UNIVERSITY OF ALBERTA MICROFUNGUS COLLECTION AND HERBARIUM (UAMH)

A Unit of the Devonian Botanic Garden, Faculty of Agriculture, Life and Environmental Sciences
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Celebrating 50 Years in 2010

SUMMARY OF ACTIVITIES FOR 2009

Staff, Volunteers

Professor (Curator) - **L. Sigler**
.66 FTE Devonian Botanic Garden/UAMH, Fac. Agriculture, Forestry & Home Economics
.33 FTE Medical Microbiology & Immunology, Fac. of Medicine
Consultant in Mycology, PLNA/UAH Microbiology & Public Health
& Adj. Prof. Biol. Sci.
Assistant Curator (.5 FTE Non-academic, .5 FTE trust, NSERC) – **C. Gibas**
Technical or laboratory assistants (trust): - **A. Anderson** (Sept 09 – present); **M. Sevigny** (part-time July 08-Aug 09); **V. Jajczay** (casual)
Volunteer- **M. Packer**

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

Academic Teaching & Graduate Supervision

L. Sigler

- MMI 427 Fungi Affecting Human and Animal Health (full responsibility, fall session)
- MLSCI 240 Pathogenic Bacteriology (4 lectures)
- BOT 306 Biology of the Fungi (1 lecture)

Graduate Supervisory Committees (Sigler)
M. Day, Biological Sciences, Supervisor, R. Currah

Cultures Received, Distributed and Accessioned

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

Cultures distributed on request or in exchange (**Table 2**)..... **305**

Culture Collection and Herbarium Accessions

New accessions **219**

Total accessions..... **11181**

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

Identification, Advisory and Depository Services

Several significant collections were received for deposit in 2009. Among these were 103 isolates representing six species of ophiostomatoid fungi arising from the Alberta / BC mountain pine beetle genomics project. PI's for this project are J. Cooke and F. Sperling from U of A Bio Sci. The deposited isolates have all been morphotyped and sequenced and represent different haplotypes detected within a species. An additional 7 isolates were received from the research group of C. Breuil at UBC. These included *Grosmannia clavigera* isolate (SLKW1407 = UAMH 11150), for which the complete genome has been recently sequenced.

The UAMH already holds large collections of mycorrhizal and root associated fungi established from different hosts, habitats and regions in Canada. These vouchers are used by researchers to determine how endophytic fungi interact with their plant hosts, and their potential to improve plant growth particularly under conditions of environmental stress. New accessions in 2009 include 20 isolates (and associated sequences) from *Cenococcum geophilum* mycorrhizae of Abies balsamea, Picea glauca or Betula papyrifera collected in Nova Scota and Quebec (G. Kernaghan), 7 isolates from aspen in Alberta (R. Currah, W. Wang), and 18 isolates from roots of threatened orchids, *Platanthera leucophaea* and *P. grandiflora*, collected from prairie grasslands in the US (L. Zettler). Host specific isolates have been shown to aid germination of seeds of orchid species.

Other isolates were received from medical laboratories or other agencies for identification or verification. Isolates received for identification are determined by morphology and/or sequencing. Agencies sending isolates in 2009 (Table 1) included: Mycotic Disease Branch, Center for Disease Control, Atlanta, GA, University of Florida College of Veterinary Medicine, Gainsville, National Veterinary Institute, Copenhagen, Denmark, National Centre for Mycotic Diseases, Edmonton, University of West Indies, Jamaica. We also receive samples of building materials for analysis of mold and provide advice regarding health risks of exposure to fungi.

Curatorial Activities

1. In 2010, the UAMH will celebrate its 50th anniversary. The collection is today recognized internationally as a Canadian fungal biorepository involved in education, conservation, distribution and research on living fungi of medical, scientific, industrial and heritage importance. The collection was officially established by the University of Alberta in 1960 under the direction of J.W. Carmichael, but its origins began in 1933 with the development of the first diagnostic service in medical mycology at the Provincial Laboratory of Public Health. The 11,000 accessions belonging to more than 3200 species are the result of almost 70 years of medical, biodiversity and taxonomic research by other scientists and us. UAMH isolates are used in diverse research applications as documented below under "Publications Citing UAMH Cultures or Assistance."
2. A major project is redevelopment of the UAMH database. The database is used for all aspects of collection work including selecting appropriate isolates for users, tracking inventories of preserved stocks, generating many types of reports, linking to digital images and sequences obtained by us. We annotate accessions by linking them to publications in which their use is cited and to GenBank sequence deposits based on UAMH isolates. Phase one 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 began in February for which a programmer was hired to rebuild the data structure and the front end application in the .net framework. A significant amount of work was required due to the need to upgrade a database that has been modified over several platforms since its inception in 1986. As well, the recent work uncovered many problems with bugs and incomplete data migration, resulting in much time being spent resolving problems, recovering or modifying data and checking its veracity. The work is still incomplete and the forthcoming testing phase will require a significant amount of time.

3. When complete, this database application will improve entry, viewing and retrieval of data in different configurations, incorporate hyperlinks to data located on other sites, e.g sequences or publications; and offer greater flexibility for updating the online catalogue which is now obsolete. An objective is to have the online catalogue illustrated with digital images.

4. Many of the isolates received in 2009 have added value because they are linked to sequence deposits. Molecular characterization of isolates is essential to the continued development of this culture collection and to its expanded use by others. We are incorporating sequencing on a more routine basis to identify isolates involved in infection and to re-assess the identity of isolates on deposit. Our sequencing program was set back this year, in part, due to the high volume of cultures received and the amount of work involved in accessioning and preserving them, and in part, due to staff turn-over and time involved in recruitment and training.

In-house and Collaborative Research

Refereed Journal Articles

1. 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 2009; 47:305-311.

   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.

2. Wang W, McGhee D, Gibas CFC, Tsuneda A, Currah RS. *Phialocephala urceolata*, sp. nov., from a commercial, water-soluble heparin solution Mycologia 2009; 101 136-141.

   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 acids 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 *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.

3. Sigler L, Sutton DA, Gibas CFC, Summerbell RC, Noel RK, Iwen PC. *Phialosimplex*, a new anamorphic genus associated with infections in dogs and having phylogenetic affinity to the Trichocomaceae. Medical Mycology Epub in advance of print. (DOI 10.1080/13693780903225805 (First published: 29 Sept 2009)

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

Abstracts - Posters

Proceedings (online only)

1. Sigler L, Peterson SW. 2009. Molecular genetic analysis supports recognition of new species among *Emmonsia* and *Blastomyces* isolates. International Journal of Antimicrobial Agents 34(s2):S593. (presented at 26th Int. Congress of Chemotherapy & Infection (ICC); AMMI Canada-CACMID Ann Mtg., Toronto, Abstr. P228, June 20.)
2. Lee TC, Richardson S, Goddard S, Sigler L, Gibas C, Castlebury L, Mohan S, Gharabaghi F, Gold W. Lessons from the soil: A subcutaneous fungal abscess caused by a yet unidentified coelomycete. International Journal of Antimicrobial Agents 34(s2):S116-117. (presented at 26th Int. Congress of Chemotherapy & Infection (ICC); AMMI Canada-CACMID Ann Mtg., Toronto, Abstr. P290, June 20).
3. Kammeyer PL, Schreckenberger PC, Petti CA, Pounder JI, Gibas CFC, Sigler L. Cross-reaction of *Blastomyces dermatitidis* Accuprobe test with *Chrysosporium carmichaelii*. International Society for Human and Animal Mycology Congress. Abstr. PP07-49.
4. Iwen PC, Peterson SW, Florescu DF, Kalil AC, Noel RK, Sigler L. 2009. Molecular identification of *Emericella echinulata* as a cause of cerebral aspergillosis in a patient following small bowel and liver transplantation. Abstr. F-009. American Society for Microbiology Ann. Mtg. Philadelphia, PA May 18

External Funding (Grants/Fees for Services)

NSERC. Major Resources Support (**continuing**). The University of Alberta Microfungus Collection and Herbarium (UAMH). (2008-2013) (Total $273,000)	54,600
NSERC Discovery (**continuing**). Systematics of Fungi in the Human Environment Sigler, L. 2006 to 2011 (Total $159,390)	31,878
U of A Small Faculties Fund. Equipment **(new)**. Barcode System Equipment	2,650
Income from all services including cultures distributed, preservation services, identifications, microbial assessments, consultation	18,000

Other Activities

Editorial work (LS): Journal of Clinical Microbiology (1), Mycologia (2), Veterinary Dermatology (1), Medical Mycology (1), Mycological Research (1), Clinical Microbiology and Infection (1), J Zoo & Wildlife Medicine (2), Canadian Journal of Microbiology (1), Mycotaxon (1)

Grant review: NSERC (1)

Committees (LS):

- Mycological Society of America Committee on Culture Collections. past-Chair 2008-09
- International Society for Human and Animal Mycology. Member of the International Advisory Committee for ISHAM Congress, Tokyo May 25-29, 2009. I was invited as organizer and co-convener of a symposium on Rapidly Changing Mycology: Perspectives on Morphological and Molecular Identification of Emerging and Classic Pathogens but I was unable to attend the congress due to family problems.
- Member of the ISHAM Global Panel of Opinion Leaders with an objective of transferring information on medical mycology. http://www.isham.org/Membership.html
- Member of the Mycology Network established in 2007 by the Canadian Public Health Laboratory, Public Health Agency of Canada to coordinate reference mycology services in Canada. Issues concerning fungal disease surveillance and outbreak investigation, development of training and quality assurance programs, and improving fungal serology and molecular identification are discussed by teleconference or email. I participated in a meeting in June at the AMMI Canada-CACMID Ann Mtg., Toronto.

Conference: LS attended joint International Congress of Chemotherapy & Infection / AMMI Canada-CACMID Ann Meeting in Toronto and presented a poster paper.

Awards: LS awarded Academic and Research Microbiologist (ARMCCM) Certification from Canadian College of Microbiologists for leadership in the education of Canadian microbiologists and for contributions to the advancement of knowledge in microbiology (May 18, 2009) and 40 year service award from U of A.

