, Wanger A, Arias CA. Cutaneous phaeohyphomycosis caused by *Paraconiothyrium cyclothyrioides*. J Clin Microbiol. 2012; 50:3795-8.

Paraconiothyrium cyclothyrioides is a recently described coelomycetous fungal species. We present a case in a renal transplant patient with chronic skin lesions of the lower extremities caused by *P. cyclothyrioide*s. Treatment with posaconazole led to complete resolution of the lesions. *P. cyclothyrioides* should be considered an opportunistic human pathogen in immunocompromised patients. [UAMH 11641]

22. Hamiduzzaman MM, Sinia A, Guzman-Novoa E, Goodwin PH. Entomopathogenic fungi as potential biocontrol agents of the ecto-parasitic mite, *Varroa destructor*, and their effect on the immune response of honey bees (*Apis mellifera* L.). J Invertebr Pathol. 2012; 111:237-43.

Three isolates of each of the entomopathogenic fungi, *Metarhizium anisopliae*, *Beauveria bassiana* and *Clonostachys rosea*, were assessed for their pathogenicity to the honey bee parasitic mite, *Varroa destructor*. The fungi were applied to varroa mites by immersing them in a spore solution, and then the inoculated mites were placed on honey bee brood inside capped cells. At 7 days post inoculation (dpi), the three fungi caused significant varroa mortality compared to non-inoculated mites. In brood treated only with varroa mites, expression of the honey bee genes, hymenoptaecin and poly U binding factor 68 Kd (pUf68), decreased over time, while expression of

blue cheese (BlCh) and single minded (SiMd) was not affected. In brood inoculated directly only with *M. anisopliae* or *B. bassiana*, the emerged adults showed reduced weight indicating infection by the fungi, which was confirmed by observation of hyphae in the brood. Fungal infection of the brood resulted in increased expression of hymenoptaecin, pUf68 and BlCh, but not SiMd. In brood treated with varroa mites that had been inoculated with the fungi, expression of hymenoptaecin, pUf68 and BlCh, but not SiMd, was even more up-regulated. While varroa mites can suppress gene expression in honey bee brood, varroa mites infected with entomopathogenic fungi induced their expression. This may be due to a low level of fungal infection of the bee, which negated the immunosuppression by the mites. Therefore, entomopathogenic fungi could reduce varroa mite damage to honey bee brood by both infecting the parasite and preventing varroa-associated suppression of honey bee immunity. [UAMH 1069, 4450, 7494, 9161, 9197, 9198, 9748]

23. Jurjevic Z, Peterson SW, Horn BW. *Aspergillus* section *Versicolores*: nine new species and multilocus DNA sequence based phylogeny. IMA Fungus 3(1):59–79 doi:10.5598/imafungus.2012.03.01.07

β-tubulin, calmodulin, internal transcribed spacer and partial lsu-rDNA, RNA polymerase 2, DNA replication licensing factor *Mcm7*, and pre-rRNA processing protein *Tsr1* were amplified and sequenced from numerous isolates belonging to *Aspergillus* sect. *versicolor.* The isolates were analyzed phylogenetically using the concordance model to establish species boundaries. *Aspergillus austroafricanus, A. creber, A. cvjetkovicii, A. fructus, A. jensenii, A. puulaauensis, A. subversicolor, A. tennesseensis* and *A. venenatus* are described as new species and *A. amoenus, A. protuberus, A. sydowii, A. tabacinus* and *A. versicolor* are accepted as distinct species on the basis of molecular and phenotypic differences. PCR primer pairs used to detect *A. versicolor* in sick building syndrome studies have a positive reaction for all of the newly described species except *A. subversicolor*. [UAMH 7651]

24. Lah L, Haridas S, Bohlmann J, Breuil C. The cytochromes P450 of *Grosmannia clavigera*: Genome organization, phylogeny, and expression in response to pine host chemicals. Fungal Genet Biol 2013; 50:72-81

Grosmannia clavigera is a fungal associate of the mountain pine beetle (*Dendroctonus ponderosae*) and pathogen of lodgepole pine (*Pinus contorta*) that must overcome terpenoid oleoresin and phenolic defenses of host trees. G. clavigera responds to monoterpene influx with complementary mechanisms that include export and the use of these compounds as a carbon source. Cytochromes P450 (CYPs) may also be involved in the metabolism of host defense compounds. We have identified and phylogenetically classified *G. clavigera* CYPs (CYPome). We show that although the *G. clavigera* CYPome has contracted in evolution, certain CYP families have expanded by duplication. We analyzed RNA-seq data for CYP expression following treatment with terpenes and pine phloem extracts to identify CYPs potentially involved in detoxification of these pine defense compounds. We also used transcriptome analysis of G. *clavigera* grown on monoterpenes, triglycerides or oleic acid as a carbon source to identify up-regulated CYPs that may be involved in the utilization of these compounds to support fungal growth. Finally, we identify secondary metabolite biosynthetic gene clusters that contain CYPs, and CYPs in clusters that may be involved in conversion of host chemicals. (UAMH 11150 =KW1407=SLKW1407 =NCBI Taxonomy ID: 655863).

