Diversity and function of fungi associated with the fungivorous millipede, *Brachycybe* lecontii

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Abstract

Fungivorous millipedes (subterclass Colobognatha) likely represent some of the earliest known mycophagous terrestrial arthropods, yet their fungal partners remain elusive. Here we describe relationships between fungi and the fungivorous millipede, *Brachycybe lecontii*. Their fungal community is surprisingly diverse, including 176 genera, 39 orders, four phyla, and several undescribed species. Of particular interest are twelve genera conserved across wood substrates and millipede clades that comprise the core fungal community of *B. lecontii*. Wood decay fungi, long speculated to serve as the primary food source for *Brachycybe* species, were absent from this core assemblage and proved lethal to millipedes in pathogenicity assays while entomopathogenic Hypocreales were more common in the core but had little effect on millipede health. This study represents the first survey of fungal communities associated with any colobognath millipede, and these results offer a glimpse into the complexity of millipede fungal communities.

Keywords

Diplopoda; Colobognatha; *Brachycybe*; millipede; mycophagy; entomopathogenicity; *Apophysomyces*; *Mortierella*; fungal diversity

1. Introduction

The Class Diplopoda, known colloquially as millipedes, represent some of the earliest known terrestrial animals, dating back to the early Devonian period *ca.* 412 million years ago (Wilson & Anderson 2004, Suarez *et al.* 2017). These early representatives were detritivores and likely played a role in early soil formation and the development of terrestrial nutrient cycling (Bonkowski *et al.* 1998, Lawrence & Samways 2003). Detritivorous millipedes continue to play a pivotal role in ecosystem processes, though herbivorous (Marek *et al.* 2012), carnivorous (Srivastava & Srivastava 1967), and fungivorous diets also exist among extant millipedes (Brewer *et al.* 2012, Marek *et al.* 2012).

Most fungivorous millipedes belong to the subterclass Colobognatha, which diverged from detritus-feeding millipedes 200-300 million years ago and possess a primitive trunk-ring architecture composed of a free sternum and/or pleurites (Brewer & Bond 2013, Rodriguez *et al.* 2018). However, these millipedes are characterized by derived rudimentary mouthparts adapted for feeding exclusively on succulent tissues such as fungi (Hopkin & Read 1992, Wilson & Anderson 2004, Wong 2018). Some taxa possess beaks composed of elongate mouthparts encompassing a fused labrum, gnathochilarium, and stylet like mandibles (Read & Enghoff 2018). Members of the Colobognatha are among the most understudied groups in Diplopoda despite their wide geographic distribution and ubiquity in natural history collections (Manton 1961, Hoffman 1980, Read & Enghoff 2009, Shorter *et al.* 2018). The ancient association between millipedes and fungi raises fascinating questions about interactions in early terrestrial ecosystems, and the possible role of fungi in diplopod success.

Most published records of fungal-millipede interactions are cases where millipedes graze on fungi in the environment (Bultman & Mathews 1996, Lilleskov & Bruns 2005) or where

parasitic fungi infect millipedes (Kudo *et al.* 2011, Hodge *et al.* 2017). Among the most studied fungal associates of millipedes are specialist ectoparasitic fungi in the Laboulbeniales (Santamaria *et al.* 2014, Enghoff & Santamaria 2015, Reboleira *et al.* 2018) and obligate arthropod gut-associated trichomycetes (Wright 1979). However, in none of these interactions does the millipede strictly depend on fungi for survival as it seemingly does in the fungivorous millipede *B. lecontii* (Diplopoda: Platydesmida: Andrognathidae).

Brachycybe lecontii is most frequently found in multigenerational aggregations in decaying wood with visible fungal growth (Gardner 1975, Shelley et al. 2005). The known geographic range of B. lecontii extends across 13 U.S. states from eastern Oklahoma to western South Carolina, south to Louisiana, and north to southern West Virginia (Shelley et al. 2005, Brewer et al. 2012). Within its known range, B. lecontii is divided into at least 4 clades that are geographically separated and may represent independent cryptic species (Brewer et al. 2012).

Historically, only one study reported *Brachycybe* feeding on an identified fungus, an unknown species of *Peniophora* (Russulales) (Gardner 1975). However, observations of *Brachycybe* species interacting with various fungi (n = 65) from community science websites such as Bugguide.net and iNaturalist.org shows that the fungal communities associated with this genus are more diverse than have been formally described (Supplemental Table 1). Recently, several basidiomycete Polyporales have been confirmed directly from *B. lecontii* and from *B. lecontii*-associated wood (Kasson *et al.* 2016). Given the discovery that Polyporales have helped facilitate the evolution of large, communal colonies with overlapping generations in other arthropods (You *et al.* 2015, Kasson *et al.* 2016, Simmons *et al.* 2016), many interesting questions are raised regarding *Brachycybe* colonies and their association with Polyporales and allied fungi.

In an attempt to uncover which fungi, if any, are consistently associated with *B. lecontii*, this study surveys fungal associates of *B. lecontii* across its known geographic range using culture-based approaches. The use of nuclear ribosomal internal transcribed spacer (ITS) barcoding on collected isolates allowed fine-scale identification and examination of culturable fungal communities. With a primary understanding of these fungal communities, we assessed diversity and applied a network analysis to determine the relationship between genetically and geographically distinct *B. lecontii* populations, their wood substrates, and associated fungal genera.

2. Materials and methods

2.1. Collection sites & field methods

Millipede collection sites were primarily identified through Brewer *et al.* (2012) and Gardner (1975), and additional sites were identified based on the known range of *B. lecontii*. Sampling was targeted to collect millipedes from all four *B. lecontii* clades. Based on previous work by Brewer (2012), individual sites were expected to contain millipedes from a single clade, with no syntopy. In total, 20 sites were sampled, with 18 yielding colonies and solitary individuals, and 2 yielding individuals only. These sites were located in Arkansas, Georgia, Oklahoma, South Carolina, Tennessee, Virginia, and West Virginia (Table 1).

At each site, decaying logs on the forest floor were overturned, examined, and replaced until colonies of *B. lecontii* were located. Colonies are defined as groups of two or more individuals, and were typically found on or near resupinate fungi covering the underside of the logs. When suitable colonies were found, individuals from single colonies were placed together in 25-ml sterile collection vials, often with a piece of the fungus-colonized wood they were on,

and stored in a cooler on ice until processing. In addition, cross-sections of logs from which colonies were collected were sampled for wood substrate identification.

2.2. Millipede processing & isolate collection

All millipedes were maintained at 4°C until processing, which typically occurred within 3 d of initial collection. After surface sterilization in 70% ethanol, individuals were sexed, sectioned with a sterilized scalpel to remove tail and gonopod sections (Macias 2017). Tail portions were preserved in 95% ethanol for millipede genotyping using custom markers previously described by Brewer et al. (2012). Gonopods were also preserved from males to permit anatomical study. The remainder of the millipede was macerated in 500 µl of sterile distilled water, and a 50-µl sample was spread on glucose yeast extract agar (GYEA) amended with antibiotics to isolate fungi (Macias 2017). GYEA was made as follows: 1000 ml distilled water, 20 g agar, 2 g yeast extract, and 0.5 g MgSO₄ (Fisher Scientific, Pittsburgh, PA, USA), 10 g dextrose (BD and Co., Franklin Lakes, NJ, USA), 1 g KH₂PO₄ (Ward's Science, Rochester, NY, USA), 50 µg thiamine, 10 µg biotin, and 1 mL of microelement solution containing 500 µg Fe₃₊, 439 μg Mn₂₊, and 154 μg Zn₂₊. Antibiotics consisted of: 100 mg tetracycline hydrochloride (Fisher Scientific, Pittsburgh, PA, USA) and 10 mg of streptomycin sulfate (Sigma-Aldrich, St. Louis, MO, USA). Cultures were sealed with parafilm and incubated at ambient conditions until growth was observed. Each colony-forming unit (CFU) was categorized by morphotype, counted, and recorded. One representative of each morphotype from each plate was retained and assigned an isolate number. Culture plates were retained for up to 3 weeks to ensure that slowgrowing fungi were counted and sampled. Depending on how rapidly fungi grew in pure culture, isolates were either grown on potato dextrose broth (PDB; BD and Co., Franklin Lakes, NJ, USA) prior to DNA extraction, or mycelium was scraped directly from plates. DNA was

extracted from all isolates using a Wizard kit (Promega, Madison, WI, USA). DNA was suspended in 75 ml of Tris-EDTA (TE) buffer preheated to 65°C. For long-term storage, isolates were kept on potato dextrose agar slants (pre-mixed PDA; BD and Co., Franklin Lakes, NJ, USA) at 4°C.

Wood samples were dried at room temperature (~21° C) for several weeks and sanded using an orbital sander equipped with 220-grit paper. Identifications were made by examining wood anatomy in cross section, based on descriptions by Panshin and de Zeeuw (1980).

2.3. Isolate identification

Isolates were identified using the universal fungal barcoding gene, the ribosomal internal transcribed spacer region (ITS), which includes ITS1, 5.8S, and ITS2 (Schoch *et al.* 2012). Primers used in this study were obtained from Integrated DNA Technologies (IDT, Coralville, IA, USA). PCR was conducted using primers ITS4 (5'-TCCTCCGCTTATTGATATGC-3') and ITS5 (5'-GGAAGTAAAAGTCGTAACAAGG-3') (White *et al.* 1990), following the protocol in Macias (2017).

PCR products were visualized via gel electrophoresis on a 1.5% w/v agarose (Amresco, Solon, OH, USA) gel with 0.5% Tris-Borate-EDTA buffer (Amresco, Solon, OH, USA). SYBR Gold (Invitrogen, Grand Island, NY, USA) was used as the nucleic acid stain, and bands were visualized on a UV transilluminator (Syngene, Frederick, MD, USA). PCR products were purified using ExoSAP-IT (Affymetrix, Santa Clara, CA). Products were Sanger sequenced with the same primers used for PCR (Eurofins, Huntsville, AL, USA). Resulting sequences were clipped using the "Clip ends" function in CodonCode Aligner v 5.1.5 and searched in the NCBI GenBank BLASTn database (Altschul *et al.* 1990) and best-match identifications recorded for each isolate.

2.4. Identification of new species

Fungal isolates were considered to represent a putative new species if three or more identical sequences were recovered with identical low percentage (threshold ≤ 95%) BLASTn matches. The large subunit of the ribosomal ITS region (LSU) was also sequenced using primers LR0R (5'-ACCCGCTGAACTTAGC-3') and LR5 (5'-TCCTGAGGGAAACTTCG-3') (Vilgalys and Hester 1990) for each putative new species. PCR conditions were as described in Macias (2017). PCR products were visualized, purified, and sequenced as above.