Publications Citing UAMH Cultures or Assistance

1. Al-Naama M, Ewaze JO, Green BJ, Scott JA. Trehalose accumulation in *Baudoinia compniacensis* following abiotic stress. International Biodeterioration & Biodegradation 2009; 63: 765-768.

   Baudoinia compniacensis is a microfungus recently described as the principal agent of fouling known as "warehouse staining", affecting building exteriors, fixtures and vegetation surfaces in areas proximate to distillery aging warehouses, commercial bakeries and other areas subject to low-level ethanol vapour exposure. The surfaces most affected tend to be highly exposed and undergo extreme diurnal temperature fluctuations. In previous work, we have demonstrated the existence of heat-inducible putative chaperone proteins that may also be induced by low-level exposures to ethanol vapour (e.g., <10 ppm). The present study investigated the cellular accumulation of trehalose, a disaccharide identified in some microorganisms to be important in the protection of cell components during adverse stress conditions, such as thermal stress. Following heat shock at 45 °C, we observed a 2.5-fold accumulation of trehalose relative to unheated controls maintained at 26 °C. Peak trehalose concentrations of 10 mg g^{-1} dry wt were seen at 90 min after heat treatment, followed by a gradual return to post-treatment by 150 min. Exposure of *B. compniacensis* cells to ethanol resulted in a similar increased accumulation of trehalose compared to unexposed controls. These findings imply that trehalose may be important in the tolerance of this fungus to abiotic stresses, such as heat and solvent exposure, and suggest future research directions for the control and prevention of warehouse staining.

2. Brockus CW, Myers RK, Crandell JM, Sutton DA, Wickes BL, Nakasone KK. Disseminated *Oxyporus corticola* infection in a German shepherd dog. Medical Mycology 2009; 47: 862-868.

   The filamentous basidiomycetous fungus, *Oxyporus corticola*, has not previously been reported in the human or veterinary medical literature. Identification of this organism as the etiologic agent of fungal

osteomyelitis and multiorgan dissemination in a German shepherd dog was confirmed by comparison of ITS and D1/D2 sequences with known isolates.

3. Calvo-Polanco M, Jones MD, Zwiazek JJ. Effects of pH on NaCl tolerance of American elm (*Ulmus americana*) seedlings inoculated with *Hebeloma crustuliniforme* and *Laccaria laccata*. Acta Physiologiae Plantarum 2009; 31:515-522.

   In the present study, we investigated the effects of pH treatments on NaCl tolerance in mycorrhizal and non-mycorrhizal American elm. American elm (*Ulmus americana*) seedlings were inoculated with *Hebeloma crustuliniforme*, *Laccaria bicolor* or with both mycorrhizal fungi and subsequently subjected to different pH solutions (pH 3, 6 and 9) containing 0 mM (control) and 60 mM NaCl for 4 weeks. Inoculation with the mycorrhizal fungi did not have a large effect on seedling dry weights when the pH and NaCl treatments were considered independently. However, when the inoculated seedlings were treated with 60 mM NaCl at pH 3 or 6, shoot to root ratios and root hydraulic conductivity were higher compared with non-inoculated plants, likely reflecting changes in seedling water flow properties. At pH 6, transpiration rates were about twofold lower in non-inoculated plants treated with NaCl compared with non-treated controls. For NaCl-treated *H. crustuliniforme*- and *L. bicolor*-inoculated plants, the greatest reduction of transpiration rates was at pH 9. Treatment with 60 mM NaCl reduced leaf chlorophyll concentrations more in non-inoculated compared with inoculated plants, with the greatest, twofold, decrease occurring at pH 6. At pH 3, root Na concentrations were higher in inoculated than non-inoculated seedlings; however, there was no effect of inoculation on root Na concentrations at pH 6 and 9. Contrary to the roots, the leaves of inoculated plants had lower Na concentrations at pH 6 and 9, but not at pH 3. The results point to an interaction between ECM fungi and root zone pH for salt tolerance of American elm.

4. Calvo-Polanco M, Zwiazek JJ, Voicu MC. Responses of ectomycorrhizal American elm (*Ulmus americana*) seedlings to salinity and soil compaction. Plant and Soil 2008; 308:189-2008.

   American elm (*Ulmus americana*) seedlings were either non-inoculated or inoculated with Hebeloma crustuliniforme, Laccaria bicolor and a mixture of the two fungi to study the effects of ectomycorrhizal associations on seedling responses to soil compaction and salinity. The seedlings were grown in the greenhouse in pots containing non-compacted (0.4 g cm^{-3} bulk density) and compacted (0.6 g cm^{-3} bulk density) soil and subjected to 60 mM NaCl or 0 mM NaCl (control) treatments for 3 weeks. All three fungal inocula had similar effects on the responses of elm seedlings to soil compaction and salt treatment. In non-compacted soil, ectomycorrhizal fungi reduced plant dry weights, root hydraulic conductance, but did not affect leaf hydraulic conductance and net photosynthesis. When treated with 60 mM NaCl, ectomycorrhizal seedlings had several-fold lower leaf concentrations of Na^+ compared with the non-inoculated plants. Soil compaction reduced Na^+ leaf concentrations in non-ectomycorrhizal plants and decreased dry weights, gas exchange and root hydraulic conductance. However, in ectomycorrhizal plants, soil compaction had little effect on the leaf Na^+ concentrations and on other measured growth and physiological parameters. Our results demonstrated that ECM associations could be highly beneficial to plants growing in sites with compacted soil such as urban areas.

5. Calvo-Polanco M, Zwiazek JJ, Jones MD, MacKinnon MD. Responses of mycorrhizal jack pine (*Pinus banksiana*) seedlings to NaCl and boron. Trees - Structure & Function 2008; 22:825-834.

   In earlier studies, we established that mycorrhizal associations protect plants against salt stress. However, elevated boron levels are often present in saline soils and little is known about the effects of boron on salt resistance of mycorrhizal plants. In the present study, we inoculated jack pine (*Pinus banksiana*) seedlings with *Hebeloma sp.*, *Suillus tomentosus* and *Wilcoxina mikolae* var. *mikolae* to study the effects of mycorrhizal associations on seedling responses to boron and salt. Seedlings were grown in the greenhouse and subjected to 60 mM NaCl, 2 mM H3BO3 or 60 mM NaCl + 2 mM H3BO3 treatments for 4 weeks. Dry weights, shoot: root ratios and chlorophyll concentrations were higher in inoculated seedlings for all treatments compared with the non-inoculated plants. When applied with NaCl, B aggravated needle necrosis while reducing Cl concentrations in shoots of non-inoculated plants. Plants treated with 2 mM H3BO3 + 60 mM NaCl had similar concentrations of Na and B to those that were treated separately with 60 mM NaCl and 2 mM H3BO3. Plants inoculated with mycorrhizal fungi had lower shoot Na concentrations compared with non-inoculated seedlings, but showed relatively little impact from elevated B concentrations.

6. Calvo-Polanco M, Zwiazek JJ, Jones MD, MacKinnon MD. Effects of NaCl on responses of ectomycorrhizal black spruce (*Picea mariana*), white spruce (*Picea glauca*) and jack pine (*Pinus banksiana*) to fluoride. Physiologia Plantarum 2009; 135: 51-61.

   Black spruce (*Picea mariana*), white spruce (*Picea glauca*) and jack pine (*Pinus banksiana*) were inoculated with Suillus tomentosus and subjected to potassium fluoride (1 mM KF and 5 mM KF) in the presence and absence of 60 mM NaCl. The NaCl and KF treatments reduced total dry weights in jack pine and black spruce seedlings, but they did not affect total dry weights in white spruce seedlings. The addition of 60 mM NaCl to KF treatment solutions alleviated fluoride-induced needle injury in ectomycorrhizal (ECM) black spruce and white spruce, but had little effect in jack pine seedlings. Both KF and 60 mM NaCl treatments reduced E values compared with non-treated control seedlings. However, with the exception of small reductions of Kr by NaCl treatments in black spruce, the applied KF and NaCl treatments had little effect on Kr in ECM plants. Chloride tissue concentrations in NaCl-treated plants were not affected by the presence of KF in treatment solutions. However, shoot F concentrations in ECM black spruce and white spruce treated with 5 mM KF + 60 mM NaCl were significantly reduced compared with the 5 mM KF treatment. The results point to a possible competitive inhibition of F transport by Cl. We also suggest that the possibility that aquaporins may be involved in the transmembrane transport of F should be further investigated.

7. Chau HW, Si BC, Goh YK, Vujanovic V. A novel method for identifying hydrophobicity on fungal surfaces. Mycological Research 2009; 113:1046-1052.

   Fungal surface hydrophobicity has many ecological functions and water contact angles measurement is a direct and simple approach for its characterization. The objective of this study was to evaluate if in growth conditions coupled with versatile image analysis allows for more accurate fungal contact angle measurements. Fungal cultures were grown on agar slide media and contact angles were measured utilizing a modified microscope and digital camera setup. Advanced imaging software was adopted for contact angle determination. Contact angles were observed in hydrophobic, hydrophilic and a newly created chronoamphiphilic class containing fungi taxa with changing surface hydrophobicity. Previous methods are unable to detect slight changes in hydrophobicity, which provide vital information of hydrophobicity expression patterns. Our method allows for easy and efficient characterization of hydrophobicity, minimizing disturbance to cultures and quantifying subtle variation in hydrophobicity.

8. Dantán-González E, Vite-Vallejo O, Martínez-Anaya C, Méndez-Sánchez M, González MC, Palomares LA, Folch-Mallol J. Production of two novel laccase isoforms by a thermotolerant strain of *Pycnoporus sanguineus* isolated from an oil-polluted tropical habitat. International Microbiology 2008; 11:163-169.