25. Madden AA, Stchigel AM, Guarro J, Sutton D, Starks PT. *Mucor nidicola* sp. nov., a fungal species isolated from an invasive paper wasp nest. Int J Syst Evol Microbiol. 2012; 62:1710-4.

A strain of a novel mucoralean fungus was isolated from a nest of the invasive paper wasp, *Polistes dominulus*. Phylogenetic analysis based on the internal transcribed spacer (ITS) regions and 5.8S rRNA gene sequences, along with physiological tests, revealed that this strain represents a novel species within the genus *Mucor*. The novel species also includes a representative that had previously been characterized as part of the *Mucor 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 propose the novel species *Mucor nidicola* sp. nov. to accommodate the isolate; the type strain of *M. nidicola* is F53(T) (=NRRL 54520(T)=UAMH 11442(T)=CBS 130359(T)). [UAMH 11442 Holotype] [Epub in 2011 report]

26. Mahmud A, Lee R, Munfus-McCray D, Kwiatkowski N, Subramanian A, Neofytos D, Carroll K, Zhang SX. *Actinomucor elegans* as an emerging cause of Mucormycosis. J Clin Microbiol. 2012; 50:1092-5.

We report an invasive mucormycosis caused by *Actinomucor elegans* in a patient with refractory aplastic anemia. The organism was isolated from a necrotic skin lesion on the patient's left arm and demonstrated angioinvasive features on histopathology examination. In contrast to three cases described previously, we describe the first case of *A. elegans* invasive fungal infection in an immunocompromised patient. This report, along with the three previously reported cases, is convincing evidence that *A. elegans* is an emerging fungal pathogen capable of causing invasive mucormycosis in humans. [UAMH 11617]

27. McMullin DR, Sumarah MW, Miller JD. Chaetoglobosins and azaphilones produced by Canadian strains of *Chaetomium globosum* isolated from the indoor environment. Mycotoxin Research. Epub Oct 2012; doi: 201210.1007/s12550-012-0144-9.

Chaetomium globosum is one of the most common species of fungi found growing on damp building materials in North America and Europe. At doses that could be experienced in a building with some mould damage, exposure to metabolites from other fungi results in inflammatory changes in vivo and in vitro. This research requires knowledge of the dominant toxins produced by fungal strains from the built environment and characterization of pure compounds for toxicity testing. We examined 25 strains of *C. globosum* isolated from the built environment in Canada. In varying amounts, these strains primarily produced chaetoglobosin A, C and F, chaetomugilin D, and chaetoviridin A. Spectroscopic data of the major isolated compounds are provided. Previous studies reported a number of metabolites from this species that we did not find. However, this appears to be due to misidentifications of the fungi they examined as well as problems with the analytical methods used. In addition, our data support the use of metabolite profiles for resolving the taxonomy of some economically important *Chaetomium* species. [UAMH 7142, 7773]

28. Miller SA, Roth-Johnson L, Kania SA, Bemis DA. Isolation and sequence-based identification of *Oxyporus corticola* from a dog with generalized lymphadenopathy. J Vet Diagn Invest. 2012; 24:178-81.

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 differentiation from other fungal pathogens. Risk factors for infection with *O. corticola* are unknown. [UAMH 11535] [Epub in 2011 report]

29. Queloz V, Duo A, Sieber TN, Grünig CR. Microsatellite size homoplasies and null alleles do not affect species diagnosis and population genetic analysis in a fungal species complex. Mol Ecol Resour 2010; 10:348-367.

The suitability of 13 microsatellite loci for species diagnosis and population genetics in 11 species of the *Phialocephala fortinii* s.l.-*Acephala applanata* species complex (PAC) was assessed. Two data sets were compared to test possible biases in species typing and clone detection resulting from null alleles and size homoplasies. The first data set was based on fragment lengths derived from a multiplex polymerase chain reaction (PCR) assay and the second data set was received from singleplex PCR at lower stringency and sequencing. Most null alleles observed in the multiplex PCR assay could be amplified during singleplex PCR under less stringent conditions. Size homoplasies resulting from mutations in flanking regions and differences in microsatellite structures were observed. For example, *Phialocephala uotolensis* possessed a (CT)(13) in addition to the (GT)(x) motif at locus mPF_0644. Despite the occurrence of null alleles and size homoplasies, species diagnosis and population genetic analysis studies were not affected. These markers will facilitate studies on population biology, ecology and biogeography of PAC species. [UAMH 11659]

30. Pedras MS, Sarma-Mamillapalle VK. Metabolism and metabolites of dithiocarbamates in the plant pathogenic fungus *Leptosphaeria maculans*. J Agric Food Chem. 2012; 60:7792-8.