In the following analyses, the default parameters of each software package were used unless otherwise noted. Two putative new species were confirmed phylogenetically by constructing ITS+LSU concatenated phylogenetic trees for each new species and its known relatives based on a combination of BLAST matches and previously published literature. MEGA7 v. 7.0.16 (Kumar et al. 2016) was used to align sequences (CLUSTAL-W, Larkin et al. 2007), select a best-fit model for estimating phylogeny, and construct maximum likelihood (ML) and maximum parsimony (MP) trees for each putative new species. For ML and MP analyses, 1000 bootstrap replicates were used. The alignments used default parameters. Initial alignments were trimmed such that all positions with less than 95% site coverage were eliminated. For maximum likelihood analyses, the Tamura 3-parameter substitution model with a gamma distribution (T92+G) was used (Tamura 1992). Both maximum parsimony analyses used the subtree-pruning-regrafting algorithm (Nei and Kumar 2000). Bayesian (BI) trees were constructed using Mr. Bayes v. 3.2.5 (Ronquist et al. 2012). Three hot and one cold independent MCMC chains were run simultaneously for 1,000,000 generations, and the first 25% were discarded as a burn-in. The average standard deviation of split frequencies statistic was checked to ensure convergence between chains (Ronquist et al. 2012) and was <0.01. Final parameter

values and a final consensus tree were generated used the MrBayes "sump" and "sumt" commands respectively. The ML tree was preferred and support for its relationships in the other analyses was determined. Reference sequences used in each phylogenetic analysis are listed in Supplemental Tables 2 and 3, respectively.

2.5. Community and diversity analyses

Community and diversity analyses were used to answer two questions: (1) Are the fungal communities of *B. lecontii* conserved across millipede clade, millipede sex, wood substrate, and/or ecoregion? (2) What genera comprise the core fungal community associated with *B. lecontii*?

The effects of *B. lecontii* clade, sex, wood substrate, and ecoregion on the fungal community composition were analyzed by perMANOVA using the vegan package (Oksanen *et al.* 2018) in R version 3.4.3 (R Core Team 2017). Multilevel pairwise comparisons were performed using the pairwiseAdonis package (Arbizu 2017). Isolates where the fungal order or wood substrate were not identified were removed from the analysis. Additionally, isolates recovered from millipedes that were not part of a colony were removed. Ecoregion 45 was deleted from the analysis because its variance was significantly different from the other ecoregions (checked using function betadisper in vegan). Pairwise comparisons were only made for groups with 20 or more millipedes sampled, and in cases where more than one pairwise comparison was made, Bonferroni-corrected p-values are reported.

In addition, diversity indices were used to provide information about rarity and commonness of genera in the fungal community of *B. lecontii*, by site. Three alpha diversity indices were chosen according to recommendations laid out in Morris *et al.* (2014): number of

genera present, Shannon's diversity index, and Shannon's equitability (evenness) index (formulae from Begon *et al.* 1990). The relationship between sample size and the three diversity metrics was examined using Spearman rank correlations.

A co-occurrence network was constructed using Gephi (Bastian *et al.* 2009) for fungal isolates obtained from *B. lecontii* at the genus level. Betweenness-centrality was used to measure relative contribution of each node (single fungal genus) to connectivity across the whole network. High betweenness-centrality values are typically associated with nodes located in the core of the network (Greenblum *et al.* 2011), which in this system are defined as fungal genera with multiple edges connecting multiple *B. lecontii* clades and multiple wood substrates. Low betweenness-centrality values indicate fungal genera with a more peripheral location in the network, with fewer edges connecting clades and wood substrates (Greenblum *et al.* 2011).

2.6. Pathogenicity testing

Twenty-one isolates (Table 2) representing the diversity of all collected isolates were initially chosen for live plating pathogenicity assay (hereafter referred to as "full-diversity assay") with *Brachycybe lecontii*. A second assay (hereafter referred to as "Polyporales assay") using nineteen isolates in the Polyporales (Table 3) were tested in a separate experiment. Three isolates from the full-diversity assay were re-tested in the second assay, for a total of 37 isolates used between both assays.

Isolates were grown on GYEA and scraped to generate inoculum suspensions in sterile water. An ~500 μl aliquot of suspension was spread onto fresh GYEA plates at incubated at room temperature (21° C). After all plates were covered by fungal growth (~3 weeks), the millipedes were introduced for 7-d pathogenicity trials. Five individuals were placed on each

plate. In the full-diversity assay, 15 millipedes were used for each treatment, while 10 were used in the Polyporales assay. For a negative control, millipedes were placed on sterile GYEA plates that were changed each time contaminating fungal growth was observed. These plates required replacement due to inadvertent inoculation by the millipede's phoretic contaminants and gut microbes. Observations were made every 12 h for the first 36 h and then every 4 h for an additional 108 h until 7 d were complete. Mortality was assessed by failure of millipedes to move in response to external stimuli (Panaccione & Arnold 2017). At the end of the assay, samples of deceased individuals were preserved for chemical analyses. Surviving millipedes were returned to laboratory colonies for future studies.

Statistical analysis of survivorship was performed using the "Survival / Reliability" function in JMP 13.1.0 (SAS Institute Inc., Cary, NC). Post-hoc pairwise comparisons to the control treatment were performed for treatments that reached at least 25% mortality by the end of the trials (five treatments in the full-diversity assay, and seven in the Polyporales assay). Both log-rank and Wilcoxon tests were used. Log-rank tests score mortality at all time points evenly, while Wilcoxon tests score early mortality more heavily. For pairwise comparisons, Bonferroni corrections were applied such that the P-value reported by the analysis was multiplied by the number of comparisons made in each experiment.

3. Results and discussion

3.1. Diversity and community structure

A total of 301 millipedes were collected from 3 of 4 known *B. lecontii* clades (Brewer *et al.* 2012) and from 20 sites across 7 states (Table 1). Our study recovered 102 males and 146 mature females. Most millipedes were engaged in feeding behavior, with their heads buried in fungus growing on the log (Figure 1).

Brachycybe lecontii was found to associate with a large and diverse community of fungi, including at least 176 genera in 39 fungal orders from four phyla (Supplemental Table 4). A majority of these fungi (59%) were members of Ascomycota. Of all the genera of fungi found in this study, 40% were represented by a single isolate, and only 13% had 10 or more isolates. The most common order was the Hypocreales, containing 26% of all isolates resolved to at least order. The five next most common orders were the Polyporales (9% of all isolates), Chaetothyriales (8%), Xylariales (6%), Capnodiales (5%), and Eurotiales (5%). All other orders contained fewer than 50 isolates (<5%).

Alpha diversity was assessed at the genus level by millipede clade, wood substrate, and site. Clade 1 included 31 fungal genera, clade 3 included 156, and clade 4 included 69. The number of fungal genera obtained from each wood substrate were as follows: *Liriodendron* (114 genera), *Quercus* (74), *Betula* (54), *Carya* (45), *Fagus* (33), *Ulmus* (19), *Acer* (18), *Pinus* (11), *Carpinus* (10), and *Fraxinus* (10). However, the number of millipedes sampled for Clade 1, and all wood substrates except *Quercus* and *Liriodendron*, are likely not sufficient to capture the full diversity of the communities with culture-based methods (n<20).

At each site, fungal alpha diversity varied from 3 genera at SC2 to 63 genera at WV1 with a mean of 23 per site (Table 4). Shannon's diversity index and Shannon's equitability were also calculated for each site. Shannon's diversity index ranged from 0.95 in SC2 to 3.79 in WV2. Shannon's equitability ranged from 0.977 in AR1 and VA2 to 0.848 in TN1 (Table 4). Sites with the five highest Shannon's diversity index values did not overlap with sites with the five highest site equitability values (Table 4). Three diversity metrics were found to be correlated with sample size (alpha diversity r = 0.70, Shannon's diversity index r = 0.58, Shannon's equitability index r = -0.28), indicating that many more millipedes would be needed to capture the full fungal

diversity using culture-based methods. The wide ranges of the three diversity metrics across sites raises questions about functional redundancies in the fungal communities.

To statistically explore relationships between fungal community composition and millipede sex, millipede clade, wood substrate, and ecoregion, perMANOVAs and pairwise multilevel comparisons were used. No relationship was found between millipede sex and fungal community composition (p = 0.353, $R_2 = 0.005$), but relationships were found for millipede clade (p = 0.045, R₂ = 0.006), wood substrate (p = 0.002, R₂ = 0.049), and ecoregion (p = 0.001, $R_2 = 0.012$). However, effect size is very small for each of these factors, indicating that while there are significant relationships between these factors and the fungal community, the strength of those relationships is weak. Pairwise multilevel corrections indicate that there are significant differences between the fungal communities of Clade 1 and 3 (p = 0.009, $R_2 = 0.015$) and 4 and 3 (p = 0.003, R₂ = 0.015), but not 1 and 4 (p = 0.096, R₂ = 0.014). For wood substrate, only the fungal communities of *Liriodendron* and *Ouercus* were compared (see Methods), and they were significantly different (p = 0.045, $R_2 = 0.015$). For ecoregion, there are significant differences between the fungal communities of ecoregions 36 and 39 (p = 0.018, $R_2 = 0.014$) and 66 and 69 $(p = 0.006, R_2 = 0.018)$, but not 36 and 37 $(p = 1.000, R_2 = 0.007)$, 36 and 66 $(p = 0.084, R_2 = 0.007)$ 0.025), 37 and 66 (p = 0.462, $R_2 = 0.029$), or 37 and 69 (p = 0.300, $R_2 = 0.010$). For all of these pairwise comparisons, the effect size was small. Increased sampling depth should help clarify whether any of these factors truly impact the fungal community composition.

A network analysis and betweenness-centrality scores were used to examine how the structure of the fungal community is affected by different millipede clades and wood substrates (Figure 2). As a whole, community structure was heterogeneous across millipede clades and wood substrates. However, some genera of fungi were consistently associated with most clades

and wood substrates, as indicated by their betweenness-centrality scores. Twelve fungal genera showed high connectivity across the whole network (betweenness-centrality values > 0.5) (Figure 2). These included 1) *Phialophora* (1.55), 2) *Ramichloridium* (1.44), 3) *Mortierella* (1.28), 4) *Trichoderma* (1.03), 5) *Mucor* (1.02), 6) *Verticillium* (0.90), 7) *Phanerochaete* (0.89), 8) *Fonsecaea* (0.84), 9) *Penicillium* (0.75), 10) *Umbelopsis* (0.73), 11) *Cosmospora* (0.68), and 12) *Xylaria* (0.63). All other fungal genera fell below a 0.5 threshold, including 144 genera with betweenness-centrality values of 0.0, indicating low presence across millipede communities.

