UNIVERSITY OF ALBERTA MICROFUNGUS COLLECTION AND HERBARIUM (UAMH)

A Division of the Devonian Botanic Garden, Faculty of Agriculture, Forestry and Home Economics
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SUMMARY OF ACTIVITIES FOR 2008

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): - **M. Sevigny** (from July); **R. Guardamano** (from Dec); **B. Bahnmann** (to Jan), **N. Fairbairn** (part-time to Mar), **V. Jajczay** (casual)
Volunteers- **M. Packer, Sharon Midbo, Carole Pierce**

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, winter session)
- MLSCI 240 Pathogenic Bacteriology (4 lectures)
- BOT 306 Biology of the Fungi (1 lecture)

Graduate Supervisory Committees (Sigler)
M. Calvo-Polanco, Renewable Resources, Supervisor, J. Zwiazek (defended July 2008)
M. Day, Biological Sciences, Supervisor, R. Currah
M. Davey, Biological Sciences, Supervisor, R. Currah (defended Dec 2008)
M. Plishka, Biological Sciences, Supervisor, R. Currah (defended July 2008)

Professional Training (Workshop)

Aug 26-27 Mycology Training Workshop given on-site for 2 employees of Epcor Water Division, Edmonton.
Program included concepts of basic fungal taxonomy and identification, learning and practicing methods for isolating, purifying, propagating and safe-handling of fungi.

Cultures Received, Distributed and Accessioned

Cultures received for identification, deposit or in exchange (**Table 1**) **67**

Cultures distributed on request or in exchange (**Table 2**)..... **247**

Culture Collection and Herbarium Accessions

New accessions **83**

Total accessions..... **10961**

Information on Accessions available through print and on-line CATALOGUES

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

In-house and Collaborative Research

Refereed Journal Articles

1. Tan DHS*, Sigler L, Gibas CFC, Fong IW. Disseminated fungal infection in a renal transplant recipient involving *Macrophomina phaseolina* and *Scytalidium dimidiatum*: case report and review of taxonomic changes among medically important members of the Botryosphaeriaceae. Medical Mycology 2008: 46: 285-292.
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   Abstract We report the first case of human infection with the fungal plant pathogen *Macrophomina phaseolina* in a Sri Lankan-born Canadian man following a renal transplant in India. The patient subsequently succumbed to invasive infection with *Scytalidium dimidiatum*. Molecular sequence analysis confirmed the identification of both fungi and revealed that they are related species within the ascomycete family Botryosphaeriaceae. We review the rationale for the recent reclassification of *S. dimidiatum* as *Neoscytalidium dimidiatum* and of *Nattrassia mangiferae* (formerly considered a synanamorph of *S. dimidiatum*) as *Neofusicoccum mangiferae*. This and other recent cases illustrate the potential for plant pathogenic fungi to cause invasive human diseases which are refractory to antifungal therapy.

2. Adam H, Groenewald M, Mohan S, Richardson S, Bunn U, Gibas CF, Poutanen S, Sigler L. Identification of a new species, *Candida subhashii*, as a cause of peritonitis. Medical Mycology 2008 (epub) **DOI:** 10.1080/13693780802380545 **First Published on:** 16 September 2008

   Abstract We report a case of fungal peritonitis from which a novel *Candida* species was isolated. Phylogenetic analysis of DNA sequences from the internal transcribed spacer (ITS) region and the D1/D2 domains of the large subunit (LSU) rRNA gene show that the *Candida* species is distinct from, but related to, the human pathogenic species, *C. parapsilosis, C. orthopsilosis, C. metapsilosis, C. tropicalis, C. albicans* and *C. dubliniensis*. *Candida subhashii* M. Groenewald, Sigler et Richardson sp. nov. is described.

3. Wang W, Tsuneda A, Gibas CF, Currah RS. *Cryptosporiopsis* species isolated from the roots of aspen in central Alberta: identification, morphology, and interactions with the host, in vitro. Can J Bot 2007; 85: 1214–1226.
   *Biol. Sci. U of A.

   Abstract: *Cryptosporiopsis* Bubák & Kabát isolates were obtained for the first time from roots of apparently healthy aspen seedlings in Alberta. These isolates were similar in all the major

morphological features previously used to separate *Cryptosporiopsis* species, but sequencing data of the ITS1-5.8S-ITS2 region indicated that they were separated into two groups, one belonging to *Cryptosporiopsis ericae* Sigler and the other to *Cryptosporiopsis radicicola* Kowalski & Bartnik. Scanning electron microscopy of ex-type cultures and selected isolates from aspen roots revealed that *C. ericae* and *C. radicicola* differed in morphogenesis and structure of conidiomata: those of *C. ericae* were either synnematous or sporodochial, whereas those of *C. radicicola* possessed a peridium-like mycelial envelope bearing amorphous adhesive material. Phialides in the hymenium of *C. radicicola* were also embedded in amorphous matrix material but such material was absent in *C. ericae*. Microscopic examination of artificially inoculated aspen roots indicated that both species are endophytes of the host. Hyphal penetration by *C. ericae* was only occasional and confined to the host epidermis, whereas *C. radicicola* was more aggressive and its hyphal ingress extended to the cortical region.