Synthetic compounds containing a dithiocarbamate group are known to have a variety of biological effects and applications including antifungal, herbicidal, and insecticidal application. *Leptosphaeria maculans* is a fungal pathogen of crucifers able to detoxify efficiently the only plant natural product containing a dithiocarbamate group, the phytoalexin brassinin. To evaluate the effects of dithiocarbamates on *L. maculans*, a number of structurally diverse S-methyl dithiocarbamates containing indolyl, biphenyl, and benzimidazolyl moieties were synthesized, and their antifungal activities and metabolism by *L. maculans* were investigated. All dithiocarbamates were transformed by *L. maculans* through hydrolysis to the corresponding amines, which were less antifungal than the parent compounds. Two dithiocarbonates were shown to be much less antifungal than the corresponding dithiocarbamates. Results of this investigation indicate that S-methyl dithiocarbamates are not useful inhibitors of *L. maculans* and that their rates of transformation by *L. maculans* did not correlate with the antifungal activity of the particular compound. [UAMH 9410]

31. Pedras MS, Sarma-Mamillapalle VK. The cruciferous phytoalexins rapalexin A, brussalexin A and erucalexin: chemistry and metabolism in *Leptosphaeria maculans*. Bioorg Med Chem. 2012; 20:3991-6.

The interactions of the cruciferous phytoalexins rapalexin A (1), brussalexin A (2) and erucalexin (3) with the fungal

plant pathogen *Leptosphaeria maculans* were analyzed and their inhibitory activities against this pathogen were determined. The reaction of *L. maculans* to N-methyl S-(indolyl-3-methyl)carbamodithioate, an analogue of brussalexin A, was also investigated. Rapalexin A was resistant to metabolism and was the most inhibitory of all compounds tested, suggesting that increasing concentrations of rapalexin A in *Brassica* species would improve their disease resistance to *L. maculans*. By contrast, erucalexin was quickly detoxified by reduction to yield 3-dihydroerucalexins. The relative configurations of the diastereomeric mixture of dihydroerucalexins were established by 1D (1)H nuclear Overhauser enhancement spectroscopy (NOE). Brussalexin A was chemically unstable decomposing mainly to indolyl-3-methanol, a product with anti-cancer properties. For this reason, brussalexin A might be of interest to use as a prodrug. [UAMH 9410]

32. Pedras MS, Khallaf I. Molecular interactions of the phytotoxins destruxin B and sirodesmin PL with crucifers and cereals: metabolism and elicitation of plant defenses. Phytochemistry. 2012; 77:129-39.

Destruxin B and sirodesmin PL are phytotoxins produced by the phytopathogenic fungi *Alternaria brassicae* (Berk.) Sacc. and *Leptosphaeria maculans* (asexual stage *Phoma lingam*), respectively. The molecular interaction of destruxin B and sirodesmin PL with cruciferous and cereal species was investigated using HPLC-ESI-MS(n). It was determined that crucifers transformed destruxin B to hydroxydestruxin B, but sirodesmin PL was not transformed. Overall, the results suggest that the five cruciferous species *Arabidopsis thaliana*, *Thellungiella salsuginea*, *Erucastrum gallicum*, *Brassica rapa* and *Brassica napus* are likely to produce a destruxin B detoxifying enzyme (destruxin B hydroxylase), similar to other cruciferous species reported previously. In addition, HPLC analyses and quantification of the phytoalexins elicited in each cruciferous species by these phytotoxins indicates that sirodesmin PL elicits a larger number of phytoalexins than destruxin B. Interestingly, transformation of destruxin B appears to occur also in the cereals *Avena sativa* and *Triticum aestivum*; however, the various destruxin metabolites detected in these cereals suggest that these reactions are non-specific enzymatic transformations, contrary to those observed in crucifers, where only a main transformation pathway is detectable. None of the toxins appear to elicit production of metabolites in either *A. sativa* or *T. aestivum*. [UAMH 4936, UAMH 9410]

33. Provost NB, Shi C, She YM, Cyr TD, Miller JD. Characterization of an antigenic chitosanase from the cellulolytic fungus *Chaetomium globosum*. Med Mycol. Epub Sep 2012; doi:10.3109/13693786.2012.715246.

We are interested in identifying human fungal allergens and antigens from species common on water-damaged or damp building materials for use as marker proteins and diagnostic tests. The cellulolytic fungus *Chaetomium globosum* is common on damp materials in the building environment worldwide. ELISA and immunoblotting tests identified two related proteins of molecular weights 45 and 47 kDa which were identified as fungal antigens found on spore surfaces and in culture filtrate. The sequences were determined by liquid chromatography tandem mass spectrometry (LC-MS/MS), which indicated that the two proteins were chitosanases, confirmed by enzyme assay. The 47 kDa protein was not glycosylated and had an acidic pI of 4.5. These proteins have not been reported from other fungi and similar antigens were not seen in other fungi common in buildings. The production of polyclonal antibodies in rabbits showed the antigenicity of the target proteins and confirmed they were not artifacts of the isolation process. The proteins isolated are useful biomarkers for the detection of *C. globosum* in the building environment. [UAMH 7142, 7773]

34. Robert T, Talarmin JP, Leterrier M, Cassagnau E, Le Pape P, Danner-Boucher I, Malard O, Brocard A, Gay-Andrieu F, Miegeville M, Morio F. Phaeohyphomycosis due to *Alternaria infectoria*: a single-center experience with utility of PCR for diagnosis and species identification. Med Mycol. 2012; 50:594-600.

