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 2003

Staff, Students

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) – vacant
(A. Flis on Long term disability)
Technical or laboratory assistants (trust): -**A. Hashimoto** (full time), **R. Gibas** (part-time continuing), **V. Jajczay** (casual)
Summer student (part-time) **S, Cowley**
Ph.D. student- **C. F. C. Gibas**
Volunteers - **R. von Tigerstrom**

Affiliate
R. Currah, Professor, Biological Sciences, Faculty of Science

Academic Teaching & Graduate Supervision

L. Sigler

- MLSCI 240 Pathogenic Bacteriology (4 lectures)
- BIOL 306 Biology of the Fungi (1 lecture)

Graduate Supervision (Sigler)
Connie Fe C. Gibas, Ph.D. candidate, Biological Sciences, Supervisors L. Sigler & R. Currah, Biol. Sci.

- Teaching Assistant for BIOL 107

Graduate Supervisory Committee (Sigler)
A. Rice, Biological Sciences, Supervisor, R. Currah

Professional Training (Workshops)

May	Invited instructor, one day workshop on "Fungi Pathogenic For Humans and Animals" for US National Laboratory Training Network /Texas Dept. of Health, San Antonio, TX (with R.C. Summerbell)

Cultures Received, Distributed and Accessioned

Cultures received for identification, deposit or in exchange (**Table 1**) **189**

Cultures distributed on request or in exchange (**Table 2**)..... **332**

Culture Collection and Herbarium Accessions

New accessions..... **134**

Total accessions..... **10385**

Information on Accessions available through print and on-line CATALOGUES

Catalogue of the University of Alberta Microfungus Collection and Herbarium. 3rd Ed. 1998
http://www.devonian.ualberta.ca/uamh/search

In-house and Collaborative Research

Refereed Journal Articles

1. Tang, P.*, S. Mohan, L. Sigler, I. Witterick, R. Summerbell, I. Campbell & T. Mazzulli. 2003. Allergic fungal sinusitis associated with *Trichoderma longibrachiatum.* J. Clin. Microbiol. 41:5333-5336.
*Dept Microbiology, Toronto Medical Laboratories & Mount Sinai Hospital, Toronto, ON

Abstract

We describe allergic fungal sinusitis caused by *Trichoderma longibrachiatum* in a patient with a history of atopy and asthma. A Gram stain of a sinus biopsy specimen was initially thought to contain yeast cells, but when *Trichoderma* was recovered in culture, these cells were subsequently recognized as chlamydospores. The patient was successfully managed with a combination of sinus lavage, oral corticosteroids, itraconazole, and allergen immunotherapy. This case also points out that careful scrutiny of direct smears is required to ensure that fungal structures are not misinterpreted.

2. Kernaghan, G.,* L. Sigler & D. Khasa. 2003. Mycorrhizal and root endophytic fungi of containerized *Picea glauca* seedlings assessed by rDNA sequence analysis. Microbial Ecology 45: 128-136. http://dx.doi.org/10.1007/s00248-002-1024-1
*Formerly Renewable Resources, U of A; currently Centre de recherche en biologice forestière (CRBF), Pavillon C.-E.-Marchand, Univ Laval, PQ

Abstract

Fungi colonizing fine roots of containerized *Picea glauca* seedlings were assessed in four large conifer nurseries in northern Alberta. PCR amplification of fungal rDNA (internal transcribed spacer and a portion of the 5? end of the large subunit gene) from random samples of fine feeder roots gave between 1 and 4 amplicons per seedling. Amplicons were either separated by electrophoresis and sequenced directly, or cloned and sequenced. The resulting sequences were compared to sequences obtained from cultures established from seedling roots and from GenBank by maximum parsimony analysis. ITS sequences formed 11 distinct clades, each including at least one reference sequence. The ectomycorrhizal basidiomycetes *Thelephora*

americana and *Amphinema byssoides* were dominant, whereas ascomycetes were less common. Fungi with sequences similar to members of the Heleotiales which form ericoid mycorrhizas were also present. Correspondence analysis revealed strong positive and negative associations among fungal taxa as well as an influence of applied fertilizer level on fungal diversity and species composition.

3. Gibas, C.F., L. Sigler, R.C. Summerbell & R.S. Currah. 2002. Phylogeny of the genus *Arachnomyces* and its anamorphs and the establishment of *Arachnomycetales*, a new eurotiomycete order in the *Ascomycota*. Stud. Mycol. 47:123-130.

Abstract
Arachnomyces is a genus of cleistothecial ascomycetes that has morphological similarities to the *Onygenaceae* and the *Gymnoascaceae* but is not accommodated well in either taxon. The phylogeny of the genus and its related anamorphs was studied using nuclear SSU rDNA gene sequences. Partial sequences were determined from ex-type cultures representing *A. minimus*, *A. nodosetosus* (anamorph *Onychocola canadensis*), *A. kanei* (anamorph *O. kanei*) and *A. gracilis* (anamorph *Malbranchea* sp.) and aligned together with published sequences of onygenalean and other ascomycetes. Phylogenetic analysis based on maximum parsimony showed that *Arachnomyces* is monophyletic, that it includes the hyphomycete *Malbranchea sclerotica*, and it forms a distinct lineage within the *Eurotiomycetes*. Based on molecular and morphological data, we propose the new order *Arachnomycetales* and a new family *Arachnomycetaceae*. All known anamorphs in this lineage are arthroconidial and have been placed either in *Onychocola* (*A. nodosetosus*, *A. kanei*) or in *Malbranchea* (*A. gracilis*). *Onychocola* is considered appropriate for disposition of the arthroconidial states of *Arachnomyces* and thus *Malbranchea sclerotica* and the unnamed anamorph of *A. gracilis* are redisposed as *Onychocola sclerotica* comb. nov. and *O. gracilis* sp. nov.

4. Sigler, L., S. Hambleton & J.A. Paré. 2002. *Chlamydosauromyces punctatus* gen. & sp. nov. (*Onygenaceae*) from the skin of a lizard. Stud. Mycol. 47:123-130.