4. Wang W*, McGhee D, Gibas CF, Tsuneda A, Currah RS. *Phialocephala urceolata*, sp. nov. from a commercial, water-soluble heparin solution. Mycologia 2009; 101:136-141.
*Biol Sci, U of A
Abstract *Phialocephala urceolata* sp. nov. was isolated from a black film that had developed on a water-soluble proprietary heparin solution (pH 2.5). Morphological and enzymatic characters, along with phylogenetic analyses of rDNA sequence data, indicated that the conidial fungus is closely related to species of *Phialocephala* known primarily as endophytes in the roots of vascular plants, e.g. *Acephala applanata*, *P. fortinii*, and *P. sphaeroides*, or as associates of persistent plant organs such as the stems and needles of woody plants (e.g. *P. compacta*, *P. dimorphospora*, and *P. scopiformis*). *Phialocephala urceolata* is distinctive in having urn-shaped phialides that are sparsely distributed along the conidiophore axis, a slow growth rate in culture, and in exhibiting a unique combination of reactions on enzymatic test media, i.e., it acidifies casamino acid medium and is gelatinase negative. Partial sequence data from the small subunit (SSU) rDNA indicated that *P. urceolata* is among the Helotiales and close to the type species of *Phialocephala*. Sequence data from the internal transcribed spacer (ITS) region places that *P. urceolata* closest to *P. sphaeroides*. The source of this contaminant is unknown but its taxonomic relationship with other root endophytic species and its ability to produce polyphenol oxidases suggest that the natural habitat of this species is possibly woody plant tissues or soil enriched with lignocellulose.

Abstracts - Posters

9. Sigler L, Gibas CFC. 2008. Onychomycosis caused by *Botryosphaeria* species: laboratory and taxonomic perspectives. ASM F-048, June 4. [poster]

10. Hambleton S, Sigler L, Molecular phylogeny of polar and alpine isolates of *Geomyces*. Polar and Alpine Microbiology, Banff, **S5-2**, May 13, 2008. (Symposium) [abstract online at http://www.polaralpinemicrobiology.com/PAM_Program.pdf]

Identification, Advisory and Depository Services

Cultures are received from medical laboratories, industry or other agencies for identification, verification or deposit. We provide advice on fungus biology or significance of mold growth, and assistance with problems of fungal contamination or deterioration. In 2008, these agencies referred isolates (see **Table 1**): Keystone Labs, Edmonton, AB; National Centre for Mycotic Diseases, Edmonton, AB; Laboratory Medicine and Microbiology, National Institutes of Health, Bethesda; Mycotic Diseases Branch, Center for Disease Control, Atlanta, GA; Centro Veterinario Madrid Exoticos, Madrid, Spain; San Diego Zoo, CA; National Wildlife Health Center, Madison, WI.

Environmental

We receive samples of building materials for analysis of mold and provide advice to public health inspectors, other agencies and the public regarding indoor air quality and health risks of exposure to fungi.

Curatorial Developments

1. A major initiative to redevelop the UAMH database began in 2008. Users acquire information about cultures and services through data transferred to the website. We use the database for all aspects of collection work including selecting isolates appropriate for particular applications, tracking inventories of preserved stocks, generating many types of reports, linking to digital images and sequences obtained by us. We annotate accessions by linking them to publications in which their use is cited and to GenBank sequence deposits based on UAMH isolates. Over the years, we have made many modifications to the database (now operating in MS SQLserver) corresponding with changes in computer hardware and software but a major redevelopment of the database is required to improve the methods for searching and updating, for adding new types of data, and for transferring information to the website.
2. Phase one of the project, completed in 2008, involved a rebuild of the storage tables to allow us better ways of entering, displaying and retrieving information on the seven different ways that we preserve isolates or their DNA. Phase two of the project, to begin in February 2009, will involve a complete rebuild of the data structure and reprogramming of the front end application to the .net framework. 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 user interface directly with the database through a secure web server.
3. Current objectives are to validate and characterizing accession holdings through DNA sequencing. With funding from NSERC (2006-07) and U of A SAS (2007-08) grants, we have established a molecular facility at the Garden which enhances both our curatorial and research programs. Sequencing is now being done more frequently to identify isolates involved in infection and to confirm the identity of isolates on deposit. Molecular characterization is essential to the continued development of this culture collection and to its expanded use by others. Many older accessions identified by phenotypic methods available at the time have not been subjected to recent re-examination, and our objectives are to reassess their classification in light of current taxonomic concepts.

Other Activities

Editorial work (LS): Journal of Clinical Microbiology (4), Medical Mycology (4), Mycologia (1)

Grant review: NSERC (1)

Committees (LS):

- National Mycology Network reporting to the National Microbiology Laboratory and the Canadian Public Health Laboratory Network. Objectives are to develop national leadership in fungal disease surveillance and outbreak investigation, training programs, quality assurance programs, molecular fungal identification and serology.
- Mycological Society of America Committee on Culture Collections. (Chair 07-08; past-Chair 08-09)

- International Society for Human and Animal Mycology: 1) Member of the International Advisory Committee for ISHAM 2009 Congress being held in Tokyo. A suggested symposium topic of Rapidly Changing Mycology: Perspectives on Morphological and Molecular Identification of Emerging and Classic Pathogens was accepted. 2) Appointed to Global Panel of Opinion Leaders. with goal of transferring information on medical mycology www.isham.org/Membership.html

Conference: LS attended the American Society for Microbiology Annual Mtgs, Boston, MA in May and presented a poster paper.