The term phaeohyphomycosis refers to a rare group of fungal infections characterized by the presence of dark-walled hyphae or yeast-like cells in affected tissues. Herein, we report on the clinical and epidemiological characteristics of six cases of phaeohyphomycosis due to *Alternaria* spp. that occurred in our hospital over a 30-month period (from January 2008 to June 2010). Interestingly, whereas histopathological examinations were positive and fungal cultures yielded molds in all cases, mycological identification using conventional phenotypic methods was never possible despite prolonged incubation of the isolates. Identification of *Alternaria infectoria* species complex was obtained for each isolate by amplification and sequencing of the internal transcribed spacer of the ribosomal DNA (ITS rDNA). All patients had favourable outcomes following the introduction of azole-based antifungal therapy. This case series describes the clinical course of these six patients and highlights the utility of molecular identification to help in the identification of the etiologic agent when classical mycological methods have failed. [UAMH 11629, 11630]

35. Robinson SC, Tudor D, Snider H, Cooper PA. Stimulating growth and xylindein production of *Chlorociboria aeruginascens* in agar-based systems. AMB Express. 2012; 2:15-21.

Four isolates of *Chlorociboria aeruginascens* were tested for possible stimulatory effects when grown on malt agar media containing wood additives. The addition of any of the four types of test wood (*Acer saccharum*, *Populus tremuloides*, spalted *P. tremuloides*, and *Ailanthus altissima*), stimulated colony growth and xylindein production in *C. aeruginascens*. Addition of any amount of wood produced more growth than no wood additions, while ground wood produced more growth than chopped wood. Of the wood types tested, *A. saccharum* wood stimulated all four isolates, while spalted *Populus tremuloides* stimulated three of the four isolates. High glucose and sucrose amounts may be partially responsible for the greater stimulatory affect of some woods over others. The development of this simple and reliable method for growth and pigment stimulation of *C. aeruginascens* in laboratory conditions will allow for further development of this fungus for decorative and commercial use. [UAMH 7614, 7615, 11655]

36. Robinson SC, Tudor D, Mansourian Y, Cooper PA. The effects of several commercial wood coatings on the deterioration of biological pigments in wood exposed to UV light. Wood Sci Technol. Epub Sep 2012; doi: 10.1007/s00226-012-0502-y.

This research subjected four wood species pigmented with the red stain of *Scytalidium cuboideum* and *Acer negundo* wood pigmented with the tree's naturally occurring red stain to natural and artificial UV light. Several commercially available coatings were applied to determine the effect of coating on the degradation of both red stains over time. The red stain of *Acer negundo* was found to be significantly less stable in UV light than the red pigment produced by *S. cuboideum* on any wood species, even *A. negundo*. None of the tested coatings significantly increased the pigment retention time of the red stain produced by *A. negundo*. The red stain of *S. cuboideum* was significantly affected by both coating and wood species; *Populus tremuloides* retained pigment significantly longer than *Fagus grandifolia* or *Acer saccharum*, and the Danish oil coating retained pigment significantly longer than the lacquer, water-based polyurethane with UV inhibitors, or the uncoated samples. Overall, lacquer increased the degradation rate of the red pigment produced by *S. cuboideum*, with the most pronounced increase occurring on *F. grandifolia*. These results indicate that the red-pigmented wood produced by *A. negundo* may not be appropriate for applications involving UV exposure, regardless of coating utilized. However, *P. tremuloides* wood pigmented with *S. cuboideum* may be appropriate for such applications, especially if Danish oil is applied. [UAMH 4802]

37. Robles-Vargas D, Montoya-Castillo SM, Avelar-González FJ, Jauregui-Rincón J, Rodríguez-Valadez FJ, Rico-Martínez R. Assessment of the quality and toxicity of the discharges of a wastewater treatment plant and alternatives to improve its operation. J Environ Sci Health A Tox Hazard Subst Environ Eng. 2012; 47:589-97.

Wastewater discharges into freshwater bodies represent a serious ecological problem worldwide. In underdeveloped and developing countries wastewater treatment plants (WTP) only count with basic treatment, leading to the pollution of important aquatic reservoirs causing critical situations. In the present work, a one year evaluation of toxicity and main physical and chemical parameters of one of the major WTP of the state of Aguascalientes was conducted fortnightly, and to assess treatment alternatives for this WTP we tested: a) three white rot fungi (WRF), b) a photo-electrochemical process, c) ion-exchangers resins and activated carbon. The 3 WRF exhibited high COD removal from influents (72 - 95 %) but only *Phanerochaete chrysosporium* reached significant toxicity removals (70 and 55 %, for an influent and an effluent, respectively). Treatments with electrochemical advanced oxidation processes resulted with the highest toxicity and COD removals (96 % for both parameters) in comparison to biological and physicochemical treatments. Adsorption with activated carbon, zeolite and chelex ion-exchange resins removed 60 - 90 % of COD and 60 - 99 % toxicity. These results could be used to improve operation of the Industrial Park WTP and to plan future modifications to the plant. [UAMH 3641, 7982, 8272]

38. Steevensz A, Al-Ansari MM, Taylor KE, Bewtra JK, Biswas N. Oxidative coupling of various aromatic phenols and anilines in water using a laccase from *Trametes villosa* and insights into the 'PEG effect'. J Chem Technol Biotechnol. 2012; 87:21–32.