Abstract
Chlamydosauromyces punctatus is described for an ascomycete producing punctate, rimmed ascospores within ascomata composed of narrow, thin-walled branched, hyphae and an anamorph of alternate arthroconidia. It is known from a single collection obtained from shed skin of a frilled lizard. DNA sequences from the small subunit (SSU) region of the nuclear ribosomal gene were obtained from the lizard isolate and two other taxa and compared with homologous sequences of onygenalean fungi obtained from GenBank. Phylogenetic analysis supports the inclusion of the genus *Chlamydosauromyces* within the *Onygenaceae*. Results also supported the separation of *Arachniotus ruber* from *Kraurogymnocarpa trochleospora* (*Pseudoarachniotus trochleosporus*), a species that at one time was considered synonymous.

5. Sigler, L., S. Hambleton, A.L. Flis & J.A. Paré. 2002. *Auxarthron* teleomorphs for *Malbranchea filamentosa* and *Malbranchea albolutea* and relationships within *Auxarthron*. Stud. Mycol. 47:111-122.

Abstract
Malbranchea filamentosa and *M. albolutea* were reexamined and connected to teleomorphs in the genus *Auxarthron*. DNA sequences were obtained from the small subunit (SSU) and internal transcribed spacer (ITS) regions of the nuclear ribosomal rRNA gene to evaluate conspecificity of the *M. filamentosa* isolates and to evaluate relationships among taxa within the *Auxarthron* clade. Five of eight isolates putatively identified as *M. filamentosa* produced fertile ascomata in matings and with F1 progeny. *Auxarthron filamentosum* sp. nov. is described for the teleomorph.

Three nonmating isolates appeared conspecific based on morphology, but one was excluded based on sequence divergence. An *Auxarthron* teleomorph was described for *M. albolutea* in 1976, but not named because of uncertainty about its distinction from *A. thaxteri* and *A. umbrinum. Auxarthron alboluteum* sp. nov. is shown to be phylogenetically distinct. Phylogenetic analysis based on newly derived sequences showed that members of the genus *Auxarthron* and *Malbranchea dendritica* formed a strongly supported monophyletic group. In the ITS analysis, most species were placed into two well supported clades that correlated with the shape of the ascospores; the position of the type species *A. californiense*, was not clearly resolved. Differences were found between newly derived SSU sequences and those on deposit in GenBank for the same strains. After re-evaluation of the strains, the following sequences are considered to be incorrect: *M. albolutea* L28063 (UAMH 2846), *A. zuffianum* L28062 (UAMH 4098), *M. dendritica* L28064 (UAMH 2731) and *M. filamentosa* L28065 (UAMH 4097). The sequence for U29389 is correct for *Malbranchea albolutea* not *M. dendritica* as stated in the GenBank record. The problems with these sequences were not uncovered in prior published analyses because insufficient representatives of *Auxarthron* species were sampled.

Refereed Articles In Press or Submitted

6. Sigler, L. Culture Collections in Canada: Perspectives and Problems. Can. J. Plant Pathology (In press; acc Dec 16/03)
7. Paré, J.A., L. Sigler, K.L. Rypien & C.F. Gibas. Cutaneous mycobiota of captive squamates reptiles with notes on the scarcity of Chrysosporium anamorph of *Nannizziopsis vriesii*. Journal of Herpetological Medicine and Surgery 13(3) (In press; acc Apr-03).
8. Untereiner, W.A., J. Scott, F.A. Naveau, L. Sigler, J. Bachewich & A. Angus. The Ajellomycetaceae, a new family of vertebrate-associated Onygenales. Mycologia (subm. Aug 18/03)
9. Tucker, D.L, C.H. Beresford & L. Sigler. Disseminated *Beauveria bassiana* infection in a patient with acute lymphoblastic leukaemia. Journal of Clinical Microbiology (subm. Dec/03).

Book Chapters Published and In Press

10. Sigler, L. & P. Verweij. 2003. *Aspergillus, Fusarium* and other opportunistic moniliaceous fungi. In: *Manual of Clinical Microbiology.* Pp 1726-1760. Chpt. 116, 8th Ed. (Eds. P.R. Murray, E.J. Baron, J.H. Jorgensen, M.A. Pfaller & R. H. Yolken) American Society for Microbiology, Washington.
11. Sigler, L. Adiaspiromycosis and other infections caused by *Emmonsia* species. IN: Topley & Wilson's Microbiology and Microbial Infections, 10th ed. (Vol Eds. R. Hay and W. Merz) Edward Arnold, London, U.K. (In press)
12. Paré, J.A. & L. Sigler. Fungal Diseases of Reptiles. (Mader, D. ed.) (In press, subm Mar, 02).

Proceedings

13. Paré, J.A., K.A. Coyle, L. Sigler, A.K. Maas III & R.L. Mitchell. 2003. Pathogenicity of the *Chrysosporium* anamorph of *Nannizziopsis vriesii* for veiled chameleons (*Chamaeleo calyptratus*). Proc. Assoc. of Reptilian and Amphibian Veterinarians, Pp. 9-10, and Proc. American Assoc. Zoo Veterinarians, p. 7, Minneapolis, MN

Abstracts († invited oral presentations; *presenter)

14. † Sigler, L. 2003. Mycological investigations of novel agents of onychomycosis. Abstr. SY02.1 MicroNZ 2003, Auckland, New Zealand.

15. †Sigler, L. 2003. Culture Collections: Perspectives and Problems. Symposium co-sponsored by Canadian Agricultural Research Council and Canadian Phytopathol. Soc. at CPS Ann. Mtgs., Montreal, June 24 (paper accepted for publication; see **Ref 6**).
16. †Sigler, L. 2003. A classical taxonomist's view of some changes in the *Onygenales* influenced by molecular data. International Society for Human and Animal Mycology (ISHAM), May 25-29, San Antonio, TX (symposium co-convenor & speaker).
17. *Gibas, C. L. Sigler, R. Currah. 2003. Relationship of *Malbranchea sclerotica* to nail associated fungi in the genus *Arachnomyces*. Abstr. 248. International Society for Human and Animal Mycology, May 25-29, San Antonio, TX. (poster)
18. *Mankowski, J.L., L.E .Craig, N.S. Miller, C.N. Morrell, J.F. Mann, A.L. Kincaid, R.C. Summerbell, L. Sigler, H.J. Schroers, W.G. Merz. 2003. *Phialemonium* sp. infections in two domestic cats: A novel fungal pathogen. American College of Veterinary Pathologists Ann. Mtg. Banff, AB, Nov 15-19. (poster)
19. *Paré, J.A., K. Coyle, L. Sigler, A. Maas Jr III & R. L. Mitchell. 2003. Pathogenicity of the Chrysos*por*ium anamorph of *Nannizziopsis vriesii* for veiled chameleons (*Chamaeleo calyptratus*). AAZV/ARAV Ann. Mtg, Minneapolis (Sept). (oral)
20. *Iwen, P.C., A.G. Freifeld, L. Sigler, S.Z. Pavletic, & S.R. Tarantolo. 2003. Molecular identification of *Rhizomucor pusillus* as a cause of sinus-orbital zygomycosis in a patient with acute myelogenous leukemia. Focus on Fungal Infections, Maui, Hawaii Mar 19-21 (oral)
21. *Rogers, K., L. Sigler, J. Matthews & M. Hudson. 2003. *Microascus cirrosus*, an uncommon agent of onychomycosis. Abst. P02.01, MicroNZ 2003, Auckland, NZ. (poster)