The betweenness-centrality scores from the network revealed that the core of the *Brachycybe*-associated fungal community is comprised of a small group of fungal genera that is fairly representative of the diversity in the broader millipede-associated fungal community. The structure of the network indicates that these core fungi are consumed by many individuals from different lineages of *B. lecontii* across its reported range and across many wood substrates. As such, these fungi may be the preferred fungal food source for *B. lecontii*. Alternatively, these fungi may readily survive gut passage, which would result in them being over-represented after culturing.

Only a single member of the order Polyporales, *Phanerochaete*, falls in the core of the fungal network, a highly unexpected result given that the majority of community science records of *Brachycybe* interacting with fungi appear to show the millipedes associating with Polyporales and closely allied decay fungi (Supplemental Table 1). It is possible that these fungi may serve a vital role, despite their near-absence from the core network. One such role may be to precondition substrates for arthropod colonization. For example, vascular wilt fungi predispose trees to attack by wood-boring ambrosia beetles (Hulcr & Stelinski 2017). The Verticillium wilt pathogen, *V. nonalfalfae*, predisposes tree-of-heaven to mass colonization by the ambrosia beetle

Euwallacea validus. However, the fungal community recovered from surface-disinfested beetles does not include *V. nonalfalfae* (Kasson *et al.* 2013). As such, *V. nonalfalfae* might be overlooked in its role to precondition substrates for arthropod colonization. A second possibility is that millipedes do actively utilize wood decay fungi but do not exhibit strict fidelity with single species or rely disproportionately on individual fungal community members (Kasson *et al.* 2013, Jusino *et al.* 2015, Jusino *et al.* 2016). Nevertheless, these results, much like studies examining fungal communities in red-cockaded woodpecker excavations, may indicate millipedes are either: (1) selecting degraded logs with a pre-established preferred fungal community, or (2) selecting fresh logs without any evidence of decay, then subsequently facilitating colonization by specific fungi (Jusino *et al.* 2015, Jusino *et al.* 2016).

3.2. Pathogenicity testing

To determine how members of the Polyporales and other fungi interact with *B. lecontii*, millipedes were challenged with pure cultures of a representative set of fungal isolates for 7 d. Only four of 21 isolates caused significant mortality after 7 d (Table 2): *Metarhizium flavoviride* (Hypocreales; Log-rank p < 0.0005), *Bjerkandera adusta* (Polyporales; Log-rank p < 0.0005), *Irpex lacteus* (Polyporales; Log-rank p = 0.014), and *Trametopsis cervina* (Polyporales; Log-rank p < 0.0005). Interestingly, the known virulent entomopathogens *Lecanicillium attenuatum*, *Pochonia bulbillosa*, and *Verticillium insectorum* caused little to no mortality to *Brachycybe* after 7 d of continuous exposure (Table 2).

Since three of the four pathogenic fungi were in the Polyporales, a follow-up experiment was performed using 18 isolates from the Polyporales, and one isolate of *Peniophora* (Russulales), the only fungus reported in the literature to be in association with *Brachycybe*

(Gardner 1975). Only three of these isolates were significantly more pathogenic than the sterile agar control (Table 3): *Gloeoporus pannocinctus* (Polyporales; Log-rank p < 0.0007), and two isolates of *Trametopsis cervina* (Polyporales; Log-rank p for both <0.0007). The *Bjerkandera* isolate and the *Irpex* isolate that were significantly pathogenic in the first assay were not significantly pathogenic in the second. However, the number of individuals used in the second assay was 10 per treatment, as compared to 15 per treatment in the first assay, and two individuals in the control treatment in the second assay were dead by the end of the assay. Together, these factors suggest that the results of the second assay are less reliable.

The results of the two pathogenicity assays indicate that several members of the Polyporales, including *Bjerkandera, Irpex, Trametopsis*, and *Gloeoporus*, may be pathogenic to *Brachycybe* millipedes (Figure 3), while three of the four entomopathogenic Hypocreales were not pathogenic. Additionally, seven other fungal orders caused little to no mortality (Table 2).

It is unclear how *B. lecontii* resists the well-documented entomopathogenic effects of many Hypocreales with the exception of *Metarhizium* (Hajek & St. Leger 1994). Parallel studies by Macias (2017) demonstrated that the Hypocrealean isolates used in the *Brachycybe* pathogenicity assays were pathogenic to insects. In contrast, the high incidence of pathogenicity among *Brachycybe*-associated Polyporales was unexpected. In a separate study, insects challenged with these same Polyporales were completely unaffected (Macias 2017).

One hypothesis is that Polyporales, depending on whether they are in a growth phase or a fruiting phase (Calvo *et al.* 2002, Lu *et al.* 2014), may produce chemicals that inadvertently harm millipedes. Since fruiting bodies were never observed in culture, it is likely that the fungi used in the pathogenicity assays were in a growth phase, which proved detrimental to *B. lecontii*. A second hypothesis that may explain pathogenicity among the Polyporales is that experiments

relying on pure cultures of a single fungus do not account for fungus-fungus interactions or interactions between fungi and other organisms (Li & Zhang 2014, Macias 2017).

3.3. New species

At least seven putative new species were identified, but only two were investigated in this study. The five not examined are "aff. *Coniochaeta*" (Coniochaetales), "aff. *Leptodontidium*" (Helotiales), "*Pseudonectria* aff. *buxi*" (Hypocreales), "aff. *Fonsecaea* sp." (Chaetothyriales) and "aff. *Oidiodendron*" (Onygenales). The two examined species were from the phylum Mucoromycota (Spatafora *et al.* 2017), in the orders Mortierellales and Mucorales.

Mortierella aff. ambigua is represented by 27 clonal isolates from seven widespread collection sites (AR1, AR3, AR4, VA3, WV2, WV4, and WV5), five wood substrates (Acer, Fagus, Fraxinus, Liriodendron, and Quercus), and two millipede clades (Clade 3 and 4). These isolates are 92% identical to strain "Mortierella ambigua CBS 450.88" and were deposited as GenBank accessions MH971275 and MK045304 (Supplemental Table 2 & 4). All isolates of "Mortierella aff. ambigua" produced large gemmae (Embree 1963, Aki et al. 2001) as the cultures aged past 7 d. These structures grew to at most half a centimeter across and were present on the surface and embedded in the media (Figure 4). Sporangia were not observed in any of the Mortierella aff. ambigua isolates so comparisons with known Mortierella sporangial morphology could not be made. More in-depth morphological studies are needed before a formal description can be made.

The initial alignment included 1149 characters and the final dataset was reduced to 834 characters, and the maximum parsimony analysis yielded 7 most-parsimonious trees with a length of 732. Phylogenetic analysis of a concatenated ITS+LSU 17-isolate dataset including 5

Mortierella aff. ambigua confirmed placement of this novel species sister to M. ambigua sensu stricto (Figure 4) and inside the previously described Clade 5 of Mortierella (Wagner et al. 2013). Clade 5 Mortierella species are common from soil but have also been associated with amphipods and invasive mycoses in humans. More distantly related species such as Mortierella beljakovae and Mortierella formicicola have known associations with ants but the nature of this relationship remains unclear (Wagner et al. 2013).

The second putative new species, aff. *Apophysomyces* sp., is represented by five isolates from one site (OK1), one wood substrate (*Quercus*), and one millipede clade (Clade 4). These isolates are 84% identical to strain "*Apophysomyces ossiformis* strain UTHSC 04-838" and were deposited as GenBank accessions MH971276 and MK045305 (Supplemental Table 3 & 4). Sporangial morphology of these isolates aligns with described features for this genus (Alvarez *et al.* 2010, Bonifaz *et al.* 2014), but more in-depth morphological studies are needed.

The initial alignment included 1258 characters and the final dataset was reduced to 935 characters, and the maximum parsimony analysis yielded 3 most-parsimonious trees with a length of 1101. Phylogenetic analysis of a concatenated ITS+LSU 16 isolate dataset including three aff. *Apophysomyces* sp. isolates confirmed placement of this novel species sister to the clade containing known species of *Apophysomyces* sp. (Figure 5). The combined branch length among all known species of *Apophysomyces* (0.0589 substitutions/site) is less than the branch length separating our putative new species and these known species (0.0903 substitutions/site), providing evidence that our novel species is in fact, a novel genus. The genus *Apophysomyces* has been isolated from soil but is also known to cause severe mycoses in immunocompetent humans (Alvarez *et al.* 2010, Etienne *et al.* 2012, Bonifaz *et al.* 2014).

Despite the use of more classical culture-based approaches, the recovery of seven putative new species highlights the vast amount of undescribed fungal biodiversity associated with millipedes. Culture-independent approaches will undoubtedly uncover many additional new species, possibly including some from unculturable lineages of fungi.

3.4. Summary

Brachycybe lecontii associates with a large and diverse community of fungi, including at least 176 genera in 39 fungal orders from four phyla. Significant differences in the fungal community among wood substrates, millipede clades, and ecoregions indicate that these factors influence the composition of millipede-associated fungal communities, while millipede sex does not. Follow-up studies will help determine if these factors remain important determinants in fungal community composition. One putative new species and one putative new genus of fungi were found and examined in this study, and there is evidence for several additional new species that remain to be assessed phylogenetically. Additional loci and morphological studies are needed to assess the phylogenetic placement of these fungal taxa.

The core fungal community of *B. lecontii* consists of fungi from at least nine orders, primarily members of phylum Ascomycota. While community science records of *Brachycybe* show the millipedes interacting with almost entirely Basidiomycota, especially Polyporales, only one genus from that order occurs in the core of the network. The disagreement between the bulk of community science records and the core network identified in this study can be explained by the fact that observers often overlook the dozens to hundreds of microfungi that co-occur on and in the large Polyporales fruiting bodies.

Four genera in the Polyporales were found to be pathogenic to *Brachycybe* in live-plating

assays, while three genera of notorious entomopathogens from the Hypocreales did not cause significant mortality in millipedes. Only a single fungus outside the Polyporales caused significant mortality. However, the results of simple culture-based experiments may not be accurate representations of what happens when these organisms interact in nature.

In less than a decade, the research on arthropod-fungus interactions has accelerated and led to the discoveries of several new associations (Voglmayr *et al.* 2011, Menezes *et al.* 2015, You *et al.* 2015). This study demonstrates that the complexity of millipede-fungus interactions has been underestimated and these interactions involve many undescribed species. This paper represents the first comprehensive survey of fungal communities associated with any member of the millipede subterclass Colobognatha. We anticipate that future studies of millipede-fungus interactions will yield countless new fungi and clarify the ecology of these interactions.

Acknowledgements

We thank Derek Hennen, Mark Double, Nicole Utano, and Toby Grapner for assistance with collection of millipedes and/or maintenance of cultured fungi. AM was supported by WVU Ruby Fellowship. MTK was supported by the West Virginia Agricultural and Forestry Experiment Station, Morgantown, WV.

Author contributions

A.M.M., P.E.M., E.M.M., M.S.B., D.G.P., R.V.M.R., and M.T.K. conceived of the study.