BACKGROUND: Studies with peroxidases (EC 1.11.1.7) have demonstrated extended lifetimes for conversion of phenolics into insoluble polymers in the presence of polyethylene glycol (PEG). Yet the mechanism of this 'PEG effect' has eluded investigators. The effectiveness of a laccase (EC 1.10.3.2) with PEGs of various average molar masses on the conversion of phenol, o-, m-, p-cresols, aniline, o-, m-, and p-toluidines was investigated. This structure-activity comparison, with and without the additive, could provide further insight into the 'PEG effect'. RESULTS: The 'PEG effect' was observed only with the cresols and only with PEGs of average molar mass ≥ 1450. Other additives capable of H-bonding, such as polyvinylpyrrolidone, had similar results. When a 'PEG effect' was observed there was a linear relationship between the amount of additive used and the amount incorporated into the precipitate, suggesting a strong interaction between products and PEG, which was confirmed by nuclear magnetic resonance spectroscopy. Optimum pH was not affected by the quantity or molar mass of the PEG added.

CONCLUSION: PEG only enhances the laccase-catalyzed oxidative coupling of certain substrates implying a product-additive relationship that may be related to the functionality and substituent positioning of the substrate. [UAMH 4103, 10067]

39. Tellenbach C, Sumarah MW, Grünig CR, Miller JD. Inhibition of *Phytophthora* species by secondary metabolites produced by the dark septate endophyte *Phialocephala europaea.* Fungal Ecology. Epub Dec 2012; doi: 10.1016/j.funeco.2012.10.003.

Dark septate fungal root endophytes of the *Phialocephala fortinii* s.l.–*Acephala applanata* species complex (PAC) are widely distributed throughout the temperate and subtropical regions of the Northern Hemisphere. Previous studies have shown that some PAC members are pathogenic, others suppress oomycete root pathogens and some have no obvious effect on their Norway spruce (*Picea abies*) host. The activity of 85 PAC isolates against *Phytophthora citricola* s.l. was investigated by co-culture on plates. We identified a strain of *Phialocephala europaea* that significantly reduced the growth of *P. citricola in vitro*. Characterization of its extracellular metabolites resulted in the identification of four major compounds, sclerin, sclerolide, sclerotinin A, and sclerotinin B. These compounds are known for their positive as well as negative effects on plant growth. We found that sclerin and sclerotinin inhibited the growth of *P. citricola in vitro* at 150 µg ml^{-1} (~1 mM). This is the first report of their production by *Phialocephala* and of activity of these compounds against an oomycete. Therefore, our data suggest that some PAC might reduce disease resulting from *P. citricola* by the production of antibiotics and plant growth promoting metabolites. [UAMH 11659]

40. Vanderwolf K. Characterizing the winter bat population, microclimate, and mycobiota of hibernating bats in New Brunswick caves. M.Sc. Thesis, The University of New Brunswick, May 2012.

Little is known regarding the overwintering population and hibernaculum conditions of bats in New Brunswick. The predicted arrival of white-nose syndrome (WNS), an invasive pathogen associated with the fungus *Geomyces destructans*, emphasized the need to establish population estimates and the fungal community on overwintering bats before WNS arrival. Known hibernacula were surveyed in autumn-spring 2009-2011 and the mycology of a sample of bats from each site was determined. The majority of hibernating bats in New Brunswick caves and mines are *Myotis lucifugus* and *M. septentrionalis*, with low numbers of *Perimyotis subflavus*. The New Brunswick hibernacula that appear to be preferred by these species have little temperature variation and average winter dark zone temperatures of 4-5°C. A total of 118 fungal species were recorded from the fur and skin of apparently healthy hibernating bats. The fungi include a core group of nine commonly-isolated taxa, and a larger secondary group, often with rare species occurring in a single sample. Less than 25 taxa had been recorded in the two previous studies on bat mycology worldwide and my work suggests that the fungal community associated with wintering bats is more diverse and complex than believed. *Geomyces destructans* was not recorded, but the isolation of *G. pannorum* sensu lato from 70% of hibernating bats sampled may complicate diagnostics for *G. destructans* in other studies. WNS was first documented in New Brunswick in March 2011, and resulted in catastrophic declines in overwintering bats in the province. (UAMH 11121, 11159-11164, 11182-11184, 11236-11251, 11296-11329, 11334-11345, 11379-11400, 11408-11436, 11438-11478, 11492-11496, 11499-11500, 11504-11516, 11528, 11529, 11594-11614, 11618, 11619, 11621-11626, 11639, 11642).[Total UAMH accessions from this study = 237].

41. Vujanovic V, Goh YK. qPCR quantification of *Sphaerodes mycoparasitica* biotrophic mycoparasite interaction with *Fusarium graminearum*: in vitro and *in planta* assays. Arch Microbiol. 2012; 194:707-17.