Identification, Advisory and Depository Services

Cultures are received for deposit, identification or verification. Additionally, we provide advice on fungus biology or significance of mold growth, and assistance with problems of fungal contamination or deterioration. Listed are some examples of individuals or agencies using these services in 2003.

- Abbott, S., akaMoldlab, Sparks, NE, deposit and identification of some isolates from environmental sampling.
- Benoit, J.B. (J. Yoder), Wittenberg University, Springfield, OH , identification of isolates from invertebrates.
- Berbee, M., Dept. of Botany, Univ. British Columbia, identification of some mycorrhizal fungi sent for deposit.
- Burleson, M., Ohio Dept. of Health Laboratories, Columbus OH, isolate identified as *Gymnascella littoralis* from BAL, female 25 yr.
- Iwen, P., Univ. Nebraska Medical Center, Omaha, NE, a *Mucor* isolate from ulcer on left calf of a 90 yr old male, for mating to confirm species identification.
- Kammeyer, P., Loyola Univ. Medical Center, Chicago, IL, identification of an isolate causing nail infection.
- Kiehn, T., Microbiology Lab., Memorial Sloan Kettering Cancer Center, New York, confirmation of an isolate as *Gymnascella hyalinospora* (see **Ref. 28**).
- Novicki, J., Laboratory Medicine, University of Washington, Fred Hutchinson Cancer Research Center, Seattle, WA, WA, deposit of case isolate from blood culture of a patient with acute myelogenous leukemia following hematopoietic stem cell transplant (see **Ref. 34**)
- Paré, J., Surgical Sciences, Veterinary Medicine, Univ. Wisconsin, Madison, WI, isolates from skin of bearded dragon lizards.
- Pelletier, R., Microbiology, Hotel Dieu de Quebec, Quebec City, identification of an isolate from

subcutaneous nodule on hand of a male gardener.
- Schulz, M. (R. Currah), Biol. Sci., Univ. Alberta, deposit and identification of isolates from dead standing leaves of *Typha latifolia*.
- Thomas, A., Dept. of Primary Industries, Oonoonba Veterinary Lab, Townsville, Queensland, Australia, identification of an isolate causing skin lesions on mouth and head of a file snake.

Medical Reference Service

The following individuals or agencies sent isolates for identification or confirmation.
- R. Rennie, National Reference Centre, Microbiology & Public Health, Univ. of Alberta Hospitals, (20)
- Sutton, D. (M. Rinaldi), Fungus Testing Laboratory, Fungus Testing Lab., Univ. Texas Health Science Center, San Antonio, TX (9)
- K. Rogers, Microbiology, Auckland Hospital, Auckland, NZ (7) including a Microascus isolate obtained twice from nail of a 64 yr old female and reported at MicroNZ (see **Ref. 21**).
- Kinahan, C., Clinical Microbiology, Royal Univ. Hospital, Saskatoon, SK (4)

Environmental

Various public and private agencies and members of the public contact us concerning assessment, significance and control of molds in the indoor environment. In addition to providing advice by telephone, we examine bulk and air samples for presence of molds and evaluate numbers and types, and potential health hazards of exposure. In 2003, about 17 reports were prepared on samples from homes and public buildings in Alberta and Saskatchewan.

Presentations, Travel

May	L. Sigler presented a paper and co-convened a session entitled "Fungal Taxonoomy: Classic Meets Molecular" at the XV Congress of the International Society for Human and Animal Mycology (ISHAM), San Antonio, TX
	C. Gibas presented a poster at the ISHAM Congress and received a travel award from ISHAM.
	L. Sigler presented a one-day workshop with R.C. Summerbell on "Fungi Pathogenic For Humans and Animals" cosponsored by US National Laboratory Training Network and Texas Dept of Health, in San Antonio.
June	L. Sigler was keynote speaker for workshop on the "Status of Microbial Genetic Resources and Culture Collections in Canada," cosponsored by the Canadian Agricultural Research Council (CARC) and the Canadian Phytopathological Society (CPS) at the CPS Annual Meeting, Montreal.
Sept.	L. Sigler presented a paper in a symposium on "Medical Mycology" at the MicroNZ Congress, Auckland NZ
May-Oct	As part of the Matsukaze Chanoyu group, Atsumi Hashimoto offered the traditional Japanese tea ceremony monthly during the summer at the DBG Ozawa Pavilion.

Visitors

January	Dr. Sarah Hambleton, Agriculture & Agri-Food Canada, Neatby Building, CEF, Ottawa, ON to discuss collaborative research
April	Dr. Jean Paré, Surgical Sciences, Veterinary Medicine, University of Wisconsin, Madison, WI to discuss collaborative research
August	Dr. Anna Lusa Ruotsalainen, Botanical Museum, Dept. of Biology, University of Oulu, Finland (visitor to laboratory of Dr. R. Currah) for tour of UAMH

Miscellaneous Activities

Editorial Boards and peer review of papers and grant applications (LS): Editorial Board, Medical Mycology (International Society for Human and Animal Mycology) (2); Journal of Clinical Microbiology, American Society for Microbiology (6); Canadian Journal of Microbiology (1); Journal of Infectious Disease (1).
NSERC individual grant (Plant Biology & Food Science) (1); Austrian Science Fund (1)

Offices in Societies and Committee work (LS)

- Member of the International Union of Biological Sciences (IUBS) World Federation of Culture Collections Committee on Postal, Quarantine and Safety, 1995- present [This committee is working to modify regulations regarding shipping of microorganisms of lower risk. This is an issue of concern to collections and their users worldwide.]
- Chair, Mycological Society of America Committee on Culture Collections, (member 1999 – present. [This committee monitors and reports on activities affecting culture collections mainly in North America; however, it plays a role in providing support for endangered world microbial collections as required.]