External Funding (Grants/Fees for Services)

NSERC. Major Resources Support (**new**). 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
U of A Small Faculties Fund. Equipment **(new)**. Cryopreservation Equipment	3,000
Income from all services cultures, services, identifications, assessments, consultation, training	14,000

Publications Citing UAMH Cultures or Assistance

1. Badali H, Carvalho VO, Vicente V, Attili-Angelis D, Kwiatkowski IB, Gerrits Van Den Ende AH, De Hoog GS. *Cladophialophora saturnica* sp. nov., a new opportunistic species of *Chaetothyriales* revealed using molecular data. Med Mycol. 2008; 7:1-12.

   Abstract While many members of the black yeasts genus *Cladophialophora* have been reported to cause diseases in humans, understanding of their natural niche is frequently lacking. Some species can be recovered from the natural environment by means of selective isolation techniques. The present study focuses on a *Cladophialophor*a strain that caused an interdigital tinea nigra-like lesion in a HIV-positive Brazilian child. The fungal infection was successfully treated with oxiconazole. Similar strains had been recovered from the environment in Brazil, Uruguay and the Netherlands. The strains were characterized by sequencing the Internal Transcribed Spacer (ITS) regions and the small subunit (SSU) of the nuclearribosomal RNA gene, as well as the elongation factor 1-alpha (EF1alpha) gene. Since no match with any known species was found, it is described as the new species, *Cladophialophora saturnica*.

2. Black JA, Dean TR, Foarde K, Menetrez M. Detection of *Stachybotrys chartarum* using rRNA, tri5, and beta-tubulin primers and determining their relative copy number by real-time PCR. Mycol Res. 2008; 112:845-51.

   Abstract Highly conserved regions are attractive targets for detection and quantitation by PCR, but designing species-specific primer sets can be difficult. Ultimately, almost all primer sets are designed based upon literature searches in public domain databases, such as the National Center for Biotechnology Information (NCBI). Prudence suggests that the researcher needs to evaluate as many sequences as available for designing species-specific PCR primers. In this report, we aligned 11, 9, and 16 DNA sequences entered for Stachybotrys spp. rRNA, tri5, and beta-tubulin regions, respectively. Although we were able to align and determine consensus primer sets for the 9 tri5 and the 16 beta-tubulin sequences, there was no consensus sequence that could be derived from alignment of the 11 rRNA sequences. However, by judicious clustering of the sequences that aligned well, we were able to design three sets of primers for the rRNA region of

S. chartarum. The two primer sets for tri5 and beta-tubulin produced satisfactory PCR results for all four strains of S. chartarum used in this study whereas only one rRNA primer set of three produced similar satisfactory results. Ultimately, we were able to show that rRNA copy number is approximately 2-log greater than for tri5 and beta-tubulin in the four strains of S. chartarum tested.

3. Davey ML, Tsuneda A, Currah RS. Evidence that the gemmae of *Papulaspora sepedonioides* are neotenous perithecia in the *Melanosporales*. Mycologia 2008; 100:626-35

   Abstract *Papulaspora sepedonioides* produces large multicellular gemmae with several, thick-walled central cells enclosed within a sheath of smaller thin-walled cells. Phylogenetic analysis of the large subunit rDNA indicates *P. sepedonioides* has affinities to the *Melanosporales* (Hypocreomycetidae). The development of gemmaein *P. sepedonioides* was characterized by light and scanning and transmissionelectron microscopy and was similar to previous ontogenetic studies of ascoma development in the *Melanosporales*. However instead of giving rise to ascogenoustissues the central cells of the incipient gemma became darkly pigmented, thick walled and filled with lipid globules while the contents of the sheath cellsautolysed, leaving them empty and deflated at maturity. Both central cells andpre-autolytic sheath cells produced both germ tubes and new gemmae primordia,suggesting microcyclic conidiogenesis occurs in this species. Mature gemmae were non-deciduous or seceded by schizolytic secession and appear to have both perennating and disseminative potential. The evolution of these neotenous perithecial propagules may be driven by life-history and ecological factors selecting for functional versatility.

4. Davis CM, Noroski LM, Dishop MK, Sutton DA, Braverman RM, Paul ME, Rosenblatt HM. Basidiomycetous fungal *Inonotus tropicalis* sacral osteomyelitis in X-linked chronic granulomatous disease. Pediatr Infect Dis J. 2007; 26:655-6.

   Abstract Osteomyelitis is a common clinical manifestation of chronic granulomatous disease, a disorder of phagocytic function. Fungal organisms account for a significant proportion of these infections. We describe the clinical presentation and subsequent destructive sacral osteomyelitis with a basidiomycetous mold, Inonotus tropicalis, in a patient with an X-linked chronic granulomatous disease.