   A thermotolerant and halotolerant strain of *Pycnoporus sanguineus* was isolated from an oil-polluted site in a tropical area located in Veracruz, Mexico. This strain was able to grow at 47°C and in culture medium containing 500 mM NaCl. The strain was also tolerant to the presence of 30,000 ppm of crude Maya oil. A 68-kDa protein purified submerged cultures exhibited laccase activity towards 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS), guaiacol, syringaldazine and o-dianisidine, for which it presented the highest affinity (Km = 43 μM). Two-dimensional gel electrophoresis analysis showed that, unusual for laccases, the enzyme has two active isoforms, with isoelectric points of 7.00 and 7.08. The purified enzyme showed high thermostability, retaining 40% of its original activity after 3 h at 60°C. This property seems to correlate with a long "shelf-life", given that at 40°C enzyme activity was only gradually lost over a 5-day period incubation. Both, the fungus and its laccase are likely to have high potential for biotechnological applications.

9. Davey ML, Currah RS. *Atradidymella muscivora* gen. et sp. nov. (*Pleosporales*) and its anamorph *Phoma muscivora* sp. nov.: a new pleomorphic pathogen of boreal bryophytes. American Journal of Botany 2009; 96:1281–1288.

   During a survey of bryophilous fungi from boreal and montane habitats, 12 isolates of a hitherto unknown plant pathogenic member of the Pleosporales were recovered from *Aulacomnium palustre*, *Hylocomium splendens*, and *Polytrichum juniperinum*, and described as *Atradidymella muscivora* gen. et sp. nov. *Atradidymella* is characterized by minute, unilocular, setose pseudothecia having 2-3 wall layers; brown, fusiform, 1-septate ascospores; and a *Phoma* anamorph. The genus is distinguished from all other

pleosporalean genera with brown, fusiform ascospores on the basis of ascospore and pseudothecium morphology and a highly reduced stroma that is localized within a single host cell. *Atradidymella muscivora* is distinguished by its minute pseudothecia (<115 m) and ascospores that are slightly allantoid and constricted at the septum with the upper cell often wider than the lower. Its anamorph, *Phoma muscivora* sp. nov., is morphologically distinguishable from *P. herbarum* in having smaller conidia. Parsimony analysis of the ITS rDNA region indicates *A. muscivora* has affinities to the *Phoma-Ascochyta-Didymella* clade that is sister to the Phaeosphaeriaceae within the Pleosporales.

10. Davey ML, Tsuneda A, Currah RS. Pathogenesis of bryophyte hosts by the ascomycete *Atradidymella muscivora*. American Journal of Botany 2009; 96: 274-1280.

    Atradidymella muscivora (Pleosporales) is a bryophyte pathogen that infects the mosses *Aulacomnium palustre*, *Hylocomium splendens*, and *Polytrichum juniperinum*. Light and scanning electron microscopy and extracellular enzyme production were used to characterize the interactions between this fungus and its native hosts and the model host *Funaria hygrometrica*. Penetration was direct via hyphae or appressoria, and hosts responded by forming layered, darkly pigmented deposits at penetration sites, similar to the papillae formed by vascular plants in response to fungal infection. Infected hosts gradually became chlorotic as hyphae grew intracellularly, presumably killing host cells. Pycnidia of the *Phoma* anamorph (*P. muscivora*) and uniloculate pseudothecia were initiated as tightly packed masses of stromatic dematiaceous hyphae within a single host cell. Mature pycnidia and pseudothecia were erumpent. A new microniche among bryophilous fungi is described, whereby *A. muscivora* supplants the gemmae of *Aul. palustre* and exploits the normal nutrient-flow of the moss gametophyte. *Atradidymella muscivora* produced both cellulases and soluble polyphenolic oxidases, allowing it to also function as a saprobe and degrade the cell walls of bryophytes. The saprophytic and pathogenic abilities of *A. muscivora* suggest it may play a role in nutrient cycling, population dynamics, and small-scale disturbances in boreal ecosystems.

11. Entz SC, Kawchuk LM, Johnson DL. Discovery of a North American genetic variant of the entomopathogenic fungus *Metarhizium anisopliae* var. *anisopliae* pathogenic to grasshoppers. BioControl 2008; 53:327-339.

    A genetic variant of the entomopathogenic fungus *Metarhizium anisopliae* var. *anisopliae*, isolated from a soil in Alberta, Canada, from a location with a history of severe grasshopper infestations, was evaluated for pathogenicity in bioassays of living grasshoppers. Mortality in treated individuals drawn from a laboratory colony was 99% (LT_{50} = 6.7 days, LT_{90} = 9.6 days) at 12 days post-inoculation compared to 100% (LT_{50} = 4.1 days, LT_{90} = 5.8 days) mortality at 8 days in insects exposed to a commercial isolate of *M. anisopliae* var. *acridum* (IMI 330189). Experimental infection of field-collected grasshoppers under laboratory conditions with the native isolate of *M. anisopliae* var. *anisopliae* resulted in 100% (LT_{50} = 4.4 days, LT_{90} = 5.4 days) mortality attained within 7 days compared to 100% (LT_{50} = 4.7 days, LT_{90} = 6.3 days) mortality in 9 days in insects treated with *M. anisopliae* var. *acridum*. Amplification of fungal genomic DNA from the indigenous isolate with primers for the specific detection of *M. anisopliae* var. *anisopliae* produced a product almost 300 bp larger than expected based on previously known isolates. This is the first demonstration of a highly virulent, indigenous non-chemical control agent of grasshoppers in North America.

12. Fujihiro S, Higuchi R, Hisamatsu S, Sonoki S. Metabolism of hydroxylated PCB congeners by cloned laccase isoforms. Applied Microbiology and Biotechnology 2009; 82:853-860.

    The white-rot fungus *T. versicolor* UAMH 8272 produced two groups of laccases, each of which included several isoforms showing different isoelectric points (p*I*). Group 1 and group 2 laccases, respectively, displayed higher p*I* 5–6 and lower p*I* 3–4. Of the four cloned full-length laccase cDNAs, Lac 1 and Lac 4 were expressed in the heterologous protein expression system using *Aspergillus oryzae*. The measured p*I* of each Lac 1 and Lac 4 expressed in *A. oryzae* was lower than that of p*I* predicted from the amino acid composition. With this regard, isoelectric focusing of Lac 1 showed the presence of multiple protein bands in the 3.0–4.0 p*I* range, although the predicted p*I* value of Lac 1 was 4.7. Similarly, Lac 4 exhibited a p*I* value which was lower than that predicted (3.6 vs. 4.3, respectively). In all tested hydroxyPCBs, higher chlorinated hydroxyPCBs were less susceptible to in vitro degradation by laccase than lower chlorinated hydroxyPCBs. Although Lac 4 showed a generally higher activity than Lac 1, the two laccases were characterized by quite different substrate specificity toward two hydroxy-tetrachlorobiphenyl congeners.

Two metabolites were obtained from the metabolism of hydroxy-pentachlorobiphenyl: a ten chlorine-substituted dimer with a C–O bond, and one with a C–C bond.

13. Gargas A, Trest MT, Christensen M, Volk TJ, Blehert DS. *Geomyces destructans* sp.nov. associated with bat white-nose syndrome. Mycotaxon 2009; 108: 147–154.

    We describe and illustrate the new species *Geomyces destructans*. Bats infected with this fungus present with powdery conidia and hyphae on their muzzles, wing membranes, and/or pinnae, leading to description of the accompanying disease as white-nose syndrome, a cause of widespread mortality among hibernating bats in the northeastern US. Based on rRNA gene sequence (ITS and SSU) characters the fungus is placed in the genus *Geomyces*, yet its distinctive asymmetrically curved conidia are unlike those of any described *Geomyces* species.

14. Grant DC, Sutton DA, Sandberg CA, Tyler RD Jr, Thompson EH, Romanella AM, Wickes BL. 2009. Disseminated *Geosmithia argillacea* infection in a German Shepherd dog. Medical Mycology 2009; 47:221-226.

    We report a systemic mycosis in a German Shepherd dog caused by *Geosmithia argillacea*. Although this etiologic agent microscopically resembles a *Penicillium* species, and is histopathologically compatible with members of the genus *Aspergillus*, morphologic features and molecular characterization clearly separate it from these genera. This appears to be the first report of disseminated disease by this species in humans or animals. In vitro antifungal susceptibility testing suggests resistance to amphotericin B and voriconazole and susceptibility to caspofungin, itraconazole, and posaconazole.

15. 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 2009: 113:207-21.

    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 degrees 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.

16. Grünig CR, Queloz V, Sieber TN, Holdenrieder O. Dark septate endophytes (DSE) of the *Phialocephala fortinii* s.l. – *Acephala applanata* species complex in tree roots: classification, population biology, and ecology. Botany 2008; 86:1355–1369.

    Dark septate endophytes (DSE), a diverse group of ascomycetes, are dominant root colonizers in many ecosystems. The most frequent DSE in natural forest ecosystems in the Northern hemisphere belong to the *Phialocephala fortinii* s.l. – *Acephala applanata* species complex (PAC). Recently, species rank was assigned to seven cryptic species (CSP) of *P. fortinii* s.l.: *Phialocephala fortinii* s. str. C.J.K. Wang & H.E. Wilcox, *Phialocephala europaea* C.R. Grünig et T.N. Sieber, *Phialocephala helvetica* C.R. Grünig et T.N. Sieber, *Phialocephala letzii* C.R. Grünig et T.N. Sieber, *Phialocephala subalpina* C.R. Grünig et T.N. Sieber, *Phialocephala turiciensis* C.R. Grünig et T.N. Sieber, and *Phialocephala uotolensis* C.R. Grünig et T.N. Sieber. PAC species occur on all parts of the root system of trees, from mycorrhizal root tips to the stem base. Up to 80% of fine roots in forest stands can be colonized by them, and up to eight species occur sympatrically. The present work is a mixture of review and reconsideration of published work in the light of the subdivision of *P. fortinii* s.l. into several species. We review the current knowledge related to taxonomy, geographical distribution, population biology, and ecology of PAC species. We identified strains of *P. fortinii* s.l. from previously published studies to species level. The reassessment of earlier studies indicates that PAC species behave in a versatile manner along the mutualism-parasitism continuum and lifestyle designation

is complicated by the use of different experimental systems. Finally we define the most promising research areas, which will contribute to elucidate the ecological role of root endophytes in general and PAC species in particular.