University Committees (LS)

- Member of advisory committee for National Reference Centre in Mycology, UAH Microbiol. & Public Health

External Funding (Grants/Fees for Services)

NSERC. Systematics of Fungi in the Human Environment	29,000
NSERC. Major Facilities Access (1999-2002). The University of Alberta Microfungus Collection and Herbarium (UAMH).	42,000
ARAV Assoc of Reptilian & Amphibian Veterinarians (**New 2003**) (J.A. Paré, J.A., D.R. Andes, D.R., L. Sigler) Susceptibility of fungal isolates from reptiles to antifungal drugs.	$2,325 US
Income from services	
cultures, safe deposit and preservation services	17,000
identifications	1,000
environmental assessments and consultation	1,500
Consultation to UAH National Reference Centre (transfer from Microbiology & Public Health)	4,500

Publications Citing UAMH Cultures or Assistance

22. Allen TR, Millar T, Berch SM, Berbee ML. 2003. Culturing and direct DNA extraction find different fungi from the same ericoid mycorrhizal roots. New Phytologist 160:255-272.

Abstract
This study compares DNA and culture-based detection of fungi from 15 ericoid mycorrhizal roots of salal (Gaultheria shallon), from Vancouver Island, BC Canada. From the 15 roots, we PCR amplified fungal DNAs and analyzed 156 clones that included the internal transcribed spacer two (ITS2). From 150 different subsections of the same roots, we cultured fungi and analyzed their ITS2 DNAs by RFLP patterns or sequencing. We mapped the original position of each root section and recorded fungi detected in each. Phylogenetically, most cloned DNAs clustered among Sebacina spp. (Sebacinaceae, Basidiomycota). Capronia sp. and Hymenoscyphus ericae (Ascomycota) predominated among the cultured fungi and formed intracellular hyphal coils in resynthesis experiments with salal. We illustrate patterns of fungal diversity at the scale of individual roots and compare cloned and cultured fungi from each root. Indicating a systematic culturing detection bias, Sebacina DNAs predominated in 10 of the 15 roots yet Sebacina spp. never grew from cultures from the same roots or from among the > 200 ericoid mycorrhizal fungi previously cultured from different roots from the same site.

23. Greif MD, Currah RS. 2003. A functional interpretation of the role of the reticuloperidium in whole-ascoma dispersal by arthropods. Mycological Research 107: 77-81.

Abstract
Auxarthron conjugatum (Onygenaceae) and Myxotrichum deflexum (Myxotrichaceae) are distantly related cleistothecial (gymnothecial) ascomycetes that form ascomata with strikingly similar peridia in which rigid, branched and anastomosed, thick-walled hyphae create a cage- or mesh-like enclosure (reticuloperidium). We tested the hypothesis that the reticuloperidium plays a role in dispersal mediated by arthropods by enclosing ascomata of these fungi together with flies from the family Sarcophagidae. Gymnothecia of both fungi were picked up easily when the stiff hairs of the flies impaled the ascomata by passing through the interhyphal spaces of the reticuloperidium. Ascospore release from the gymnothecia then occurred during grooming activities during which the limbs of the flies caught the ascoma appendages causing the peridium to be torn apart. This adaptation to arthropod morphology and behaviour is interpreted as the driving force behind the evolution of reticuloperidia in unrelated groups of cleistothecial ascomycetes.

24. Gupta AK, Kohli Y. 2003. Clinical and Laboratory InvestigationsIn vitro susceptibility testing of ciclopirox, terbinafine, ketoconazole and itraconazole against dermatophytes and nondermatophytes, and in vitro evaluation of combination antifungal activity. British Journal of Dermatology 149:296-305.

Abstract
With the development of newer antifungal agents with activity against both yeasts and filamentous fungi, there is an increased need to develop and standardize in vitro assays that will evaluate the activity of antimycotics against filamentous fungi. In vitro analysis of antifungal activity of these agents would also allow for the comparison between different antimycotics, which in turn may clarify the reasons for lack of clinical response or serve as an effective therapy for patients with chronic infection.

25. Hambleton S, Tsuneda A, Currah RS. 2003. Comparative morphology and phylogenetic placement

of two microsclerotial black fungi from Sphagnum Mycologia 95:959-975.

Abstract
Capnobotryella renispora and Scleroconidioma sphagnicola form black, irregularly shaped microsclerotia that are indistinguishable in gross morphology on leaves of Sphagnum fuscum. In culture, microsclerotia of these fungi were similar, in that mature component cells possessed thick, highly melanized cell walls, poorly defined organelles, large lipid bodies and simple septa. They were different in morphogenesis, in the way their component cells were organized and in disseminative propagules. Microsclerotia of S. sphagnicola formed phialidic conidiogenous cells on their surface, whereas in C. renispora, adjacent cells in mature microsclerotia often separated from each other by septum schizolysis and formed chlamydospores. The identification of C. renispora from Sphagnum is provisional despite a 100% ITS sequence match with data for a culture derived from the type strain. No holoblastic, reniform conidia typical of the species were formed in nature or in culture, and the SSU sequence for a separately preserved culture of the ex-type strain was markedly divergent. Parsimony analyses of nuclear ribosomal DNA sequences showed that these two fungi were related to separate orders of Dothideomycetes. Both SSU and ITS data supported a close relationship for S. sphagnicola to the Dothideales sensu stricto, while the closest ITS match was to Rhizosphaera spp. In the SSU analyses, C. renispora was nested within the Capnodiales.

26. Jany JL, Bousquet J, Khasa PD. 2003. Microsatellite markers for Hebeloma species developed from expressed sequence tags in the ectomycorrhizal fungus Hebeloma cylindrosporum. Molecular Ecology Notes 3:659-661.

Abstract
The increasing number of expressed sequence tag (EST) projects dedicated to ectomycorrhizal fungi is translating into the release of large sets of ESTs. The aim of this study was to develop and test simple sequence repeat (SSR) markers from EST databases of the model ectomycorrhizal fungus Hebeloma cylindrosporum. Six SSR markers were found to be both unambiguously scorable and polymorphic among 12 H. cylindrosporum isolates. Two SSR markers were transferable to other Hebeloma species and one marker was interestingly found to be polymorphic among seven H. crustuliniforme isolates.