A.M.M., D.P.G.S., C.M.S., K.L.W., M.C.B., A. M. M., V.W., T.H.J., and M.T.K. performed laboratory work with the help/advice of P.E.M., M.C.B., D.G.P., J.E.S., G.R.B. A.M.M., P.E.M.,

E.M.M., and M.T.K. analyzed data. A.M.M., P.E.M., E.M.M., M.S.B., J.E.S., G.R.B, R.V.M.R., and M.T.K. wrote the manuscript with input from all coauthors.

Supplementary data

Supplementary data related to this article include Tables S1-S4.

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Figure Legends

Figure 1. *Brachycybe lecontii* colony feeding on the white-rot fungus *Irpex lacteus* (Basidiomycota: Polyporales). Mature adults (larger individuals in the photo) range from 1.5 cm

– 2 cm in length.

Figure 2. Fungal community network across *B. lecontii* clades and wood substrates. Small unlabeled nodes represent fungal genera, color-coded by taxonomic order. Orders with fewer than 10 isolates are lumped into "Other". Genus nodes with betweenness-centrality scores >0.5 are labeled with the rank of their betweenness-centrality score (1-12). White and black nodes represent clades and wood substrates, respectively. For these, the size of the node represents the relative sample size. Edges represent interactions between a fungal genus and a wood substrate/clade. Edge boldness indicates the strength of the interaction.

Figure 3. Representative outcomes of live-plating assay with Polyporales. A-C show *B. lecontii* with no outward disease symptoms after 7 d of exposure to the indicated fungus, and D-F show millipedes that were killed by the indicated fungus. In all three examples of mortality, fungal hyphae are growing over the millipede. A: *Phlebia livida* (BC0629), B: *Ceriporia lacerata* (BC1158), C: *Scopuloides rimosa* (BC1046), D: *Trametopsis cervina* (BC0494), E: *Bjerkandera adusta* (BC0310), F: *Irpex lacteus* (BC0523).

Figure 4. Concatenated ITS+LSU phylogenetic tree of *Mortierella* aff. *ambigua* and close relatives. Bootstrap support and posterior probabilities are indicated near each node (ML/MP/BI), and nodes with >50% support are labeled. Dashes indicate that a particular node did not appear in the indicated analysis. The grey box indicates the isolates belonging to *Mortierella* aff. *ambigua*. A representative culture of the fungus with gemmae is shown in the upper left.

Figure 5. Concatenated ITS+LSU phylogenetic tree of aff. *Apophysomyces* sp. and close relatives. Bootstrap support and posterior probabilities are indicated near each node (ML/MP/BI), and nodes with >50% support are labeled. Dashes indicate that a particular node did not appear in the indicated analysis. The grey box indicates the isolates belonging to aff. *Apophysomyces* sp. A representative culture of the fungus is shown in the upper left.

Figure 1



Figure 2

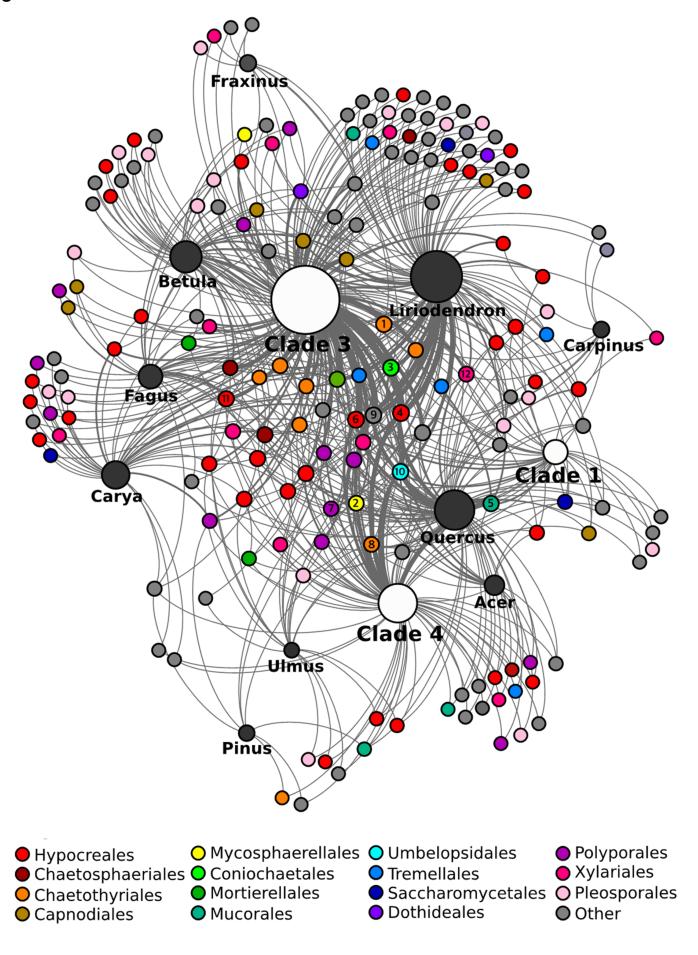


Figure 3

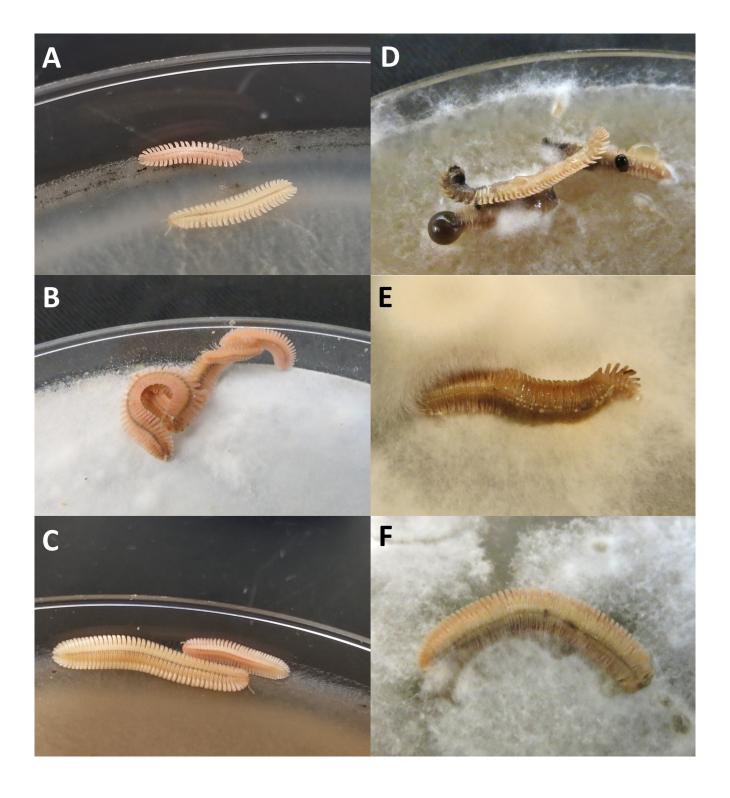


Figure 4

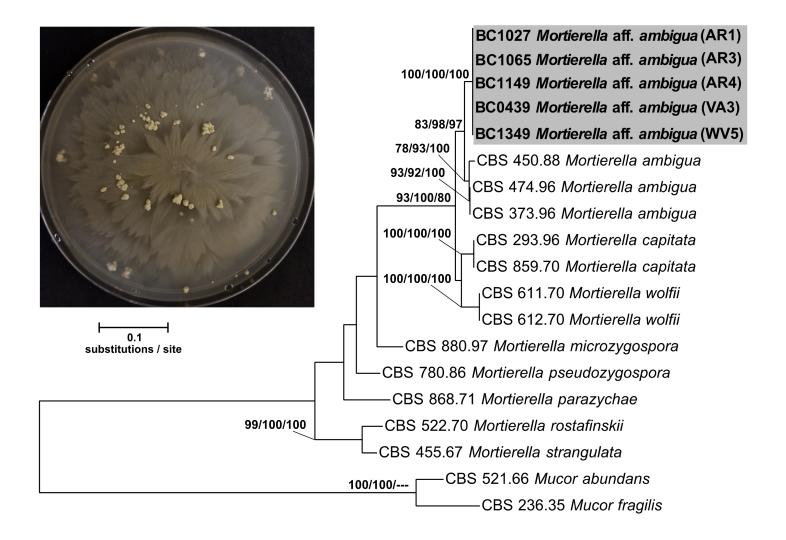


Figure 5

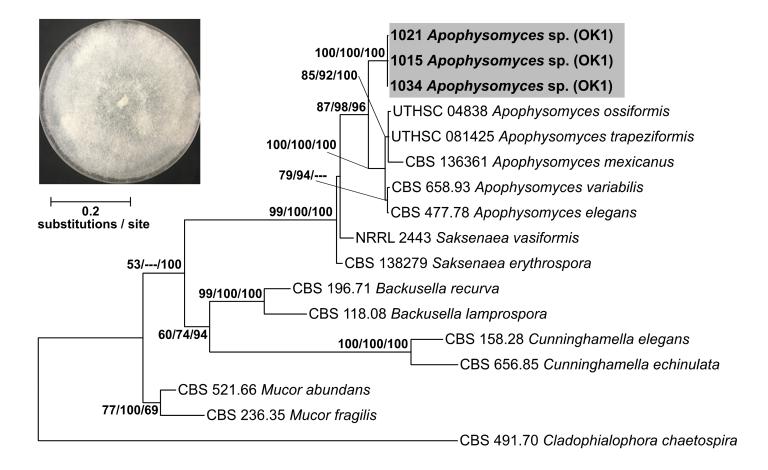


Table 1. Brachycybe lecontii collection sites.

Site	Collection reference	Millipede	Level 4	# millipedes
		clade	ecoregion	sampled
AR1	Gardner 1975	4	37A	6
AR2		4	36B	6
AR3		4	36C	13
AR4	Brewer et al. 2012	4	37A	22
AR5		4	36B	14
AR6		4	36B	12
GA1	Gardner 1975	1	66D	9
OK1	Brewer et al. 2012	4	36D	14
SC1	Brewer <i>et al.</i> 2012, Gardner 1975	1	66D	22
SC2	Gardner 1975	1	45E	4
TN1	Gardner 1975	3	69D	42
VA1	Brewer <i>et al.</i> 2012, Gardner 1975	3	69D	4
VA2		3	67I	8
VA3	Gardner 1975	3	69D	15
VA4		1	67H	5
WV1	Brewer <i>et al.</i> 2012, Gardner 1975	3	69D	29
WV2	,	3	69D	24
WV3		3	69D	4
WV4		3	69D	12
WV5		3	69D	36

Table 2. Results of pathogenicity assays using a representative set of fungal community members isolated from *B. lecontii*. HPP = Hours post-plating. Asterisks denote significantly faster and greater mortality in a treatment, compared to the negative control: * = p < 0.05, ** = p < 0.01, *** = p < 0.001. Both Log-rank P and Wilcoxon P are Bonferroni-corrected. † Denotes isolates tested again in the Polyporales pathogenicity assay.

