

ABSTRACT

Title of Dissertation: DIVERSITY AND DISTRIBUTION OF
FUNGAL ENDOPHYTES IN TWO
AMAZONIAN HARDWOOD GENERA

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Hevea brasiliensis (Euphorbiaceae) is the primary species for tapped natural rubber and an economically important crop since the 1870's. Plantation-grown trees of *H. brasiliensis* are susceptible to numerous pathogens, some which are resistant to traditional chemical control. Fungal endophytes obtained from the wild are often considered ideal candidates for developing biological controls for pathogens, however little knowledge of the fungal endophytes associated with wild rubber and related hosts exists. The objectives of this study were the following: 1) determine the composition of the fungal endophyte communities associated with wild *H. brasiliensis* and its close relatives in *Micrandra* using cultures and culture-independent methods; 2) determine the species identities of endophytes in the genus

Diaporthe associated with the two host genera; and 3) assess the overall utility of automated and manual methods for curating operational taxonomic unit (OTU) characterization of endophytes. To accomplish these objectives, fungal isolates and DNA from 381 seedlings and 144 adults of *Hevea* and *Micrandra* from three Amazon Peru locations were characterized using sequences from the internal transcribed spacer regions (ITS) of the ribosomal DNA repeat unit for both cultures and culture-independent samples, the latter using metagenomics methods. To determine the species identities of the *Diaporthe* isolates, four loci were analyzed using phylogenetic methods. A comparison of the effects of manual and automated operational taxonomic unit (OTU) classification was performed by using four different methods. *Trichoderma* species were most frequently identified from adult trees while *Diaporthe* species were the most abundant from seedlings, suggesting host developmental stage may be a key determinant of tropical endophytic community assemblage. Twenty-one distinct *Diaporthe* lineages were recovered with seven described as new species. Manual OTU curation methods were less error prone suggesting that algorithm adjustments are needed for currently used automated methods. This study resulted in a greater understanding of the diversity of endophytes, particularly *Diaporthe* spp., associated with wild rubber. Knowledge of fungal diversity, host life stage associations, and spatial distribution of *Hevea* and *Micrandra* endophytes will provide additional tools for integrated disease management approaches and aid development of successful biocontrol methods.

DIVERSITY AND DISTRIBUTION OF FUNGAL ENDOPHYTES IN TWO
AMAZONIAN HARDWOOD GENERA

by

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Dedication

To my husband Matthew Allen, for joining me on this journey. You infused each day with warmth and joy, even when the dreary winters seemed impenetrable. You never complained about my long hours in the lab, and even longer hours in the field. You stood beside me, a quiet strength, never pushing, always inspiring, and providing me with absolutely anything I needed to succeed.

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FIGURE 1.14. Diversity results from culture-independent approach. Species accumulation and diversity curves for endophytes sampled from (A) seedling and (B) adult trees separated by host species (HEGU: *Hevea guianensis*, HENI: *Hevea nitida* and MISP: *Micrandra spruceana*). Trees were sampled from the Amazon Conservatory for Tropical Studies Biological Station (NAPO). Metrics include richness (q=0), Shannon (q=1), Simpson's (q=2).

FIGURE 1.15. Community similarity results from culture-independent approach. Nonmetric Multidimensional Scaling (NMDS) analyses using presence/absence data with stress values for all trees sampled from the Amazon Conservatory for Tropical Studies Biological Station (NAPO). Data partitioned by (A) developmental stage (ADULT: Adult, JUVI: Seedling), and (B) tree species (HEGU: *Hevea guianensis*, HENI: *Hevea nitida*, and MISP: *Micrandra spruceana*).

FIGURE 2.1. Phylogenetic tree resulting from combined multilocus (ITS, TEF1, TUB, HIS) alignment. RAxML bootstrap values (bs) and Bayesian probabilities (pp) are displayed at each node (bs/pp). Only those with percentages above 70% are shown. Ex-type and ex-epitype isolates are in bold. Culture collection numbers are given for downloaded sequences and isolate codes for the newly generated sequences. *Diaporthe* from this study isolated from wild trees are indicated in green, while isolates from plantation trees are indicated in red.

FIGURE 2.2. *Diaporthe amazonica* (GPB18-1a). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 10 μm , C = 5 μm .

FIGURE 2.3. *Diaporthe heveicola* (AHGB25-8b). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 20 μm , C = 10 μm .

FIGURE 2.4. *Diaporthe napoensis* (GXB11-4b2). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 10 μm , C = 10 μm .

FIGURE 2.5. *Diaporthe neotropica* (JMGB04-6b). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 10 μm , C = 10 μm .

FIGURE 2.6. *Diaporthe peruviensis* (JMGB13-6a). A) Sporulation on alfalfa stem in Wag, B) pycnidial wall lined with paraphyses, C) conidiophores, D) alpha conidia, E) alpha conidia — Scale bars: A = 2,000 μm , B = 10 μm , C = 20 μm , D) 5 μm , E) 5 μm .

FIGURE 2.7. A) *Diaporthe ubiqueta* (AHGB7-9a1), and B) *Diaporthe umbrina* (JHGB2-8a) on potato-dextrose-agar (PDA) after seven days incubation at room temperature.

FIGURE 3.1. Venn diagram showing overlap of fungal centroid sequences among datasets curated using three different methods (CLU REP: Clustered GenBank Representatives method, PIPE OTU: Pipeline BLASTn method, RDP WAR: RdP

classifier with Warcup Fungal training set method). MAN PER (Manual BLAST Percent Based method), not pictured, had the same centroid sequences as CLU REP.

FIGURE 3.2. Species accumulation and diversity curves for fungal communities partitioned by dataset (Clustered GenBank Representatives [CLU REP], Manual BLAST Percent Based [MAN PER], Pipeline BLASTn OTUs [PIPE OTU], and the RdP classifier with Warcup Fungal training set [RDP WAR]) within location (A. Allpahuayo-Mishana National Reserve [ALPE], B. The Jenaro Herrera Research Center [JEHE], and C. the Amazon Conservatory for Tropical Studies Biological Station [NAPO], and host tree genus (1. *Hevea* and 2. *Micrandra*). Species accumulation metrics include richness ($q=0$), Shannon ($q=1$), Simpson's ($q=2$).

FIGURE 3.3. Distribution of operational taxonomic units (OTUs) at the phylum level for each dataset generated using one of the four OTU classification methods: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn (PIPE OTU), and the RdP classifier with Warcup Fungal training set (RDP WAR).

FIGURE 3.4. Proportion of operational taxonomic units (OTUs) assigned to each function guild per dataset: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn (PIPE OTU), and the RdP classifier with Warcup Fungal training set (RDP WAR).

Introduction

Hevea brasiliensis is the primary species for tapped natural rubber and an increasingly economically important crop since the 1870's. *Micrandra*, another latex producing genus of trees, is a close relative of *Hevea*, and sister to the clade of *Hevea* + *Glycydendron* (Wurdack et al. 2005). *Micrandra* has been a source of food, medicine and lamp fuel for the indigenous people of the Amazon (Schultes 1945, 1977, 1978), but its latex is not suitable for rubber production. Commercially tapped latex is used for a wide range of products essential to modern daily life ranging from the biomedical field (surgical equipment, rubber gloves, prophylactics) to industrial parts (tubes, pipes, connectors, tires) and it is a potential source for biodegradable plastics (Cotter et al. 2009; Mooney 2009). Latex was traditionally harvested directly from wild rubber trees within the Amazon Basin. As the demand for rubber grew, plantations were first established in South America and in India and Malaysia in the late 1800's (Priyadarshan 2011). Today the top rubber producing plantations are located in Southeast Asia and Africa, with demand continuing to grow (FAO 2009).

Plantation grown trees suffer from a variety of diseases that reduce production or destroy entire plantation areas, including White Root Disease (*Rigidoporus microporus*), Leaf Fall Disease (*Corynespora cassiicola*), Pod Rot (*Phytophthora meadii*), Abnormal Leaf Fall Disease (*Phytophthora* sp.) and South American Leaf Blight (*Microcyclus ulei*). South American Leaf Blight (SALB) is the major reason that rubber plantations have failed in South America and SALB has remained resistant to chemical fungicides. To date, the disease is endemic to South and Central

America, but the threat of proliferation to Old World production areas is of great concern (Lieberei 2007; Onokpise and Louime 2012). Breeding efforts have focused on incorporating genetic resistance for diseases such as SALB; however, genetic resistance is often overcome (Rivano et al. 2013). Biocontrol methods have been successful for other tropical commodities. For example, fungal endophytes have been extensively studied and successfully deployed in *Theobroma cacao* (Bailey et al. 2009; Evans et al. 2003). In particular, the fungal genus *Trichoderma* has been successfully incorporated into a commercial biofungicide (Mukherjee et al. 2012). Hanada et al. (2010) observed that *Trichoderma* spp. were not only the dominant endophytes collected from branches of cultivated *Theobroma cacao* and wild *Theobroma grandiflorum* in Brazil, but that these endophytes were antagonistic to *Phytophthora palmivora*, an important cacao disease. Coupled with these findings and their own observations, Gazis and Chaverri (2015) proposed that *Trichoderma* spp. are important or even essential components for protection against pathogens in natural forests.

Efforts for developing methods for the biological control of diseases for *Hevea* have been largely unsuccessful, however those studies have focused on non-endophytic fungi or endophytes isolated from healthy plantation trees outside the native range of *Hevea* (Abraham et al. 2013; Evueh and Ogbebor 2008; Sudirman et al. 1992). Endophytes obtained from the wild that have a highly specialized relationship with their hosts are generally considered to be ideal candidates for developing biological controls against diseases of that host (Thomas et al. 2008). As a preliminary effort toward the development of biological control methods for *H.*

brasiliensis, a fungal endophyte study utilizing culture-based techniques was conducted in Peru (Gazis and Chaverri 2010, 2015). Leaves and sapwood from a total of 190 trees of *H. guianensis* and both wild- and plantation-grown *H. brasiliensis* were collected in eight locations. Sapwood endophytes were found to be more diverse than leaf endophytes and species composition of the endophytic community differed between the two tissue types. However, endophytes were recovered from only 66% of the samples. The most frequently isolated taxa from all hosts were species of *Penicillium*, *Pestalotiopsis* and *Trichoderma*. *Trichoderma* spp. were the dominant endophytic fungi in wild *Hevea* trees (Gazis and Chaverri 2015).

This study, in consideration of the potential for a greater diversity of beneficial endophytes to be found in wild *Hevea*, targeted adults and seedlings of four species (*H. brasiliensis*, *H. guianensis*, *H. nitida*, *H. pauciflora*) and two species of the related host genus, *Micrandra* (*M. elata*, *M. spruceana*), from remote and underexplored areas of the Amazonian Peru. Few studies of other plant species have directly compared the fungal endophytic communities of adults to those of their offspring. In those studies, differences in community composition and diversity were reported (Espinosa-Garcia and Langenheim 1990, Rodrigues 1994, Gure and Birhanu 2014, Oono et al. 2015). For that reason, two developmental stages, adult and seedling trees, were sampled in this study. Lastly, due to the low recovery rate reported by Gazis and Chaverri (2010) when culture-based identification methods were used exclusively, both culture-dependent and culture-independent approaches through high-throughput DNA sequencing were compared for one location in this study. Additionally, this study targeted sapwood and stem tissue, rather than leaf

tissue, due to the greater diversity of endophytes reported in those tissues by Gazis and Chaverri (2010).

During the larger endophyte discovery project presented here and that of Gazis and Chaverri (2010, 2015), a large number of *Diaporthe* isolates were recovered. *Diaporthe* includes a wide array of species that are endophytes, saprobes, opportunistic pathogens, as well as aggressive pathogens of economically important crops. However, morphological species identification remains problematic and past reliance on host species or genus in describing fungal species has resulted in a proliferation of species names. Little is currently known about the distribution of *Diaporthe* spp. on *Hevea*, and reports of *Diaporthe* spp. in Peru are lacking (Rocha et al. 2011, Gomes et al. 2013).

Isolates generated by both Gazis and Chaverri (2010, 2015) and this project were used in the present study to: 1) resolve the identity of the endophytic *Diaporthe* of *Hevea* and *Micrandra*; 2) place these isolates in a phylogenetic context with known pathogenic and non-pathogenic *Diaporthe* spp.; and 3) determine the geographic and host distribution of endophytic *Diaporthe* clades compared with that known from other hosts. Four nuclear loci including the ribosomal internal transcribed spacer region (ITS, comprised of ITS1, 5.8S, ITS2), partial translation elongation factor 1-alpha (TEF1), beta-tubulin (TUB) and histone H3 (HIS) were sequenced and analyzed to identify phylogenetic species. Since *Diaporthe* spp. are common endophytes, and because choice of genetic barcode has major implications for ecological hypotheses, the utility of each locus for species identification was investigated (Gotelli & Colwell 2001, Agapow et al. 2004, Magurran 2008, Gazis et

al. 2011). Accurate means of identification will aid in monitoring the geographical range and hosts of known *Diaporthe* spp. and allow reporting on previously unknown *Diaporthe* species from the Amazonian Peru.

Metabarcoding data analysis of the samples collected led to an examination of operational taxonomic unit (OTU) classification methods on endophyte distribution, diversity estimates, and ecological function role assignment. Metabarcoding has become an important tool for exploring communities across multiple systems (Gao et al. 2008, Bellemain et al. 2013, Cox et al. 2016, Miller et al. 2016, Núñez et al. 2016, Durand et al. 2017). There are, unfortunately, many inherent errors or biases when using next generation sequencing that may lead to incorrect inferences regarding community composition and diversity: initial amplicon library preparation, PCR and sequencing artifacts, chimera detection methods, and absence of well-curated fungal reference sequences (Nilsson et al. 2015, Brown et al. 2015, Hibbett et al. 2011, Nagy et al. 2011, Dighton and White 2017). Lastly, errors occur during the analyses of clustering and classifying sequences (Gazis et al. 2011, Nguyen et al. 2015, Yahr et al. 2016, Raja et al. 2017a). Multiple methods are accepted for classifying OTUs in environmental metabarcoding studies. In this study, four different methods were used to classify OTUs with the dataset of endophytes collected from multiple hosts in multiple locations. The effect of those different methods on endophyte distribution, endophyte diversity estimates, and endophyte ecological function roles were examined.

This is one of the first studies comparing adult to seedling stem tissue in a systematic manner, the majority of prior studies used fungal communities recovered

from leaves. Metabarcoding is an increasingly standard method used in modern studies, and streamlined data analysis is vitally important. Development of successful biocontrol methods and integrated disease management strategies for *H. brasiliensis* will likely benefit from further understanding fungal diversity, host associations, and spatial distribution of their endophytes.

Objectives

- Determine the influence of host identity on community species composition and abundance in *Hevea* and *Micrandra* adult trees and seedlings.
- Determine the influence of geography on community species composition and abundance in adult and seedlings.
- Investigate whether the patterns observed between adult and seedlings agree when using culture vs. culture independent approaches.
- Determine and quantify the species of *Diaporthe* associated with wild *Hevea* and *Micrandra* in Peru.
- Determine the effect of manual curation vs. automated methods for OTU classification of metabarcoding data.

Chapter 1: Developmental stage as a primary force driving fungal endophytic community assemblage in two Amazonian hardwood genera

Abstract

Euphorbiaceae contains economically and ethnologically important Amazonian hardwood species *Hevea brasiliensis* and *Micrandra inundata*. Recent fungal endophyte research has focused on *H. brasiliensis* due to its global importance as a commodity but almost no data exists about the fungal community harbored within other *Hevea* species or its sister genus *Micrandra*. In addition to expanding host sampling to include four *Hevea* spp. and two *Micrandra* spp., we recovered endophytes at two developmental stages of the host. The latter represents a novel approach in endophyte research that will contribute to a better understanding of the dynamics involved in community assemblage of tropical endophytes. Through a culture-based approach, we sampled a total of 381 seedlings and 144 adults distributed across three remote areas within the Amazonian Peru. In addition, at one site we used culture-independent approaches through high-throughput DNA sequencing to test if the patterns in community composition and abundance agreed. Our results from both sampling approaches indicate that host development stage has a greater influence in community assemblage than host taxonomy or locality. *Trichoderma* was the most abundant genus recovered from adult trees, while *Diaporthe* prevailed in seedlings. Potential explanations for the disparity of abundance between *Trichoderma* and *Diaporthe* are discussed. Finally, we found that anthropogenic influence has a negative impact on species richness and diversity.

These results are in accordance with previous studies that have suggested that human disturbances could have a strong influence on the establishment of fungal species assemblages

Keywords: Next Generation Sequencing (NGS), ITS nrDNA, mycobiome, phytobiome, Janzen-Connell hypothesis, negative density dependence (NDD).