5. de Repentigny L, St-Germain G, Charest H, Kokta V, Vobecky S. Fatal zygomycosis caused by *Mucor indicus* in a child with an implantable left ventricular assist device. Pediatr Infect Dis J. 2008; 27:365-9

   Abstract *Mucor indicus* is a rare, emerging cause of zygomycosis with 7 cases previously reported since 1975. We report the first case of endovascular M. indicus infection in a pediatric recipient of the Incor (Berlin Heart AG, Germany) implantable left ventricular assist device, and review the literature to describe the broadening clinical spectrum of zygomycosis caused by this emerging fungal pathogen.

6. Ewaze JO, Summerbell RC, Scott JA. Ethanol physiology in the warehouse-staining fungus, *Baudoinia compniacensis*. Mycol Res. 2008; 112:1373-80.

   Abstract The fungus *Baudoinia compniacensis* colonizes the exterior surfaces of a range of materials, such as buildings, outdoor furnishings, fences, signs, and vegetation, in regions subject to periodic exposure to low levels of ethanol vapor, such as those in the vicinity of distillery aging warehouses and commercial bakeries . Here we investigated the basis of ethanol metabolism in *Baudoinia* and investigate the role of ethanol in cell germination and growth.

Germination of mycelia of *Baudoinia* was enhanced by up to roughly 1d exposure to low ethanol concentrations, optimally 10ppm when delivered in vapour form and 5mm in liquid form. However, growth was strongly inhibited following exposure to higher ethanol concentrations for shorter durations (e.g., 1.7m for 6h). We found that ethanol was catabolized into central metabolism via alcohol dehydrogenase (ADH) and acetaldehyde dehydrogenase (ACDH). Isocitrate dehydrogenases (IDHs) were activein cells grown on glucose, but these enzymes were not expressed when ethanol was provided as a sole or companion carbon source. The glyoxylate cycle enzymesisocitrate lyase (ICL) and malate synthase (MS) activities observed in cells grown on acetate were comparable to those reported for other microorganisms. By replenishing tricarboxylic acid (TCA) cycle intermediates, it is likely that the functionality of the glyoxylate cycle is important in the establishment of luxuriant growth of *Baudoinia compniacensis* on ethanol-exposed, -deprived, exposed surfaces. In other fungi, such as *Saccharomyces cerevisiae*, ADH II catalyses the conversion of ethanol to acetaldehyde, which then can be metabolized via the TCA cycle. ADH II is known to be strongly repressed in the presence of glucose.

7. Ewaze JO, Summerbell RC, Scott JA. Semiselective isolation of the ethanol-imbibing sooty mould *Baudoinia* of distillery aging warehouses. Can J Microbiol. 2008; 54:331-3.

Abstract *Baudoinia compniacensis* is a darkly pigmented microfungus that grows conspicuously on environmental surfaces around warehouses where alcoholic spirits are stored in wooden casks. This fungus has long been ignored because its primary isolation is very difficult. The present study describes a new semiselective isolation medium for this fungus based on the use of ethanol as a sole carbon source and low levels of nitrogen and trace elements.

8. Grünig CR, Queloz V, Duo A, Sieber TN. Phylogeny of *Phaeomollisia piceae* gen. sp. nov.: a dark, septate, conifer-needle endophyte and its relationships to *Phialocephala* and *Acephala*. Mycological Research, doi:10.1016/j.mycres.2008.10.005; available from: http://www.sciencedirect.com/science/article/B7XMR-4TTHWK3-1/2/ad357cd017f25d0094f6c3482775b7b3)

Abstract Dark, septate endophytes (DSE) were isolated from roots and needles of dwarf *Picea abies* and from roots of *Vaccinium* spp. growing on a permafrost site in the Jura Mountains in Switzerland. Two of the isolates sporulated after incubation for more than one year at 4 °C. One of them was a hitherto undescribed helotialean ascomycete *Phaeomollisia piceae* gen. sp. nov., the other was a new species of *Phialocephala*, *P. glacialis* sp. nov. Both species are closely related to DSE of the *Phialocephala fortinii s. lat.–Acephala applanata* species complex (PAC) as revealed by phylogenetic analyses of the ITS and 18S rDNA regions. Morphologically dissimilar fungi, such as *Vibrissea* and *Loramyces* species, are phylogenetically also closely linked to the new species and the PAC. *Cadophora lagerbergii* and *C. (Phialophora) botulispora* are moved to *Phialocephala* because *Phialocephala dimorphospora* and *P. repens* are the closest relatives. Several *Mollisia* species were closely related to the new species and the PAC according to ITS sequence comparisons. One DSE from needles of *Abies alba* and one from shoots of *Castanea sativa* formed *Cystodendron* anamorphs in culture. Their identical 18S sequences and almost identical ITS sequences indicated *Mollisia* species as closest relatives, suggesting that *Mollisia* species are highly euryoecious.

9. Grünig CR, Duo A, Sieber TN, Holdenrieder O. Assignment of species rank to six reproductively isolated cryptic species of the *Phialocephala fortinii s.l.-Acephala applanata* species complex. Mycologia 2008; 100:47–67.