17. Gupta AK, Williams JV, Zaman M, Singh J. In vitro pharmacodynamic characteristics of griseofulvin against dermatophyte isolates of *Trichophyton tonsurans* from tinea capitis patients. Medical Mycology 2009; 47:796–801.

    Tinea capitis is the most commonly observed fungal infection in childhood and is primarily caused by the dermatophyte species *Trichophyton tonsurans*, *Microsporum canis*, and *Trichophyton violaceum*. In North America and the United Kingdom T. tonsurans is responsible for more than 90% of cases. Griseofulvin has been the treatment of choice for tinea capitis for more than 40 years and is the sole oral antifungal agent approved by the FDA for the management of tinea capitis. Some researchers have expressed concern about the possibility of emerging resistance in tinea capitis isolates, especially when there is clinical failure to treatment. A total of 151 isolates of *T. tonsurans* (142), *M. canis* (7), and *T. violaceum* (2) collected from tinea capitis patients were evaluated for their susceptibility to griseofulvin using the CLSI M38-A method. MIC ranges and geometric means in parenthesis were observed for *T. tonsurans* 0.125-16 microg/ml (1.1 microg/ml), *M. canis* 0.25-2 microg/ml (0.61 microg/ml), and *T. violaceum* 2-4 microg/ml (2.82 microg/ml), respectively. In a time kill assay with *T. tonsurans* UAMH 9334, 50% and 90% reduction was observed in the number of colony forming units with >2x MIC after 6 h and 12 h of exposure to the griseofulvin, respectively. Of 142 *T. tonsurans* isolates studied, only three could grow on SDA containing 4 times to their griseofulvin MIC, representing resistance frequencies of 1.3x10(-6), 6.9x10(-7), and 9.7x10(-7). Furthermore a two-fold increase in MIC was observed in isolates collected at two time intervals in only one of eight patients. Interestingly, these isolates did not show the same increase in their in vitro resistance as exhibited by the three isolated mentioned above. In light of this data, we could not confirm any correlation between increased MIC and therapy failure.

18. Hernández-Luna CE, Gutiérrez-Soto G, Salcedo-Martínez SM. Screening for decolorizing basidiomycetes in Mexico. World Journal of Microbiology and Biotechnology 2008; 24:465-473.

    A survey to isolate native white rot basidiomycetes from Northeast Mexico was conducted in the forests of the Sierra Madre Oriental in the state of Nuevo León. A total of 92 isolates from at least 20 different genera, were screened on Bran-Flakes solid plate cultures for the production of ligninolytic oxidases and/or peroxidases with guaiacol and o-anisidine as substrates; their lignin depolymerizing potential using the polymeric dye Poly R 478; their ability to decolorize anthraquinonic (Remazol Brilliant Blue Reactive), azo (Acid Red 44) and triphenylmethane (Crystal Violet) dyes. Among all fungi tested, 15 isolates showed extensive decolorization of the three dyes within a week and gave a positive reaction in guaiacol and o-anisidine tests. Nine of them were also efficient degraders of Poly R-478. Two isolates (CS5 and CU1) showed decolorization of all dyes within 5 days, comparing favorably with reference strains of *P. chrysosporium*, *Pleurotus ostreatus*, and *Bjerkandera adusta*. Decolorization was associated with laccase activity in both isolates and reached 90% or more for all dyes within 24 h in 8-day-old liquid cultures. The coupling of pairs 2,4-dichlorophenol + 4-aminoantipyrine and 3-dimethylaminobenzoic acid + 3-methyl-2-benzothiazolinone hydrazone, strongly suggest that the laccases of both strains correspond to those considered of high redox potential. These strains are considered good candidates for bioremediation of dye polluted effluents due to their ligninolytic potential and decolorizing performance.

19. Hickey PW, Sutton DA, Fothergill AW, Rinaldi MG, Wickes BL, Schmidt HJ, Walsh TJ. *Trichosporon mycotoxinivorans*, a novel respiratory pathogen in patients with cystic fibrosis. Journal of Clinical Microbiology 2009; 47:3091-3097.

    This report describes the molecular epidemiology, in vitro susceptibility, colonial and microscopic morphologies, and biochemical features of *Trichosporon mycotoxinivorans*, a newly recognized pathogen that appears to have a propensity for patients with cystic fibrosis. The index patient died with histologically documented *Trichosporon* pneumonia complicating cystic fibrosis. This is also the first report of disease caused by a *Trichosporon* species in a nontransplant patient with cystic fibrosis. As *T. mycotoxinivorans* has not previously been recognized as a respiratory pathogen, the significance of its recovery from sputum samples was not initially appreciated. Genetic analysis of archived clinical samples found three additional cases of *T. mycotoxinivorans* infection which had previously been identified as other members of the genus. An additional isolate of *T. mycotoxinivorans* was identified from a clinical sample on initial testing. Three of

these four cases were also patients with cystic fibrosis. All isolates had MICs at 48 h of amphotericin B of ≥1 μg/ml and of echinocandins of ≥16 μg/ml, but they displayed various susceptibilities to the triazoles. In summary, *Trichosporon mycotoxinivorans* is a newly recognized human pathogen that is associated with cystic fibrosis.

20. Hildén K, Hakala TK, Lundell T. Thermotolerant and thermostable laccases. Biotechnology Letters 2009; 31:1117-1128.

    Laccases are phenol-oxidizing, usually four-copper containing metalloenzymes. For industrial and biotechnological purposes, laccases were among the first fungal oxidoreductases providing larger-scale applications such as removal of polyphenols in wine and beverages, conversion of toxic compounds and textile dyes in waste waters, and in bleaching and removal of lignin from wood and non-wood fibres. In order to facilitate novel and more efficient bio-catalytic process applications, there is a need for laccases with improved biochemical properties, such as thermostability and thermotolerance. This review gives a current overview on the sources and characteristics of such laccases, with particular emphasis on the fungal enzymes.

21. Husain Q, Husain M, Kulshrestha Y. Remediation and treatment of organopollutants mediated by peroxidases: a review. Critical Reviews in Biotechnology 2009; 29:94-119.

    In this paper an effort has been made to review the literature on the role of peroxidases in the remediation and treatment of a wide spectrum of aromatic pollutants. Peroxidases can catalyse degradation/transformation of polycyclic aromatic hydrocarbons, polychlorinated biphenyls, organochlorines, 2,4,6-trinitrotoluene, phenolic compounds and dyes. These enzymes are also capable of treating various types of recalcitrant aromatic compounds in the presence of redox mediators. Immobilised peroxidases from plant and fungal sources have been used for the remediation of such types of industrial pollutants on a large scale.

22. Inderbitzin P, Mehta YR, Berbee ML. *Pleospora* species with *Stemphylium* anamorphs: a four locus phylogeny resolves new lineages yet does not distinguish among species in the *Pleospora herbarum* clade. Mycologia 2009; 101: 329-339.

    Stemphylium is a genus of plant pathogens and saprobes in the Pleosporaceae (Pleosporales, Dothideomycetes, Ascomycetes). The teleomorphs of *Stemphylium*, where known, are in *Pleospora*, with *Pleospora herbarum* as the type. The goal of this study was to present a rigorous phylogenetic analysis of the relationships among *Stemphylium* isolates with particular emphasis on species delimitation in the *P. herbarum* clade, on possible new species and on the relationship of clades to cultures from type specimens. Our taxon sampling comprised 110 *Stemphylium* strains collected worldwide from various hosts and DNA sequences from four loci, from the ITS, the protein encoding GPD and EF-1 alpha genes and the intergenic spacer between vmaA and vpsA. A large EF-1 alpha intron delimited by noncanonical splice sites and encoding putative proteins was present in three unrelated isolates and was excluded from analyses. Isolates comprised 23 representatives derived from type strains, compared to type strains or otherwise connected to type material, 40 unnamed strains morphologically similar to the type *P. herbarum*, four strains from an outbreak of *Stemphylium* leaf blight of cotton in Brazil and eight strains collected in British Columbia mainly from nonagricultural hosts. Our findings provided strong support for the main groupings of *Stemphylium* obtained earlier and also revealed six possible new species. Other variation within morphological species might point to additional cryptic species. On the other hand, even with four loci, cultures ex-type of five species including *P. herbarum* were inseparable. We speculate that being self-fertile the clade including *P. herbarum* might represent a group of highly inbred, morphologically distinct lineages that have yet to accumulate detectable species-specific sequence variation.

23. Koster B, Wong B, Straus N, Malloch D. A multi-gene phylogeny for *Stachybotrys* evidences lack of trichodiene synthase (tri5) gene for isolates of one of three intrageneric lineages. Mycological Research 2009; 113:877-886.

    Members of the mitosporic fungal form-genus *Stachybotrys*, including common indoor contaminants *Stachybotrys chartarum*, *Stachybotrys echinata* and *Stachybotrys chlorohalonata*, are capable of producing potent, protein synthesis-inhibiting, trichothecene mycotoxins. A combined multi-gene approach was used to investigate relationships among species of *Stachybotrys* against which the presence/absence of the trichothecene biosynthetic pathway gene, trichodiene synthase (tri5), was evaluated. Phylogenetic analyses

partitioned species of *Stachybotrys* into three strongly supported lineages, two of which contained common indoor taxa. No tri5 PCR product was amplified from members of the third clade, which included the only member of the group with a known sexual state, *Stachybotrys albipes*. Isolates grouped with *S. albipes* also tested negative for tri5 in Southern analyses. The phylogenetic distribution of tri5 was consistent with known toxin production for the group. For isolates with tri5 product, Bayesian analysis suggested that signal from amino acid determining sites conflicted with the combined phylogeny. Incongruence however, was not supported by either SH-test results or maximum likelihood analyses. Moreover, sites rates analysis showed that tri5 was highly conserved at the amino acid level suggesting that identity at variable sites, among otherwise divergent taxa, might be the result of chance events.