Introduction

Fungal endophytes are found in almost every plant species and tissue type (Verma and Gange 2014) and have been the topic of a plethora of research articles (2,746 articles in the last decade) (Web of Science Database, Accessed: September 12, 2017). Nevertheless, information regarding turnover of fungal endophytes from one developmental stage of a plant to another (i.e., from seed to seedling to adult) is limited. Characterizing communities from one host at different developmental stages can shed light into community dynamics and can provide the first clues on how these highly complex communities are assembled and change through time. The few studies regarding the effects of developmental stages on endophytic fungal community assemblages have focused on endophytes isolated from seeds and/or emerging seedlings (Johnston-Monje and Raizada 2011, Hodgson et al. 2014, Parsa et al. 2016, (Sarmiento et al. 2017) as compared to older or newly flushed leaves on a single adult plant (Fröhlich et al. 2000, Arnold and Herre 2003, Nascimento et al. 2015), or often involved inoculation of seedlings with fungal endophytes recovered from taxonomically unrelated adult plants with the objective to gauge the effect on plant growth (Fernandes et al. 2013, Leite et al. 2013), disease resistance (Nichol and

Walker 2013, Romeralo et al. 2015, Martínez-Álvarez et al. 2016), or tolerance to abiotic stresses (Hubbard et al. 2014, Navarro-Torre et al. 2016, Barra et al. 2017).

Few studies have directly compared the fungal endophytic communities of adults to that of their offspring. Predominantly, these studies isolated fungal endophytes from adult leaves and leaves of their offspring to evaluate the effect of developmental stage on endophytic communities (Espinosa- Garcia and Langenheim 1990, Rodrigues 1994, Gure and Birhanu 2014, Oono et al. 2015). Espinosa-Garcia and Langenheim (1990) isolated endophytic fungi from adult *Sequoia sempervirens* leaves and their basal sprouts, reporting higher fungal diversity in basal sprouts. Rodrigues (1994) sampled 10 adult trees and 20 saplings (6 to 18 months old) of *Euterpe oleracea* (Arecaceae) from an island located within the Amazon Basin of Brazil. Three leaf-growth stages were examined: unopened leaves, newly expanded leaves, and mature leaves. Rodrigues (1994) also found that isolation frequencies increased with leaf age and that saplings had a higher fungal isolation frequency than adults.

Diversity was not measured in this study; however, Rodrigues (1994) observed that the composition of fungal communities differed between saplings and adults. Gure et al. (2014) isolated fungal endophytes from juvenile (dbh 13.5-16.5 cm) and adult (dbh 68-90cm) *Afrocarpus falcatus* (Podocarpaceae) needles and observed that endophytic communities from juveniles tended to have a higher diversity. Oono et al. (2015) used culture-based and culture-independent methods to assess the fungal communities of *Pinus taeda* pine needles (9 adults and 18 seedlings)

in a temperate forest and, as in the previously mentioned studies, the endophytic communities from seedlings had a higher fungal diversity than the surrounding adults.

Prior to the work conducted by Gazis and Chaverri (2010), few studies had evaluated the fungal community harbored within inner bark tissue (phloem + cambium). Therefore, even less is known about the dynamics of community assemblage associated with this tissue. Many tropical trees that have been investigated for endophytes are deciduous and so communities living within the trunk/stem are expected to be more stable but still vary with host age. Tree diameter has been used to gain insight into the relationship between host age and endophyte richness and abundance. For instance, Meaden et al. (2016) used tree diameter as an estimation of host age for *Quercus robur* (Fagaceae) and observed a negative correlation between tree age and the number of endophytic bacterial OTUs (Operational Taxonomic Units) recovered from sapwood, as well as a negative correlation between tree age and abundance of particular bacterial taxa. On the other hand, Gazis and Chaverri (2015) observed a positive correlation between the number of fungal OTUs recovered from *H. brasiliensis* sapwood and tree diameter, but no significant correlation between tree diameter and abundance of particular taxa. Although these studies yielded conflicting results, tree age (inferred from tree diameter) was found to influence endophytic richness.

The main challenges in the study of community dynamics is that tropical fungal endophytes are mainly transmitted horizontally and highly complex (hundreds of genotypes inhabiting a single host), with the surrounding environment acting as the main source of inoculum (Clay 1993, Arnold and Herre 2003, Santamaría and

Bayman 2005). The composition and abundance of these communities are thought to be a function of environmental factors such as light, rainfall, elevation, soil type, salinity and forest type rather than host taxonomy (Arnold and Herre 2003, Arnold 2007, Krishnamurthy et al. 2009, Azad and Kaminskyj 2016, Soares et al. 2016). A survey of leaves of an endemic tree species across the varied environments of Hawaii reported that endophytic communities differed along rainfall and temperature gradients (Zimmerman and Vitousek 2012). Similarly, when four tree species were surveyed across three different tropical forest types, their endophytic communities were found to be significantly different for each forest type, suggesting that the environment structured the endophytic communities rather than host taxonomy (Suryanarayanan et al. 2011).

Surrounding vegetation has been shown to be one of the most important variables driving endophyte species composition and abundance. In the tropics, where plant diversity is high and species density is low, host specificity among endophytes has rarely been reported (May 1991, Bailey et al. 2006, Suryanarayanan et al. 2011). Specific relationships may not be advantageous as host encounters would be more difficult, and a specialized relationship could reduce endophytic reproductive and dispersal success (Cannon and Simmons 2002, Ferrer and Gilbert 2003).

Although host specificity has rarely been reported in the tropics, several studies have shown that host identity does influence endophytic communities (Solis et al. 2016, Vincent et al. 2016, Del Olmo-Ruiz and Arnold 2017). Solis et al. (2016) sampled leaves from three species of *Ficus* (*F. benjamina*, *F. elastica* and *F. religiosa*,) within two forests in the Philippines and in both sampling sites as the

phylogenetic distance of hosts increased, the similarity of endophytic communities decreased. Vincent et al. (2016) isolated leaf fungal endophytes from two more closely related tree genera (*Ficus* [Moraceae], *Macaranga* [Euphorbiaceae]), along with three more distantly related genera (*Psychotria* [Rubiaceae], *Syzygium* [Myrtaceae], *Gnetum* [Gnetaceae]) distributed at three sites in Papua New Guinea. In contrary to the previous study, the authors found that while host identity influenced composition of endophytic communities, dissimilarity among the communities was not correlated to host plant phylogeny.

In this study, we targeted four species of *Hevea* and two species of *Micrandra* distributed in remote and underexplored areas of the Amazonian Peru. In addition to characterizing the endophytic community of the targeted species, this study had three main objectives: 1) determine the influence of host identity on community species composition and abundance in adult and seedlings; 2) determine the influence of geography on community species composition and abundance in adult and seedlings; and 3) investigate whether the patterns observed between adult and seedlings agree when using culture vs. culture-independent approaches. We compared our findings with previous studies and discussed the factors that can be contributing to the differences and similarities among hosts, sites, and developmental stages.

Material and Methods

Collection sites

Samples were collected from three localities within the Loreto Region of Amazonian Peru (Figure 1.1): 1) Amazon Conservatory for Tropical Studies (ACTS) Biological

Station (NAPO; 3°14'57.20"S, 72°54'33.60"W), 2) Allpahuayo-Mishana National Reserve (ALPE; 3°58'1.16"S, 73°25'8.11"W), and 3) Jenaro Herrera Research Center (JEHE; 4°53'54.29"S, 73°38'59.80"W). All three locations are high terraced lowland forests (elevation: 103 m to 146 m) (Aquino et al. 2013, Box 2016).

NAPO was the most remote location with no industrial presence, and very little development. The forest surrounding this region is inhabited by indigenous people as well as small villages along the riverbanks. ALPE is located off of a two-lane road that connects the cities of Iquitos and Nauta. This small road is surrounded by a river and forested areas and there are no other roads connecting this region to the rest of the country. Although the population is growing on one side of the road, on the other side the forest is well preserved and unfragmented. Many of the trees in this locality were sampled from inaccessible, almost pristine, areas of the forest. JEHE had the highest anthropogenic influence of the three sites. The large research center is 1.6 km (0.99 mi) from the community of Jenaro Herrera, population of 5,632 (Thomas Brinkhoff: City Population, <http://www.citypopulation.de/php/peru-distr.php?adm1id=1605>), off of an unpaved road approximately 12-17 m (39-55 ft) wide leading away from the nearby community and deep into the forest. The surrounding forest is heavily fragmented by small farms, and pastures. Human activity, such as farming, hunting and gathering of natural resources, is prevalent throughout. The community has public electricity and paved roads that are heavily used by motorcyclists, pedestrians and cattle.

Adult endophyte isolation

Endophytic fungi were isolated from stem tissues of a total of 143 adult trees. Four species of *Hevea* (*H. brasiliensis*, *H. guianensis*, *H. nitida*, *H. pauciflora*) and two species of *Micrandra* (*M. elata*, *M. spruceana*) were opportunistically sampled.

Vouchers for each host tree were collected, and deposited at the Universidad Nacional de la Amazonía Peruana (AMAZ).

Geographical coordinates were recorded for each sampled tree using a handheld GPS unit (GPSmap 62sc, Garmin Inc., Schaffhausen, Switzerland). Trunk diameter (dbh) was measured at 1.4 meters above the ground (*Hevea* spp.) or 1.4 meters above the swell of buttressed prop roots (*Micrandra* spp.). Trees with dbh of 23 – 100 cm were targeted for sampling. The number of individual trees sampled, per species and site, varied due to their natural low abundance and scatter distribution (Table 1.1). Inner bark tissue (wood containing functioning vascular tissue) samples were collected by shaving the outer tree bark and exposing a 10 cm² area. Using a smaller flame-sterilized knife, three pieces of wood (~4 x 5 mm) were excised and transferred individually to Petri plates containing BBL™ cornmeal-agar (Sigma-Aldrich, St Louis, Missouri, USA) with 2 % dextrose and 2 mL of 1 % neomycin-penicillin-streptomycin solution to suppress bacterial growth (CMD+). Each tree had this procedure replicated three times, at different points around the tree's circumference, yielding a total of nine subsamples per tree. CMD+ plates were incubated at room temperature and emerging colonies were sub-cultured onto BBL™ potato-dextrose-agar (PDA) until pure cultures were obtained. Cultures are stored at the University of Maryland (College Park, Maryland, USA) in 20% glycerol cryovials

at -80° C and in CMD test tubes at 4° C. Representative isolates obtained in this study, with their corresponding GenBank accession numbers, are listed in Supplementary Table 1.1. The endophyte recovery rate was calculated by dividing the number of subsamples with endophytes divided by the number of subsamples (Evans et al. 2003).

Seedling endophyte isolation

Three seedlings, all within approximately 3 m of the parent tree and ranging from 30 to 60 cm in length, were randomly collected per adult tree. From each seedling stem, 3 segments (~ 5mm long) that included the entire stem with all the inner primary tissues (cortex and vascular, both phloem and xylem), were excised in the field station using sterile surgical blades and surface-sterilized through sequential immersion in 2 % sodium hypochlorite solution (2 min), 70 % ethanol (2 min) and sterilize water (Gazis and Chaverri 2010). Each segment was transferred to an individual Petri dish containing CMD+. This procedure was replicated three times, yielding a total of nine subsamples per seedling.

Environmental sample collection for direct sequencing

To investigate whether the recovered endophytic community from adults and seedlings varies when using culture-independent versus direct sequencing approaches, additional samples were collected from adults and seedlings of *H. guianensis*, *H. nitida*, and *M. spruceana* in NAPO. For adult trees, three pieces of inner bark tissue were excised from each individual (as described for the culture-based method) and transferred into individual cryovials containing 500 µL of MoBio

Bead Solution Buffer (MoBio Laboratories, Carlsbad, California, USA). Each adult tree had this procedure replicated three times, yielding a total of nine subsamples divided into three cryovials (each containing 3 inner bark tissue pieces) for direct sequencing. For seedling tissue, three stem segments (~ 5mm long) from each individual were transferred into individual cryovials with 500 μ L of MoBio Bead Solution Buffer after surface sterilization (described for culture-based method). Each seedling had this procedure replicated three times, yielding a total of nine subsamples divided in three cryovials (each containing 3 seedling stem pieces) for direct sequencing.

DNA extraction, PCR and sequencing

Isolates were sub-cultured onto PDA and incubated at 25° C for a minimum of 4 days. Mycelial mats were harvested directly from PDA plates and suspended in a microcentrifuge tube containing 60 μ L of PrepMan® Ultra Reagent (Applied Biosystems, California, USA). DNA was extracted following the manufacturer's protocol. The Internal Transcribed Spacer regions (ITS) 1 and 2 of the nuclear ribosomal DNA, including the 5.8S, were amplified and sequenced using the primers ITS5 and ITS4 (White et al. 1990). PCR conditions followed Gazis et al. (2015) and were performed on a Bio-Rad Dyad Peltier thermal cycler (Bio-Rad Laboratories, Inc., Hercules, California, USA). PCR products were sequenced at the Systematic Mycology and Microbiology Laboratory (USDA-ARS, Beltsville, Maryland, USA.) and at Macrogen USA (Rockville, Maryland, USA) as outlined by (Udayanga et al. 2014).

For culture-independent samples, excised plant tissues were placed into tubes prefilled with 500- μ m garnet sand and a 6-mm zirconium grinding satellite bead (OPS Diagnostics LLC, New Jersey, USA.). The tube contents were ground using a FastPrep® beadmill (MP Biomedicals, Santa Ana California, USA.). Each tube was treated to three cycles of grinding (speed: 5.0 m/s, time: 43 seconds) or until no visually recognizable fragments remained. Total DNA was extracted using the Qiagen® DNeasy Plant Mini Kit according to the manufacturer's instructions (Qiagen, Hilden, Germany). The fungal ITS 2 region was amplified using fITS7 (Ihrmark et al. 2012) and ITS4 (White et al. 1990) primers. To allow multiplexing of samples, unique 6-bp barcode tags were added to the ITS primers, according to the individual tree or seedling sample (Dowd et al. 2008). PCR amplification was performed using HotStarTaq Plus Master Mix Kit (Qiagen®, Hilden, Germany) under the following conditions: 94°C for 3 minutes, followed by 28 cycles of 94°C for 30 seconds, 53°C for 40 seconds and 72°C for 1 minute, after which a final elongation step at 72°C for 5 minutes was performed. Three aliquots from each sample were amplified and PCR amplification products were then pooled in equal proportions based on their molecular weight and DNA concentrations, and purified using AMPure® XP beads (Agencourt Bioscience, Massachusetts, USA). PCR amplification and sequencing was performed on an Illumina MiSeq platform at MR DNA (www.mrdnalab.com, Shallowater, TX, USA) using MiSeq Reagent Kit v2 with paired end sequencing read lengths of 150 base pairs. Forward and reverse sequences of each sample were merged into contigs. For quality control and optimization of downstream analyses, contigs with lengths smaller than 300 bp were

discarded and sequences larger than 300 bp were truncated to 300 bp (Puente-Sánchez et al. 2015). Sequences were removed when less than 90% of their base calls fell below the Q30 quality score (Manley et al. 2016). Singletons, contigs with abundance equal to one, were removed from the dataset and the UCHIME database were used to retrieve and remove chimeras from the dataset (Edgar et al. 2011).

OTU delimitation and classification

Full-length ITS sequences (~600 bp) from Sanger sequencing of fungal isolates were aligned using the MAFFT aligner version 7.305 (Katoh and Toh 2008) in CIPRES (Miller et al. 2015). Default parameters were selected, along with the adjust direction option. Sequences were clustered into operational taxonomic units (OTUs) using the furthest neighbor method in MOTHUR version 1.36.1 (Schoch et al. 2014) with a 99 % similarity criterion (Gazis et al. 2011). One representative from each putative species was chosen for OTU taxonomic classification and, when possible, well-curated sequences (sequences from published studies, with voucher/culture collection numbers) were added to the MOTHUR analysis. OTUs will be considered as putative species hereafter. BLAST (Madden 2002) was used to compare sequences against the National Center for Biotechnology Information Nucleotide database (<https://www.ncbi.nlm.nih.gov/nucleotide>) excluding uncultured/environmental sample sequences. GenBank sequences of the matched taxa for all OTUs were collected and aligned with all representative sequences from this study using the MAFFT aligner with the default parameters (Katoh and Toh 2008) in CIPRES (Miller et al. 2010). Sequences were then clustered into OTUs using the furthest neighbor

method in MOTHUR (Schoch et al. 2014), and the percent similarity at which all the GenBank representative sequences clustered together exclusively (meaning no other representative sequences from other genera were clustered with them) was considered the genus limit for the OTU.

Sequences (contigs) obtained from environmental samples were ~300 bp in length. Most reference sequences in the NCBI nuclear database are full ITS (<550 bp), thus shorter sequences have less resolution, and differences in percent divergence would be partly correlated with sequence length (Monard et al. 2013, Nilsson et al. 2008). To deal with this challenge when assigning OTUs the following steps were completed: 1) a preliminary BLAST search and gathered representative sequences of the matched taxa; 2) dataset constructed that contained 1,835 taxa; 3) sequences aligned using MAFFT aligner with the default parameters (Katoh and Toh 2008) in CIPRES (Miller et al. 2015); 4) reference sequences truncated to 300 bp; and 5) sequences clustered into OTUs using the furthest neighbor method in MOTHUR (Schoch et al. 2014). The percent similarity at which all the GenBank representative sequences clustered together exclusively (meaning no other representative sequences from other genera were included in the group) was considered the genus limit for the environmental OTU.