Abstract Phialocephala fortinii s.l. and Acephala applanata are the dominant dark septate endophytes (DSE) in roots of many trees and shrubs. Population genetic analysis led to the

discovery of morphologically indistinguishable but reproductively isolated cryptic species (CSP) within Phialocephala fortinii s.l. In the present study we show that sequence data of two coding (beta-tubulin and translation elongation factor [EF-1alpha]) and three noncoding DNA loci confirm subdivision of P. fortinii s.l. and allow to differentiate seven CSP of P. fortinii. In addition we show that strains collected throughout Europe can be classified correctly based on these sequence markers. Statistically significant differences in growth response on different media were observed among CSP of P. fortinii and A. applanata. Growth inhibition on MEA amended with 100 mgl21 cycloheximide had the strongest differential effect of all physiological traits examined. In contrast exoenzyme production (laccase, proteinase, pectinase, phenol-oxidase, amylase, cytochrome oxidase and tyrosinase) rarely helped to differentiate CSP of P. fortinii. However A. applanata was a strong producer of amylases, laccases and proteinases. Based on these data we propose to assign species rank to six CSP of P. fortinii: P. turiciensis, P. letzii, P. europaea, P. helvetica, P. uotolensis, P. subalpina spp. nov. and P. fortinii s.s.

10. Hausner G, Reid R, Eyjólfsdóttir GG, Iranpour M, Loewen PC. *Basidiopycnides albertensis* gen. et sp. nov., a new anamorphic fungus with phylogenetic affinities in the *Atractiellales* (Basidiomycota). Mycotaxon 2008; 103: 279-297.

    Abstract A new anamorphic genus, *Basidiopycnides*, and its type species, *Basidiopycnides albertensis*, are described. Strains of *Basidiopycnides albertensis* produce what superficially appeared to be a *Graphium*-like conidial state with percurrently proliferating annellophores. Detailed morphological and molecular data analysis showed these isolates represent a new taxon that belongs to the *Atractiellales* (Basidiomycota).

11. Li, D-W, Cowles RS, Vossbrinck CR. *Metarhiziopsis microspora* gen. et sp. nov. associated with the elongate hemlock scale. Mycologia 2008; 100: 460-466

    Abstract A sporodochial fungus collected from the elongate hemlock scale, *Fiorinia externa* (Ferris) in Coventry, Connecticut, is described. This fungus has characteristics of both *Metarhizium* and *Myrothecium* but develops setae surrounding white to buff sporodochia and dry conidia in chains, a combination of characters found in neither genus. Phylogenetic analyses of the complete small subunit ribosomal DNA (*ssu*), partial *ef1*-alpha , and complete 5.8S ribosomal DNA and internal transcribed spacers (ITS) 1 and 2 shows that the fungus is allied with a subclade within *Cordyceps* including the species *C. agriota*, which places this fungus in the Hypocreales, Clavicipitaceae *sensu lato* or the newly erected Ophioclavicipitaceae. Morphological observation and molecular analysis indicate that this fungus is sufficiently different from *Metarhizium* and *Myrothecium* to warrant the erection of a new anamorphic genus. Therefore *Metarhiziopsis microspora* gen. et sp. nov. is proposed.

12. Montero CI, Shea YR, Jones PA, Harrington SM, Tooke NE, Witebsky FG, Murray PR. Evaluation of Pyrosequencing technology for the identification of clinically relevant non-dematiaceous yeasts and related species. Eur J Clin Microbiol Infect Dis. 2008; 27:821-30.

    Abstract Pyrosequencing was used to identify 133 isolates of clinically relevantnon-dematiaceous yeasts. These included 97 ATCC strains (42 type strains), seven UAMH strains, and 29 clinical isolates. Isolates belonged to the following genera: *Candida* (18 species), *Trichosporon* (10), *Cryptococcus* (7), *Malassezia* (3), *Rhodotorula* (2), *Geotrichum* (1), *Blastoschizomyces* (1), and *Kodamaea* (1). Amplicons of a hyper-variable ITS region were obtained and analyzed using Pyrosequencing technology. The data were evaluated by a BLAST search against the GenBank database and correlated with data obtained by conventional cycle sequencing of the ITS1-5.8S-ITS2 region. Cycle sequencing identified 78.9% of the isolates to the species level. Pyrosequencing technology identified 69.1%. In 90.1% of all of the strains tested, the

identification results of both sequencing methods were identical. Most *Candida* isolates can be identified to the species level by Pyrosequencing. *Trichosporon* species and some *Cryptococcus* species cannot be differentiated at the species level. Pyrosequencing can be used for the reliable identification of most commonly isolated non-dematiaceous yeasts, with a reduction of cost per identification compared to conventional sequencing.

13. Plishka MJ, Tsuneda A, Currah RS. Evidence of apothecial ancestry in the cleistothecial ascomata of *Pleuroascus nicholsonii*. Mycol Res. 2008; 112:1319-26.

Abstract Ascomata of *Pleuroascus nicholsonii*, a rarely reported cleistothecial ascomycete, show little overt evidence of a putative affiliation with the *Leotiomycetes*. However, close examination of the plectomycetous centrum reveals a distorted hymenium arising from a system of branched ascogenous hyphae, and twisted or coiled uniseriate ascospores enclosed within what appears to be the remains of the spore investing membrane of a clavate ascus precursor. Abundant sterile elements arising from the inner wall layer of the peridium and interspersed throughout the centrum are interpreted as representing vestiges of apically branched paraphyses. Whole ascomata show limited signs of polarity, although the characteristic, tightly coiled appendages generally arise along or below the equatorial region and there is a marked thinning of subicular hyphae over the crown of the cleistothecium. The mature peridium, which consists of a thin, melanized outer layer of squamulose cells, splits irregularly along intercellular grooves when disturbed. The adaptive significance of these characteristics is unknown, but the persistent paraphyses, the easily fractured and darkly pigmented membranous peridium, an ascospore mass that is dry at maturity, and the tendency for ascomata to cling together in clumps can be rationalized in the context of a coprophilous life-style. Collection data for *P. nicholsonii* provide further support for this supposition because five of the six reported specimens are from rodent dung.