Sphaerodes mycoparasitica, a biotrophic mycoparasite of *Fusarium* species, improved wheat seed germination and seedling growth in vitro compared to *Trichoderma harzianum*, a necrotrophic mycoparasite. However, under phytotron conditions, both *S. mycoparasitica* and *T. harzianum* had positive impact on wheat seedlings growth in the presence of *F. graminearum*. Once exposed to the mycoparasites, the DNA quantity of *F. graminearum* in wheat root decreased. Observed shifts in DNA quantity using qPCR, a set of newly designed *Sphaerodes*-specific SmyITS primers, as well as *Trichoderma*-TGP4 and *Fusarium*-Fg16 N primers, demonstrated the mycoparasite's biocontrol effectiveness *in planta*. In the presence of *F. graminearum*, the concentration of *S. mycoparasitica* DNA remained stable in the root, whereas the amount of *T. harzianum* DNA decreased. The toxicity assays indicated that *S. mycoparasitica*'s mycelia withstand higher concentrations of deoxynivalenol, 3-acetyldeoxynivalenol, and zearalenone mycotoxins than *T. harzianum* mycelia. This study compares the ability of two fungi to improve the wheat growth, decrease the root colonization of *Fusarium*, and withstand mycotoxins. [UAMH 5512, 9089, 10033]

42. Zaffarno PL, Duo A, Grünig CR, Characterization of the mating type (MAT) locus in the *Phialocephala fortinii* s.l. - *Acephala applanata* species complex. Fungal Genet Biol 2010; 47(9):761-72. doi: 10.1016/j.fgb.**2010**.06.001.

Members of the *Phialocephala fortinii* sensu lato -*Acephala applanata* species complex (PAC) are the dominant root endophytes of woody plants in temperate and boreal forests. In the present study, the mating type (MAT) idiomorphs of eight species belonging to the PAC were cloned. Because direct cloning of MAT idiomorphs was not possible, species phylogenetically placed between the PAC and other helotialean species with characterized MAT locus were used for an intermediate cloning step. Whereas *A. applanata* showed a homothallic organization structure of the MAT locus, all other species either contained the MAT1-1 or MAT1-2 idiomorph indicative of heterothallism. A Tc1-like transposable element was found within the MAT locus of *A. applanata*. Analysis of *A. applanata* strains collected over a broad geographical range showed that the transposable element was present in all *A. applanata* strains, suggesting an ancient transposition event. Moreover, a partial MAT1-1-1 gene was identified within MAT1-2 idiomorphs, a common phenomenon in the order Helotiales. However, this partial gene was not fixed in all populations of the species. The evolution of the MAT locus with regard to different mating systems is discussed for the species complex. [UAMH 10855, 11659 accessioned in 2012]

43. Zaffarano PL, Queloz V, Duo A, Grünig CR. Sex in the PAC: a hidden affair in dark septate endophytes? BMC Evol Biol 2011; 11:282 doi: 10.1186/1471-2148-11-282.

BACKGROUND: Fungi are asexually and sexually reproducing organisms that can combine the evolutionary advantages of the two reproductive modes. However, for many fungi the sexual cycle has never been observed in the field or in vitro and it remains unclear whether sexual reproduction is absent or cryptic. Nevertheless, there are indirect approaches to assess the occurrence of sex in a species, such as population studies, expression analysis of genes involved in mating processes and analysis of their selective constraints. The members of the *Phialocephala fortinii* s. l. - *Acephala applanata* species complex (PAC) are ascomycetes and the predominant dark septate endophytes that colonize woody plant roots. Despite their abundance in many ecosystems of the northern hemisphere, no sexual state has been identified to date and little is known about their reproductive biology, and how it shaped their evolutionary history and contributes to their ecological role in forest ecosystems. We therefore aimed at assessing the importance of sexual reproduction by indirect approaches that included molecular analyses of the mating type (MAT) genes involved in reproductive processes. RESULTS: The study included 19 PAC species and > 3, 000 strains that represented populations from different hosts, continents and ecosystems. Whereas *A. applanata* had a homothallic (self-fertile) MAT locus structure, all other species were structurally heterothallic (self-sterile). Compatible mating types were observed to co-occur more frequently than expected by chance. Moreover, in > 80% of the populations a 1:1 mating type ratio and gametic equilibrium were found. MAT genes were shown to evolve under strong purifying selection. CONCLUSIONS: The signature of sex was found in worldwide populations of PAC species and functionality of MAT genes is likely preserved by purifying selection. We hypothesize that cryptic sex regularely occurs in the PAC and that further field studies and in vitro crosses will lead to the discovery of the sexual state. Although structurally heterothallic species prevail, it cannot be excluded that homothallism represents the ancestral breeding system in the PAC. [UAMH 10855, 11659]

44. Zhang H, Ren J, Wang Y, Sheng C, Wu Q, Diao A, Zhu D. Effective multi-step functional biotransformations of steroids by a newly isolated *Fusarium oxysporum* SC1301. Tetrahedron. 2013; 69:184–9.