27. Kernaghan G, Hambling B, Fung M, Khasa D. 2002. In Vitro selection of boreal ectomycorrhizal fungi for use in reclamation of saline-alkaline habitats. Restoration Ecology 10:43-51.

Abstract
To identify appropriate species of ectomycorrhizal fungi for use in the reclamation of saline-alkaline sites, such as the composite tailings (alkaline, with high sodium, sulfate, and calcium) produced by the Canadian tar sands industry, pure cultures of nine fungal species indigenous to the Canadian boreal forest were grown on media containing different levels of CaCl2, CaSO4, NaCl, or Na2SO4, as well as on medium containing composite tailings (CT) release water, and on media at four different pH levels. Members of the Boletales (Suillus brevipes, Rhizopogon rubescens, and Paxillus involutus) and Amphinema byssoides (Aphyllophorales) were sensitive to alkalinity, and their growth was completely inhibited by CT release water. Laccaria and Hebeloma spp. (Agaricales) as well as Wilcoxina mikolae (Pezizales) were tolerant to alkalinity and survived on the medium containing CT release water. Calcium chloride proved to be the most toxic of the salts tested. Growth of seven isolates of Laccaria bicolor and three isolates of Hebeloma crustuliniforme on media containing CaCl2 and release water showed low intraspecific variation. A combination of fungal species, each with its own beneficial characteristics, is recommended for the inoculation of seedlings to be outplanted onto composite tailings.

28. Kiehn TE. 2003. Pythium insidiosum Reidentified as Gymnascella hyalinospora. Clinical Infectious Disease 36:1350-1351.

Letter

Amy M. Grooters, a veterinary internist at Louisiana State University (Baton Rouge) who fairly frequently encounters pythiosis in young dogs in the southeastern United States, questioned the identification of Pythium insidiosum as the fungus that caused endocarditis in a patient with leukemia who my colleagues and I described in an electronic article in Clinical Infectious Diseases. The isolate, which had originally been sent to Michael G. Rinaldi at the University of Texas Health Science Center (San Antonio) for antifungal susceptibility testing, was subsequently correctly identified as Gymnascella hyalinospora by Dr. Grooters, Dr. Deanna A. Sutton, who works with Dr. Rinaldi, and Lynne Sigler (Curator of the University of Alberta Microfungus Collection and Herbarium in Edmonton, Canada). Correct identification was based on the organism's morphological features, including good growth at both 30°C and 37°C, characteristic production of yellow and green tufts of aerial hyphae within which ascospores were produced, and electron micrograph imaging of the ascospore characteristics, when compared with known isolates of G. hyalinospora. Structures described in the original report (see figure 3*C* and 3*D* in as zoosporangia and zoospores were, in fact, subspherical asci (each containing 8 discoid ascospores within a membrane) and ascospores that were induced to germinate by overnight incubation in water. There is one other reported case of infection in a human caused by G. hyalinospora, which was a case of pulmonary infection in a patient with acute myelogenous leukemia. As was mentioned in the latter report, sporulation may be absent on standard media, leading to difficulties in identification. Subculture onto sporulation media may be required to demonstrate the salient characteristics required for identification of G. hyalinospora and other ascomycetes.

29. Kim JJ, Kim SH, Lee S, Breuil C. 2003. Distinguishing Ophiostoma ips and Ophiostoma montium, two bark beetle-associated sapstain fungi. FEMS Microbiol. Lett. 222:187-192.

Abstract

Two synonymous sapstain species, Ophiostoma montium and Ophiostoma ips, which are vectored by Dendroctonus ponderosae and various bark beetles, respectively, were differentiated into separate species using growth and molecular characteristics. Analysis of 32 isolates of the two species from different countries showed that O. ips was able to grow at 35 degrees C while O. montium was not. This growth-based differentiation was strongly supported by sequence data for the internal transcribed spacer (ITS), 5.8S and partial 28S rDNA, and the beta-tubulin genes. The beta-tubulin gene sequence data indicate that the two species can easily be differentiated with a single polymerase chain reaction (PCR) assay.

30. Koster B, Scott J, Wong B, Malloch D, Neil Straus N. 2003. A geographically diverse set of isolates indicates two phylogenetic lineages within Stachybotrys chartarum. Canadian Journal of Botany 81:633-643.

Abstract

Stachybotrys chartarum is a black mitosporic fungus capable of dense colonization of cellulose-based building materials such as drywall. The presence of S. chartarum in indoor environments has been reported as linked to a variety of alleged environment-related illnesses including infant acute idiopathic pulmonary hemorrhage, although there continues to be insufficient (especially exposure) data to support such associations. We investigated genetic variation among 52 morphologically and geographically diverse, indoor and outdoor isolates of S. chartarum sensu lato using molecular markers based on □-tubulin, calmodulin, elongation factor-1 alpha, and trichodiene synthase genes, as well as the internal transcribed spacer region of nuclear

ribosomal DNA. Gene genealogies proved concordant in dividing all isolates into two strongly supported clades. The majority of the variable sites separating these lineages were fixed within each of these clades, and there was no evidence of recombination between genotypes. The results of this study therefore provide strong support for the recognition of two phylogenetic species within S. chartarum sensu lato, and further demonstrate the limitations of morphological characters in delineating monophyletic taxa among morphologically simple fungi.

31. Kristiansen KA, Taylor DL, Kjøller R, Rasmussen HN, Rosendahl, S. 2001. Identification of mycorrhizal fungi from single pelotons of Dactylorhiza majalis (Orchidaceae) using single-strand conformation polymorphism and mitochondrial ribosomal large subunit DNA sequences. Molecular Ecology 10:2089-2093.

Abstract
The mitochondrial ribosomal large subunit (LS) DNA was used to identify the orchid mycorrhizal fungi found in roots of Dactylorhiza majalis. The gene was amplified using DNA extracted from single pelotons obtained from fresh and silica gel dried roots. Furthermore, sequencing a variety of well-characterized orchid isolates expanded the fungal database of the mitochondrial ribosomal LsDNA. Polymerase chain reaction product length variants present in D. majalis were sequenced and identified using the expanded database. These analyses revealed two different peloton-forming fungi in samples from D. majalis, which sometimes occurred together as a single two-taxa peloton within the same cortex cell. The first taxon belonged to the genus Tulasnella and the second taxon was distantly related to Laccaria.

32. Lacourt I, Girlanda M, Perotto S, Del Pero M, Zuccon D, Luppi AM. 2001. Nuclear ribosomal sequence analysis of Oidiodendron: towards a redefinition of ecologically relevant species. New Phytologist 149:565-576.