14. Sutton DA, Wickes BL, Thompson EH, Rinaldi MG, Roland RM, Libal MC, Russell K, Gordon S. Pulmonary *Phialemonium curvatum* phaeohyphomycosis in a Standard Poodle dog. Med Mycol. 2008; 46:355-359.

Abstract *Phialemonium curvatum*, frequently misidentified as an *Acremoniu*m species, is reported here as a new agent of pulmonary phaeohyphomycosis in a Standard Poodle dog, and added as a new species in the genus to cause mycoses in canines. In vitro susceptibility data, for both human and animal isolates, suggests resistance to amphotericin B and susceptibility to the triazole agents itraconazole, voriconazole, and posaconazole.

15. Untereiner WA, Angus A, Réblová M, and Orr M. Systematics of the *Phialophora verrucosa* complex: new insights from analyses of β-tubulin, large subunit nuclear rDNA and ITS sequences Can. J. Bot. 2008; 86:742–750

Abstract *Phialophora* Medlar, as defined currently, is a genus encompassing melanized, anamorphic Ascomycota that produce one-celled conidia from phialides with distinct, darkened collarettes. The type species, *Phialophora verrucosa* Medlar, is closely related to *Phialophora americana* (Nannf.) S. Hughes, the anamorph of *Capronia semiimmersa* (Candoussau & Sulmont) Untereiner & Naveau (Herpotrichiellaceae, Chaetothyriales). To confirm that *P. americana* and *P. verrucosa* are distinct taxa, and to examine their phylogenetic relationships to species of *Capronia* and other representatives of the Chaetothyriales, we sequenced portions of the β-tubulin gene and nuclear ribosomal RNA cistron (ITS and LSU rDNA). We also compared isolates of *P. americana* grown on a number of media. Isolates of *C. semiimmersa*, *Capronia svrcekiana* Réblová, and *P. americana* produced phialides bearing deep, vase-shaped collarettes and formed a strongly supported clade that did not include *P. verrucosa* in a

phylogeny inferred from the combined β-tubulin–ITS–LSU dataset. *Capronia svrcekiana* was found to be conspecific with *C. semiimmersa* based on the comparison of cultural, micromorphological, and molecular characters. In the LSU phylogeny, three recently described species of *Phialophora* (*Phialophora europaea* de Hoog et al., *Phialophora reptans* de Hoog, and *Phialophora sessilis* de Hoog) were grouped outside of the clade containing sampled members of the Herpotrichiellaceae. While the position of these species in the Chaetothyriales remained unresolved, it was evident that *P. europaea*, *P. reptans*, and *P. sessilis* are not members of the *P. verrucosa* complex.

16. Tsuneda A, Davey ML, Hambleton S, Currah RS.*Endosporium*, a new endoconidial genus allied to the Myriangiales. Can J Bot. 2008; 86(9): 1020–1033 doi:10.1139/B08-054

Abstract A new endoconidial genus, *Endosporium* gen. nov., is reported from Alberta, Canada. Two species are described: *Endosporium populi-tremuloidis* Tsuneda sp. nov. (type species) isolated from a heavily colonized bud of *Populus tremuloides* Michx., and *Endosporium aviarium* Tsuneda sp. nov. isolated from the skin of *Bombycilla garrulus* (L.) (Bohemian waxwing) and a twig of *Populus balsamifera* L. This genus is morphologically similar to *Phaeotheca* in forming black, slow-growing colonies (conidiomata) containing numerous, conidiogenous, cellular clumps, but different in that (*i*) colonies possess aerial, determinate hyphae on the surface; (*ii*) mature colonies eventually collapse to release a mixture of conidiogenous cellular clumps, endoconidia, and blastic conidia in slimy liquid; and (*iii*) endoconidia are hyaline. Phylogenetic analyses of nuclear rDNA SSU, LSU, and ITS sequences indicate that *Endosporium* is phylogenetically distant from other endoconidial taxa, including *Phaeotheca*, and is most closely related to the Myriangiales (Dothideomycetes). Similarities in stroma and conidioma development as well as ecology between the two taxa suggest that *Endosporium* can be accommodated within this order, making it the first endoconidial and first black meristematic genus reported in the Myriangiales.

17. Vohník M, Fendrych M, Albrechtová J, Vosátka M. Intracellular colonization of *Rhododendron* and *Vaccinium* roots by *Cenococcum geophilum*, *Geomyces pannorum* and *Meliniomyces variabilis*. Folia Microbiol (Praha). 2007; 52:407-14.