Diversity estimates of individual and combined datasets

Three orders of Hill numbers (HN) were used to interpolate and extrapolate species richness and diversity for all endophyte communities at tree host level within each locality (species richness, $q=0$), common species (Shannon's entropy, $q=1$) and

dominant species (inverse Simpson's, $q=2$), decreasingly sensitive to rare species (Jost 2006, Chao et al. 2014). Chao1 was calculated to extrapolate asymptotic richness using iNext package version 2.0.14. Hill numbers are expressed as the number of equally abundant species that would be needed to return the same value given by a diversity measure (Jost 2016, Chao et al. 2014). Accumulation and diversity curves were built using iNext package version 2.0.14. A 95 % confidence interval was obtained by applying 1,000 bootstrap iterations. Non-overlapping confidence intervals denote a significant difference between samples.

Comparative analysis among host species

Nonmetric Multidimensional Scaling (NMDS) analyses were conducted to visualize the trends and groupings of the fungal endophytes, at individual host tree level and developmental stage, using Euclidean distance for quantitative (abundance) data. NMDS was run under a random starting configuration using the metaMDS function in Vegan package version 2.4-2. To obtain a global solution (minimum global stress) and avoid termination of convergence upon recovery of two minimum stress solutions (local minimum), a minimum (20) and maximum (1,000) number of iterations were set according to metaMDS developer recommendations (Oksanen 2016). Stress values were interpreted according to Clarke's (1993) recommendations, where <0.05 indicates an excellent representation of the observed distances among the samples by the ordination, <0.1 indicates a good representation, <0.2 indicates a good but potentially misleading representation at the upper limits, and >0.3 indicates a poor representation.

The rate of distance decay of the fungal endophyte communities was calculated according to Nekola and White (1999), with the assumption that community similarities decrease with increasing geographical distance. In this study, endophytic turnover patterns within site and across sites were examined by constructing two distance matrices, one based on the presence/absence of an OTU (Jaccard), and the other based on geographic distances between samples (Euclidean). In this way, we are evaluating the change of community similarity across all pairwise samples. The geographic distance between individual tree hosts, within and across collection sites, was determined by first converting their geographic coordinates (latitude and longitude) into Cartesian points and then calculating the Euclidean distance between them. The distance decay relationship was calculated as the slope of a least-squares linear regression on the geographic distance and the fungal endophyte community similarity measured by the Jaccard index). In addition, we tested whether the slope of the distance decay curve of each collection site was significantly different from zero using a randomization with 1,000 iterations (Vegan package version 2.4-2). The slope of the distance similarity relationship is one of the most common measures of beta diversity in ecological studies (Soininen et al. 2007, Goldmann et al. 2016, Oono et al. 2017)

The distribution of fungal richness for each site, tree species and age group was visualized as a Venn diagram using the VIB-UGENT Venn Diagram Tool (Chen and Boutros 2011). Species abundances were ranked for each site, tree species and age group using the Rankabundance function in BiodiversityR package version 2.8-0. Fungal taxa were considered core (abundant) species if they occurred in more than 50

% of the individuals within a tree species within a site (Unterseher et al. 2011).

Putative species were parsed into 6 ecological guilds based on genus level using the FunGuild database (Nguyen et al. 2016) including: 1. entomopathogenic (parasitic or causes disease in insects), 2. fungicolous (parasitic or grows on other fungi), 3. plant pathogen (causes disease in plants), 4. saprotroph (rots plant litter), 5. wood decay (rots wood) or 6. undetermined for taxa with no established ecological lifestyle.

Fine scale comparative analysis

For three host tree species in NAPO (*H. guianensis*, *H. nitida*, and *M. spruceana*), both sampling techniques were applied and endophytic diversity, richness and distribution were examined as described above. Sequence data produced by next generation sequencing present more challenges than the ones produced by Sanger sequencing. Customarily, proportional read abundance is correlated to the proportional abundance of an organism within a sample, but often this assumption is incorrect due to factors such as variation of gene copy number among fungal taxa (especially of multi-copy ITS), and amplification artifacts such as biases due to differential primer binding efficiencies among taxa, and stochastic effects (Amend et al. 2010, Kebschull and Zador 2015). Therefore, both sequence reads (number of reads per OTU) and species incidence frequency (number of samples from which an OTU was captured) were analyzed.

Results

Endophyte Isolates

A total of 2,061 endophyte fungi were isolated from 271 trees belonging to four different species of *Hevea* (*H. brasiliensis*, *H. guianensis*, *H. nitida* and *H. pauciflora*) and two of *Micrandra* (*M. elata* and *M. spruceana*). Samples (stem and inner bark tissue) were obtained from trees in two developmental stages (seedling and adult) from three different geographic localities in the Amazonian Peru: Napo (NAPO), Allpahuayo (ALPE) and Jenaro Herrera (JEHE) (Figure 1.1). The recovery rate differed greatly between the two developmental stages across all three locations. From seedlings, 1,237 fungi were recovered (average recovery rate of 83%); and from adults, 824 (average recovery rate of 66%) (Table 1.1).

There were 356 putative species from 136 genera recorded. Endophyte communities from adult trees were composed of 255 species, while endophyte communities from seedlings were composed of 153 species, there were 52 fungal species recorded from both adult and seedling hosts. Eighteen percent of the putative species were resolved at the genus level while the rest (82%) were only resolved to higher taxonomic ranks (Supplementary Table 1.1). In all three locations, and for all tree species examined, Ascomycota dominated the fungal endophytic community in seedlings and adults, 97% and 89% of the isolates respectively. Basidiomycota were found in lower amounts for both seedling (3%) and adult (8%) fungal communities. Mucoromycota were only isolated from adult tree samples (2.7% of the isolates). Most abundant fungal orders for endophytic communities in adult trees were

Hypocreales (46% of isolates), Eurotiales (13%) and Xylariales (11%) (Figure 1.2A). Most abundant orders for communities in seedlings were Diaporthales (61% of isolates), Glomerales (11%), and Xylariales (10%) (Figure 1.2B). Three genera were most prevalent in adult trees: *Trichoderma* (26% of isolates), *Penicillium* (9%), and *Tolypocladium* (6%) while all the other genera isolated (142 out of 148) were found in lower quantities (relative abundances below 6%). In seedlings, *Diaporthe* represented 61% of isolates with *Colletotrichum* the second most abundant genus (12%); 86 genera were isolated in abundances below 3%. *Diaporthe* was the most abundant genus recovered from *Hevea* and *Micrandra* seedlings, excepting *M. elata* (sampled only in ALPE), where *Pezizula* (28%) and *Colletotrichum* (26%) prevailed.

Diversity estimates of individual and combined datasets

Richness and diversity (estimated using Shannon and Simpson indices) for endophytic communities of adult trees was not significantly different within each location, regardless of host taxonomy (Table 1.2). Similarly, richness and diversity for endophytes isolated from seedlings were similar for all hosts within location (Table 1.2). Richness and diversity for fungi isolated from adult trees were greater than those isolated from seedling in both NAPO and ALPE (Figure 1.3AB). However, in JEHE the pattern differed from the other regions; fungal richness and diversity for seedlings were greater than for the adult trees (Figure 1.3C).

Species accumulation curves increased steeply and did not reach asymptote for either seedling or adult tree fungal communities (Figures 1.4-1.6). Curves for Shannon HN and Simpson HN diversity, reached or nearly reached asymptote for all

seedling fungal communities (Figure 1.4A, Figure 1.5A, Figure 1.6A). For adult tree fungal communities, Simpson HN diversity curves reached or neared asymptote at all three locations. Shannon HN diversity curves, however, did not near or reach asymptote at any location, despite the slopes being less steep than the species accumulation curves (Figure 1.4B, Figure 1.5B, Figure 1.6B).

Based on projected diversity, some samples were nearly complete while others were insufficiently sampled (Table 1.2). The difference between the estimated number of species (Chao and Jost 2015) and observed richness for seedling fungal communities ranged from 8 to 168 (ALPE 24 to 167, NAPO 8 to 30, JEHE 11 to 67), while for adult tree fungal communities it ranged from 23 to 258 (ALPE 70 to 129, NAPO 127 to 213, JEHE 23 to 258). The difference between the estimated diversity and observed Shannon HN ranged from 0.53 to 26 (ALPE 4 to 16, NAPO 0.53 to 4, JEHE 4 to 26) for seedling fungal communities and 23 to 125 (ALPE 30 to 43, NAPO 38 to 125, JEHE 23 to 34) for adult tree fungal communities. The difference between the estimated diversity and observed Simpson HN ranged from 0.04 to 5 (ALPE 0.18 to 4, NAPO 0.04 to 0.14, JEHE 0.41 to 5) for seedlings fungal communities and 2 to 46 (ALPE 6 to 10, NAPO 6 to 46, JEHE 2 to 11) for adult tree fungal communities.

Comparative analyses among host species

Non-metric multidimensional scaling (NMDS) analysis revealed distinctiveness between fungal communities associated with the two developmental stages of host trees (stress = 0.1313) (Figure 1.7A). Seedling and adult trees had different fungal communities across hosts (stress value range 0.1055–0.1742), and across sampling

sites (stress value range 0.1129–0.1269) (Figures 8 and 9). There was no clear distinction between the endophytic communities from different host species when the data was not partitioned by developmental stage within each locality (stress value range 0.1129–0.1265) (Figure 1.10).

Across all three sampling sites, the fungal endophytic community similarity decreased when the geographic distances between the pairwise set of samples increased, except for adult *H. nitida* (Table 1.3). Within sites, the rate of distance decay indicated that there was no significant increase in community dissimilarity with increasing geographic distance except for Adult MISP in ALPE, adult HEBR in JEHE and seedling HENI in NAPO. There were very few fungal species that overlapped between seedling and their adult counterparts; overlapped species ranged from two to four, with the exceptions of HEGU in NAPO (6) and MIEL in ALPE (1) (Table 1.4). For adult trees within each location, there were more species unique to a host than overlapped with other adult species, largely due to the high percentage of singletons and doubletons (Figure 1.11). The exceptions, where host species had more endophyte species that overlapped between hosts than unique, were HEGU and MISP in ALPE and HENI in NAPO. For seedling trees within each location, the trend was reversed; there were generally more endophyte species that overlapped between hosts than were unique to a single host species.

Core species (those occurring in more than 50% of individuals within a tree species within a site) were only identified from adult HEGU, HEPA and MISP in ALPE, HENI in NAPO, and MISP in JEHE (Table 1.5). No pattern of host preference was observed across the three sites for adults. MISP in ALPE had a different core

species (*Neopestalotiopsis* species 3) than MISP in JEHE (*Trichoderma* species 21), while there were no core species recovered from MISP in NAPO (Table 1.5). In all three locations *Trichoderma* species 11 and *Trichoderma* species 21 were the most abundant endophyte species recovered from adult trees. *Trichoderma* species 21 was a core species for HEGU and HEPA in ALPE, while *Trichoderma* species 11 was a core species for MISP adults in JEHE. Seedlings from NAPO had the most fungal species that met core criteria (NAPO 5, ALPE 4, JEHE 3). In ALPE and NAPO, three of the identified core species met the core criteria in multiple hosts, while in JEHE only one core species (*Diaporthe* species 1) met the core criteria in all three host species (Table 1.5). *Diaporthe* species 7 was the most abundant in all three seedlings locations and was also a core species in all seedlings except for MIEL in ALPE, and HENI and MISP in JEHE. *Diaporthe* species 9 and *Diaporthe* species 4 were the second and third most abundant species found in seedlings.

The ecological guilds differed greatly between seedling and adult tree endophytic communities (Figure 1.12). In seedlings, endophytes in the plant pathogen guild were isolated in a higher percentage (79%) than from adult trees (10%). Less than 2% of guilds that would be considered beneficial to plant hosts, entomopathogenic (0.24%) and fungicolous (2%), were isolated from seedlings. A higher percentage of endophytes in saprotrophic (35%), fungicolous (29%), entomopathogenic (9%), undetermined (9%) and wood decay (8%) guilds were isolated from adult trees. The distribution of ecological guilds differed in JEHE. Adults trees in this region harbored more potentially plant pathogenic fungi (JEHE 15%, ALPE 11%, NAPO 7%) and less saprotrophic fungi than what was found in

ALPE and NAPO (JEHE 32%, ALPE 34%, NAPO 37%). In seedlings, the overwhelming majority of fungi recovered were members belonging to potentially plant pathogenic taxa, however, in JEHE there were less isolates under this guild recovered (JEHE 67%, ALPE 85%, NAPO 84%) as well as less fungicolous fungi (JEHE 0.5%, ALPE 2%, NAPO 2%).

Fine scale comparative analysis at NAPO

A total of 1,086,242 reads from 91 trees belonging to two different species of *Hevea* (*H. guianensis* and *H. nitida*) and one species of *Micrandra* (*M. spruceana*) met bioinformatic quality control measures for further analysis. Samples (stem and inner bark tissue) were obtained from trees in two developmental stages (seedling and adult). There were 1,039 putative fungal species identified from 436 genera. Generated sequences have been archived in the NCBI Sequence Read Archive (SRA) database (project # pending). When considering the number of OTUs, the number of reads, and incidence frequencies, Ascomycota dominated the fungal endophytic community for both seedlings (57% of OTUs, 61% of reads, 62% incidence frequency) and adult trees (73% of OTUs, 87% of reads, 89% incidence frequency). For adult tree samples, the proportion of Basidiomycota comprising fungal communities (13% of sequence reads, 10% incidence frequency) was similar to that observed using culture-based methods, in which 8% of the isolates recovered from NAPO were Basidiomycota. A higher proportion of Basidiomycota were observed in seedlings using culture-independent methods (32% sequence reads, 37% incidence frequency) than what was recovered from cultured samples (0.7 %). Mucoromycota

taxa were captured from both seedling and adult tree samples at low incidence frequencies (0.23% seedlings, 0.48% adults), whereas Mucoromycota fungal isolates were recovered solely from adult tree samples and at a higher proportion than what was captured using culture-independent methods (3% of the isolates).

Fungal genera identified using culture methods were underrepresented in culture-independent methods. For seedling endophytic communities, 50% of the recovered genera were represented in the culture-independent dataset, for adult tree endophytic communities only 23% of the recovered genera were represented. For all adult trees hosts in NAPO, four endophytic genera were the most prevalent:

Acremonium (18% of sequence reads, 10% incidence frequency), *Debaryomyces* (14% of sequence reads, 10% incidence frequency), *Tolypocladium* (14% of sequence reads, 9% incidence frequency), *Sarocladium* (1% of sequence reads, 8% incidence frequency). *Tolypocladium* was also one of the most abundant genera recovered using culture-dependent methods. No *Sarocladium* species were recovered from cultured samples and less than 1% of recovered isolates were members of *Debaryomyces* and *Acremonium*. *Trichoderma*, the most abundant genus recovered using culture methods, was captured from only one tree sample (HEGU), at a very low abundance (2 reads). For all seedling species in NAPO the two most prevalent genera, *Debaryomyces* and *Tricholomataceae* species 1, were not recovered from seedling in NAPO using culture methods. *Diaporthe*, the most abundant genus recovered using culture methods, was captured in 26% of seedling trees at a low abundance (0.14% reads) and incidence frequency (0.61%). *Colletotrichum*, the second most abundant

genus recovered from cultured samples, was captured in 43% of seeding trees, also at low abundance (0.56% reads) and incidence frequency (3.60%).

Richness and diversity, based on Shannon HN and Simpson HN indices, of endophytic communities captured using culture-independent methods were significantly different among adult trees with HEGU having the greatest endophytic (richness 318) and diversity (Shannon HN 221, Simpson HN 134), followed by HENI (Richness 133, Shannon HN 105, Simpson HN 76), and MISP (Richness 122, Shannon HN 72, Simpson HN 42) (Table 1.6). Richness and diversity of endophytic communities from HEGU and HENI seedlings were similar, however the endophytic community from MISP (Richness 562, Shannon HN 385, Simpson HN 222) was significantly more diverse than HEGU (Richness 72, Shannon HN 45, Simpson HN 32) and HENI (Richness 53, Shannon HN 37, Simpson HN 27). Richness and diversity of endophytic communities captured from adult trees were greater than those captured from seedlings except for MISP, which was significantly more diverse than communities captured from all adult tree species (Figure 1.13). The number of species captured per MISP seedling sample ranged from 33 to 111 with a mean/median of 56/50, whereas the number of species captured from HEGU and HENI seedlings ranged from 8 to 24 with a mean/median of 15/13.

Species accumulation curves increased steeply and did not asymptote for either seedlings or adults (Figure 1.14). Curves for Shannon HN and Simpson HN diversity reached or nearly reached asymptote for HEGU and HENI seedlings while the curve for MISP seedlings remained steep (Figure 1.14A). For all adult tree species, Simpson diversity curves approached asymptote. Shannon HN diversity

curves, however, did not near or reach asymptote, despite the slopes being less steep than the species accumulation curves.

The difference between the estimated number of species (Chao and Jost 2015) and observed richness ranged from 32–1,490 (HEGU 32, HENI 108, MISP 1,490) for seedlings, whereas for adult tree communities it ranged from 269–527, (HEGU 526, HENI 527, MISP 269) (Table 1.6). The difference between the estimated diversity and observed Shannon HN ranged from 12–554 (HEGU 12, HENI 29, MISP 554) for seedlings 62–241 (HEGU 225, HENI 241, MISP 62) for adult tree communities. The difference between the estimated and observed Simpson HN ranged between 4 to 67 (HEGU 4, HENI 8, MISP 67) for seedlings and 8 to 47 (HEGU 40, HENI 47, MISP 8) for adult tree communities.