Abstract
Nuclear ribosomal sequence analysis was performed to investigate delimitation of common Oidiodendron species comprising endomycorrhizal symbionts and close associates of ectomycorrhizal plants. Neighbour-joining, maximum likelihood and parsimony analyses were used to compare 35 ribosomal DNA (internal transcribed spacer (ITS) and 5.8S) sequences (including sequences available in databases) from 15 putative species. Oidiodendron citrinum formed a monophyletic group nested within O. maius, whereas O. tenuissimum and O. griseum did not appear either as distinct groups or as a single complex. Pairwise nucleotide divergence values between O. citrinum and O. maius were very low and comparable to intraspecific values obtained for both species; values for O. griseum and O. tenuissimum, although higher, overlapped those observed at the intraspecific level for the two species. Molecular data indicate that O. maius and O. citrinum, which were described as distinct, though related species, could be moved to a subspecific level; however, the delimitation of O. griseum and O. tenuissimum is still open to question. Taxonomic rank assignment to groups determined from sequence data analysis is discussed.

33. Lilleskov EA, Hobbie EA, Fahey TJ. 2002. Ectomycorrhizal fungal taxa differing in response to nitrogen deposition also differ in pure culture organic nitrogen use and natural abundance of nitrogen isotopes. New Phytologist 154:219-231

Abstract
Ectomycorrhizal fungal species vary in their response to nitrogen (N) availability and ability to use organic N. We hypothesized that taxa dominant at sites with high soil inorganic N would be less likely to use organic N than taxa dominant at low soil inorganic N. We also asked whether these taxa differed in natural abundance of N isotopes. Pure culture N use for taxa from an N

deposition gradient in Alaska was examined and N isotopes of sporocarps, soils and foliage collected over this gradient were quantified. Taxa common in low inorganic N soils grew on protein, glutamine and serine, whereas dominant taxa in high inorganic N soils grew on glutamine, but poorly on protein and serine. Sporocarp delta15N was highest in protein users, and lowest in nonprotein users. With increasing soil inorganic N, sporocarps became more isotopically enriched relative to foliage. The importance of organic N use might decline with increasing N availability, although field tests are required. The relationship between organic N use and N isotopes also merits further study. However, sporocarp isotopic enrichment may be a useful indicator of soil N availability.

34. Novicki TJ, LaFe K, Bui L, Bui U, Geise R, Marr K, Cookson BT. 2003. Genetic diversity among clinical isolates of Acremonium strictum determined during an investigation of a fatal mycosis. J Clin Microbiol. 41:2623-2628

Abstract

Primarily saprophytic in nature, fungi of the genus Acremonium are a well-documented cause of mycetoma and other focal diseases. More recently, a number of Acremonium spp. have been implicated in invasive infections in the setting of severe immunosuppression. During the course of routine microbiological studies involving a case of fatal mycosis in a nonmyeloablative hematopoietic stem cell transplant patient, we identified a greater-than-expected variation among strains previously identified as Acremonium strictum by clinical microbiologists. Using DNA sequence analysis of the ribosomal DNA intergenic transcribed spacer (ITS) regions and the D1-D2 variable domain of the 28S ribosomal DNA gene (28S), the case isolate and four other clinical isolates phenotypically identified as A. strictum were found to have <99% homology to the A. strictum type strain, CBS 346.70, at the ITS and 28S loci, while a sixth isolate phenotypically identified only as Acremonium sp. had >99% homology to the type strain at both loci. These results suggest that five out of the six clinical isolates belong to species other than A. strictum or that the A. strictum taxon is genetically diverse. Based upon these sequence data, the clinical isolates were placed into three genogroups.

35. Pryce TM, Palladino S, Kay ID, Coombs GW. 2003. Rapid identification of fungi by sequencing the ITS1 and ITS2 regions using an automated capillary electrophoresis system. Medical Mycology 41:369-381.

Abstract

We developed a standardized DNA sequence-based approach for the accurate and timely identification of medically important fungi by sequencing polymerase chain reaction (PCR) products with a rapid automated capillary electrophoresis system. A simple DNA extraction method and PCR amplification using universal fungal primers was used to amplify ribosomal DNA from a range of clinical isolates and reference strains. The entire internal transcribed spacer (ITS) 1-5.8S-ITS2 ribosomal DNA region was sequenced using automated dye termination sequencing for 89 clinical isolates. These had previously been identified by traditional methods and included 12 ascomycetous yeast species, three basidiomycetous yeast species, eight dermatophyte species and two thermally dimorphic fungi, Scedosporium prolificans and S. apiospermum. Furthermore, 21 reference strains representing 19 different Candida species, Geotrichum candidum and Malassezia furfur were also sequenced as part of this study and were used either as standards for sequence-based comparisons, or as assay controls. Sequence-based identification was compared to traditional identification in a blinded manner. Of the clinical isolates tested, 88/89 had DNA sequences that were highly homologous to those of reference strains accessioned in GenBank, and 87/89 gave a sequence-based identification result that correlated with the traditional identification. In contrast to relatively slow conventional

methods of identification, a sequence-based identification from a pure culture can be obtained within 24 h of a DNA extraction carried out after a minimal period of culture growth. We conclude that this approach is rapid, and may be a more accurate cost-effective alternative than most phenotypic methods for identification of many medically important fungi frequently encountered in a routine diagnostic microbiology laboratory.

36. Seifert KA., Louis-Seize G, Sampson G. 2003. Myrothecium acadiense, a new hyphomycete isolated from the weed Tussilago farfara. Mycotaxon 87:317 – 327.

Abstract
Myrothecium acadiense, isolated from leaves of the weed Tussilago farfara collected in Nova Scotia, Canada, is described as a new anamorph species. It produces sporodochial conidiomata, percurrently proliferating conidiogenous cells, a green, slimy conidial mass and unusual cylindrical conidia that are swollen and convex at the base. Despite the fact that most species of Myrothecium have phialidic conidiogenous cells, a phylogenetic analysis of aligned DNA sequences of the 5 ′ end of the large subunit (LSU) rDNA suggest that M. acadiense is closely related to the type of the genus, M. inundatum, tentatively placed in the Bionectriaceae, Hypocreales. Some comments are included on the relationships and generic concept of Trichothecium roseum

37. Sharma J, Zettler LW, van Sambeek JW, Ellersieck MR, Starbuck CJ.2003. Symbiotic seed germination and mycorrhizae of federally threatened Platanthera praeclara (Orchidaceae). The American Midland Naturalist 149: 104–120.