24. Larena I, Melgarejo P. Development of a method for detection of the biocontrol agent *Penicillium oxalicum* Strain 212 by combining PCR and a selective medium. Plant Disease 2009; 93:919-928.

The registration of biological control agents requires the development of monitoring systems to detect and quantify the agent in the environment. *Penicillium oxalicum* strain 212 (PO212) is being developed for the control of tomato pathogens. In this study, we demonstrated that PO212 was more effective for controlling *Fusarium oxysporum* f. sp. *lycopersici* in tomato plants than 13 other *P. oxalicum* strains. A new semiselective medium was developed as a preliminary screen for *P. oxalicum* from soil. This semiselective medium was a modified Fusarium selective medium that contained 0.006 g of nystatin per liter. The growth of *P. oxalicum* strain 212 was not inhibited on this medium, but it did inhibit the growth of 11 fungal species. Specific identification of the biocontrol strain and its quantification were achieved using a polymerase chain reaction with a strain-specific pair of primers (POITS1F/POITS2R1) and dilution plating. This primer set differentiated the biocontrol strain from 13 other strains of *P. oxalicum*. There were differences in the nucleotide sequences of the internal transcribed spacer (ITS) regions of the ribosomal DNA of 25 strains of *P. oxalicum* and those of PO212. Based on the differences in the nucleotide sequences of the ITS regions in rDNA of PO212 and other *P. oxalicum* strains, a relationship between the nucleotide sequences in the ITS region and biocontrol efficacy is postulated.

25. Mahnaz, F, Khosravi AR, Yadegari MH. Comparison of the cytoplasmic proteins of *Fusarium solani* isolate, obtained from air and food sources in Iran by SDS – PAGE. Scientific-Research Iranian Veterinary Journal 2009; 4:42-48.

Studies have shown that various species of *Fusarium* grow well in food resources, specially in agricultural crops like cotton meal, rough rice, potato and wheat. Also by distributing conidia in air and inhaling them, they can act as pathogen, saprophyte or allergenic agents. *Fusarium solani* is known as soil saprophytic and it has allergenic components in cell wall and cytoplasm of conidia and hyphae, used for diagnostic and allergy therapy purposes. The goal of this study was to identify the cytoplasmic proteins of *Fusarium solani* isolates under study and evaluate the correlation and differention of the antigens between isolates. In the present study, 12 samples of *Fusarium solani*, with sources of air and foods, were maintained at collection of mycology center of faculty of Veterinary Medicine of Tehran University. They were broken by Freez and Taw and mechanical methods, and after centrifuging, supernatants which consist of most cytoplasmic proteins were assessed by SDS-PAGE technique. The results showed that 12 *Fusarium solani* isolates have common and uncommon protein bands and some isolates have special protein bands such as 87, 40 and 108 KD, in which specifics for isolates were 3, 4 and 10 respectively. Also, the bands of 24 and 32 KD were presented on the all isolates. In comparison with two standard strains, UAMH 7419 and UAMH 3317, the 24 KD band is specific for Iranian isolates, but 32 KD band was presented in standard strains. Therefore, the 24 KD band is special protein in Iran's native samples. This study suggests that for diagnostic and vaccine preparation and allergy therapy, the specific native *Fusarium solani* antigens should be used by researchers.

26. Massoumi Alamouti S, Tsui CK, Breuil C. Multigene phylogeny of filamentous ambrosia fungi associated with ambrosia and bark beetles. Mycological Research 2009; 113:822-35.

Most 'ambrosia' fungi are members of a heterogeneous group of ophiostomatoids that includes the anamorph genera *Ambrosiella*, *Raffaelea* and *Dryadomyces*. The taxonomy of these fungi based on morphological features has been complicated by these features being poorly descriptive and having evolved convergently. In this work we report maximum parsimony and Bayesian phylogenetic analysis of a multigene dataset (nSSU rDNA, nLSU rDNA and beta-tubulin gene) from sixty-seven taxa that include members of genera *Ambrosiella*, *Raffaelea* and *Dryadomyces* and a diverse set of ophiostomatoid relatives. We discuss the phylogenetic status of genus *Ambrosiella* and its relationships with representatives of *Ophiostomatales*

teleomorph and anamorph genera. Our analysis shows that ten of the thirteen species that had been assigned to the genus *Ambrosiella* are related to the teleomorph genera *Grosmannia* or *Ophiostoma*, within the *Ophiostomatales*. The multigene analysis and expanded taxon samplings provide a higher resolution for the species phylogeny and clarify detailed relationships between *Ambrosiella* associates of ambrosia and bark beetles and the closely related species of genera *Raffaelea* and *Dryadomyces*. We discuss difficulties in using the morphology of conidiophores and the mode of conidiogenesis to re-define the phylogenetic classification of *Ambrosiella* species. Finally, we report a correlation between the molecular classification of *Ophiostomatales*-related species of *Ambrosiella* and *Raffaelea* and their ecological niches.

27. Mullineux T, Hausner G. Evolution of rDNA ITS1 and ITS2 sequences and RNA secondary structures within members of the fungal genera *Grosmannia* and *Leptographium.* Fungal Genetics and Biology 2009; 46:855-867.

    The two internal transcribed spacers (ITS) of the nuclear ribosomal (r) DNA tandem repeat were examined in ophiostomatoid fungi belonging to the genera *Grosmannia* and *Leptographium* and closely-related taxa. Although the DNA sequence of the ITS region evolves rapidly, core features of the RNA secondary structure of the ITS1 and ITS2 segments are conserved. The results demonstrate that structural conservation of GC-rich helical regions is facilitated primarily through compensatory base changes (CBCs), hemi-CBCs, and compensating insertions/deletions (indels), although slippage of the RNA strand is potentially an additional mechanism for maintaining basepairing interactions. The major conclusion of the structural analysis of both ITS segments is that two factors appear to be involved in limiting the type of changes observed: a high GC bias for both ITS1 and ITS2 and structural constraints at the RNA level.

28. Peterson RL, Wagg C, Pautler M. Associations between microfungal endophytes and roots: do structural features indicate function? Botany 2008; 86:445-456.

    Roots encounter a plethora of microorganisms in the soil environment that are either deleterious, neutral, or beneficial to plant growth. Root endophytic fungi are ubiquitous. These include dark septate endophytes whose role in plant growth and the maintenance of plant communities is largely unknown. The objectives of this review were to assess the structural features of the interactions between dark septate endophytic fungi and the roots of both angiopsperms and conifers, and to suggest avenues for further research. Several light microscopy studies of endophyte–root interactions have revealed a variety of structural features, depending on host species and plant growth conditions. In some cases, when fungal hyphae enter roots they cause cell breakdown, whereas in other situations there is little noticeable effect. In some tree species, associations with these endophytes may mimic ectomycorrhizas or ectendomycorrhizas. The few ultrastructural studies indicate that intracellular hyphae lack a host-derived perifungal membrane and interfacial matrix material, features typical of biotrophic fungus – plant cell interactions. This raises questions concerning nutrient exchange between these fungi and plant cells. Further research in this area is needed. New approaches that include molecular cytology and live-cell imaging are needed to determine early changes in plant cells when challenged with these fungi.

29. Pietarinen V, Rintala H, Hyvärinen A, Lignell U, Kärkkäinen P, and Nevalainen A. Quantitative PCR analysis of fungi and bacteria in building materials and comparison to culture-based analysis. Journal of Environmental Monitoring 2008; 10:655–663.

    Prolonged moisture on building materials can lead to microbial growth on them. Microbes can emit spores, metabolites and structural parts into the indoor air and thus, cause adverse health effects of people living and working in these buildings. So far, culture methods have been used for assessment of microbial contamination of building materials. In this work, we used quantitative PCR (qPCR) for the detection of selected fungal and bacterial groups in 184 building materials of different types and compared the results with culture-based analysis. Nine either commonly found species, genera or groups of fungi, or those considered as moisture damage indicators, and one bacterial genus, *Streptomyces*, were determined using qPCR. Fungi and mesophilic actinomycetes were also cultivated using standard media and conditions of the routine analysis. The bacterial genus *Streptomyces* and the fungal group *Penicillium/ Aspergillus/ Paecilomyces* were the most prevalent microbial groups in all building material types, followed by *Stachybotrys chartarum* and *Trichoderma viride/atroviride/koningii*. The highest prevalences, concentrations and species diversity was observed on wooden materials. In general, the results of the two methods did not correlate well, since concentrations of fungi and streptomycetes were higher and their

occurrence more prevalent when determined by qPCR compared to culture-based results. However, with increasing concentrations, the correlation generally increased. The qPCR assay did not detect *Aspergillus versicolor* and *Acremonium strictum* as often as culture.

30. Plishka MJ, Tsuneda A, Currah RS. Morphology and development of *Nigrosabulum globosum*, a cleistothecial coprophile in the *Bionectriaceae* (*Hypocreales*). Mycological Research 2009; 113:815-821.

    Recent DNA sequence analyses indicated that *Nigrosabulum globosum* is a cleistothecial representative of the *Bionectriaceae* in the *Hypocreales*, but morphological characters supporting this relationship are unknown. Using light and electron microscopy we followed the development of the ascomata of this species, from the formation of gametangia through to the development of mature ascospores, and observed a series of characters that confirmed its hypocrealean affinities. These included the formation of a gel-filled centrum during early stages of ascoma development, the subsequent appearance of hyaline peridial tissue enclosed within a layer we interpret as representing a melanized uniloculate stroma, apically derived paraphyses, and an ascogenous system that gives rise to asci that were both cylindrical to clavate and globose. Ascospores, previously reported to be smooth, were ornamented with a honeycomb-like reticulum and were able to germinate within the ascoma. The carbonaceous outer (stromatic) walls of the mature, grit-like cleistothecia indicate possible resistance to UV radiation and desiccation. Furthermore, the complement of germinated ascospores would enable mature ascomata to function as propagules that could quickly initiate new growth when transferred to fresh substrate. Our reexamination of *N. globosum* also provides data that support the hypothesized close relationship with other bionectriaceous, cleistothecial coprophiles, i.e., species of *Hapsidospora*, and *Bulbithecium* in particular.