Non-metric multidimensional scaling (NMDS) analysis revealed distinctiveness between fungal communities associated with the two developmental stages of host trees (Figure 1.15A). Clear separation between the endophytes captured from seedlings and adult tree communities was observed when either presence/absence data (stress=0.1388) or sequence read data (stress=0.2183) was analyzed. There was no significant distinction between the different host species (Figure 1.15B). Core species were identified from all adult and seedling host species (Table 1.7). As with culture-dependent results, seedling endophytic communities had the most fungal species that met core criteria (16 species), six of the species identified met the core criteria in all three seedling host species. In adult endophytic communities seven species were identified as core species, four of which met the criteria in all three host species.

As with culture-dependent methods, the ecological guilds differed greatly between seedling and adult tree endophytic communities; however, the proportions of fungal guilds comprising the endophytic communities differed between the two methods (Table 1.8). A higher percentage of endophytes in entomopathogenic guild (31% of incidence frequency, 30% of sequence reads) and a lower percentage of fungicolous guild (10% of incidence frequency, 19% of sequence reads) were captured from adult tree communities than from seedlings. On the other hand, endophytes in the plant pathogen guild were equally captured from seedling (9% of incidence frequency, 3% of sequence reads) and adult trees (10% of incidence frequency, 3% of sequence reads). A higher percentage of endophytes with unknown functions (39% of incidence frequency, 25% of sequence reads) were detected in seedling communities, than in adult tree communities (16% of incidence frequency, 23% of sequence reads). Similar to results from the culture-based approach, seedlings harbored less than 1% of guilds that would be considered beneficial to plant hosts, entomopathogenic (0.61% of incidence frequency) and fungicolous (0.08% of incidence frequency), which is similar to the results using culture dependent methods.

Discussion

Different fungal communities, in terms of abundance and species composition, were recovered from seedlings and adult tree tissues. A greater number of endophytic fungi were recovered from seedlings (83% of isolates) than from adult trees (66% of isolates). Higher isolation rates have been reported in younger host tissues in other host systems as well. Espinosa-Garcia and Langenheim (1990) observed that in

Sequoia sempervirens endophyte isolation frequency increased with leaf age and then decreased after the leaves reached full maturity in both adult and basal sprout leaves; however, a higher isolation frequency was recorded from basal sprout leaves.

Rodrigues (1994) observed higher isolation frequency from sapling leaves of *Euterpe oleracea* than adult leaves, and Gure et al. (2014) observed a higher isolation frequency from juvenile *Afrocarpus falcatus* needles than adults.

The known and described dominance of Ascomycota in plant endophytic communities (Neubert et al. 2006, Higgins et al. 2007, Hoffman and Arnold 2008, Gazis and Chaverri 2010, 2015) was confirmed in this study, as they represented 89% of isolates recovered from adult trees and 97% of isolates recovered from seedling stems. *Trichoderma* and *Penicillium* were the most commonly cultured fungi from adult trees but were rarely isolated from seedling stems (0.2%). An opposite pattern was observed for *Diaporthe* and *Colletotrichum*, which were more abundant in seedling stems than in adult trees (0.6 and 0.2%, respectively). This pattern of one taxon being isolated more frequently from one host developmental stage rather than another has been reported for other tree hosts and tissue types as well, suggesting that host developmental stage is key to shaping endophytic communities (Espinosa-Garcia and Langenheim 1990, Rodriguez et al. 2009, Gure and Birhanu 2014, Oono et al. 2015).

Specificity to the host developmental stage was found to have greater influence on the assemblage of endophytic communities, than host identity or locality. The fungal genera recovered from seedling and adult trees using culture-dependent methods were not the same than the ones captured using next generation

sequencing, and yet the pattern was similar in that the two developmental stages harbored distinctly different communities regardless of method used. There are several factors that may be contributing to the differences: 1) fungal endophytes might be adapted to particular “microenvironments” (*e.g.*, host cells and tissues) (Vujanovic and Brisson 2002, Kumaran and Hur 2009, Feinstein and Blackwood 2012); 2) seedlings may be more susceptible to the colonization by fungi that belong to plant pathogenic groups than adults (Lieberei et al. 1996, Ballhorn et al. 2005); and 3) the Negative Density Dependence (NDD) effect may be occurring due to an accumulation of pathogenic taxa surrounding the parent tree (Janzen 1970, Connell 1971).

Because seedlings and adult trees in natural forests are generally exposed to the same surrounding *ex-planta* fungal inoculum, there are likely other factors influencing differences between developmental stages. Therefore, one hypothesis to explain the differences observed between seedling and adult trees maybe micro-niche specialization (Vujanovic and Brisson 2002, Kumaran and Hur 2009, Feinstein and Blackwood 2012). Studies have shown that different tissues types (*e.g.*, twig, leaf, flower and fruit) from a single plant may harbor distinct endophytic communities, thus the observed dissimilarity between adult and seedling tissues may be determinant to fungal colonization mechanisms (Huang et al. 2008, Martinson et al. 2012, Wu et al. 2013). For instance, many *Trichoderma* thrive on lignin/hemicellulose rich plant tissues (Kubicek 2012, Navarro et al. 2012) and this may explain their low abundances in young tissues and leaves.

A second hypothesis to explain the observed differences between seedlings and adults is that seedlings are more susceptible to the colonization by fungi that belong to plant pathogenic groups than adult trees. Seedling stems and new leaves of *Hevea* lack some of the physical and chemical properties that make colonization of adult trees difficult for certain fungal taxa (Fang et al. 2016). The immature tissues are tender, lack lignin, and have not fully developed defensive biochemical pathways that produce fungitoxic compounds such as the coumarin scopoletin (Lieberei 2007). Alternatively, younger leaves contain higher levels of gaseous hydrogen cyanide (HC), which protect against herbivores but negatively affects fungicidal enzymes (Lieberei et al. 1996, Ballhorn et al. 2005). It is in these juvenile foliar growth stages that *Hevea* is most susceptible to fungal diseases such as *Pseudocercospora ulei*, the causal agent of South American leaf blight (Chee and Holliday 1986, Jayasuriya et al. 2003).

Gazis and Chaverri (2015) found *Trichoderma* spp. to be the dominant culturable endophytic fungi in wild adult *Hevea* trees. The same study found a negative correlation between the presence of *Trichoderma* spp. and the abundance of potentially pathogenic fungi, *Diaporthe* in particular. Likewise, Hanada et al. (2010) observed that *Trichoderma* spp. were not only the dominant endophytes collected from branches of cultivated *Theobroma cacao* and wild *Theobroma grandiflorum* in Brazil, but that these endophytes were antagonistic to *Phytophthora palmivora*, an important cacao disease. Coupled with these findings and their own observations, Gazis and Chaverri (2015) proposed that this taxon is an important or even an essential component for host protection against pathogens in natural forests. The

opportunistic plant pathogenic *Diaporthe* was more abundant in seedlings (61% of isolate), whereas *Trichoderma* was almost absent (0.2% of isolates). The absence of *Trichoderma* spp. may be one of the reasons for the successful colonization of pathogenic strains (Gazis and Chaverri 2015). As was suggested by Evans et al. (2003) upon observing a high proportion of mycoparasitic hypocrealean fungi in asymptomatic wild pods of *Theobroma gileri*, and none of the usual opportunistic pod pathogens normally colonizing diseased pods such as *Fusarium*, *Colletotrichum*, and *Xylaria*. The negative correlation observed between the presence of *Trichoderma* and potentially pathogenic fungi may be due to competitive exclusion mechanisms or to the antifungal properties of *Trichoderma* (Harman et al. 2004, Hanada et al. 2010, Hermosa et al. 2012).

A third hypothesis to explain the differences between fungal communities of seedling and adult trees may be explained by the Negative Density Dependence (NDD) hypothesis. Janzen and Connell hypothesized that specialized natural enemies (herbivores, pathogens) maintain high tree diversity in tropical forests (Janzen 1970, Connell 1971). Areas nearest the parent plant have accumulated a high inoculum load, making the surrounding area inhospitable for seedlings. The resulting high rates of seedling mortality prevent dominant plant species from competitively excluding others. Both *Hevea* and *Micrandra* produce abundant crops of seedlings around the bases of parent trees from seeds that germinate immediately after localized dispersal via their explosive fruits. Few of these seedlings appear to survive beyond the first season with few saplings observed except near light gaps. It is hypothesized that plant species richness is maintained by allowing rarer tree species to accumulate more than

the dominant species. Eventually the “rarer” species become more common and the situation is reversed. Bagchi et al. (2014) demonstrated that although insects help structure plant communities, fungi are the natural enemies that maintain high tropical diversity. Classical NDD pathogens involved with seedling mortality are thought to be specialists; however, host specificity has rarely been observed and the agents of seedling mortality are more likely generalists (Augspurger and Kelly 1984, Peters 2003, Gilbert 2005, Bell et al. 2006, Freckleton and Lewis 2006). NDD may partly account for the observed division of functional groups between seedling stem endophytes and adult tree endophytes.

When examining the patterns of diversity, richness and community composition across sampling locations, JEHE differed from both ALPE and NAPO. Adult trees generally had a higher endophytic richness than seedlings (Table 1.2), except in JEHE where endophytic richness of adult trees was not only lower than the richness of seedlings, but also lower than the endophytic richness of adults in the other two locations. Although we did not measure disturbance, the latter may have an influence on fungal endophyte diversity based on our personal observations of the sites. NAPO was the most remote location, ALPE was easily accessible but well preserved, and JEHE had the most anthropogenic pressures such as forest fragmentation due to small scale farming and conversion of forested areas into pastures. Expansion of human activities into natural forests may be one explanation for the observed differences among locations as they lead to changes in host microclimate, soil chemistry (due to pollutants and agricultural practices) and forest fragmentation and isolation (Helander et al. 2007, Jumpponen and Jones 2010,

Hossain and Sugiyama 2011, Matsumura and Fukuda 2013, Sikes et al. 2017). Forest fragmentation exposes the landscape to sunlight which has a strong effect on leaf endophytes. Several studies have shown that incidence frequencies significantly increase or decrease for particular fungal taxa depending on a leaf's position in tree canopy (light vs shade) (Osono and Mori 2004, Unterseher et al. 2007, Gure and Birhanu 2014, Harrison et al. 2016, Kato et al. 2016). Furthermore, Alvarez-Loayza et al. (2011) observed that light can regulate how an endophyte affects the fitness of its host by triggering an endophyte's mutualistic or pathogenic response.

The degree to which a taxon or functional grouping is impacted by urbanization varies according to an endophyte's taxonomy (Ochimaru and Fukuda 2007). While examining fungal communities recovered from soil and leaf litter in urban and rural Japanese forests, Ochimaru and Fukuda (2007) found that the abundance of amanitaceous (Agaricales, Basidiomycota) species was lower in urban and suburban forests than in the rural forest. In contrast, the frequency of Russulaceae (Russulales, Basidiomycota) species was higher in the urban forest than in the rural forest. We also found that the most common species/genera in mainly undisturbed areas were either absent or not as dominant in JEHE. For seedling stems, *Diaporthe* species 7 was the most recovered species in all three locations. However, in JEHE, the abundance of this species was almost half of what was recovered from the other two locations (ALPE 40%, NAPO 46%, and JEHE 23%). *Diaporthe* species 4 was the second most recovered species in ALPE and NAPO but in JEHE it was not one of the top ten abundant species. Conversely, the dominance of *Trichoderma* 11, the most abundant species recovered from adult trees, did not significantly change. The impact

of anthropogenic activities on the richness and diversity of fungal communities has been well documented (Ochimaru and Fukuda 2007, Jumpponen and Jones 2010, Matsumura and Fukuda 2013, Robles et al. 2015). Our data are in accordance with these studies, suggesting that human disturbances could have a strong influence on the establishment of fungal species even in communities living within trees.

All of the results discussed so far have been based on culture-dependent methods. For one collection site (NAPO), both culture-independent and -dependent methods were utilized. Results of culture-independent methods concur with culture-dependent methods in that a clear distinction between the taxonomic community composition and abundance of fungal endophytes of adult and seedlings was observed. However, endophytes identified with culture-dependent and culture-independent methods had very little overlap. We obtained drastic differences in the abundance of some of the common isolated genera. For instance, *Trichoderma* was found to be the most abundant genus recovered through the culture-based approach from adult trees, but was one of the least abundant (number of reads and incidence in individual samples/sub-samples) when culture-independent approaches were applied. Some of the explanations are that *Trichoderma* is a relative fast-growing genus that grows readily on artificial media and so tends to overgrow other fungi that may colonize the sapwood. Previous reports in other systems have also shown that these two approaches recover different endophytes and have suggested that both approaches are needed for a comprehensive exploration of these highly diverse communities (Allen et al. 2003, Arnold 2007, Stenström et al. 2014). Culture-independent methods detect species that are not able to grow in artificial culture

medium, or that have low growth rates and are easily overgrown by other co-inhabitants.

This is one of the first studies comparing adult tissue to seedling stem tissue. The majority thus far had compared fungal communities recovered from adult tree leaves and offspring leaves. Differences between seedling and adult tree fungal communities as well as differences among locations were expected; however, this is the first study to address the question in a systematic manner. Results from this study suggest that host developmental stage, more than host taxonomy or locality, is a key determinant of community assemblage of tropical endophytes. We believe that anthropogenic activities can also influence species richness and diversity as reflected by the lower metrics in the location with highest anthropogenic impact.

TABLE 1.1. Summary of locations, host tree species and the number of trees and developmental stages sampled from Amazon Conservatory for Tropical Studies Biological Station (NAPO), Allpahuayo-Mishana National Reserve (ALPE), and Jenaro Herrera Research Center (JEHE), as well as the total number of endophytes recovered per tree species, location and developmental stage.

	Host Tree Species	No. of Adult trees that had seedlings	No. of seedlings sampled (Stem)/ No. subsamples/ No. of subsamples with endos	No. of adult trees sampled (Sapwood) / No. subsamples/No. of subsamples with endos	No. of endos recovered		Recovery Rates (%)	
					Seedling	Adult	Seedling	Adult
Site	<i>Hevea guianensis</i>	16	48 /144/ 127	13/81/53	180	69	88%	65%
	<i>Hevea pauciflora</i>	15	45/ 135/103	16/117/70	132	81	76%	60%
	<i>Micrandra elata</i>	10	30 / 63/38	15/126/84	54	92	60%	67%
	<i>Micrandra spruceana</i>	5	15/45/41	9 /54/45	58	52	91%	83%
	Total sampled	46	141/396/309	55/387/256	424	294	78%	66%
JEHE	<i>Hevea brasiliensis</i>	13	39 /126/105	13 /54/23	121	51	83%	43%
	<i>Hevea nitida</i>	10	30 /99/80	10 /45/27	94	30	81%	60%
	<i>Micrandra spruceana</i>	14	42 /126/112	15 /108/70	181	74	89%	65%
	Total sampled	37	114/351/297	38/207/120	396	155	84%	58%
NAPO	<i>Hevea brasiliensis</i>	-	-	-	-	-	-	-
	<i>Hevea guianensis</i>	16	48 /144 /133	21/189/153	197	201	92%	81%
	<i>Hevea nitida</i>	9	27/72/54	11/ 72/45	64	58	75%	63%
	<i>Micrandra spruceana</i>	17	51/ 144 /121	19/ 162/99	156	116	84%	61%
	Total sampled	42	126/360/308	51/423/297	417	375	86%	70%
Totals	Total sampled	125	381/1107/914	144/1017/673	1237	824	83%	66%

TABLE 1.2. **Culture dependent method:** Observed and estimated species richness (SR) and diversity (Shannon Hill numbers and Simpson Hill numbers), including upper (UCL) and lower (LCL) confidence intervals, of endophytes per location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]), tree species and tree developmental stage. Non-overlapping confidence levels signify a significant difference in richness or diversity, while partially overlapping confidence levels do not guarantee non-significance (Chao et al. 2014).

Site	Host tree species	Dev. stage	Observed							Estimated								
			SR	Shannon	LCL	UCL	Simpson	LCL	UCL	SR	LCL	UCL	Shannon	LCL	UCL	Simpson	LCL	UCL
ALPE	<i>H. guianensis</i>	Adult	39	29	20	38	20	12	27	168	77	480	70	29	113	27	20	44
		Seedling	43	15	11	19	6	4	8	91	59	183	19	15	25	6	6	8
	<i>H. pauciflora</i>	Adult	44	32	26	38	22	15	30	132	74	301	66	33	100	31	22	45
		Seedling	39	16	11	21	8	6	10	206	80	715	27	16	39	9	8	12
	<i>M. elata</i>	Adult	53	39	30	49	26	19	33	138	89	256	82	54	110	36	26	52
		Seedling	23	17	11	23	13	9	17	119	39	597	33	17	53	16	13	23
	<i>M. spruceana</i>	Adult	32	22	14	31	15	10	21	102	53	259	53	22	90	21	15	35
		Seedling	19	8	6	11	4	2	6	43	25	118	12	8	18	4	4	6
JEHE	<i>H. brasiliensis</i>	Adult	28	23	18	28	19	15	24	46	33	87	38	27	49	30	19	43
		Seedling	57	38	30	47	23	15	31	124	84	225	64	45	83	28	23	39
	<i>H. nitida</i>	Adult	17	13	7	18	9	4	15	40	23	114	25	13	42	13	9	24
		Seedling	40	25	20	30	15	10	20	62	48	101	36	27	45	17	15	24
	<i>M. spruceana</i>	Adult	39	23	14	32	12	6	18	197	86	572	58	23	103	14	12	22
		Seedling	45	19	15	23	9	7	11	56	49	80	23	19	28	9	9	12

Site	Host tree species	Dev. stage	Observed							Estimated								
			SR	Shannon	LCL	UCL	Simpson	LCL	UCL	SR	LCL	UCL	Shannon	LCL	UCL	Simpson	LCL	UCL
NAPO	<i>H. guianensis</i>	Adult	90	55	45	64	32	25	38	218	150	359	93	72	114	37	32	48
		Seedling	35	12	10	15	6	5	7	51	40	89	14	12	17	6	6	8
	<i>H. nitida</i>	Adult	43	35	25	46	26	14	37	170	88	400	117	38	197	46	26	84
		Seedling	19	10	7	14	7	5	9	49	25	162	15	10	22	7	7	10
	<i>M. spruceana</i>	Adult	79	67	55	79	54	42	66	292	175	550	192	119	265	100	63	136
		Seedling	18	6	4	7	3	2	4	26	20	60	6	6	8	3	3	4

TABLE 1.3. The rate of distance decay (DD) of the fungal endophyte communities for each tree host across and within sampling locations (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]). P values in red indicate a significant increase in community dissimilarity with increasing geographic distance.