Abstract
In vitro culture of mycotrophic leaf-bearing seedlings of federally threatened Platanthera praeclara Sheviak and Bowles, a terrestrial orchid native to the midwestern prairies, is reported for the first time. Symbiotic germination was evaluated to: (1) determine need for cold moist stratification to enhance seed germination and seedling development and (2) identify the mycobionts that support in vitro germination and development. Germination was improved by exposing seeds to both 4- and 6-mo stratification periods; whereas seeds without stratification failed to germinate in a pilot study. Pretreatment of seeds with 6 mo of stratification combined with inoculation with mycorrhizal fungus derived from a seedling (Ceratorhiza sp., UAMH 9847) supported development of higher stage protocorms and some leaf-bearing seedlings of P. praeclara. Protocorms with developing leaf primordia were also obtained by coinoculation with strains of Epulorhiza and Ceratorhiza. Fungi derived from mature P. praeclara plants failed to promote seedling development to advanced growth stages. Results indicate that in vitro development of P. praeclara is best supported when stratified seeds are cultured with fungi isolated from young seedlings.

38. Taylor DL, Bruns TD, Szaro TM, Hodges SA.2003. Divergence in mycorrhizal specialization within Hexalectris spicata (Orchidaceae), a nonphotosynthetic desert orchid. American Journal of Botany 90:1168-1179.

Abstract
Evidence is accumulating for specialized yet evolutionarily dynamic associations between orchids and their mycorrhizal fungi. However, the frequency of tight mycorrhizal specificity and the phylogenetic scale of changes in specificity within the Orchidaceae are presently unknown. We used microscopic observations and PCR-based methods to address these questions in three taxa of nonphotosynthetic orchids within the Hexalectris spicata complex. Fungal ITS RFLP analysis and sequences of the ITS and nuclear LSU ribosomal gene fragments allowed us to identify the

fungi colonizing 25 individuals and 50 roots. Thanatephorus ochraceus (Ceratobasidiaceae) was an occasional colonizer of mycorrhizal roots and nonmycorrhizal rhizomes. Members of the Sebacinaceae were the primary mycorrhizal fungi in every *Hexalectris* root and were phylogenetically intermixed with ectomycorrhizal taxa. These associates fell into six ITS RFLP types labeled B through G. Types B, C, D, and G were found in samples of H. spicata var. spicata, while only type E was found in H. spicata var. arizonica and only type F was found in H. revoluta. These results provide preliminary evidence for divergence in mycorrhizal specificity between these two closely related orchid taxa. We hypothesize that mycorrhizal interactions have contributed to the evolutionary diversification of the Orchidaceae.

39. Vujanovic V, Hamel C, Jabaji-Hare S, St-Arnaud M.2003. A new species of Pseudorobillarda from an asparagus field in Quebec, Canada. Mycotaxon 87: 351 – 357

Abstract

A new species of coelomycetes in genus Pseudorobillarda is described and illustrated. Pseudorobillarda *asparagis* sp. nov. is a saprophyte isolated from the soil litter of an asparagus field in Quebec, Canada. This fungus is typical of the genus in morphology, but clearly different from other known species in Pseudorobillarda by distinct size and form of conidiomata and paraphyses, and by shape, size, and colour of conidia. Its taxonomic placement is discussed.

40. Yoder JA, Hanson PE, Zettler LW, Benoit JB, Ghisays F, Piskin KA. 2003. Internal and External Mycoflora of the American Dog Tick, Dermacentor variabilis (Acari: Ixodidae), and Its Ecological Implications. Applied and Environmental Microbiology 69: 4994-4996.

Abstract

Scopulariopsis brevicaulis, the anamorph of Microascus brevicaulis (Microascaceae, Ascomycota), has been identified in the body contents of the tick Dermacentor variabilis. After topical application of the fungal inoculum, tick mortality was marked. This is the first account describing the internal mycoflora of D. variabilis with a novel technique used to recover potential biological control agents.

Table 1. Cultures Received in 2003

Person or industry or culture collection and address	*Reason for shipment*	*Total*
1. Abbott, S.A., aka Moldlab, Sparks, NV	D/ID	25
2. Berbee, M. (P. Inderbitzin), Botany, Univ. British Columbia, Vancouver, BC	D/ID	28
3. Berg, G., Univ. Tennessee, Knoxville, TN	ID	16
4. Burleson, M., Ohio Dept. of Health, Columbus, OH	ID	1
5. CBS, Ultrecht, The Netherlands	D	1
6. Currah, R. S. (M. Schulz, B. Wilson), Biological Sciences, Univ. Alberta, Edmonton	D/ID	21
7. Di Salvo, A., P.O. Box 18220, Reno, NV	D	1
8. Hambleton, S., Agriculture & Agri Food Canada, Ottawa, ON	ID	4
9. Herrera, J., Division of Science, Truman State University, Kirksville, MO	ID	1
10. Iwen, P., Univ. Nebraska Medical Center, Omaha, NE	ID	1
11. Jang, S., Veterinary Medical Teaching Hospital, Univ. California-Davis, Davis, CA	ID	1
12. Kammeyer, P., Loyola Univ. Medical Center, Chicago, IL	ID	1
13. Kiehn, T., Microbiology Lab., Memorial Sloan-Kettering Cancer Center, NY	ID	1
14. Kinahan, C., Clinical Microbiology, Royal Univ. Hospital, Saskatoon. SK	D/ID	4
15. Kong, H., Agricultural Environment, Chungcheongbuk-do Agricultural Research & Extension Services, Seoul, South Korea	D	2
16. Narisawa, K., Plant Biotechnology Institute, Ibaraki Agricultural Center, Iwama, Japan	D	3
17. Novicki, J., Laboratory Medicine, Univ. Washington, Seattle, WA	D	1
18. Pare, J., Veterinary Medicine, Univ. Wisconsin, Madison, WI	D/ID	6
19. Pelletier, R., Microbiology, Hotel Dieu de Quebec, Quebec, QC	ID	1
20. Pivkin, M.V., Pacific Institute of Bioorganic Chemistry, Vladivostok, Russia	ID	1
21. Reid, J., Microbiology, Univ. Manitoba, Winnipeg, MB	D	12
22. Rennie, R., National Center for Mycology, Univ. Alberta Hospital, Edmonton, AB	ID	20
23. Rinaldi, M. (D. Sutton), Fungus Testing Lab., Univ. Texas Health Science Center, San Antonio, TX	D	9
24. Rogers, K., Auckland Hospital, Auckland, New Zealand	ID	7
25. Tewari, J.P., Agric. Food & Nutri. Sci., Univ, Alberta, Edmonton, AB	ID	2
26. Thomas, A., Primary Industries, Oonoonba, Townsville, Australia	ID	1
27. Tsuneda, A., Biological Sciences, Univ. Alberta, Edmonton, AB	D	3
28. Udagawa, S., Nodai Research Institute, Tokyo, Japan	D	3
29. Untereiner, W., Brandon Univ., Brandon. MB	D	5
30. Yoder, J.A. (J.B. Benoit), Wittenberg Univ., Springfield, OH	ID	7