A fungus *Fusarium oxysporum* SC1301 was isolated from soil samples, which could transform androst-4-ene-3,17-dione, androst-1,4-diene-3,17-dione, dehydroepiandrosterone, progesterone, testosterone, and pregnenolone to give testolactone in 76–98% yields. Especially, for progesterone and pregnenolone, multi-step functional transformations, including oxygenative esterification of 20-ketosteroids, hydrolysis of ester, oxidation of C-17 OH group, oxygenative lactonization of 17-ketosteroids, 1-dehydrogenation, oxidation of C-3 OH group and $\Delta^{5\rightarrow4}$ C$=$C bond migration, could proceed effectively to yield testolactone as a single product. This is the first example that a *F. oxysporum* species shows catalytic capability of ring-D lactonization. The results are remarkably distinguished from those previously reported for the closely-related fungus *F. oxysporum* var. *cubense*, which predominantly mediates the hydroxylations at different positions of steroids. In addition, *F. oxysporum* SC1301 may serve as a valuable biocatalyst for the production of testolactone. [UAMH 9013]

Table 1. Cultures Received in 2012

	Person or industry or culture collection and address	Purpose	Total
1.	Atuku E (Hamel C), Agriculture & Agri-Food Canada, Swift Current, SK	D	1
2.	Bemis DA, Comparative Medicine, Univ of Tennessee College of Veterinary Medicine, Knoxville, TN	D	1
3.	Breuil C, Forest Sciences Centre, Univ of British Columbia, Vancouver, BC	D	1
4.	Clough R (Jackson B), Investigation & Diagnostic Centre and Response, MAF Biosecurity NZ, Upper Hutt, New Zealand	ID	4
5.	Dynalife Diagnostic Lab Services (Majewski K), Edmonton, AB	ID	1
6.	Fuller J (Woods J), Mycology, Microbiology and Public Health, Univ of Alberta Hospitals, Edmonton, AB	ID	2
7.	Keystone Labs Inc. (McDonald J, Zimmer M), Edmonton, AB	ID	26
8.	Microsynth AG (Grunig C), Balgach, Switzerland	D	1
9.	Porter R (Facey P), Dept of Chemistry, Univ of West Indies, Kingston, Jamaica	ID	2
10.	Seifert K (Tanney J), Biodiversity (Mycology and Botany), Agriculture & Agri-Food Canada, Ottawa, ON	D	1
11.	Sutton DA, Fungus Testing Lab, Dept of Pathology, Univ of Texas Health Science Center, San Antonio, TX	D	7
12.	Suzuki K, National Institute of Technology and Evaluation, Biological Resource Center (NBRC), Chiba, Japan	EX	1
13.	Tudor D (Cooper P), Fac of Forestry, Univ of Toronto, Toronto, ON	D	9
14.	Vederas J (Dietrich D, McKinnie S), Dept of Chemistry, Univ of Alberta, Edmonton, AB	D	3
15.	Zettler L, Biology Dept, Illinois College, Jacksonville, IL	D	3
16.	Zhang S (Lee R), Medical Microbiology, Johns Hopkins Hospital, Baltimore, MD	D	1

Cultures received from:

Internal (Univ Alberta/UA Hospitals)	7
North America	49
International	8
Total cultures received	**64**

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

Table 2. Cultures Distributed in 2012

	Person or industry or culture collection and address	Purpose	Total
1.	20/20 Seed Labs Inc. (Morton D), Nisku, AB	MR	1
2.	ARUP Laboratories (Slechta S), Institute for Clinical and Experimental Pathology, Salt Lake City, UT	RD	1
3.	CanBiocin Inc. (Sai M), Edmonton, AB	RD	2
4.	Clay O, Unidad Biologia Celular y Molecular, Corporacio Para Investigaciones Biologicas, Medellin, Columbia	MS	7
5.	Coelho A (Hamelin R), Durability & Protection Dept, FPInnovations (Univ of British Columbia), Vancouver, BC	MS/BD	3
6.	Day M, Centre for Research & Innovation, Grande Prairie Regional College, Grande Prairie, AB	BD/BR	3
7.	Dlusskaya E, Civil and Environmental Engineering, Univ of Alberta, Edmonton, AB	BD/BR	7
8.	Douhan G (Uribe G, Braga J), Dept of Plant Pathology, Univ of California Riverside, Riverside, CA	MP	3
9.	Environmental Safety Technologies Inc. (Koebel A), Louisville, KY	RD	1
10.	Gene J, Unitat de Microbiologia, Facultat de Medicina I Ciencies de la Salut, Universitat Rovira I Virgili, Reus, Spain	EX	1
11.	Hambleton S, Biodiversity (Mycology and Botany), Agriculture & Agri-Food Canada, Ottawa, ON	CR/MS	12
12.	Hausner G (Berg S), Dept of Microbiology, Univ of Manitoba, Winnipeg, MB	MS	4
13.	Hijri M, Sciences Biologiques, IRBV, Univ de Montreal, Montreal, QC	MR	6
14.	Hill J, Dept of Radiology, New England Baptist Hospital, Roxbury Crossing, MA	TE	1
15.	Hobak W (Shaw D, Nelson M), Biology Dept, Univ of Nebraska at Kearney, Kearney, NE	MR	2
16.	Kai K, Graduate School of Life and Environmental Sciences, Univ of Osaka Prefecture, Osaka, Japan	PP	1
17.	Kim SH (Yun YH), Dept of Microbiology, Dankook Univ, Cheonan, Korea	MS/RD	13
18.	Klironomos J (Pakpour S), Biology, Univ of British Columbia, Okanagan, Kelowna, BC	MT	9
19.	Lab'Eau-Air-Sol Ltd. (Dubois-Bouchard C), Aerobiology, St-Charles-Borromee, QC	IAQ	10
20.	Lawrey J, Dept of Environmental Science & Policy, George Mason Univ, Fairfax, VA	MS	2
21.	Luminex Molecular Diagnostics (Fernandes S), Early Product Development, Toronto, ON	RD	1
22.	Malloch D (Bremner A), Dept of Botany, New Brunswick Museum, Saint John, NB	CR	4
23.	McCluskey K, Fungal Genetic Stock Center, Biological Sciences, Univ of Missouri, Kansas City, MO	EX	1
24.	McInerney N, Science Dept, Red Deer College, Red Deer, AB	TE	1
25.	O'Donnell K, National Center for Agricultural Utilization Research, USDA-Agricultural Research Services, Peoria, IL	MS/EX	4
26.	Overy D (Kerr R), Dept of Chemistry, Duffy Research Centre, Univ of Prince Edward Island, Charlottetown, PEI	CR/MS	11
27.	PBR Laboratories Inc. (Pietruch S), Edmonton, AB	IAQ	1