Location	Developmental stage	Host Tree species	Slope Intercept	Rate of DD	P value
ALPE	Adult tree	<i>Hevea guianensis</i>	0.978	-0.042	0.129
		<i>Hevea pauciflora</i>	0.947	-0.009	0.250
		<i>Micrandra elata</i>	0.950	-0.001	0.965
		<i>Micrandra spruceana</i>	1.015	-0.078	0.017
	Seedling tree	<i>Hevea guianensis</i>	0.797	-0.014	0.399
		<i>Hevea pauciflora</i>	0.786	0.013	0.208
		<i>Micrandra elata</i>	0.906	-0.004	0.899
		<i>Micrandra spruceana</i>	0.612	0.054	0.179
NAPO	Adult tree	<i>Hevea guianensis</i>	0.959	-0.010	0.097
		<i>Hevea nitida</i>	0.946	0.003	0.699
		<i>Micrandra spruceana</i>	0.984	-0.002	0.563
	Seedling tree	<i>Hevea guianensis</i>	0.705	-0.033	0.249
		<i>Hevea nitida</i>	0.681	0.060	0.001
		<i>Micrandra spruceana</i>	0.612	0.001	0.952
JEHE	Adult tree	<i>Hevea brasiliensis</i>	0.989	-0.034	0.010
		<i>Hevea nitida</i>	0.993	-0.011	0.310
		<i>Micrandra spruceana</i>	0.896	0.008	0.420
	Seedling tree	<i>Hevea brasiliensis</i>	0.900	-0.004	0.563
		<i>Hevea nitida</i>	0.898	0.010	0.366
		<i>Micrandra spruceana</i>	0.788	-0.001	0.926
All locations	Adult tree	<i>Hevea guianensis</i>	0.965	-0.00054	0.000
		<i>Micrandra spruceana</i>	0.973	-0.00031	0.000
		<i>Hevea nitida</i>	0.982	-0.00017	0.078
	Seedling tree	<i>Hevea guianensis</i>	0.758	-0.00048	0.011
		<i>Micrandra spruceana</i>	0.814	-0.00134	0.000
		<i>Hevea nitida</i>	0.914	-0.00046	0.004

TABLE 1.4. The number and percent of endophyte species overlap within and across developmental stages (seedling, adult), per tree species, method (culture dependent and culture independent), and location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]). Percentages of shared endophytes were calculated with singletons included and excluded from the datasets.

Site	Dev. stage	Tree host species	No. endophyte species	No. Singletons	No. shared endo species within dev. stage	No. shared endo species across dev. stage	% endophyte overlap within developmental stages		% endophyte overlap across developmental stages	
							with singletons	without singletons	with singletons	without singletons
ALPE	Adult trees	<i>H. guianensis</i>	39	16	21	4	54%	91%	10%	17%
		<i>H. pauciflora</i>	44	21	21	2	48%	91%	5%	9%
		<i>M. elata</i>	53	26	22	1	41%	79%	2%	4%
		<i>M. spruceana</i>	32	14	17	2	53%	94%	6%	12%
	Seedling trees	<i>H. guianensis</i>	43	14	25	4	58%	86%	9%	14%
		<i>H. pauciflora</i>	39	16	23	2	59%	100%	5%	9%
		<i>M. elata</i>	23	7	15	1	65%	94%	4%	6%
		<i>M. spruceana</i>	19	3	15	2	79%	94%	11%	13%
JEHE	Adult trees	<i>H. brasiliensis</i>	28	12	12	3	43%	75%	11%	19%
		<i>H. nitida</i>	17	8	8	2	47%	89%	12%	22%
		<i>M. spruceana</i>	39	24	12	3	31%	80%	8%	20%
	Seedling trees	<i>H. brasiliensis</i>	57	25	31	3	54%	97%	5%	9%
		<i>H. nitida</i>	40	12	25	2	63%	89%	5%	7%
		<i>M. spruceana</i>	45	9	28	3	62%	78%	7%	8%

Site	Dev. stage	Tree host species	No. endophyte species	No. Singletons	No. shared endo species within dev. stage	No. shared endo species across dev. stage	% endophyte overlap within developmental stages		% endophyte overlap across developmental stages	
							with singletons	without singletons	with singletons	without singletons
NAPO	Adult trees	<i>H. guianensis</i>	90	40	38	6	42%	76%	7%	12%
		<i>H. nitida</i>	43	16	26	4	60%	96%	9%	15%
		<i>M. spruceana</i>	79	47	27	3	34%	84%	4%	9%
	Seedling trees	<i>H. guianensis</i>	35	11	15	6	43%	63%	17%	25%
		<i>H. nitida</i>	19	7	11	4	58%	92%	21%	33%
		<i>M. spruceana</i>	18	3	14	3	78%	93%	17%	20%
NAPO Culture Independent	Adult trees	<i>H. guianensis</i>	317	225	31	3	10%	34%	1%	3%
		<i>H. nitida</i>	133	108	20	3	15%	80%	9%	15%
		<i>M. spruceana</i>	122	87	23	2	19%	66%	4%	9%
	Seedling trees	<i>H. guianensis</i>	72	32	35	3	49%	88%	4%	8%
		<i>H. nitida</i>	53	33	20	3	38%	100%	21%	33%
		<i>M. spruceana</i>	562	430	30	2	5%	23%	17%	20%

TABLE 1.5. The distribution of core species per location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]), separated by developmental stage, and tree species. Columns denote a core species and an “X” indicates that the endophyte species was identified as a core species within a particular location, dataset and tree host. Core species: *Annulohypoxylon* species 1 (Annul 1), *Colletotrichum* species 11 (Colle 11), *Diaporthe* species 1 (Diapo 1), *Diaporthe* species 14 (Diapo 14), *Diaporthe* species 19 (Diapo 19), *Diaporthe* species 4 (Diapo 4), *Diaporthe* species 5 (Diapo 5), *Diaporthe* species 7 (Diapo 7), *Diaporthe* species 8 (Diapo 8), *Diaporthe* species 9 (Diapo 9), *Neopestalotiopsis* species 3 (Neope 3), *Pezicula* species 1 (Pezic 1), *Trichoderma* species 11 (Trich 11), and *Trichoderma* species 21 (Trich 21).

Site	Tree host species	Adult tree endophyte core species					Seedling tree endophyte core species								
		Trich 21	Neope 3	Diapo 19	Annul 1	Trich 11	Diapo 4	Diapo 7	Diapo 14	Pezic 1	Diapo 5	Diapo 8	Colle 11	Diapo 1	Diapo 9
ALPE	<i>H. guianensis</i>	x	-	-	-	-	x	x	-	-	-	-	-	-	-
	<i>H. pauciflora</i>	x	-	-	-	-	x	x	-	-	-	-	-	-	-
	<i>M. elata</i>	-	x	-	-	-	x	x	x	x	-	-	-	-	-
	<i>M. spruceana</i>	-	-	-	-	-	-	-	-	x	-	-	-	-	-
JEHE	<i>H. brasiliensis</i>	-	-	-	-	-	-	x	-	-	-	-	-	x	-
	<i>H. nitida</i>	-	-	-	-	-	-	-	-	-	-	-	-	x	-
	<i>M. spruceana</i>	-	-	-	-	x	-	-	-	-	-	-	-	x	x
NAPO	<i>H. guianensis</i>	-	-	-	x	-	x	x	-	-	x	-	-	-	-
	<i>H. nitida</i>	-	-	-	-	-	-	x	-	-	-	-	x	-	-
	<i>M. spruceana</i>	-	-	-	-	-	-	x	-	-	x	x	-	-	-

TABLE 1.6. Culture independent method: Observed and estimated species richness (SR) and diversity (Shannon Hill numbers and Simpson Hill numbers), including upper (UCL) and lower (LCL) confidence intervals, of endophytes for Amazon Conservatory for Tropical Studies Biological Station [NAPO], tree species and tree developmental stage. Partially overlapping confidence levels do not guarantee non-significance (Chao et al. 2014).

Site	Host tree species	Dev. stage	Observed							Estimated								
			SR	Shannon	LCL	UCL	Simpson	LCL	UCL	SR	LCL	UCL	Shannon	LCL	UCL	Simpson	LCL	UCL
NAPO	<i>H. guianensis</i>	Adult	318	221	199	242	134	112	156	844	674	1096	446	389	502	174	138	210
		Seedling	72	45	39	50	32	27	36	104	85	148	57	49	64	36	32	43
	<i>H. nitida</i>	Adult	133	105	88	122	76	56	96	660	399	1179	346	239	452	123	76	173
		Seedling	53	37	31	43	27	21	34	161	91	361	66	45	87	35	27	45
	<i>M. spruceana</i>	Adult	122	72	60	83	42	32	53	391	261	645	134	102	165	50	42	60
		Seedling	562	385	351	418	222	192	252	2052	1649	2602	938	816	1061	289	234	344

TABLE 1.7. The distribution of core species recovered from tree hosts in Amazon Conservatory for Tropical Studies Biological Station (NAPO) using culture independent method. HEGU: *Hevea guianensis*, HENI: *Hevea nitida* and MISP: *Micrandra spruceana*. Columns denote a core species and an “X” indicates that the endophyte species was identified as a core species within a particular location, dataset and tree host. Core species: *Acremonium* species 3 (Acre 3), Agaricales species 15.2 (Agar 15.2), Basidiomycota species 21 (Basta 21), *Beltrania* species 1 (Beltr 1), *Beltraniella* species 1 (Belta 1), *Beltraniella* species 5 (Bella 5), *Colletotrichum* species 1 (Colle 1), *Colletotrichum* species 2 (Colle 2), *Cyphellophora* species 1 (Cyphe 1), *Debaryomyces* species 1 (Debar 1), *Debaryomyces* species 6 (Deb 6), *Debaryomyces* species 16 (Debar 16), *Debaryomyces* species 18 (Debar 18), *Graphidaceae* species 2.2 (Grap 2.2), Hypocreales species 3 (Hyp 3), *Sarocladium* species 1 (Saro 1), *Tolypocladium* species 1 (Tolyp 1), *Tolypocladium* species 2 (Tolyp 2), Tricholomataceae 1.1 (Mycen 1.1), Tricholomataceae 1.3 (Mycen 1.3), Xylariales species 4.1 (Xylal 4.1), and *Xylodon* species 5 (Xlod 5).

Tree host species	Adult tree endophyte core species							Seedling tree endophyte core species																
	Deb 6	Hyp 3	Toly 2	Saro 1	Toly 1	Acre 3	Agar 1	Debar 1	Debar 16	Debar 18	Grap 2	Mycen 1.3	Mycen 1.1	Colle 1	Colle 2	Xlod 5	Basta 21	Bella 5	Belta 1	Beltr 1	Cyphe 1	Debar 6	Xylal 4	
HEGU	x	x	x	x	x	-	-	x	x	x	x	x	x	x	x	x	-	-	-	-	-	-	-	-
HENI	x	x	x	x	-	-	-	x	x	x	x	x	x	-	-	-	-	-	-	-	-	-	-	-
MISP	x	x	x	x	-	x	x	x	x	x	x	x	x	-	-	-	x	x	x	x	x	x	x	x

TABLE 1.8. The proportion of function guilds separated by developmental stage, method (culture dependent and culture independent), and tree host species sampled from Amazon Conservatory for Tropical Studies Biological Station (NAPO).

Developmental stage	Method	Tree host species	Proportion of function guild					
			Entomopathogenic	Fungicolous	Plant pathogen	Saprotroph	Undetermined	Wood decay
Adult	Culture dependent	<i>H. guianensis</i>	7%	36%	5%	34%	9%	8%
		<i>H. nitida</i>	9%	19%	5%	34%	17%	16%
		<i>M. spruceana</i>	6%	14%	11%	42%	13%	13%
		Site total	7%	27%	7%	37%	12%	11%
	Culture independent	<i>H. guianensis</i>	29%	11%	10%	32%	15%	2%
		<i>H. nitida</i>	22%	11%	9%	46%	12%	0%
		<i>M. spruceana</i>	40%	6%	5%	27%	19%	2%
		Site total	31%	10%	9%	33%	16%	2%
Seedling	Culture dependent	<i>H. guianensis</i>	1%	1%	79%	19%	0%	1%
		<i>H. nitida</i>	2%	6%	77%	16%	0%	0%
		<i>M. spruceana</i>	0%	3%	95%	2%	1%	0%
		Site total	1%	2%	84%	12%	0.2%	0%
	Culture independent	<i>H. guianensis</i>	0%	0%	23%	37%	38%	2%
		<i>H. nitida</i>	19%	10%	10%	48%	13%	1%
		<i>M. spruceana</i>	1%	0%	7%	39%	45%	9%
		Site total	3%	2%	10%	40%	39.2%	7%

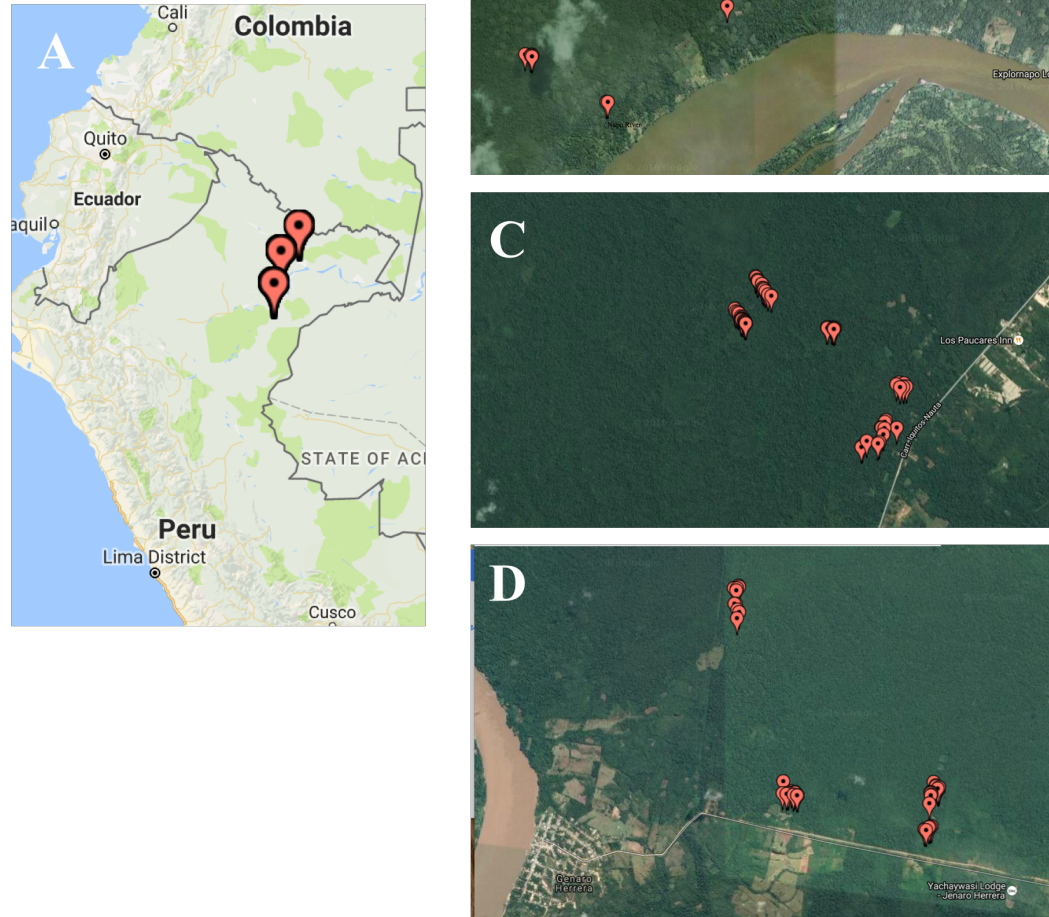


FIGURE 1.1. Research sites. (A) The three sampling localities demarcated in red. (B) Google Earth 7.1.5.1557 ACTS Biological Station ($3^{\circ}14'57.20''\text{S}$, $72^{\circ}54'33.60''\text{W}$), (C) Google Earth 7.1.5.1557 Allpahuayo-Mishana National Reserve ($3^{\circ}58'1.16''\text{S}$, $73^{\circ}25'8.11''\text{W}$), D) Google Earth 7.1.5.1557. Jenaro, Herrera Research Center ($4^{\circ}53'54.29''\text{S}$, $73^{\circ}38'59.80''\text{W}$), viewed 26 September 2016.