Abstract Four in vitro experiments were set up to verify the colonization potential of ectomycorrhizal (EcM) *Cenococcum geophilum* FR. (strain CGE-4), saprotrophic *Geomyces pannorum* (LINK) SIGLER & CARMICHAEL (GPA-1) and a frequent root-associated, potentially ericoid mycorrhiza (ErM)-forming Meliniomyces variabilis Hambleton & Sigler (MVA-1) in roots of *Rhododendron* and *Vaccinium*. A typical ErM fungus, *Rhizoscyphus ericae* (Read) Zhuang & Korf (RER-1), was included for comparison. All fungal strains intracellularly colonized rooted *Vaccinium* microcuttings: GPA-1 occasionally produced hyphal loops similar to ErM, MVA-1 and RER-1 exhibited a typical ErM colonization pattern. CGE-4 hyphae grew vigorously on and around newly formed roots and rarely penetrated turgescent rhizodermal cells forming intracellular loose loops. Rooting of *Rhododendron sp*. microcuttings was not promoted by any fungal strain except CGE-4, which also promoted the most vigorous growth of *Rhododendron ponticum* L. seedlings. The widespread EcM fungus *C. geophilum* has a potential to colonize non-EcM roots and support their development which may influence overall growth of ericaceous plants. As shown for *G. pannorum*, structures resembling ErM may be formed by fungi that are to date not regarded as ericoid mycorrhizal.

Table 1. Cultures Received in 2008

	Person or industry or culture collection and address	Purpose	Total
1.	Blehert, D., US Geological Survey, National Wildlife Health Center, Madison, WI	D	4
2.	Brandt, M., Mycotic Diseases Branch, Center for Disease Control, Atlanta, GA	ID	1
3.	Centraalbureau voor Schimmelcultures, (Snippe-Clause, F.B.), Utrecht, Netherlands	R	1
4.	Currah, R.S. (Tsuneda, A., Davey, M., Wang, W.), Dept. of Biological Sciences, Univ of Alberta, Edmonton, AB	D	11
5.	Gallego, M., Centro Veterinario, Madrid Exoticos, Madrid, Spain	ID	6
6.	Hsiang, T., Univ of Guelph, GuelpH, ON	SD	1
7.	Iwen, P., Univ of Nebraska Medical Center, Omaha, NE	ID/CR	6
8.	Keystone Labs Inc. (Chieng, J., McDonald, J.), Edmonton, AB	ID	5
9.	Li, D.W., Connecticut Agricultural Experimental Station, Valley Laboratory, Windsor, CT	D	1
10.	Plattner, A., (Breuil, C.), Forest Science Center, Dept. Wood Science, UBC, Vancouver, BC	D	3
11.	Rennie, R. (Sand, C.), National Center for Mycotic Diseases, Univ of Alberta Hospitals Microbiology & Public Health, Edmonton, AB	ID/D	15
12.	San Diego Zoo (Keener, L.), San Diego, CA	ID	1
13.	Scully, L., Dept. of Biology, Brock University, St. Catharines, ON	D	1
14.	Shea, Y., Dept. of Laboratory Medicine & Microbiology Service, National Institutes of Health, Bethesda, MD	ID	2
15.	Sutton, D.A., Fungus Testing Lab., Dept. of Pathology, Univ Texas Health Science Center, San Antonio, TX	D	8
16.	Zettler, L. (Stice, A.), Depts. of Biology and Chemistry, Illinois College, Jacksonville, IL	D	2
17.	Zhou, J., Mycology Program, American Type Culture Collection, Manassas, VA	EX	1

Cultures received from:

1. Internal (Univ Alberta/UA Hospitals) **26**

2. External (North America, International) **43**

Total cultures received **69**

Codes: **CR** = Collaborative Research; **D**= Deposit; **EX**= Exchange; **ID**= Identification; **SD**= Safe Deposit; **R**= Requested