Table 2. Cultures Distributed in 2012

	Person or industry or culture collection and address	Purpose	Total
28.	Pedras S (Reynaud D, Surtees C), Bioorganic and Agricultural Chemistry, Dept of Chemistry, Univ of Saskatchewan, Saskatoon, SK	M/PP	7
29.	Peterson S, National Center for Agricultural Utilization Research, USDA-Agricultural Research Services, Peoria, IL	MS/EX	4
30.	Precision Microslides, LLC (Ricklefs K, Killen R), Cottonwood, AZ	RD	1
31.	RealTime Laboratories Inc. (Hooper D), Carrolton, TX	RD	2
32.	Sain M (Ung T, Jeng R), Center of Biocomposites & Biomaterials Processing, Faculty of Forestry, Univ of Toronto, Toronto, ON	BD/EZ	11
33.	Schroers H, Agricultural Institute of Slovenia, Ljubljana, Slovenia	CR/MS	1
34.	Seifert K (Tanney J), Biodiversity (Mycology and Botany), Agriculture & Agri-Food Canada, Ottawa, ON	EX/MS	5
35.	Shan S (Hsiang T), Pest Diagnostic Clinic, Laboratory Services Division, University of Guelph, Guelph, ON	RD/MS	7
36.	Siciliano S (Nanh R), Soil Science, Univ of Saskatchewan, Saskatoon, SK	BD/BR	3
37.	Smith B, Western Ecology Division, US Environmental Protection Agency, Corvallis, OR	RD	1
38.	Sporometrics Inc. (Guardiola YG, Summerbell RC, Hollis E), Toronto, ON	RD/PT	6
39.	Strelkov S (Dunfield K, Strelkov I, Ziesman B), Agriculture, Food & Nutritional Sciences, Univ of Alberta, Edmonton, AB	PP/P	2
40.	Sullivan M (Liebig P), Ecology &d Evolutionary Biology, Univ of Arizona, Tucson, AZ	TE	1
41.	Toyama Chemical Co. Ltd. (Kaeriyama M), Research Laboratories, 3rd Research Dept, Toyama City, Japan	RD	9
42.	Vederas J (Dietrich D, McKinnie S, Cochrane R, Gao Z), Dept of Chemistry, Univ of Alberta, Edmonton, AB	M	9
43.	Whiteside M (Jones M), Biological and Physical Geography Unit, Irving K Barber School of Arts and Science, Univ of British Columbia, Okanagan, Kelowna, BC	MR	6
44.	Winegarden M (Cywinska A), Microarray Centre, Univ Health Network, Toronto, ON	MS/IAQ	6
45.	Woo J (Zhang J), Agriculture, Food & Nutritional Sciences, Univ of Alberta, Edmonton, AB	EZ	2
46.	Woo PC (Tsang C), Dept Microbiology, Queen Mary Hospital Compound, Univ Hong Kong, Pokfulam, Hong Kong	T	1
47.	Zhang S, Medical Microbiology, Dept of Pathology, Johns Hopkins Univ, School of Medicine, Baltimore, MD	RD	3

Cultures distributed to:

Internal (Univ Alberta/UA Hospitals)	20
North America	146
International	33
Total cultures distributed	**199**

Codes: **BD** – Biodegradation/ Bioremediation; **CR** – Collaborative Research; **EX** – Exchange; **EZ** – Enzyme; **IAQ** – Indoor Air Quality; **M** – Metabolites; **MP** – Mycoparasites; **MR** – Mycorrhizae; **MS** - Molecular Systematics; **MT** – Mycotoxicology; **P** – Pathogenicity; **PP** – Plant Pathology; **PT** – Proficiency Testing; **RD** – Research Diagnostics; **T** – Taxonomy; **TE** – Teaching.