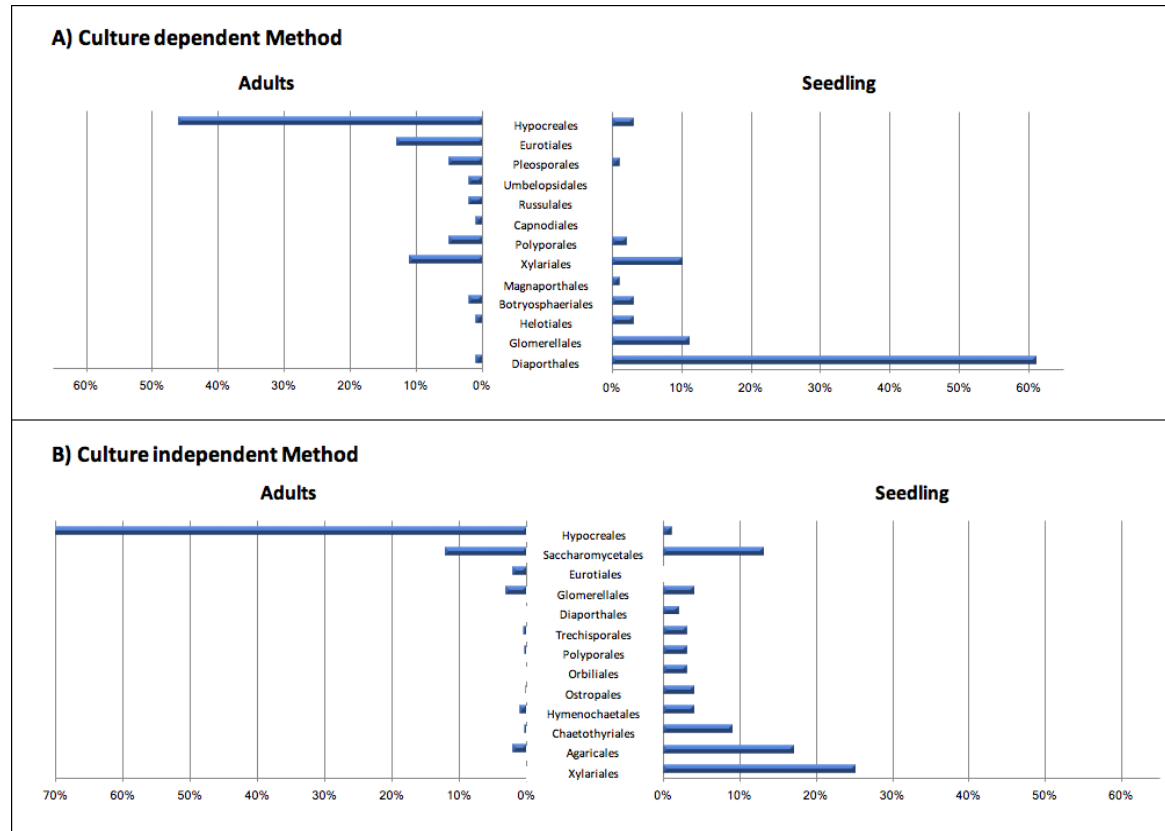


FIGURE 1.2. Relative abundance of orders present in each developmental stage under the two different sampling approaches. (A) The most abundant taxonomic orders recovered from seedling stems and adult sapwood using culture dependent method. (B) The taxa with the highest incidence frequency captured using culture independent method.

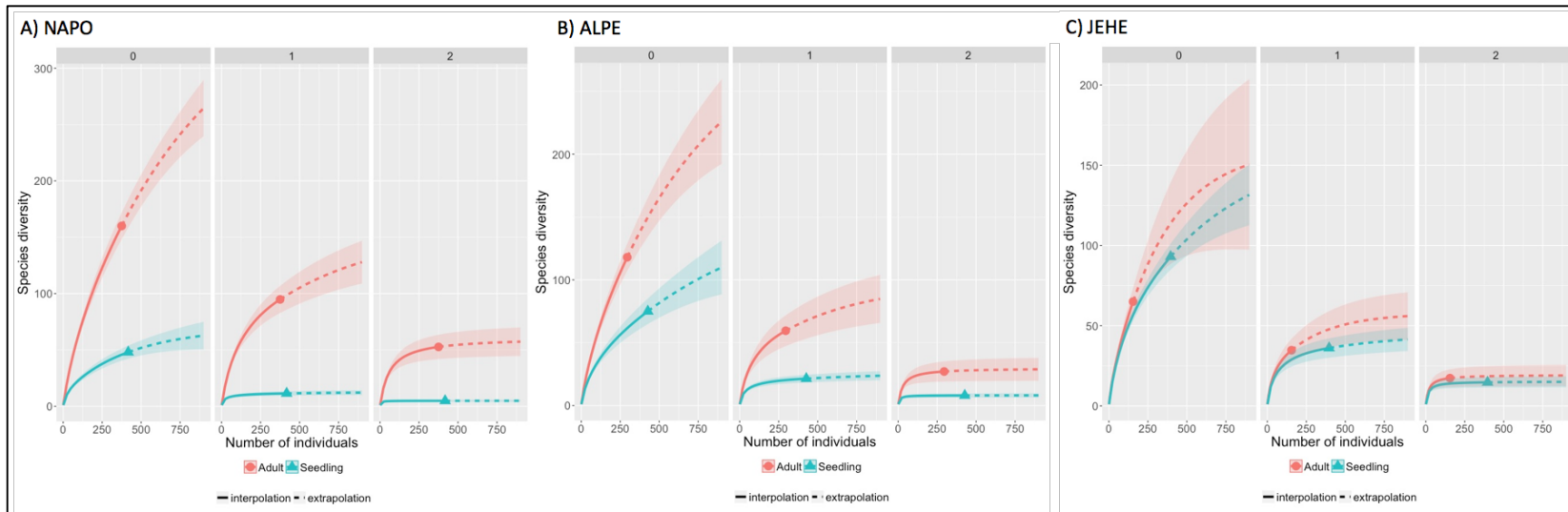


FIGURE 1.3 Species accumulation and diversity curves for endophytes sampled from adult and seedling trees separated by location. (A) the Amazon Conservatory for Tropical Studies Biological Station (NAPO), (B) Allpahuayo-Mishana National Reserve (ALPE), and (C) The Jenaro Herrera Research Center (JEHE). Metrics include richness ($q=0$), Shannon HN ($q=1$), Simpson's HN ($q=2$).

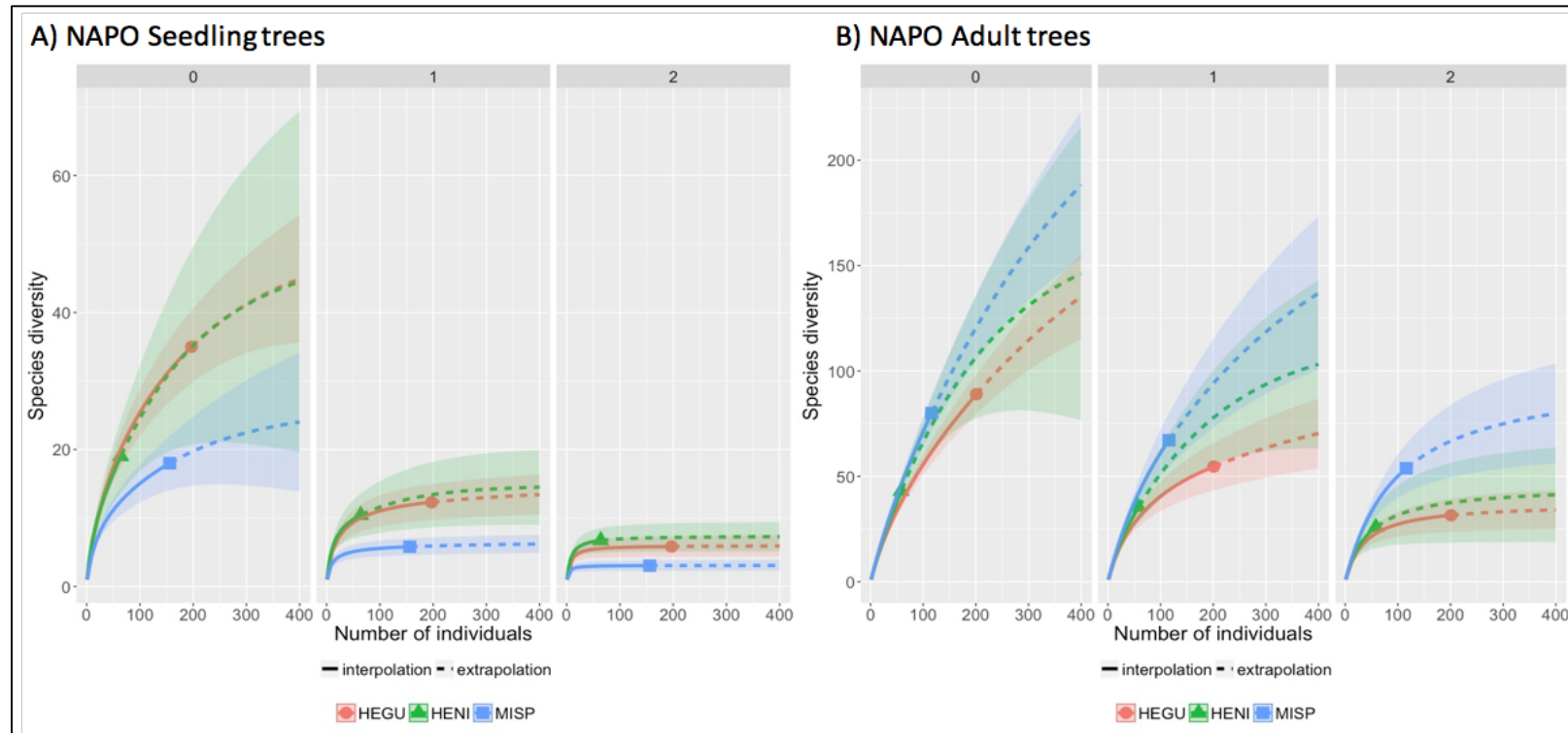


FIGURE 1.4. Diversity results from culture dependent approach from trees distributed in Amazon Conservatory for Tropical Studies Biological Station (NAPO). Species accumulation and diversity curves for endophytes sampled from (A) seedling and (B) adult trees separated by host species (HEGU: *Hevea guianensis*, HENI: *Hevea nitida* and MISP: *Micrandra spruceana*). Metrics include richness ($q=0$), Shannon HN ($q=1$), Simpson's HN ($q=2$).

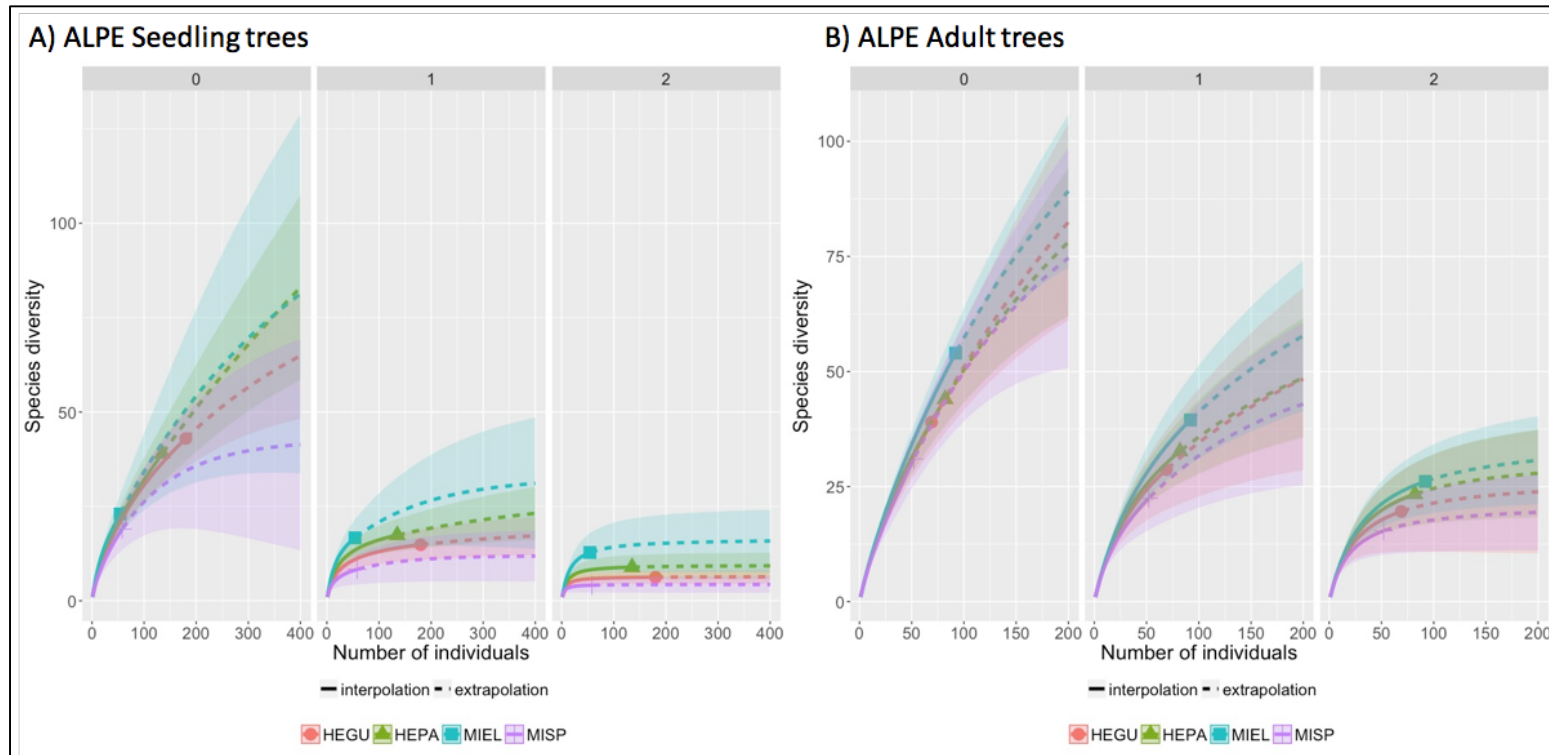


FIGURE 1.5. Diversity results from culture dependent approach from trees distributed in Allpahuayo-Mishana National Reserve (ALPE). Species accumulation and diversity curves for endophytes sampled from (A) seedling and (B) adult trees separated by host species (HEGU: *Hevea guianensis*, HEPA: *Hevea pauciflora*, MIEL: *Micrandra elata* and MISP: *Micrandra spruceana*). Metrics include richness ($q=0$), Shannon HN ($q=1$), Simpson's HN ($q=2$).

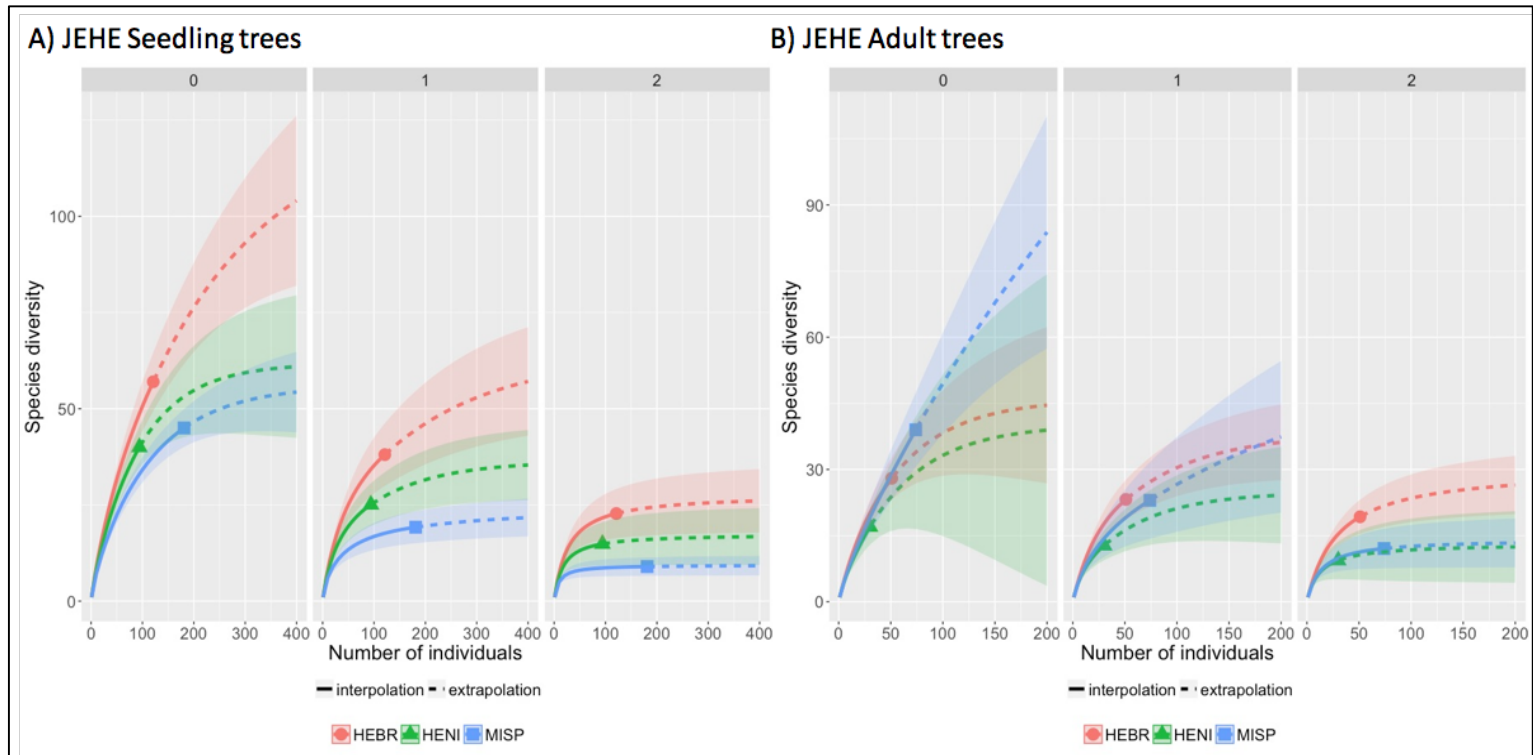


FIGURE 1.6. Diversity results from culture dependent approach from trees distributed in Jenaro Herrera Research Center (JEHE). Species accumulation and diversity curves for endophytes sampled from (A) seedling and (B) adult trees separated by host species (HEBR: *Hevea brasiliensis*, HENI: *Hevea nitida* and MISP: *Micrandra spruceana*). Metrics include richness ($q=0$), Shannon HN ($q=1$), Simpson's HN ($q=2$).