Name	Order	Isolate	Time to 50% mortality	% dead at 7 days HPP	Log-rank P	Wilcoxon P
Negative control				0%		
Pestalotiopsis microspora	Amphisphaeriales	BC0630		20%		
Chaetosphaeria myriocarpa	Chaetosphaeriales	BC0320		0%		
Capronia dactylotricha	Chaetothyriales	BC1244		0%		
Fonsecaea sp.	Chaetothyriales	BC1147		0%		
Phialophora americana	Chaetothyriales	BC1193		7%		
Lecanicillium attenuatum	Hypocreales	BC0678		0%		
Metarhizium flavoviride	Hypocreales	BC1163	136 HPP	87%	<.0005***	<.0005***
Pochonia bulbillosa	Hypocreales	BC0029		0%		
Trichoderma viride	Hypocreales	BC1216		7%		
Verticillium insectorum	Hypocreales	BC0482		0%		
Mortierella aff. ambigua	Mortierellales	BC1150		0%		
Mortierella sp.	Mortierellales	BC0530		27%	0.173	0.175
aff. Apophysomyces sp.	Mucorales	BC1015		0%		
Mucor abundans	Mucorales	BC1010		0%		
Ramichloridium anceps	Mycosphaerellales	BC0329		0%		
Bjerkandera adusta†	Polyporales	BC0310	36 HPP	80%	<.0005***	<.0005***
Irpex lacteus †	Polyporales	BC0523	72 HPP	47%	0.014*	0.0155*
Trametopsis cervina†	Polyporales	BC1143	36 HPP	100%	<.0005***	<.0005***
Umbelopsis angularis	Umbelopsidales	BC0529		13%		
Umbelopsis isabellina	Umbelopsidales	BC1290		0%		
Umbelopsis ramanniana	Umbelopsidales	BC1028		0%		
Overall					<.0001***	<.0001***

Table 3. Results of pathogenicity assays using a representative set of Polyporales isolated from *B. lecontii*. HPP = Hours post-plating. Asterisks denote significantly faster and greater mortality in a treatment, compared to the negative control: * = p < 0.05, ** = p < 0.01, *** = p < 0.001. Both Log-rank P and Wilcoxon P are Bonferroni-corrected. † Denotes isolates used in initial pathogenicity assay.

Name	Order	Isolate	Time to 50% mortality	% dead at 7 days HPP	Log-rank P	Wilcoxon P
Negative control				20%		
Bjerkandera adusta†	Polyporales	BC0310	36 HPP	50%	0.8484	0.4907
Ceriporia lacerata	Polyporales	BC1158		10%		
Ceriporiopsis gilvescens	Polyporales	BC0174		0%		
Gloeoporus pannocinctus	Polyporales	BC0042	12 HPP	100%	<.0007***	<.0007***
Irpex lacteus	Polyporales	BC1038		30%	1.0000	1.0000
Irpex lacteus †	Polyporales	BC0523	72 HPP	50%	0.7119	0.5033
Junghuhnia nitida	Polyporales	BC0528		10%		
Phanerochaete cumulodentata	Polyporales	BC0709		0%		
Phanerochaete sordida	Polyporales	BC0691	84 HPP	60%	0.2352	0.1603
Phlebia acerina	Polyporales	BC1331		0%		
Phlebia fuscoatra	Polyporales	BC1014		0%		
Phlebia livida	Polyporales	BC0629		0%		
Phlebia subserialis	Polyporales	BC0054		0%		
Phlebiopsis flavidoalba	Polyporales	BC1426		10%		
Phlebiopsis gigantea	Polyporales	BC1049		0%		
Scopuloides rimosa	Polyporales	BC1046		0%		
Trametopsis cervina†	Polyporales	BC1143	36 HPP	100%	<.0007***	<.0007***
Trametopsis cervina	Polyporales	BC0494	36 HPP	100%	<.0007***	<.0007***
Peniophora pithya	Russulales	BC1467		0%		
Overall					<.0001***	<.0001***

Table 4. Collection information and genus-level diversity indices for each site.

for each site.					
Site	# millipedes	Alpha	Shannon's	Shannon's	
5110	sampled	diversity	diversity index	equitability	
AR1	6	11	2.342	0.977	
AR2	6	14	2.497	0.946	
AR3	13	17	2.590	0.914	
AR4	22	26	3.064	0.941	
AR5	14	19	2.801	0.951	
AR6	12	18	2.583	0.894	
GA1	9	13	2.378	0.927	
OK1	14	18	2.737	0.947	
SC1	22	14	2.262	0.857	
SC2	4	3	0.950	0.865	
TN1	42	42	3.170	0.848	
VA1	4	34	3.301	0.936	
VA2	8	11	2.342	0.977	
VA3	15	24	3.043	0.957	
VA4	5	7	1.787	0.918	
WV1	29	63	3.784	0.913	
WV2	24	57	3.790	0.938	
WV3	4	16	2.599	0.937	
WV4	12	24	3.033	0.954	
WV5	36	34	3.045	0.864	

Supplemental Table 1. Community science records of Brachycybe from BugGuide and iNaturalist websites. Habit and fungus columns were based on subjective

Species	Database	URL	Year	Contributor	Habit	Fungus?
B. lecontii	BugGuide	https://bugguide.net/node/view/45/bgpage	2002	Troy Bartlett	Colony on bark	Not apparent
B. lecontii	BugGuide	https://bugguide.net/node/view/49/bgpage	2000	Troy Bartlett	Colony on bark	Not apparent
B. lecontii	BugGuide	https://bugguide.net/node/view/57554/bgpage	1969	Steven Barney	Individual on dead leaf	Not apparent
B. lecontii	BugGuide	https://bugguide.net/node/view/213351/bgpage	2008	Tim Nichols	Colony on bark (?)	Not apparent
B. lecontii	BugGuide	https://bugguide.net/node/view/595215/bgpage	2011	David J. Thomas	Individual on rock	Not apparent
B. lecontii	BugGuide	https://bugguide.net/node/view/1178937/bgpage	2016	Jonathan Carpenter	Individual on dead wood	Not apparent
B. lecontii	BugGuide	https://bugguide.net/node/view/1517909/bgpage	2018	John Lampkin	Individual on rock	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/17512358	2018	"wjneely"	(Individual in collection)	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/17283380	2018	"rhinoclemmys"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/13439380	2018	"kevinfitzpatrick"	(Individual in collection)	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/12280088	2018	"cavemander17"	Individual on rock	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/10718361	2018	"paulmarek"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/8057119	2017	"hazelsnail"	(Individual in collection)	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/6737379	2017	"beschwar"	Colony on rotten wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/6604286	2017	"mark_swanson"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/6537354	2017	"libbing_life"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/6451167	2017	"reallifeecology"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/6451129	2017	"muir"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/5524007	2017	"chinquapin"	Individual on wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/5012087	2017	"reallifeecology"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/4534657	2016	"reallifeecology"	Individual on rock	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/3402635	2016	"mhedin"	Colony on rotten wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/3007821	2016	"reallifeecology"	(Individual in collection)	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/2877858	2016	"damontighe"	Large colony on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/453193	2013	"eric_hunt"	Individual on dead wood	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/134815	2009	"rcurtis"	(Individual in collection)	Not apparent
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/4308248	2014	"michaelskvarla"	Colony on dead wood	Yes; grey phlebioid crust
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/11292069	2018	"teriyaki12"	Colony on rotten wood	Yes; tan poroid crust
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/2360344	2015	"eric_hunt"	Colony on dead wood	Yes; Terana caerulea
B. lecontii	iNaturalist	https://www.inaturalist.org/observations/13127260	2018	"rdandekar"	Large colony on dead wood	Yes; <i>Trichoderma</i> -infected white phlebioid crust

		27		2010	U 1U		Yes; well-rotted black
	lecontii		https://www.inaturalist.org/observations/11265140	2018	"goody"	Large colony on dead wood	fungus
	lecontii		https://www.inaturalist.org/observations/12606811	2018	"jeremysouthers1"	Individual on pine bark	Yes; white crust
	lecontii		https://www.inaturalist.org/observations/9988932	2017	"rdandekar"	Large colony on dead wood	Yes; white crust
В.	lecontii	iNaturalist	https://www.inaturalist.org/observations/5322157	2005	"larry14"	Colony on dead wood	Yes; white crust
В.	lecontii	iNaturalist	https://www.inaturalist.org/observations/5212886	2017	"muddynaturalist"	Colony on dead wood	Yes; white hyphal cords
_					W 1 1 104W		Yes; white hyphal mat and
	lecontii		https://www.inaturalist.org/observations/3915382	2016	"chris184"	Large colony on dead wood	cup fungus
	lecontii		https://www.inaturalist.org/observations/13292468	2018	"daniel_folds "	Large colony on snag	Yes; white poroid bracket
В.	lecontii	BugGuide	https://bugguide.net/node/view/53529/bgimage	2006		Large colony on dead wood	Yes; white-grey crust
В.	petasata	BugGuide	https://bugguide.net/node/view/270869/bgimage	2009	Rob Craig	Colony under rotten log	Yes; phlebioid white crust
В.	producta	BugGuide	https://bugguide.net/node/view/1027823/bgimage	2014	Sam McNally	Individual on dead wood	Not apparent
В.	producta	i Naturalist	https://www.inaturalist.org/observations/10618906	2018	"damarisb"	Individual on wood	Not apparent
В.	producta	iNaturalist	https://www.inaturalist.org/observations/9480009	2018	"kueda"	Individual on dead wood	Not apparent
В.	producta	$i \\ Natural is t$	https://www.inaturalist.org/observations/9465211	2018	"tiwane"	Individual on dead wood	Not apparent
В.	producta	iNaturalist	https://www.inaturalist.org/observations/8771365	2017	"mazer"	Colony on rotten wood	Not apparent
В.	producta	iNaturalist	https://www.inaturalist.org/observations/5540144	2017	"richardwasson"	(Individual in collection)	Not apparent
В.	producta	iNaturalist	https://www.inaturalist.org/observations/5536177	2017	"dominic"	Colony on rotten wood	Not apparent
В.	producta	iNaturalist	https://www.inaturalist.org/observations/4502473	2016	"icosahedron"	Colony on dead wood	Not apparent
В.	producta	iNaturalist	https://www.inaturalist.org/observations/1404122	2015	"loarie"	Individual on dead wood	Not apparent
В.	producta		https://www.inaturalist.org/observations/1117299	2014	"biosam"	Individual on dead wood	Not apparent
В.	producta		https://www.inaturalist.org/observations/1108594	2011	"temminicki"	Individual on dead wood	Not apparent
В.	producta	BugGuide	https://bugguide.net/node/view/514775/bgimage	2011	Timothy Boomer	Colony on rotten wood	Yes; brown crust
В.	producta	iNaturalist	https://www.inaturalist.org/observations/4551536	2016	"m_patton"	Colony on dead wood	Yes; brown crust
В.	producta		https://www.inaturalist.org/observations/5406781	2017	"catchang"	Colony on rotten wood	Yes; grey hyphae
В.	producta		https://www.inaturalist.org/observations/5471277	2017	"loarie"	Colony on rotten wood	Yes; tan phlebioid crust
В.	producta		https://www.inaturalist.org/observations/10189738	2018	"katewread"	Colony on rotten wood	Yes; white crust
	producta		https://www.inaturalist.org/observations/9556670	2018	"lisahug"	Individual on dead wood	Yes; white crust
	producta		https://www.inaturalist.org/observations/2701345	2016	"loarie"	Individual on dead wood	Yes; white hyphal mat
	1						Yes; white-green hyphal
В.	producta	iNaturalist	https://www.inaturalist.org/observations/6908225	2017	"biosam"	Individual on rotten wood	mat
В.	producta	iNaturalist	https://www.inaturalist.org/observations/4784269	2016	"icosahedron"	Colony on dead wood	Yes; white-tan crust
В.	rosea		https://bugguide.net/node/view/169590/bgpage	2007	Jim McClarin	Rotting oak wood	Not apparent
В.	rosea	BugGuide	https://bugguide.net/node/view/418663/bgpage	2010	Debbi Brusco	Individual on dead wood	Not apparent