31. Quiroz-Castañeda RE, Balkcázar-López E, Dantán-González E, Martinez A, Folch-Mallol J, Martínez-Anaya C. Characterization of cellulolytic activities of *Bjerkandera adusta* and *Pycnoporus sanguineus* on solid wheat straw medium. Electronic Journal of Biotechnology [online] October 15, 2009, vol. 12, no. 4.

    Cellulolytic properties of two white rot fungi, *Bjerkandera adusta* and *Pycnoporus sanguineus*, cultivated on wheat straw agar medium, were characterized and compared. Optimal growing parameters for maximum enzyme production for both fungi were wheat straw medium pH 5 and 28°C. *B. adusta* showed, on the 6th day of culture, carboxymethylcellulose (CMC)ase activity levels 1.6 times higher than maximal *P. sanguineus* activity, achieved on the 8th day. *B. adusta* supernatants also displayed higher activity levels towards xylan (3.6-fold) compared to those of *P. sanguineus*. However, enzymes from *P. sanguineus* were more robust resisting one hour incubation at high temperatures (up to 80°C), and exhibiting activity and stability in pH range from 2 to 8. Cellulolytic activities, with molecular masses ranging from 25 to 90 kDa, from the two species were detected in zymograms.

32. Quoreshi AM, Khasa DP. Effectiveness of mycorrhizal inoculation in the nursery on root colonization, growth, and nutrient uptake of aspen and balsam poplar. Biomass and Bioenergy 2008; 32:381-391.

    Aspen and balsam poplar seedlings were inoculated with six species of ectomycorrhizal fungi (*Hebeloma longicaudum*, *Laccaria bicolor*, *Paxillus involutus*, *Pisolithus tinctorius*, *Rhizopogon vinicolor*, and *Suillus tomentosus*), one species of endomycorrhizal fungus (*Glomus intraradices)*, two species of bacteria (*Agrobacterium sp.* and *Burkholderia cepacia*), treated with a growth hormone (SR3), and co-inoculated with a combination of *Paxillus* and *Burkholderia*. The seedlings were grown in a greenhouse under three different fertility regimes. Bacterial inoculation alone did not affect seedling growth and nutrition as observed when co-inoculated with ectomycorrhizal fungus. The biomass and root collar diameter of aspen and balsam poplar were significantly increased when adequate mycorrhizas are formed and more prominent when co-inoculated with *P. involutus* and *B. cepacia* and grown at the 67% fertilizer level. Except for *R. vinicolor* and *S. tomentosus*, the other four species of ectomycorrhizal fungi and *G. intraradices* formed symbiotic associations with both plant species. Both ectomycorrhizal and endomycorrhizal colonization were observed at all fertilizer levels and fertilizer applications did not affect the colonization rates. Nitrogen and phosphorus concentrations were significantly improved in both aspen and balsam poplar compared with control only when co-inoculated with *P. involutus* and *B. cepacia*. However, plant net nitrogen uptake (content) increased significantly in all successful inoculation treatments and co-inoculated treatment when

compared with control. These results hold promise for incorporation of inoculation of *Populus sp.* with appropriate mycorrhizal fungi and selected bacteria into commercial nursery system to improve the establishment of *Populus* in various sites.

33. Rice V, Thormann MN Langor DW. Mountain pine beetle-associated blue-stain fungi are differentially adapted to boreal temperatures. Forest Pathology 2008; 38:113–123.

Mountain pine beetles (MPB) are the most serious pest of lodgepole pine in Canada and are likely to invade boreal jack pine forests. MPB vector three blue-stain fungi, *Grosmannia clavigera*, *Ophiostoma montium* and *Leptographium longiclavatum*, which contribute to beetle success. Fungal survival at extreme boreal temperatures will contribute to their success in jack pine. Growth, sporulation and survival of the three fungi at -20 to 37°C were tested in vitro. Overwintering survival of *G. clavigera* and *O. montium* was assessed in vivo. All species grew at 5–30°C, with optimal growth at 20–25°C. *Grosmannia clavigera* and *L. longiclavatum* survived at -20°C, but *O. montium* died. Growth of *G. clavigera* and *L. longiclavatum* was inhibited at 30°C, but *O. montium* grew well. *Grosmannia clavigera* and *O. montium* overwintered in living pines. These results suggest that *G. clavigera* and *L. longiclavatum* were adapted to cold boreal winters but not hot summers, with the converse true for *O. montium*. Temperature tolerance varied among *G. clavigera* isolates. British Columbian and Californian isolates grew faster at 25°C than Albertan isolates. Isolates from Alberta and Idaho / Montana grew optimally at 20°C, while British Columbian and Californian isolates grew optimally at 25°C.

34. Schulz B, Draeger S, de la Cruz TE, Rheinheimer J, Siems K, Loesgen S, Bitzer J, Schloerke O, Zeeck A, Kock I, Hussain H, Dai J, Krohn K. Screening strategies for obtaining novel, biologically active, fungal secondary metabolites from marine habitats. Botanica Marina 2008; 51:219–234.

To determine the best sources of novel, biologically active metabolites, both endophytic fungi (plant isolates) and fungi associated with algae were isolated from plants and algae from marine habitats of the North, Baltic and Mediterranean Seas, Atlantic Ocean, and Gulf of Mexico. Following preselection of the isolates according to taxon and metabolic profiles, almost all were active in at least one of the tests for antibacterial, antifungal, and/or herbicidal activities. Metabolites isolated from the culture extracts belonged to diverse structural groups; 42% were previously unknown structures. Compared to fungi associated with algae, endophytic fungi were a better source of novel metabolites and antifungal culture extracts; they produced a higher number of metabolites per fungus. *Microsphaeropsis* spp. and *Coniothyrium* spp. synthesized the highest numbers of novel metabolites per isolate, and *Geniculosporium*, *Nodulisporium* and *Phomopsis* the greatest numbers of metabolites per isolate. Based on the proportion of novel to known metabolites, endophytic fungi from marine environments equalled endophytes from terrestrial habitats. Metabolic profiles (HPLC-DAD) of the saprophytic, marine fungi belonging to *Dendryphiella* spp. from diverse temperate and subtropical locations revealed that geographical source of the isolates had little qualitative effect on secondary metabolite production in this genus.

35. Scully LR, Bidochka MJ. An alternative insect pathogenic strategy in an *Aspergillus flavus* auxotroph. Mycological Research 2009; 113:230-239.

In order to study fungal pathogen evolution, we used a model system whereby the opportunistic fungus *Aspergillus flavus* was serially propagated through the insect (*Galleria mellonella*) larvae, yielding a cysteine/methionine auxotroph of *A. flavus* with properties of an obligate insect pathogen. The auxotroph exhibited insect host restriction but did not show any difference in virulence when compared with the wild-type (Scully LR, Bidochka MJ, 2006. Microbiology 152, 223–232). Here, we report that on 1 % insect cuticle medium and synthetic *Galleria* medium, the auxotroph displayed increased extracellular protease production, a virulence factor necessary for insect pathogenesis. In the wild-type strain, protease production was deregulated during carbon (glucose), nitrogen (nitrate), or sulphate deprivation. If all three were present, protease production was vastly reduced. However, in the cysteine/methionine auxotroph, protease production was deregulated in complete medium. We suggest that the deficiency in sulphate assimilation in the auxotroph resulted in deregulation of protease production. The auxotroph exhibited delayed germination and slower hyphal growth when compared to the wild-type but there were no differences in virulence or cuticle penetration, suggesting a shift in pathogenic strategy that compensated decreased growth with increased virulence factor (extracellular protease) production. We concluded that the biosynthetic deficiency that mediated insect host restriction also increased protease production in the slow-growing auxotroph, resulting in an alternate, more host-specific pathogenic strategy. However, we

argue that transmission is not necessarily correlated with virulence as competition bioassays in insect larvae showed that the wild-type generally out-competed the auxotroph by producing the majority of the conidia on the sporulating cadavers. This is one of the few examples that highlight the effect of genome decay on nutrition acquisition, virulence, and transmission in fungal pathogen evolution.

36. Siemens JA, Zwiazek JJ. Root hydraulic properties and growth of balsam poplar (*Populus balsamifera*) mycorrhizal with *Hebeloma crustuliniforme* and *Wilcoxina mikolae* var. *mikolae*. Mycorrhiza 2008; 18:393-401.

    The effects of an E-strain fungus (*Wilcoxina mikolae* var. *mikolae*) and an ectomycorrhizal fungus (*Hebeloma crustuliniforme*) on growth and water relations of balsam poplar were examined and compared in the present study. Balsam poplar roots inoculated with *W. mikolae* var. *mikolae* (Wm) exhibited structures consistent with ectendomycorrhizal (EEM) associations, including a mantle surrounding the outside of the root and an extensive Hartig net that was located between cortical cells and extended to the vascular cylinder. Roots colonized with *H. crustuliniforme* (Hc) developed a mantle layer, indicative of an ectomycorrhizal (ECM) association, around the outer part of the root, but no distinct Hartig net was present. Wm-colonized balsam poplar also showed increased shoot growth, stomatal conductance (g s), and root volumes compared with non-inoculated and Hc-inoculated plants. However, Hc-inoculated plants had higher root hydraulic conductivity (L pr) compared with non-inoculated plants and Wm-inoculated plants. These results suggest that L pr was not a growth-limiting factor in balsam poplar and that hyphal penetration of the root cortex in itself may have little influence on root hydraulic properties.

37. Srinivasan A, Wickes BL, Romanelli AM, Debelenko L, Rubnitz JE, Sutton DA, Thompson EH, Fothergill AW, Rinaldi MG, Hayden RT, Shenep JL. Cutaneous Infection Caused by *Macrophomina phaseolina* in a Child with Acute Myeloid Leukemia. Journal Clinical Microbiology Epub 22 April 2009,doi:10.1128/JCM.02397-08.