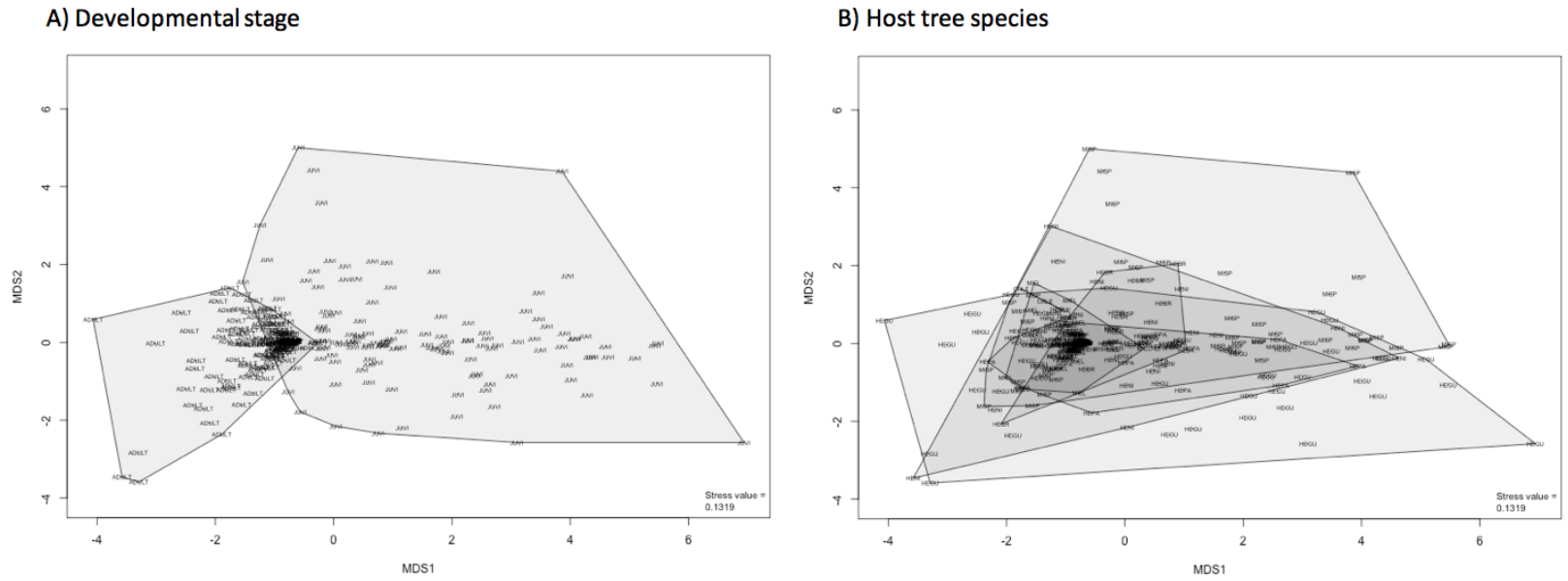


FIGURE 1.7. Nonmetric Multidimensional Scaling (NMDS) analyses with stress values for all three locations and data partitioned by (A) developmental stage (ADULT: Adult, JUVI: Seedling), and (B) tree species (HEBR: *Hevea brasiliensis*, HEGU: *Hevea guianensis*, HENI: *Hevea nitida*, HEPA: *Hevea pauciflora*, MIEL: *Micrandra elata*, and MISP: *Micrandra spruceana*).

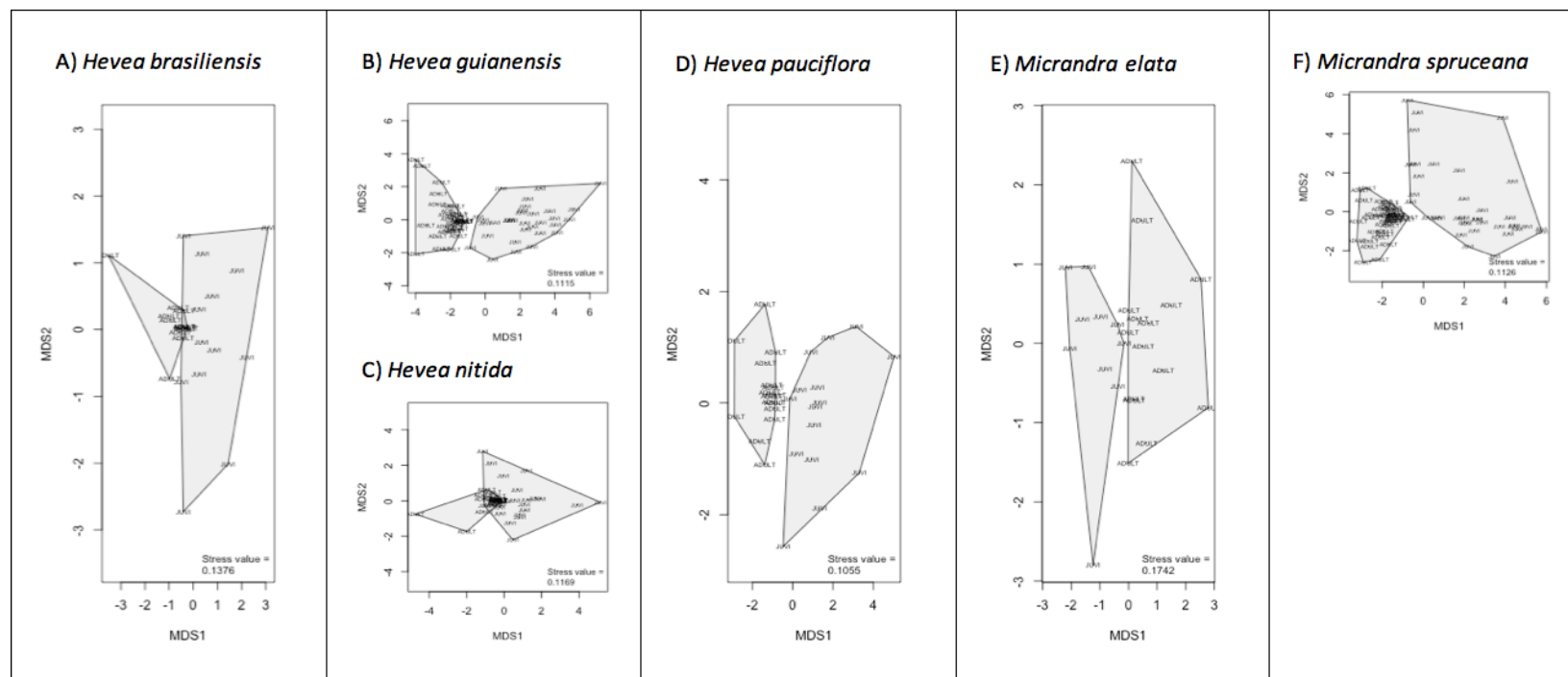


FIGURE 1.8. Nonmetric Multidimensional Scaling (NMDS) analyses with stress values. Data partitioned by developmental stage (ADULT: Adult, JUVI: Seedling) for each tree host species (A) HEBR: *Hevea brasiliensis*, (B) HEGU: *Hevea guianensis*, (C) HENI: *Hevea nitida*, (D) HEPA: *Hevea pauciflora*, (E) MIEL: *Micrandra elata*, and (F) MISPR: *Micrandra spruceana*.

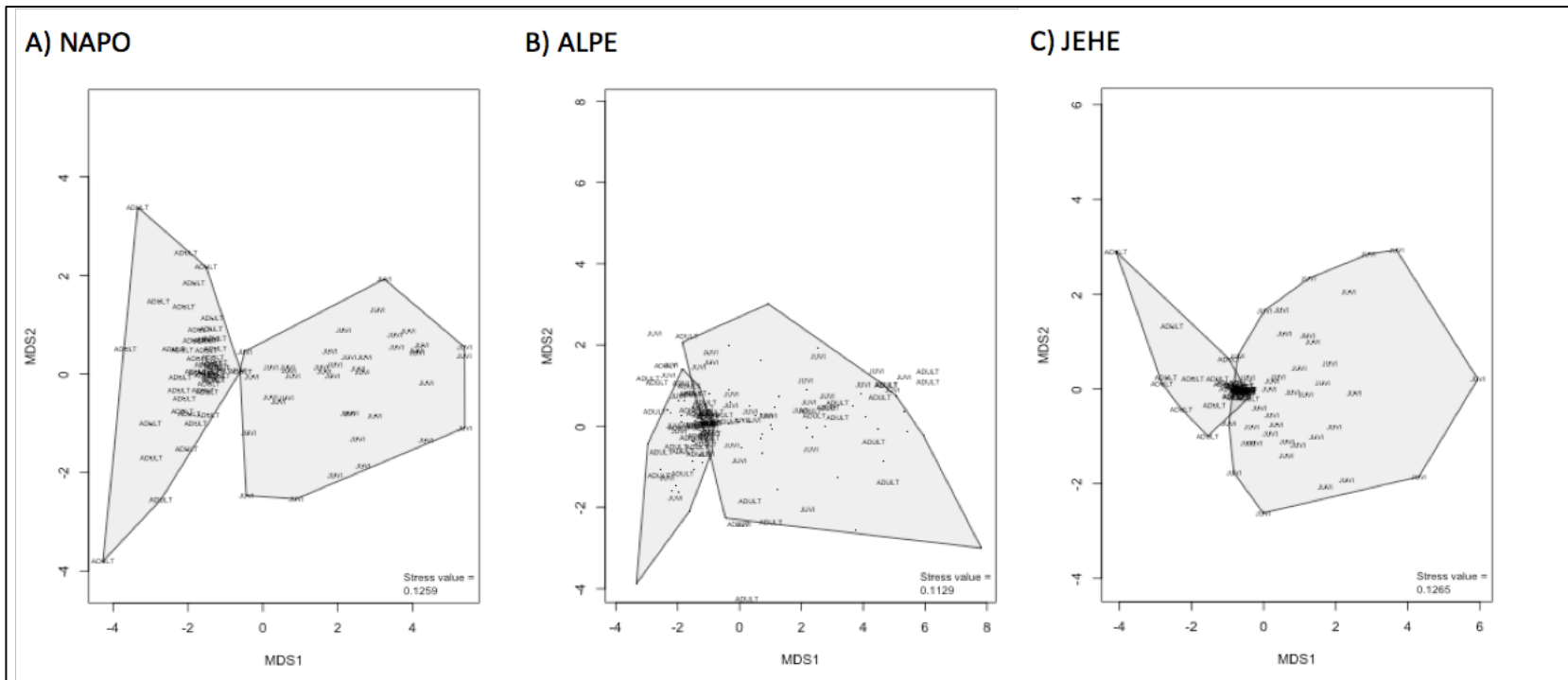
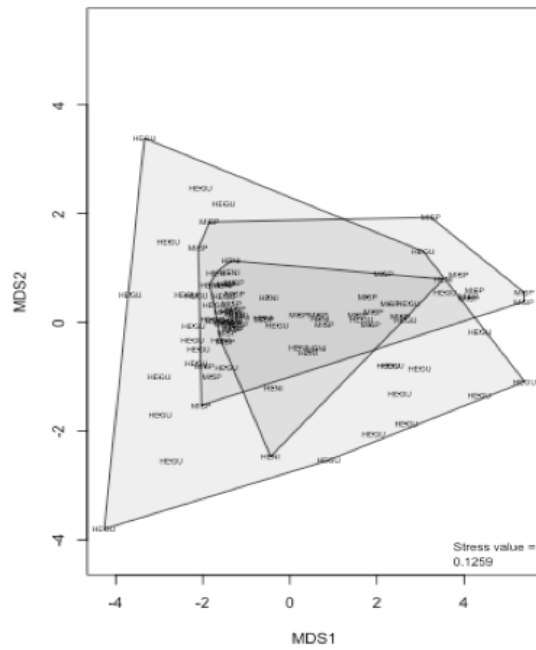
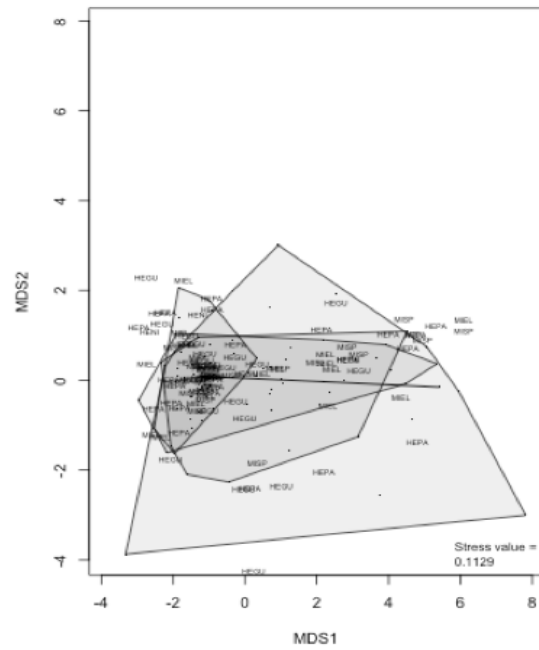


FIGURE 1.9. Nonmetric Multidimensional Scaling (NMDS) analyses with stress values. Data partitioned by developmental stage (ADULT: Adult, JUVI: Seedling) within each location (A) the Amazon Conservatory for Tropical Studies Biological Station (NAPO), (B) Allpahuayo-Mishana National Reserve (ALPE), and (C) Jenaro Herrera Research Center (JEHE).

A) NAPO



B) ALPE



C) JEHE

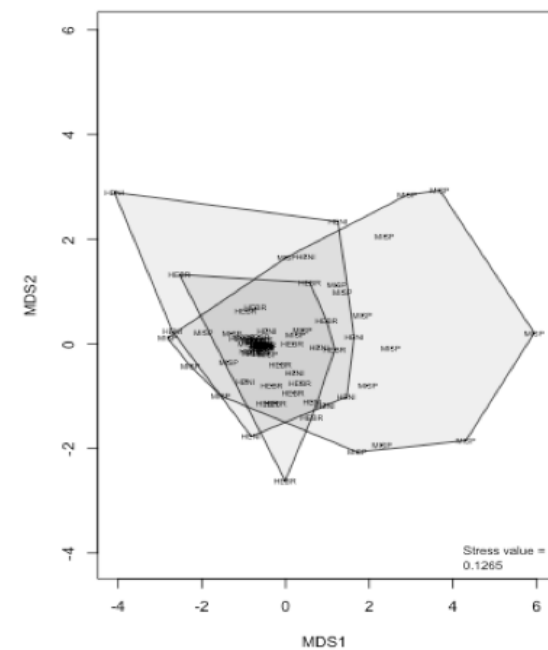


FIGURE 1.10. Nonmetric Multidimensional Scaling (NMDS) analyses with stress values. Data partitioned by tree host species (HEBR: *Hevea brasiliensis*, HEGU: *Hevea guianensis*, HENI: *Hevea nitida*, HEPA: *Hevea pauciflora*, MIEL: *Micrandra elata*, and MISP: *Micrandra spruceana*) and location (A) the Amazon Conservatory for Tropical Studies Biological Station (NAPO), (B) Allpahuayo-Mishana National Reserve (ALPE), and (C) Jenaro Herrera Research Center (JEHE).