В.	rosea	BugGuide	https://bugguide.net/node/view/1508463/bgimage	2018	"Madratter"	Individual on dead leaf	Not apparent
В.	rosea		https://bugguide.net/node/view/904123/bgimage	2014	Sharon Hadley	Individual on dead wood	Not apparent
В.	rosea	iNaturalist	https://www.inaturalist.org/observations/6543298	2017	"biosam"	(Colony in collection)	Not apparent
В.	rosea		https://www.inaturalist.org/observations/5914163	2017	"leptonia"	Individual on dead wood	Not apparent
В.	rosea	iNaturalist	https://www.inaturalist.org/observations/3067933	2016	"rebeccafay"	Colony on rotten wood	Not apparent
В.	rosea	iNaturalist	https://www.inaturalist.org/observations/2896872	2016	"mhedin"	Individual on wood	Not apparent
В.	rosea	iNaturalist	https://www.inaturalist.org/observations/1310859	2015	"kueda"	Colony on dead wood	Not apparent
В.	rosea	iNaturalist	https://www.inaturalist.org/observations/1205992	2015	"kueda"	Individual on dead wood	Not apparent
В.	rosea	iNaturalist	https://www.inaturalist.org/observations/23559	2011	"biosam"	Colony on dead wood	Not apparent
В.	rosea	iNaturalist	https://www.inaturalist.org/observations/4039035	2016	"damontighe"	Individual on dead wood	Yes; white hyphal mat
В.	sp.	BugGuide	https://bugguide.net/node/view/1459279/bgimage	2017	Bob Kipfer	Individual on dead wood	Not apparent
					"Hobo Joe A.K.A.		
	sp.	BugGuide	https://bugguide.net/node/view/1421004/bgimage		Insect Lover"	Individual on dead wood	Not apparent
	sp.	BugGuide	https://bugguide.net/node/view/1104425/bgimage		Jonathan Carpenter	(Individual in collection)	Not apparent
	sp.	BugGuide	https://bugguide.net/node/view/865459/bgimage	2013	Mark H Brown	Individual on rock	Not apparent
В.	sp.	BugGuide	https://bugguide.net/node/view/843152/bgimage	2013	William Hull	Individual on dead wood	Not apparent
В.	sp.	BugGuide	https://bugguide.net/node/view/784265/bgimage	2013	"BugCatcher10"	(Individual in collection)	Not apparent
В.	sp.	BugGuide	https://bugguide.net/node/view/620056/bgimage	2012	Marvin Smith	Colony on soil	Not apparent
В.	sp.	BugGuide	https://bugguide.net/node/view/413806/bgimage	2010	Scott Cox	Individual on wood	Not apparent
В.	sp.	BugGuide	https://bugguide.net/node/view/176887/bgimage	2008	Natalie McNear	Individual on dead wood	Not apparent
В.	sp.	BugGuide	https://bugguide.net/node/view/172005/bgimage	2008	Natalie McNear	Colony on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/17666548	2018	"sageharmon"	(Individual in collection)	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/17422879	2018	"ecology2"	(Individual in collection)	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/17418303	2018	"jainitastic"	(Individual in collection)	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/12322132	2018	"apteryxrowi"	(Individual in collection)	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/12152016	2018	"lorri-gong"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/11718802	2018	"magicicada"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/11510349	2018	"kestrel"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/11095607	2018	"garmonb0zia"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/10940260	2018	"christopher13"	Colony on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/10178482	2018	"christopher13"	Individual on wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9963155	2018	"10000_hz_legend"	Colony on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9307728	2017	"irislane"	Individual on dead wood	Not apparent

В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9307713	2017	"irislane"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9281269	2017	"temminicki"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/8993568	2017	"easmeds"	Colony on bark	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/7609652	2017	"tonytravlos"	Colony on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/6937088	2017	"biosam"	Colony on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/6253831	2017	"chinquapin"	Colony on soil	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/6207443	2017	"friel"	Individual on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5722971	2017	"geodani"	(Individual in collection)	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5714347	2017	"lorri-gong"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5534690	2017	"christopher13"	Colony on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5282983	2016	"sclerobunus"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5228142	2017	"vermfly"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5189159	2017	"christopher13"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/2936552	2016	"allisonpeters"	Individual on rotten wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/2730609	2016	"marionanoiram"	Individual on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/1522694	2015	"beeboy"	Colony on dead wood	Not apparent
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/1333933	2015	"damontighe"	Individual on dead leaf	Not apparent
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/158981	2007	"kucycads"	Individual on dead wood	Not apparent
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/18981	2010	"tapbirds"	Individual on dead wood	Not apparent
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/10674619	2006	"henkwallays2"	Individual on wood	Yes; black-orange crust
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/1275824	2015	"robberfly"	Colony on dead wood	Yes; cup fungus
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/9013075	2017	"easmeds"	Individual on dead wood	Yes; gelatinous grey crust
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/14057280	2018	"clinchriverdreams"	Individual on dead wood	Yes; grey crust
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/363144	2013	"tonyg"	Colony on dead wood	Yes; grey crust
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/9722536	2018	"kookamongus"	Individual on dead wood	Yes; grey phlebioid crust
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/5823516	2017	"leenash"	Individual on dead wood	Yes; large brown crust
В.	sp.	$i \\ Natural is t$	https://www.inaturalist.org/observations/12265670	2018	"athensalive"	Colony on rotten wood	Yes; Phlebia sp.
							Yes; phlebioid crust and
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/595969	2014	"moonlittrails"	Colony on dead wood	cup fungus
R	sp.	iNaturalist	https://www.instrumlist.ong/ohapmations/5409722	2017	"damontighe"	Individual on dead wood	Yes; phlebioid grey crust and white hyphal mat
υ.	ъ р.	11 vatu141181	https://www.inaturalist.org/observations/5408733	201/	Gamonogne	marviduai on dead wood	Yes; pink-white hyphal
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/11719631	2018	"magicicada"	Individual on dead wood	mat

_							Yes; tan bracket fungus and
	sp.		https://www.inaturalist.org/observations/8870068	2017	"debk"	Individual on rotten wood	white poroid crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/12367836	2018	"dgreenberger" "eccentric_entomop	Colony on rotten wood	Yes; tan crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5257850	2016	hile"	Individual on dead wood	Yes; tan crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/10698727	2006	"henkwallays2"	Large colony on dead wood	Yes; tan poroid crust
							Yes; very rotten yellow
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5452255	2017	"damontighe"	Individual on dead wood	crust
В.	sp.	BugGuide	https://bugguide.net/node/view/851644/bgimage	2011	Sam McNally	Large colony on dead wood	Yes; white crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9736972	2018	"twillrichardson"	Colony on pine log	Yes; white crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9281266	2017	"temminicki"	Individual on dead wood	Yes; white crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5920644	2017	"leslie_flint"	Colony under rotten log	Yes; white crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5229632	2017	"tomv"	Colony on dead wood	Yes; white crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/2801341	2016	"robberfly"	Colony on rotten wood	Yes; white crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5095109	2016	"mazer"	Colony on dead wood	Yes; white crust and phlebioid grey crust Yes; white hyphae and
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9964190	2018	"l0000_hz_legend"	Large colony on dead wood	orange crust
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5408600	2017	"robberfly"	Colony on rotten wood	Yes; white hyphal cords
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/3520995	2016	"biosam"	Colony on rotten wood	Yes; white hyphal cords
					"eccentric_entomop		
	sp.	iNaturalist	https://www.inaturalist.org/observations/3198564	2014		Colony on rotten wood	Yes; white hyphal cords
	sp.	iNaturalist	https://www.inaturalist.org/observations/1110059	2014	"lindynik"	Colony on dead wood	Yes; white hyphal cords
	sp.	iNaturalist	https://www.inaturalist.org/observations/1066156	2014	"bapeck8"	Individual on dead wood	Yes; white hyphal cords
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/9812105	2018	"amacedo"	Colony on rotten wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/8858584	2008	"robirwin"	Individual on dead wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/7489413	2008	"robirwin"	Individual on dead wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/6682063	2017	"biosam"	Colony on rotten wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5278798	2017	"jessefurrow"	Individual on dead wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/5225939	2017	"lenaz"	Individual on dead wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/4780656	2016	"lorri-gong"	Colony on dead wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/1275884	2015	"metsa"	Colony on dead wood	Yes; white hyphal mat
В.	sp.	iNaturalist	https://www.inaturalist.org/observations/4505555	2016	"dutchflatterry"	Large colony on dead wood	Yes; white hyphal mat, tan bracket, slime mold

<i>B</i> . sp.	BugGuide https://bugguide.net/node/view/945769/bgimage	2014 Jonathan Carpenter	Colony on rotten wood	Yes; white poroid crust
<i>B</i> . sp.	BugGuide https://bugguide.net/node/view/633418/bgimage	2012 Alan Rockefeller	Colony on rotten wood	Yes; Xylodon sp.
				Yes; yellow slime mold
<i>B</i> . sp.	iNaturalist https://www.inaturalist.org/observations/5786153	2017 "daniam"	Individual on dead wood	and white hyphal cords
				Yes; yellow slime mold or
<i>B</i> . sp.	iNaturalist https://www.inaturalist.org/observations/4902929	2017 "grayson"	Colony on dead pine wood	cup fungus
<i>Б.</i> вр.	inaturalist https://www.inaturalist.org/observations/4902929	2017 grayson	Colony on dead plife wood	cap rangas

Supplemental Table 2. Strains and their associated NCBI Genbank reference numbers for isolates of *Mortierella* aff. *ambigua* and close relatives used in phylogenetic analysis.