    We report a case of *Macrophomina phaseolina* skin infection in an immuno-compromised child with acute myeloid leukemia, which was treated successfully with posaconazole, without recurrence after a hematopoietic stem cell transplant. The fungus was identified by DNA sequencing using both the internal transcribed spacer (ITS) and D1/D2 region of the 28S rDNA gene.

38. Sutton DA, Wickes BL, Anna M. Romanelli AM, Rinaldi MG, Elizabeth H. Thompson EH, Fothergill AW, Dishop MK, Elidemir O, Mallory GB, Moonnamakal SP, Adesina AM, Schecter MG. Cerebral aspergillosis caused by *Aspergillus granulosus*. Journal of Clinical Microbiology 2009; 47: 3386-3390.

    Disseminated disease by *Aspergillus granulosus* has been reported only once previously in a cardiac transplant recipient. We report a fatal central nervous system infection in a lung transplant recipient. Key features of this species in the section *Usti* include growth at 37°C and large, randomly spaced aggregates of variably shaped Hülle cells.

39. Taylor DL, McCormick MK. Internal transcribed spacer primers and sequences for improved characterization of basidiomycetous orchid mycorrhizas. New Phytologist 2008; 177:1020-1033.

    Despite advances owing to molecular approaches, several hurdles still obstruct the identification of fungi forming orchid mycorrhizas. The Tulasnellaceae exhibit accelerated evolution of the nuclear ribosomal operon, causing most standard primers to fail in polymerase chain reaction (PCR) trials. Insufficient sequences are available from well characterized isolates and fruitbodies. Lastly, taxon-specific PCR primers are needed in order to explore the ecology of the fungi outside of the orchid root. Here, progress in overcoming these hurdles is reported. Broad-spectrum basidiomycete internal transcribed spacer (ITS) primers that do not exclude most known Tulasnellaceae are presented. BLAST searches and empirical PCR tests support their wide utility within the Basidiomycota. Taxon-specific ITS primers are presented targeted to orchid-associated Tulasnella, and a core component of the *Thelephora–Tomentella* complex. The efficiency and selectivity of these primer sets are again supported by BLAST searches and empirical tests. Lastly, ITS DNA sequences are presented from several strains of *Epulorhiza*, *Ceratorhiza*, *Ceratobasidium*, *Sistotrema*, *Thanatephorus* and *Tulasnella* that were originally described in the landmark mycorrhizal studies of Currah and Warcup. Detailed phylogenetic analyses reveal some inconsistencies in species concepts in these taxonomically challenging resupinate basidiomycetes, but also help to place several

sequences from environmental samples.

40. Torres-Duarte C, Roman R, Tinoco R, Vazquez-Duhalt R. Halogenated pesticide transformation by a laccase–mediator system. Chemosphere 2009; 77:687-692.

The transformation of organic halogenated pesticides by laccase–mediator system has been investigated. Twelve pesticides were assayed in the presence of nine different mediators. Acetosyringone and syringaldehyde showed to be the best mediators. The halogenated pesticides bromoxynil, niclosamide, bromofenoxim and dichlorophen were transformed by the laccase-syringaldehyde system showing catalytic activities of 48.8, 142.0, 166.2 and 1257.6 nmol min^{-1} U^{-1}, respectively. The highest pesticide transformation rates were obtained with a mediator–substrate proportion of 5:1, one of the lowest reported so far for the laccase–mediator systems. The analysis of the main product from the dichlorophen transformation showed that an oxidative dehalogenation is involved in the catalytic mechanism. Adduct formation between the mediator syringaldehyde and the pesticides dichlorophen or bromoxynil was also found after enzymatic oxidation. The main goal of this work is to evaluate environmental-friendly mediators for the pesticide transformation, and the potential of laccase–mediator system to efficiently reduce the environmental impact of organic halogenated pesticides is discussed.

41. Tsuneda A, Wang W, Tsuneda I, Currah RS. Endomembrane system of aspen root cells plays a key role in defense against a common fungal root endophyte, *Cryptosporiopsis radicicola.* Mycologia 2009; 101:182-189.

The host-endophyte interaction between roots of aspen (*Populus tremuloides*) and *Cryptosporiopsis radicicola* was examined primarily by transmission electron microscopy. Hyphae growing on the exterior of the inoculated roots had a thick, electron-dense, adhesive sheath. At hyphal contact and penetration, host epidermal cells exhibited a series of defense responses (viz. formation of papillae and partition walls, general wall thickening and walling-off of internal hyphae). In papilla formation, loop-shaped, rough endoplasmic reticula (rER) gave rise to globose secretory vesicles that accumulated around and then fused to the developing papilla. Unlike papillae, general wall thickening was associated with the Golgi apparatus (GA) that produced cell wall materials; 1–3 layers of Golgi cisternae were in contact with or in the immediate proximity (mostly within 0–0.5 μm) of and lying parallel to the host cell wall, where they budded out numerous subglobose vesicles that fused directly to the host cell wall and made it thicker. Partition wall formation and walling-off of internal hyphae also were common; the former was associated with an extended single cisterna, which was indistinguishable from rER or individual cisternae of GA, and in the latter phenomenon internal hyphae were encased by electron-dense material containing numerous ribosomes and membranous elements that were derived apparently from proliferated rER. These pronounced defense responses protected the stele and contributed to making *C. radicicola* endophytic rather than pathogenic.

42. Tully CC, Romanelli AM, Sutton DA, Wickes BL, Hospenthal DR. Fatal *Actinomucor elegans* var. *kuwaitiensis* infection following combat trauma. Journal Clinical Microbiology 2009;46:3394-99.

We report the first case of invasive mucormycosis secondary to *Actinomucor elegans* infection. A severely injured soldier with a fatal *A. elegans* var. *kuwaitiensis* infection is described. The identification of this fungus was performed by classical and molecular methods, and this report documents the pathogenicity of the recently described variety *Actinomucor elegans* var. *kuwaitiensis.*

43. Vohník M, Burdíková Z, Albrechtová J, Vosátka M. Testate amoebae (Arcellinida and Euglyphida) vs. ericoid mycorrhizal and DSE fungi: A possible novel interaction in the mycorrhizosphere of ericaceous plants? Microbial Ecology 2009; 57:203-214.

Common occurrence of testate amoebae (TA) in the rhizosphere of mycorrhizal plants indicates existence of yet undocumented ecological interactions, involving three distinct groups of organisms: soil protists, mycorrhizal fungi, and their host plants. This tripartite relationship was to date investigated only to a limited extent, despite its probable importance for processes taking place in the mycorrhizosphere. In this study, we (1) explored spectra of different TA genera naturally associated with the rhizoplane of three autochthonous European *Rhododendron* species, (2) screened natural fungal colonization of the TA shells occupying the rhizoplane of selected rhododendrons, and (3) carried out two in vitro experiments addressing the question whether TA shells may serve as a nutrient source for ericoid mycorrhizal fungi (ErMF) and dark septate endophytes (DSE). Our field observations indicated that TA regularly associated

with the rhizoplane of all screened rhododendrons and that ErMF and/or DSE associated with their roots possibly exploited the TA shells as a nutrient source. We were unable to detect any major differences among the TA spectra from the rhizoplanes with respect to the three *Rhododendron* species. The spectra were dominated by *Diplochlamys*, *Centropyxis*, *Cyclopyxis*, *Euglypha*, *Trinema*, and *Assulina*. Positive, neutral, and negative associations were found for various TA genera × *Rhododendron* species combinations. The highest fungal colonization was observed in *Centropyxidae* and *Trigonopyxidae*, reaching up to 45% of the shells in the case of *Trigonopyxis*. In the in vitro experiments, both ErMF *Rhizoscyphus ericae* and DSE *Phialocephala fortinii* regularly colonized TA shells, utilizing them as a source of nutrients. We hypothesize a complex relationship between ErMF–DSE and TA. If corroborated, it would represent an interesting nutrient loop in the mycorrhizosphere of ericaceous plants.

44. Yi H, Calvo-Polanco M, MacKinnon MD, Zwiazek JJ. Responses of ectomycorrhizal P*opulus tremuloides* and *Betula papyrifera* seedlings to salinity. Environmental and Experimental Botany 2008; 62:357-363.

    Roots of trembling aspen (*Populus tremuloides* Michx.) and paper birch (*Betula papyrifera* Marsh.) seedlings were inoculated with *Hebeloma crustuliniforme* or *Laccaria bicolor* and treated with 25 mM NaCl for 6 weeks. Both tree species appeared to be relatively tolerant of the applied NaCl treatment and did not develop visible leaf symptoms that are characteristic of salt injury. Salt treatment reduced total dry weights in aspen and birch, but did not significantly affect transpiration rates and root hydraulic conductance. Salt-treated ectomycorrhizal aspen maintained higher root hydraulic conductance compared with non-mycorrhizal plants. Na and Cl concentrations increased in shoots and roots of mycorrhizal and non-mycorrhizal aspen and birch in response to NaCl treatment. Roots of NaCl-treated aspen inoculated with H. crustuliniforme had over twofold higher concentrations of Na compared with non-mycorrhizal NaCl-treated plants. Similarly to aspen, Na and Cl concentrations increased in roots and shoots of NaCl-treated birch seedlings. However, in birch, there were no significant differences in Na and Cl concentrations between mycorrhizal and non-mycorrhizal plants. The results suggest that salt exclusion by the ectomycorrhizal associations is host-specific or/and that the processes leading to salt exclusion are activated in ectomycorrhizal plants by a threshold salt level which may vary between plant species.

45. Yoder JA, Benoit JB, Denlinger DL, Tank JL, Zettler LW. An endosymbiotic conidial fungus, *Scopulariopsis brevicaulis*, protects the American dog tick, *Dermacentor variabilis*, from desiccation imposed by an entomopathogenic fungus. Journal of Invertebrate Pathology 2008; 97:119-127.