Table 2. Cultures Distributed in 2008

Person or industry or culture collection and address	Purpose	Total
1. Addy, H. (Cusack, F.), Dept. of Biological Sciences, Univ of Calgary, Calgary, AB	BD/EZ	3
2. Becker, D. (Dannenman, S.), Dept. of Biology, Northern Michigan University, Marquette, MI	T	1
3. Bio-Chem Consulting Services Ltd. (Sheppard, M.), Analytical Services Div., Calgary, AB	PT	6
4. Brzezinski, R., Dept. de Biologie, Faculte des Sciences, Universite de Sherbrooke, Sherbrooke, QC	IAQ	2
5. Chaturvedi, V., New York State Dept. of Health, Albany, NY	MS	24
6. Chau, H.W. (Si, B.C.), Dept. of Soil Science, Univ of Saskatchewan, Saskatoon, SK	MR	3
7. Cooper, P. (Tudor, D.), Faculty of Forestry, Univ of Toronto, Toronto, ON	BD	8
8. Currah, R. (Plishka, M.), Dept. of Biological Sciences, Univ of Alberta, Edmonton, AB	T	1
9. EMSL Analytical Inc. (Williams, K., Kaminski, A.), Indianapolis, IN	T	1
10. Farrel, R., Soil Sciences, Univ of Saskatchewan, Saskatoon, SK	BD	2
11. Gagne, A. (Khasa, D.), Center for Forest Research, Microbial and Genomic Collections, Univ. Laval, Laval, QC	MR	1
12. Gruenig, C., Dept of Forest Pathology and Dendrology, Swiss Fed. Institute of Technology, Zurich, Switzerland	EX/MS	40
13. Hambleton, S., ECORC, Agriculture & Agri-Food Canada, Ottawa, ON	CR	18
14. Isotechnika Inc. (Freitag, D.), Edmonton, AB	M	1
15. Iwen, P., Dept. of Pathology and Microbiology, Univ of Nebraska Medical Center, Omaha, NE	CR	4
16. Jones, M. (Brooks, D.), Faculty of Forestry, Univ of British Columbia, Vancouver, BC	MR	2
17. Kapsanaki-Gotsi, E., Dept. of Ecology and Systematics of Biology, ATHUM Culture Collection of Fungi, Univ of Athens, Athens, Greece	T	5
18. Koukol, O., Dept. of Botany, Charles University in Prague, Prague 2, Czech Republic	TE	3
19. Kulka, M., National Research Council of Canada, Charlottetown, PEI	ST	2
20. Zobbe, D. (Hoegh, S.), Labkemi Denmark A/S, Brondby, Denmark	RD	1
21. Lauer, C.K. (Volk, T.), Dept. of Biology, Univ of Wisconsin La Crosse, La Crosse, WI	MS	4
22. Levac, S. (Miller, D.), Dept. of Chemistry, Carleton University, Ottawa, ON	IAQ	3
23. Lievens, B., Molecular Diagnostics and Metagenomics, Scientia Terrae Research Institute, Antwerp, Belgium	MR	18
24. –Liu, Yu-Chen, Bioresource Collection and Research Center, Food Industry Research and Development Institute, Hsinchu, Taiwan	T	1
25. Luminex Molecular Diagnostics (Pitsikas, P.), Toronto, ON	RD	5
26. Markham, J., Dept. of Biological Sciences, Univ of Manitoba, Winnipeg, MB	BD	2
27. Martin, J., Pavillion de l'Envirotron, Univ of Laval, Ste Foy, QC	PP	1
28. Nuutinen, J., Dept. of Applied Biology, Univ of Helsinki, Helsinki, Finland	MR	14
29. Pedras, M.S.C. (Surtees, C.), Dept. of Chemistry, Univ of Saskatchewan, Saskatoon, SK	PP	2
30. Pickard, M., Dept. of Biological Sciences, Univ of Alberta, Edmonton, AB	EZ	2

Table 2. Cultures Distributed in 2008

Person or industry or culture collection and address	Purpose	Total
31. Reese, P. , Dept. of Chemistry, Univ of the West Indies, Mona, Kingston 7, Jamaica, West Indies	M/PS	15
32. Reid, J. (Hausner, G.), Dept. of Microbiology, Univ of Manitoba, Winnipeg, MB	T	3
33. Rennie, R. (Sand, C.), National Center for Mycotic Diseases, Microbiology & Public Health, Univ of Alberta Hospitals, Edmonton AB	CR	1
34. Sadowsky, J., Dept. of Plant Pathology, Michigan State University, East Lansing, MI	MR	3
35. Shahzadi, A. (Bressler, D., Gaenzle, M.), Dept. of Agriculture, Food and Nutritional Science, Univ of Alberta, Edmonton, AB	BD	6
36. Solazyme Inc. (Acena, J.), San Francisco, CA	M	1
37. Sporometrics Inc. (Ronson, K., Hollis, E., Saleh, M.), Toronto, ON	PT	11
38. Sutton, D.A., Fungus Testing Lab., Dept. of Pathology, Univ Texas Health Science Center at San Antonio, San Antonio, TX	MS	4
39. Taylor, J. W. (Whiston, E.), Univ of California Berkeley, Berkeley, CA	MS	1
40. Untereiner, W., Dept. of Botany, Brandon University, Brandon, MB	TE	2
41. VanHamme, J., Dept. of Biological Sciences, Thompson Rivers University, Kamloops, BC	EZ	5
42. Verenium Corp. (Kustedjo, K., Powell, K.), San Diego, CA	EZ	1
43. Wei, T. (Berch, S.), Chinese Academy of Sciences, Kunming Institute of Biology, Kunming, Yunnan, China	MR	2
44. Wing, L. (Sinia, A.), Dept. of Environmental Biology, Univ of Guelph, Guelph, ON	B	7
45. Zettler, L. (Stice, A.), Depts. of Biology and Chemistry, Illinois College, Jacksonville, IL	MR	4
46. Zhou, J., Mycology Program, American Type Culture Collection, Manassas, VA	EX	1

Cultures distributed to:

1. Internal (Univ Alberta/UA Hospitals)	**10**
2. North America	**138**
3. International	**99**

Total cultures distributed **247**

Codes: **BD** – Biodegredation/ Bioremediation; **CR** – Collaborative Research; **EX** – Exchange; **EZ** – Enzyme; **IAQ** - Indoor Air Quality; **M** – Metabolites;**MR** – Mycorrhizae; **MS** - Molecular Systematics; **PP** – Plant Pathology; **PS-** Preservation Service; **PT** – Proficiency Testing; **RD** – Reference Diagnostics; **ST** - Susceptibility Testing; **T** – Taxonomy; **TE** - Teaching