Total cultures received from:

Internal (Univ. Alberta/UA Hospitals)	46
External (North America & International)	143

Total cultures received 189

Codes: D - Deposit, ID - Identification

Table 2. Cultures Distributed in 2003

	Person or industry or culture collection and address	*Reason for shipment*	Total
1.	Berbee, M. (C.K.M. Tsui), Botany, Univ. British Columbia, Vancouver, BC	MB	9
2.	Blenis, P., Renewable Resources, Univ. Alberta, Edmonton, AB	BD	4
3.	Bush, S., Coastal Carolina Univ., Conway, SC	REQ	1
4.	Caldwell, B., Forest Science, Oregon State Univ., Corvallis, OR	MR	3
5.	Corrigan, J., Microbiologics, St. Cloud, MN	IAQ	1
6.	Currah, R., (A. Rice) Biological Sciences, Univ. Alberta, Edmonton, AB	T	22
7.	Enviro-Test Lab (Scholcz, J. / B. Bayer), Winnipeg, MB	IAQ	20
8.	From, M., Lab. for Rare & Endangered Plants, Omaha's Henry Doorly Zoo, Omaha, NE	MR	2
9.	GeneVision Inc. (N. Lacombe), Laval, QC	MB	61
10.	Hambleton, S., Agriculture & Agri-Food Canada, Ottawa, ON	MB/CR	24
11.	Hasselquist, N., Biological Sciences, Idaho State Univ., Pocatello, ID	MR	1
12.	Horner, E., Air Quality Services, Marietta, GA	IAQ	8
13.	Iwen, P., Pathology & Microbiology, Univ. Nebraska Medical Center, Omaha, NE	MB	11
14.	Jacobs, K. (M. Wingfield), Forestry & Agriculture Biotechnology Institute, Univ. Pretoria, Hatfield, South Africa	T	4
15.	Jany, J.L.(L. Sylvain), Centre de Reserche en Biologie Forestiere, Laval, Quebec	MB/MR	33
16.	Kim, J.J., Wood Science, Univ. British Columbia, Vancouver, BC	BD/T	5
17.	Kim, S.H., (C. Breuil) Wood Science, Univ. British Columbia, Vancouver, BC	BD	4
18.	Kim, S.H., Graduate School of Biotechnology; Korea Univ., Seoul, South Korea	FM	4
19.	Kong, H., Agricultural Environment, Chungcheongbuk-do Agricultural Research & Extension Services, Seoul, South Korea	T	3
20.	Koster, B. (D.W. Malloch), Botany, Univ. Toronto, Toronto, ON	MB	4
21.	Kroeger, P., Botany & Zoology Stores, Univ. British Columbia, Vancouver, BC	M	2
22.	Microbial Insights Inc., (Y. Piceno), Rockford, TN	IAQ/MB	2
23.	Mitchell, J., Biology, Ball State Univ., Muncie, IN	TE	5
24.	Nishimura, K., Research Center for Pathogenic Fungi, Chiba Univ., Tokyo, Japan	MB/P	21
25.	O'Donnell, K., Microbial Properties Research, NCAUR, ARS-USDA, Peoria, IL	MB	1
26.	Patel, S., Engineering & Fire Investigation, Technical Support Services, Kingwood, TX	MB	2
27.	Peterson, S., Microbial Properties Research, NCAUR, ARS-USDA, Peoria, IL	MB	3
28.	Pickard, M., Biological Sciences, Univ. Alberta, Edmonton, AB	EZ	4
29.	Reid, J. (J. Hausner), Microbiology, Univ. Manitoba, Winnipeg, MB	MB	7
30.	Rennie, R., National Center for Mycotic Disease, Univ. Alberta Hospital, Edmonton, AB	PH	2
31.	Schar, G., Institut fur Med. Mikrobiologie, Zurich, Switzerland	MB/T	14
32.	Seifert, K., Eastern Cereal & Oilseed Research, Agriculture & Agri-Food Canada, Ottawa	MB/T	3
33.	Stadler, M., Bayer Health Care, Wuppertal, Germany	MB/T	1
34.	Surya, P., Dimethaid Mfg. Inc., Vavennes, QC	ST	1
35.	Strassner, R. (T. Lubken), Inst. Plant Biochemistry/Fungal Metabolites, Halle, Germany	M	4
36.	Summerbell, R.C., CBS, Ultrecht, The Netherlands	MB	1
37.	Tewari, J.P., Agricultural, Food & Nutritional Sci., Univ. Alberta, Edmonton, AB	IAQ	2
38.	Thorn, G., Biology, Univ. Western Ontario, London, ON	TE	1
39.	Truksa, L., Insultech, Weston, ON	BD	5
40.	Tsang, A. (T. John), Biology, Concordia Univ., Montreal, PQ	MB	1
41.	Udagawa, S., Japan Food Research Laboratories, Tama-shi, Tokyo, Japan	T	3
42.	Zwiazek, J., Renewable Resources, Univ. Alberta, Edmonton, AB	MR	23

Total cultures distributed to:

Internal (Univ. Alberta/UA Hospitals)	57
External (North America & International)	275

Total cultures distributed 332

Codes: BD - Biodeterioration, CR – Collaborative Research, EZ - Enzyme, FM – Food Microbiology, IAQ - Indoor Air Quality; M – Metabolites; MB – Molecular Biology; ME - Microbial Ecology; MR - Mycorrhizae, PH – Physiology; ST - Susceptibility Testing; T - Taxonomy, TE - Teaching