    The functional role of an endosymbiotic conidial fungus (*Scopulariopsis brevicaulis*) prevalent within the integumental glands and hemocoel of the American dog tick (*Dermacentor variabilis*) was investigated to explore the nature of this tick/fungus association. *D. variabilis* is normally highly resistant to *Metarhizium anisopliae*, a widely-distributed entomopathogenic fungus, but when mature female ticks harboring *S. brevicaulis* were fed a solution containing a mycotoxin (Amphotericin B) to purge this mycobiont internally, the ticks inoculated with *M. anisopliae* displayed classic signs of pathogenicity, as evidenced by recovery of *M. anisopliae* from ticks by internal fungus culture, greatly accelerated net transpiration water loss rates (nearly 3× faster than ticks containing *S. brevicaulis* naturally) and elevation of critical equilibrium humidity (CEH) closer to saturation, implying a reduced capacity to absorb water vapor and disruption of water balance (water gain ≠ water loss) that resulted in tick death. The presence of *S. brevicaulis* within the tick was previously puzzling: the fungus is transmitted maternally and there is no apparent harm inflicted to either generation. This study suggests that *S. brevicaulis* provides protection to *D. variabilis* ticks against *M. anisopliae*. Thus, the *S. brevicaulis*/tick association appears to be mutualistic symbiosis. Given that both organisms are of medical–veterinary importance, disruption of this symbiosis has potential for generating novel tools for disease control.

Table 1. Cultures Received in 2009

	Person or industry or culture collection and address	Purpose	Total
1.	Brandt, M., Mycotic Diseases Branch, Center for Disease Control, Atlanta, GA	ID	1
2.	Breuil, C. (Alamouti, S.M.), Dept of Wood Science, Univ of British Columbia, Vancouver, BC	D	7
3.	Cardamone, J., Wool Research, USDA-ARS Eastern Regional Res. Center, Wyndham, PA	ID	1
4.	Centraalbureau voor Schimmelcultures, (Snippe-Clause, F.B.), Utrecht, Netherlands	D	10
5.	Conley, K. (Douglass, T.), College of Veterinary Medicine, Veterinary Medical Center, Univ of Florida, Gainesville, Fl.	ID	1
6.	Currah, R.S. (Day, M.,Tsuneda, A., Davey, M., Wang, W.), Dept. of Biological Sciences, Univ of Alberta, Edmonton, AB	D	21
7.	Iwen, P. (Biehle, J. Creighton Univ), Univ of Nebraska Medical Center, Omaha, NE	D	1
8.	Kernaghan, G., Biol. Dept., Mount Saint Vincent Univ, Halifax, NS	D	22
9.	Kokotovic, B., National Veterinary Institute, Technical Univ of Denmark, Copenhagen, Denmark	ID	2
10.	National Institute of Technology and Evaluation, Biological Resource Center, (Nakagiri, A.), Kisarazu-shi, Japan	EX	3
11.	Reese, P., Dept of Chemistry, Univ of the West Indies, Mona, Jamaica	ID	14
12.	Rennie, R. (Sand, C.), National Center for Mycotic Diseases, Univ of Alberta Hospitals Microbiology & Public Health, Edmonton, AB	ID	1
13.	Rice, A. (Sperling, F.), Dept. of Biological Sciences, Univ of Alberta, Edmonton, AB	D	103
14.	Sutton, D.A., Fungus Testing Lab., Dept. of Pathology, Univ Texas Health Science Center, San Antonio, TX	D	3
15.	Swiss Federal Institute of Technology, Dept of Forest Pathology and Dendrology (Gruenig, C.), Zurich, Switzerland	D	2
16.	Untereiner, W., Brandon Univ, Brandon, MB	D	7
17.	Vanderwolf, K., (Malloch, D.), New Brunswick Museum, Saint John, NB	D	13
18.	Woodgyer, A., Microbiological Diagnostic Unit, Univ of Melbourne, Melbourne, Australia	D	4
19.	Zettler, L. (Stice, A.), Depts. of Biology and Chemistry, Illinois College, Jacksonville, IL	D	18
			234

Cultures received from:

1. Internal (Univ Alberta/UA Hospitals)	**125**
2. North America	**74**
3. International	**35**

Total cultures received **234**

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

Table 2. Cultures Distributed in 2009

	Person or industry or culture collection and address	Purpose	Total
1.	Artz, R., The Macaulay Institute, Soils Group, Aberdeen, Scotland	MS	9
2.	Assured Biotechnology Corporation, (Pope, L., Whelon, J.), Oak Ridge, TN	RD	9
3.	Basque Institute of Agriculture, Research and Development, (Romon Ochoa, P.), Vitoria-Gasteiz, Spain	B	13
4.	BD-Diagnostics, Diagnostic Systems, (White, V.), Sparks, MD	RD	59
5.	Bidochka, M., Dept of Biological Sciences, Brock Univ, St. Catherines, ON	IAQ	20
6.	Bio-Chem Consulting Services Ltd. (Sheppard, M.), Analytical Services Div., Calgary, AB	IAQ	7
7.	Bio-Connect, (Verplanke, C., Burgers, C.), Huissen, The Netherlands	PP	1
8.	Bouarab, K., Biology Dept, Univ of Sherbrooke, Sherbrooke, QC	PP	3
9.	Brandt, M., Mycotic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA	TE	6
10.	Briere, S., Canadian Food Inspection Agency, Plant Pathology Lab., Nepean, ON	MS	2
11.	Brown, E. (Zhang, S., Richardson, S.), Ontario Agency for Health Protection, Public Health Laboratories, Toronto, ON	RD	8
12.	Centraalbureau voor Schimmelcultures, (Verkley, G.), Utrecht, The Netherlands	EX	4
13.	Chaturvedi, V., New York Dept of Health, Mycology Laboratory, Albany, NY	MS	4
14.	Chen, M., Civil Engineering, Univ of Alberta, Edmonton, AB	CR	4
15.	Christians, J., Biological Sciences, Simon Fraser Univ, Burnaby, BC	MS	12
16.	Currah, R. (Day, M., Romanyk, K.), Dept. of Biological Sciences, Univ of Alberta, Edmonton, AB	T/MS	21
17.	Fratpietro, S., PaleoDNA Lab, Lakehead Univ, Thunder Bay, ON	MS	2
18.	Guertin, C., Inst. national de la recherché scientifique, Univ du Quebec, Laval, QC	RD	6
19.	Hambleton, S, Agriculture & Agri-Food Canada, Biodiversity (Mycology & Botany), Ottawa, ON	CR	20
20.	Harris, S., Dept of Plant Pathology, Univ of Nebraska, Lincoln, NE	MS	4
21.	Hausner, G., Dept of Microbiology, Univ of Manitoba, Winnipeg, MB	MS	1
22.	Island Mushrooms, (Sprungman, K.), Duncan, BC	E	3
23.	Kang, H.J., Agriculture Environment, Chungcheongbuk-do Agricultural Research & Extension Services, Cheongwon, Korea	CR	5
24.	Luminex Molecular Diagnostics (Pitsakis, P.), Toronto, ON	RD	6
25.	Lyew, D., Bioresource Engineering, McGill Univ, Ste-Anne-de-Bellevue, QC	ST	1
26.	Masters, E., Chemical Engineering and Applied Chemistry, Univ of Toronto, Toronto, ON	FG	1
27.	Nakagiri, A., Biological Research Center, National Institute Technology & Evaluation, Chiba, Japan	EX	3
28.	Pinto, L. (Moore, M.), Biological Sciences, Simon Fraser Univ, Burnaby, BC	MS	6
29.	Poinar, H., McMaster Univ, Hamilton, ON	MS	2
30.	Proctor, R., US Dept of Agriculture, Mycotoxin Research Unit, Peoria, IL	MT	4
31.	Reese, P. , Dept. of Chemistry, The Univ of the West Indies, Mona, Jamaica, West Indies	M	9
32.	Sadowsky, J., Dept. of Plant Pathology, Michigan State Univ, East Lansing, MI	MR	1

33.	Sage Biosciences Inc., (Rode, L.), Edmonton, AB	BD	1
34.	Sinia, A. (Wing, L.), Enviromental Biology Dept, Univ of Guelph, Guelph, ON	B	7
35.	Sorensen, J., Dept of Chemistry, Univ of Manitoba, Winnipeg, MB	M	2
36.	Spatafora, J. (Schoch, C.), Botany and Plant Pathology, Oregon State Univ, Corvallis, OR	M	1
37.	Sporometrics Inc. (Saleh, M.), Toronto, ON	PT/TE	16
38.	Stefani, F., National Research Council, Canadian Forest Services, Quebec, QC	MR	4
39.	Strobel, S., Molecular Biophysics and Biochemistry, Yale Univ, New Haven, CT	MS	3
40.	Vederas, J. (Campbell, C.), Chemistry Dept, Univ of Alberta, Edmonton, AB	M	2
41.	Villani, P., Dept Biology, Butler Univ, Indianapolis, IN	BD	3
42.	Walkling-Ribeiro, M., Canadian Research Institute for Food Safety, Univ of Guelph, Guelph, ON	FM	2
43.	Whiston, E. (Taylor, J.), Plant & Microbial Biology, Univ of California Berkeley, Berkeley, CA	MS	5
44.	Wu, J. (Sen, L.), Agricultural, Food and Nutritional Science, Univ of Alberta, Edmonton, AB	FM	2
45.	Zilberman, D., Plant & Microbial Biology, Univ of California Berkeley, Berkeley, CA	MS	1

Cultures distributed to:

1. Internal (Univ Alberta/UA Hospitals)	**29**
2. North America	**241**
3. International	**35**

Total cultures distributed **305**

Codes: **B** – Biocontrol; **BD** – Biodegredation/ Bioremediation; **CR** – Collaborative Research; **E** – Edible Fungus; **EX** – Exchange; **FG** – Fungal Genetics; **FM** – Food Mycology; **IAQ** - Indoor Air Quality; **M** – Metabolites;**MR** – Mycorrhizae; **MS** - Molecular Systematics; **MT** – Mycotoxicology; **PP** – Plant Pathology; **RD** – Reference Diagnostics; **ST** - Susceptibility Testing; **T** – Taxonomy; **TE** - Teaching