Name	Strain	ITS	LSU
Mortierella ambigua	CBS 450.88	JX976067	KC018411
Mortierella ambigua	CBS 474.96	JX976056	KC018416
Mortierella ambigua	CBS 373.96	JX976062	JX976147
Mortierella capitata	CBS 293.96	JX976123	KC018334
Mortierella capitata	CBS 859.70	JX976008	KC018395
Mortierella microzygospora	CBS 880.97	NR_111569	HQ667394
Mortierella parazychae	CBS 868.71	HQ630283	HQ667362
Mortierella pseudozygospora	CBS 780.86	JX975880	JX976143
Mortierella wolfii	CBS 611.70	JN943806	JN940863
Mortierella wolfii	CBS 612.70	MH859876	HQ667381
Mortierella rostafinskii	CBS 522.70	NR_111586	NG_042570
Mortierella strangulata	CBS 455.67	HQ630359	HQ667437
Mucor abundans	CBS 521.66	JN206110	JN206457
Mucor fragilis	CBS 236.35	JN205979	FN650671

Supplemental Table 3. Strains and their associated NCBI Genbank reference numbers for isolates of aff. *Apophysomyces* sp. and close relatives used in phylogenetic analysis.

Name	Strain number	ITS	LSU
Apophysomyces variabilis	CBS 658.93	NR_130683	HM849695
Apophysomyces elegans	CBS 477.78	JN206280	JN206536
Apophysomyces ossiformis	UTHSC 04-838	NR_137035	FN554252
Apophysomyces trapeziformis	UTHSC 08-1425	NR_137034	FN554261
Apophysomyces mexicanus	CBS 136361	HG974255	HG974256
Saksenaea vasiformis	NRRL 2443	FR687327	HM776679
Saksenaea erythrospora	CBS 138279	KM102733	KM102734
Mucor abundans	CBS 521.66	JN206110	JN206457
Mucor fragilis	CBS 236.35	JN205979	FN650671
Backusella circina	CBS 128.70	NR_103649	JN206529
Backusella recurva	CBS 196.71	JN206265	JN206523
Backusella lamprospora	CBS 118.08	NR_145291	JN206531
Cunninghamella echinulata	CBS 656.85	JN205896	JN206598
Cunninghamella elegans	CBS 158.28	JN205888	JN206602
Cunninghamella bertholletiae	CBS 190.84	JN205878	HM849701
Cladophialophora chaetospira	CBS 491.70	EU035405	EU035405

Supplemental Table 4. Fungi recovered from *B. lecontii* based on ITS barcoding and arranged taxonomically. †LSU sequences are deposited for *Mortierella* aff. *ambigua* (NCBI Genbank accession MK045304) and aff. *Apophysomyces* sp. (NCBI Genbank accession MK045305).

		Example		Query	Identity	Deposited ITS
Name		isolate	Best match	coverage (%)	(%)	sequence #
Ascomycota						
Amphisphaeriales						
Discosia	sp.					
Neopestalotiopsis	sp.					
Pestalotiopsis	crassiuscula	BC1288	AY687868.1	100	99	
	jesteri	BC1501	KT000165.1	95	99	
	knightiae	BC0084	KM199311.1	99	99	
	mangiferae	BC1427	KP074973.1	100	100	
	microspora	BC1439	MH707065.1	100	100	
	sp.					
Annulatascales						
Conlarium	duplumascospora	BC1222	JN936997.1	98	85	
Rhodoveronaea	varioseptata	BC0645	KF823603.1	99	82	
Capnodiales						
Acrocalymma	aquatica	BC0359	JX276951.1	83	83	
Cladosporium	cladosporioides	BC1475	MH714552.1	100	100	
	sp.					
Passalora	brachycarpa	BC1621	GU214664.1	100	98	
Ramularia	coryli	BC1480	KX287391.1	100	98	
	endophylla	BC1635	KP894243.1	98	98	
	interstitiales	BC1540	KX287458.1	98	98	
	rumicicola	BC1601	KX287503.1	100	96	
	sp.					
Septoria	hyperici	BC1571	NR_147271.	99	97	
Sphaerulina	berberidis	BC1578	LC206672.1	100	99	
Trichomerium	foliicola	BC0315	NR 144963.	100	95	
Chaetosphaeriales	-		_			

Chaetosphaeria	chloroconia	BC1533	AF178542.1	98	99
	myriocarpa	BC0320	MH107883.1	98	99
Chloridium	virescens	BC1507	EF029220.1	99	100
	sp.				
Codinaea	acaciae	BC1318	KY965397.1	100	96
Chaetothyriales					
Capronia	dactylotricha	BC1244	NR 137136.	91	86
	leucadendri	BC0548	NR 156212.	98	98
	pilosella	BC1634	DQ826737.1	98	96
	sp.				
Cladophialophora	chaetospira	BC1539	KF359558.1	100	92
	potulentorum	BC1241	EU035410.1	99	90
	sp.				
Cyphellophora	gamsii	BC1562	NR 156306.	100	95
	olivacea	BC1633	KX302010.1	95	98
	oxyspora	BC0325	MF196874.1	99	99
	sp.				
Exobasidium	otanianum	BC1069	AB180343.1	96	96
Exophiala	moniliae	BC1410	HE605213.1	100	97
_	xenobiotica	BC1574	KY434151.1	97	92
	sp.				
Fonsecaea	pedrosoi	BC1176	AB114131.1	98	98 MH971241
	sp. (new)	BC1045	JN999999.1	93	94 MH971242
	sp.				
Phialophora	americana	BC1388	U31840.1	99	99 MH971243
_	sessilis	BC1631	GU981736.1	100	99 MH971244
	sp.				
Rhinocladiella	anceps	BC0327	AF050284.1	100	99 MH971245
	atrovirens	BC0550	AB091215.1	98	98 MH971246
	quercus	BC1534	NR 155728.	97	99 MH971247
Coniochaetales	•				
Coniochaeta	cephalothecoides	BC0639	KY064029.1	97	99
	sp.				

Cordanales					
Cordana	pauciseptata	BC0927	HE672147.1	93	99
Diaporthales					
Cryptodiaporthe	hystrix	BC0433	KX776446.1	100	98
Diaporthe	phaseolorum	BC0083	FJ441609.1	99	98
Gnomonopsis	sp.				
Phaeoacremonium	iranianum	BC1423	KF764529.1	100	98
	mortoniae	BC1555	EU427312.1	82	99
Togninia	minima	BC0539	KP083231.1	100	100
Dothideales					
Aureobasidium	pullulans	BC1444	MF497401.1	100	100
	sp.				
Dothiora	sorbi	BC0422	KY929146.1	100	98
	pyrenophora	BC1629	KU728514.1	97	98
Eurotiales					
Aspergillus	versicolor	BC1564	KU318416.1	98	99
Paecilomyces	carneus	BC1457	HQ660442.1	100	99
	inflatus	BC0451	KU702692.1	99	99
	javanicus	BC1300	AB099944.1	100	100
Penicillium	carneum	BC1278	NR 111551.	100	100 MH971248
	chrysogenum	BC1254	MH778149.1	99	100 MH971249
	daleae	BC1205	MH854984.1	100	100 MH971250
	fellutanum	BC1326	HM469425.1	100	100 MH971251
	glabrum	BC1095	MF803957.1	100	100 MH971252
	herquei	BC1214	MF663569.1	100	100 MH971253
	nodositatum	BC1031	NR 103703.	100	100 MH971254
	oxalicum	BC1327	MG733762.1	100	100 MH971255
	pancosmium	BC1499	MF803943.1	100	100 MH971256
	pinophilum	BC0544	EF488397.1	100	99 MH971257
	steckii	BC0778	MG554368.1	100	100 MH971258
	sumatraense	BC1530	JX140874.1	100	100 MH971259
	sp.				
Thysanophora	penicilloides	BC1421	JQ272462.1	99	100

Glomerellales					
Glomerella	acutata	BC1479	JN697577.1	100	100
Helotiales					
Cadophora	malorum	BC0073	DQ404350.1	100	98
Catenulifera	brachyconia	BC1570	AB190384.1	100	97
Hyalodendriella	sp.				
Hymenoscyphus	dehlii	BC0543	LC206621.1	94	94
Hyphodiscus	hymeniophilus	BC0581	DQ227258.1	99	97
Idriella	rara	BC1306	KC775737.1	91	98
Leptodontidium	elatius	BC1257	AM981224.1	100	95
	sp.				
Leptodontium	sp.				
Pezicula	cinnamomea	BC1553	KR859145.1	98	83
Pilidium	concavum	BC1478	MF776047.1	100	100
Rhexocercosporidium	sp.				
Scytalidium	lignicola	BC1391	GQ272634.1	98	99
	sp.				
Synchaetomella	acerina	BC1299	NR 111811.	99	93
Xenopolyscytalum	sp.				
Hypocreales					
Acremonium	variecolor	BC0031	HE608648.1	99	99
	sp.				
Atractium	stilbaster	BC1404	KM231792.1	100	87
Beauveria	brongniartii	BC0062	JX110373.1	99	99
	caledonica	BC1250	DQ350137.1	100	99
Calcarisporium	arbuscula	BC1182	LC145810.1	100	99
Clonostachys	rosea	BC1297	KX421414.1	99	99
·	sp.				
Cordyceps	militaris	BC1419	KY407763.1	100	99
	sp.				
Cosmospora	butyri	BC1580	JQ070093.1	99	100 MH97126
•	flavoviridis	BC0394	HQ897791.1	100	99 MH97126
	berkeleyana	BC0428	MH859583.1	99	96 MH971262

	sp.				
Cylindrium	elongatum	BC1446	KM231852.1	100	99
Dialonectria	sp.				
Fusarium	equiseti	BC1447	GQ365157.1	100	100
	tricinctum	BC1510	JX045791.1	99	100
	sp.				
Fusicolla	melogramma	BC0649	NR 155096.	99	99
Geosmithia	sp.				
Gibberella	sp.				
Gliomastix	murorum	BC0156	AB540558.1	100	98
Hirsutella	sp.				
Нуростеа	lutea	BC1265	AF359264.1	99	99
	pachybasioides	BC0321	AY240843.1	100	98
Hypomyces	aurantius	BC1020	AB591044.1	100	98
Isaria	farinosa	BC0416	MH191137.1	100	99
	fumosorosea	BC0014	FJ177460.1	100	99
Lasionectria	sp.				
Lecanicillium	araneogenum	BC0675	KX845704.1	99	98
	attenuatum	BC1503	MH231313.1	100	100
	fungicola	BC1022	KX379184.1	99	100
	fusisporum	BC1518	AB378517.1	99	100
	psallotiae	BC0015	AB360367.1	99	99
	saksenae	BC1455	KY320616.1	100	97
Mariannaea	elegans	BC1489	KX028787.1	99	99
	samuelsii	BC1156	KM231757.1	99	100
Metacordyceps	chlamydosporia	BC0618	AB214654.1	100	99
Metarhizium	anisopliae	BC1203	MG786739.1	100	100
	flavoviride	BC1163	KX380789.1	100	99
Monocillium	sp.				
Nectria	sp.				
Niesslia	pulchriseta	BC0033	MG827040.1	96	99
Pochonia	bulbillosa	BC1436	AB709835.1	100	99
	chlamydosporia	BC1165	AB713184.1	99	100

	suchlasporia	BC0017	AB214658.1	99	99
Protocrea	sp.				
Pseudonectria	sp.				
Purpureocillium	lilacinum	BC1070	FJ765024.1	100	98
Sepedonium	chalcipori	BC1058	KT946847.1	100	90
Simplicillium	lamellicola	BC1496	KT004573.1	100	97
	lanosoniveum	BC0027	AB758126.1	99	99
	sp.				
Stilbella	sp.				
Tolypocladium	album	BC1113	MH137667.1	100	98
	inflatum	BC0499	KT693271.1	100	99
Trichoderma	atroviride	BC1215	MF871528.1	100	100 MH971263
	harzianum	BC1204	MG132085.1	100	100 MH971264
	lixii	BC1322	MF782824.1	100	100 MH971265
	melanomagnum	BC1271	KU738454.1	100	100 MH971266
	pleuroticola	BC1277	MF687194.1	100	100 MH971267
	viride	BC1433	AJ230676.1	99	100 MH971268
	sp.				
Verticillium	fungicola	BC0488	FJ810136.1	100	99 MH971269
	insectorum	BC1005	AB214655.1	100	99 MH971270
	leptobactrum	BC1341	EF641871.1	99	99 MH971271
	sp.				
Xenoacremonium Mycosphaerellales	falcatus	BC1488	MH062972.1	98	100
Mycosphaerella	sp.				
Ramichloridium	sp.				
Onygenales	sp.				
Oidiodendron	sp.				
Ophiostomatales	sp.				
Ophiostoma	dentifundum	BC1140	AY495435.1	97	93
Opinosionia	grandicarpum	BC1638	NR 147600.	99	90
Sporothrix	inflata	BC0434	AY495432.1	100	99
sporoun m	sp.	DC0434	A1 475452.1		
	2P.				

Pleosporales					
Coniothyrium	fuckelii	BC0181	AB665314.1	100	100
Curvularia	geniculata	BC1177	MH517581.1	100	100
	senegalensis	BC1151	MH517581.1	100	100
Dictyosporium	australiense	BC0100	DQ018092.1	97	98
Helminthosporium	asterinum	BC1248	AF073917.1	99	99
_	velutinum	BC1385	AB551948.1	98	99
Leptosphaerulina	chartarum	BC0086	GU566269.1	100	99
Lophiostoma	sp.				
Neocucurbitaria	vachellia	BC1535	NR 156363.	100	95
	acerina	BC1494	MF795767.1	99	98
Paraconiothyrium	brasiliense	BC1485	JF502455.1	99	99
·	hawaiiense	BC1456	HM751092.1	100	99
	sp.				
Paraphaeosphaeria	neglecta	BC1617	JX496038.1	99	99
Periconia	pseudobyssoides	BC0452	KC954161.1	100	99
	sp.				
Peyronellaea	glomerata	BC0592	MG832565.1	99	99
Phaeosphaeria	sp.				
Phoma	bellidis	BC1498	JF502444.1	100	100
	sp.				
Preussia	sp.				
	sp.				
Stagonosporopsis	cucurbitacearum	BC1500	LC168795.1	100	99
Teichospora	quercus	BC1412	MH107920.1	98	96
Saccharomycetales	1				
Candida	aglyptina	BC1600	FJ196775.1	76	98
	boleticola	BC1585	KY102001.1	100	99
	sp.				
Pichia	jadinii	BC0555	FJ865435.1	100	95
	sp.				
Yamadazyma	mexicana	BC0590	KY105944.1	100	99
Sordariales					-

Apodus	deciduus	BC1170	NR 145141.	100	96
Cercophora	sulphurella	BC1619	AY587913.1	99	96
Chaetomium	sp.				
Fimetariella	rabenhorstii	BC1129	KX869958.1	98	98
	sp.				
Phialemonium	dimorphosporum	BC0511	FJ441614.1	100	98
Spadicoides	bina	BC0107	JF340260.1	97	99
Trichosphaetiales					
Nigrospora	oryzae	BC1017	HQ608152.1	100	100
Tubeufiales					
Thaxteriellopsis	lignicola	BC1594	JN865207.1	99	78
Venturiales					
Venturia	viennotii	BC0500	KF793787.1	97	96
Xylariales					
Ascovirgaria	occulta	BC0589	AB740957.1	100	97
Biscogniauxia	atropunctata	BC0106	JX507799.1	97	99
	sp.				
Diatrype	disciformis	BC1565	KR092795.1	99	99
Eutypella	vitis	BC1453	KU320620.1	99	99
Hansfordia	nebularis	BC1173	KF893290.1	99	100
Hypoxylon	crocopeplum	BC0178	JN673047.1	99	99
	fendleri	BC1400	JN979417.1	100	92
	fuscum	BC1159	JN979424.1	100	96
	lenormandii	BC1352	KM610287.1	99	96
	perforatum	BC1305	JQ009308.1	100	99
	rubiginosum	BC1438	MH178694.1	91	99
	truncatum	BC1079	AF201716.2	98	99
	sp.				
Nemania	diffusa	BC1521	MH633932.1	99	91
	serpens	BC1093	KU683860.1	99	99
	sp.				
Spegazzinia	sp.				
Virgaria	nigra	BC1406	AB670716.1	100	98

Xylaria	heliscus	BC1355	JQ761642.1	96	95 MH971272
	sp.				
incertae sedis					
Acrodontium	crateriforme	BC1302	KX287270.1	99	97
Barbatosphaeria	dryina	BC1060	KM492892.	92	96
	varioseptata	BC1188	NR 132089.	92	97
Geomyces	sp.				
Leohumicola	sp.				
Pseudogymnoascus	sp.				
Ramimonilia	apicalis	BC1546	NR 144959.	89	93
Veronaea	japonica	BC1623	NR 111277.	98	97
Xylomelasma	sp.				
Basidiomycota	•				
Agaricales					
Schizophyllum	commune	BC1449	MF554593.1	100	99
Cantharellales					
Sistotrema	brinkmanii	BC1078	KX527870.1	99	99
	oblongisporum	BC1508	KP814309.1	99	99
Tulasnella	sp.				
Dacrymycetales	_				
Calocera	sp.				
Dacrymyces	australis	BC1195	MH858261.1	96	84
Exobasidiales					
Meira	sp.				
Hymenochaetales	•				
Hydnochaete	olivacea	BC1560	KJ140712.1	100	82
Peniophorella	pubera	BC1138	KP715565.1	97	84
Malasseziales	-				
Malassezia	sp.				
Microbotryales	_				
Curvibasidium	cygneicollum	BC1606	KY102973.1	98	98
	pallidicorallinum	BC0542	JX188149.1	100	99
Microstromatales	-				

Microstroma	juglandis	BC1607	EU069498.1	95	90
Polyporales					
Bjerkandera	adusta	BC1316	MF161298.1	100	99
Ceriporia	lacerata	BC1158	KP135024.1	99	100
	sp.				
Ceriporiopsis	gilvescens	BC0174	KY948761.1	100	100
Gloeoporus	pannocinctus	BC0042	JQ673102.1	100	100
Irpex	lacteus	BC1038	JX290579.1	100	99
	sp.				
Junghuhnia	nitida	BC0528	KP135323.1	97	99
Phanerochaete	cumulodentata	BC0709	KP994373.1	100	100 MH971273
	sordida	BC0691	KP135074.1	100	100 MH971274
	sp.				
Phlebia	acerina	BC1331	KP135373.1	100	99
	fuscoatra	BC1014	KY948754.1	99	97
	lividina	BC0629	KY948756.1	100	99
	subserialis	BC0054	HQ607954.1	100	99
	tremellosa	BC0184	GU062266.1	99	99
Phlebiopsis	flavidoalba	BC1426	KP135401.1	100	100
1	gigantea	BC1049	KX028786.1	100	100
Scopuloides	rimosa	BC1046	KP135348.1	99	100
Trametopsis	cervina	BC1143	JX463662.1	99	99
Russulales					
Peniophora	pithya	BC1467	MH857635.1	100	95
1	sp.				
Stereum	complicatum	BC1428	MF161283.1	98	100
	sp.				
Sporidiobolales	1				
Rhodotorula	eucalyptica	BC1579	EU075186.1	99	87
	sp.				
Tremellales	1				
Cryptococcus	dimennae	BC0392	KM246197.1	98	98
V1	sp.				
	1				

Kockovaella	fuzhouensis	BC1536	KY103850.1	97	93
	sichuanensis	BC1542	KY103859.1	100	99
Tremella	subalpina	BC1424	NR 155908.	91	85
incertae sedis					
Acaromyces	ingoldii	BC1417	HM595575.1	100	100
Hamamotoa	singularis	BC1050	AF444600.1	100	87
Mucoromycota	<u> </u>				
Mortierellales					
Mortierella	aff. ambigua†	BC1065	JX976067.1	100	92 MH971275
	sp.				
Mucorales					
aff. Apophysomyces	sp.†	BC1021	NR 137035.	91	78 MH971276
Backusella	circina	BC1287	JQ979443.1	100	94
	recurva	BC1267	JN206265.1	99	98
Cunninghamella	elegans	BC1044	MH857146.1	99	99
Mucor	abundans	BC1003	MH855716.1	99	99 MH971277
	circinelloides	BC1285	MH856522.1	99	100 MH971278
	fragilis	BC1294	KY047150.1	100	99 MH971279
	genevensis	BC1002	JN206046.1	97	98 MH971280
	luteus	BC1107	MH859851.1	98	98 MH971281
	mucedo	BC1056	JQ319046.1	100	98 MH971282
	racemosus	BC1295	MF356581.1	100	99 MH971283
	sp.				
Umbelopsidales	_				
Umbelopsis	angularis	BC0529	MH859191.1	99	99 MH971284
-	isabellina	BC1080	KM044070.1	100	99 MH971285
	ramanniana	BC1097	MH864647.1	100	100 MH971286
	sp.				
Zoopagomycota	-				
Entomophthorales					
Basidiobolus	ranarum	BC1232	EF392530.1	100	99