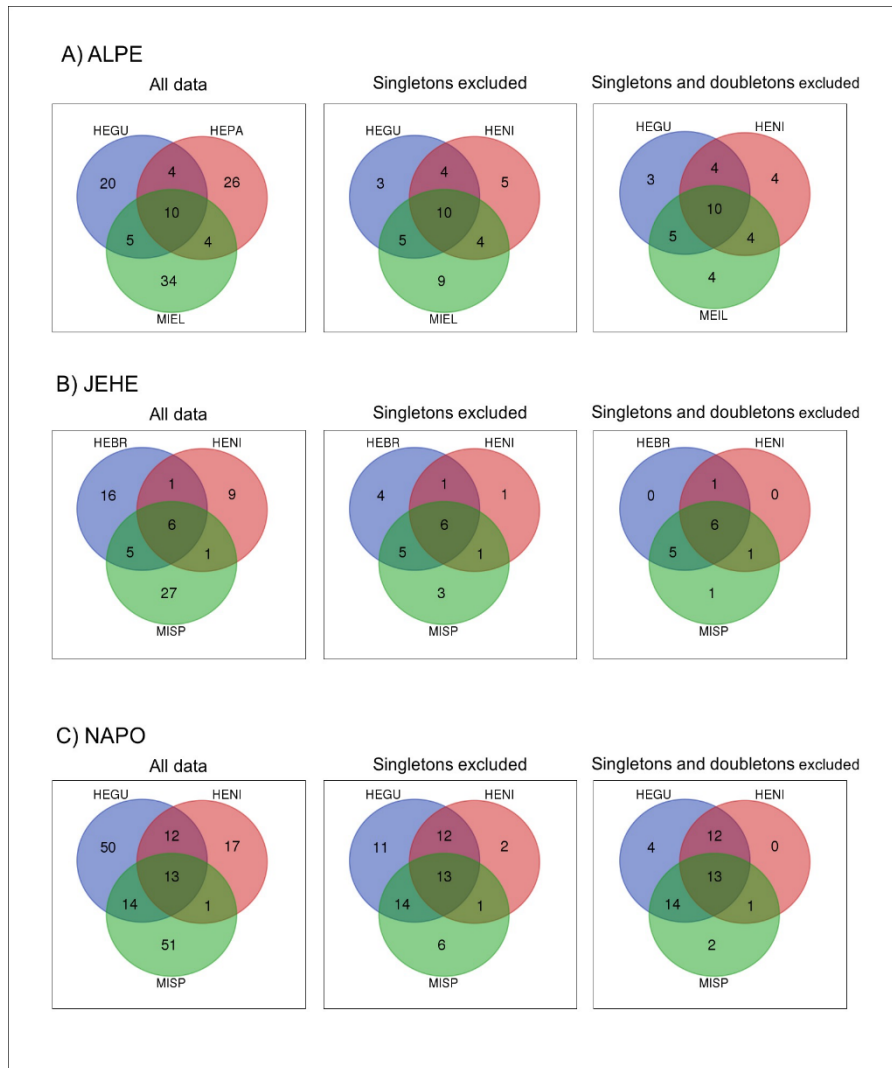


FIGURE 1.11. Venn diagrams showing the overlap of fungal species among adult tree communities (HEBR: *Hevea brasiliensis*, HEGU: *Hevea guianensis*, HENI: *Hevea nitida*, HEPA: *Hevea pauciflora*, MIEL: *Micrandra elata*, and MISP: *Micrandra spruceana*) per location (A) the Amazon Conservatory for Tropical Studies Biological Station (NAPO), (B) Allpahuayo-Mishana National Reserve (ALPE), and (C) Jenaro Herrera Research Center (JEHE).

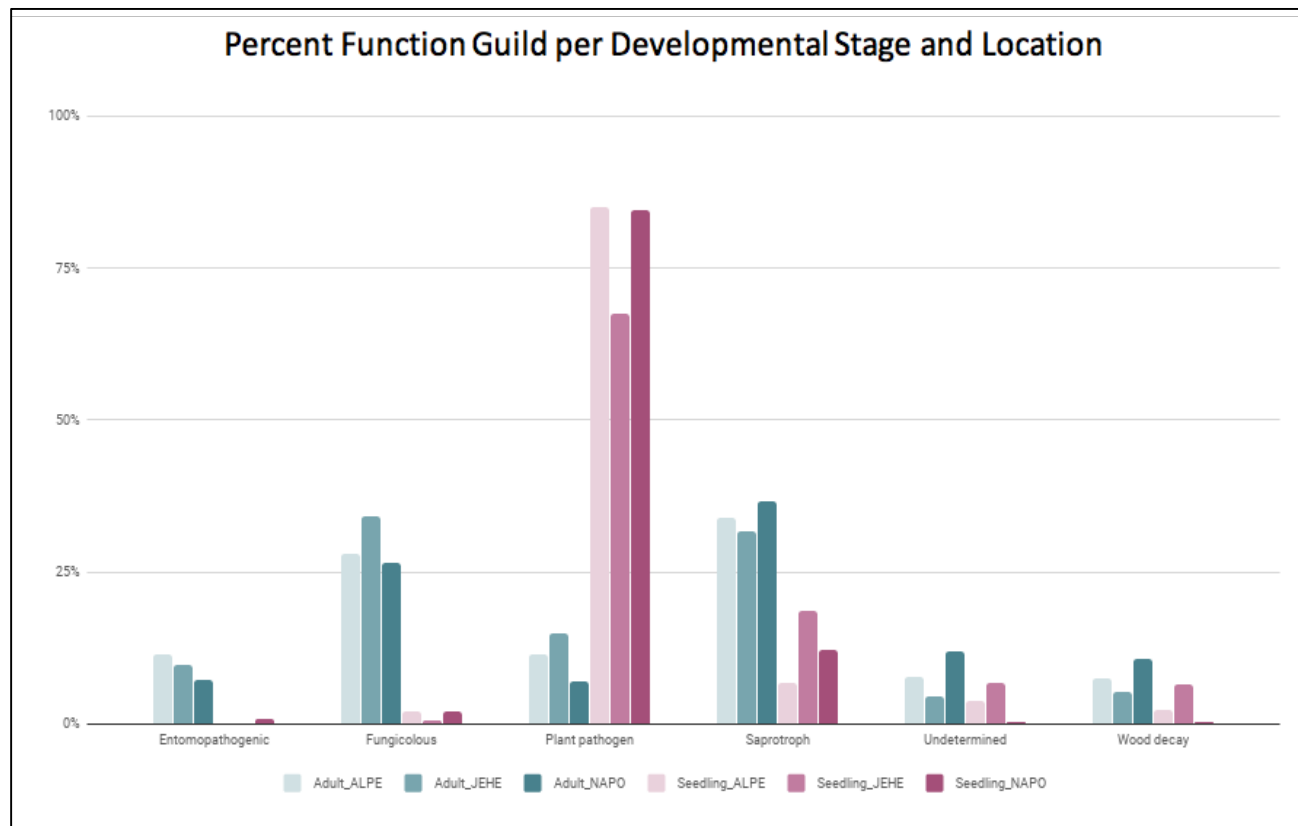


FIGURE 1.12. Distribution of function guilds separated by developmental stage and location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]).

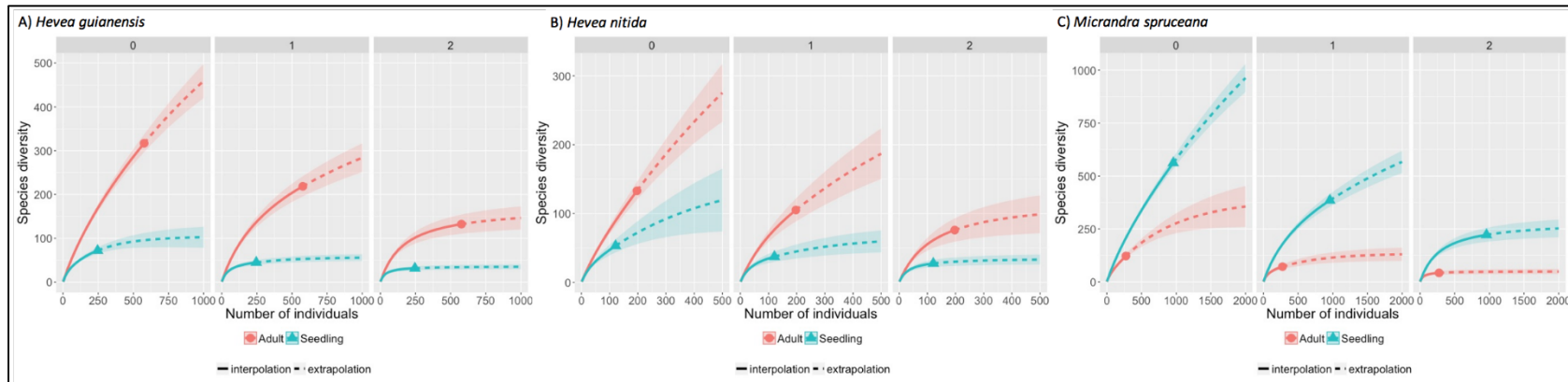


FIGURE 1.13. Diversity results from culture-independent approach. Species accumulation and diversity curves for endophytes sampled from seedling and adult trees separated by host species. Trees were sampled from the Amazon Conservatory for Tropical Studies Biological Station (NAPO). Metrics include richness ($q=0$), Shannon HN ($q=1$), Simpson's HN ($q=2$).

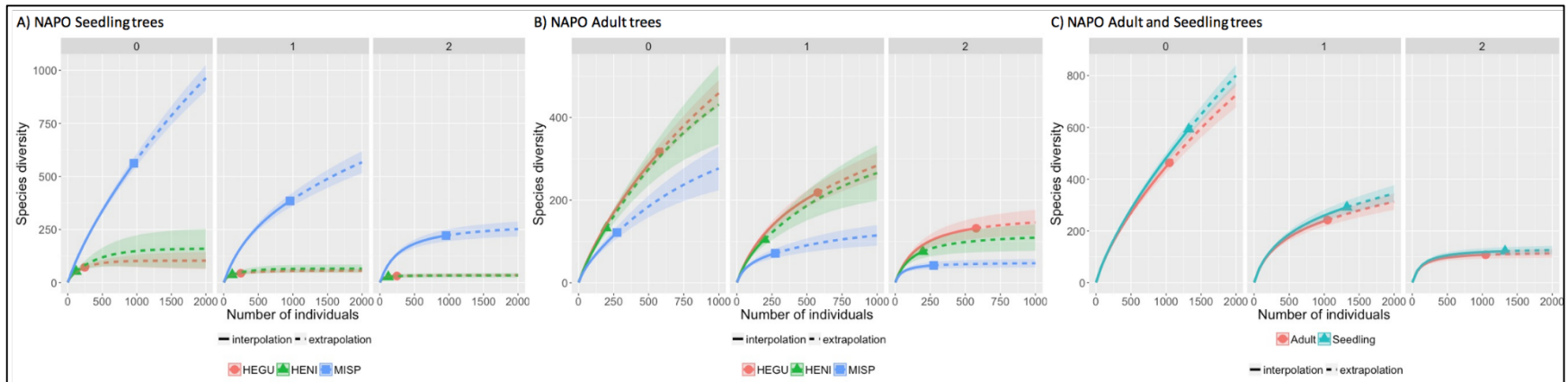


FIGURE 1.14. Diversity results from culture-independent approach. Species accumulation and diversity curves for endophytes sampled from (A) seedling and (B) adult trees separated by host species (HEGU: *Hevea guianensis*, HENI: *Hevea nitida* and MISP: *Micrandra spruceana*). Trees were sampled from the Amazon Conservatory for Tropical Studies Biological Station (NAPO). Metrics include richness ($q=0$), Shannon HN ($q=1$), Simpson's HN ($q=2$).

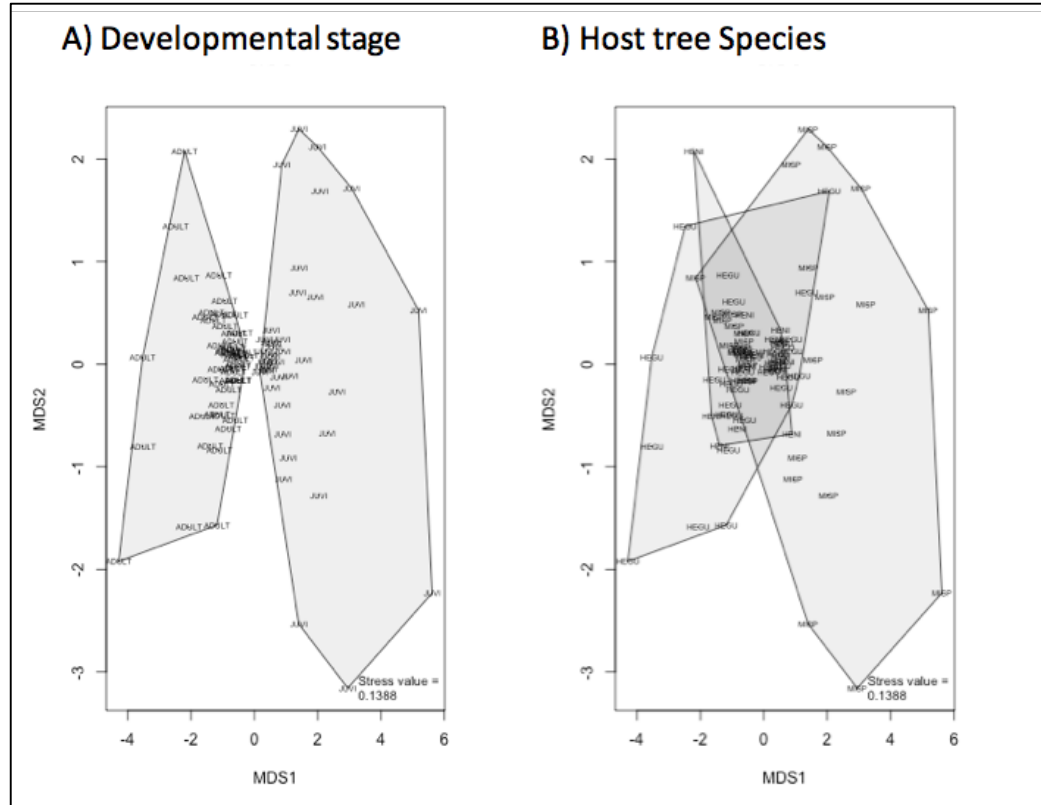


FIGURE 1.15. Community similarity results from culture-independent approach. Nonmetric Multidimensional Scaling (NMDS) analyses using presence/absence data for all trees sampled from the Amazon Conservatory for Tropical Studies Biological Station (NAPO). Data partitioned by (A) developmental stage (ADULT: Adult, JUVI: Seedling), and (B) tree species (HEGU: *Hevea guianensis*, HENI: *Hevea nitida*, and MISP: *Micrandra spruceana*).

Chapter 2: Cryptic diversity of endophytic *Diaporthe* spp. in *Hevea* and *Micrandra* (Euphorbiaceae)

Abstract

Diaporthe (Diaporthaceae, Diaporthales, Ascomycota) includes a wide array of species that are endophytes, saprobes, and opportunistic pathogens as well as aggressive pathogens of economically important crops. Unfortunately, species identification in *Diaporthe* remains troublesome due to the lack of meaningful diagnostic morphological and the historically and current reliance on host species for species identification. As part of a larger endophyte discovery project in Peru, 970 *Diaporthe* isolates were recovered from asymptomatic tissues of two Euphorbiaceae genera, *Hevea* (wild and plantation-grown) and *Micrandra* (wild). Four loci [internal transcribed spacer region (ITS1, 5.8S, ITS2), partial translation elongation factor 1-alpha (TEF1), beta-tubulin (TUB) and histone H3 (HIS)] were used to identify species. In addition, reference sequences from GenBank were included in the; most of which derived from ex-type specimens. For each locus, a standard clustering method was used to cluster sequences into OTUs and results were compared with species delimited through multilocus phylogenetic analyses. TEF1 was the most efficient locus for initial clustering of sequences into OTUs. Although TEF1 overestimated the number of putative species by 18, it did not incorrectly group different species into a single OTU as did the other loci used in this analysis. The commonly used fungal barcode, ITS, performed the poorest. Multilocus analysis revealed 21 distinct lineages of endophytic *Diaporthe*, 15 of which represent novel species. Seven

of these novel lineages are described in this study, and morphological, ecological, and molecular data is provided. The results of this study have major implications for ecological hypotheses since the number of OTUs affects diversity estimates. This is especially problematic for endophyte studies, since *Diaporthe* is a common endophyte.

Keywords: Morphology, Peru, *Phomopsis*, Phylogenetic analysis, Rubber trees

Introduction:

Diaporthe Nitschke 1870 (= *Phomopsis* (Sacc.) Bubák, 1905) (Diaporthaceae, Diaporthales, Sordariomycetes, Pezizomycotina, Ascomycota) includes a broad diversity of species that are endophytes, saprophytes, and opportunistic as well as aggressive pathogens of economically important crops (Murali et al. 2006, Santos et al. 2011, Elfar et al. 2013, Mathew et al. 2015). Although progress in understanding their systematics has been made recently using multilocus phylogenetic analyses (Gomes et al. 2013, Huang et al. 2013, Tan et al. 2013, Thompson et al. 2015, Udayanga et al. 2014a, Udayanga et al. 2014b, Dissanayake et al. 2015, Fan et al. 2015, Gao et al. 2016, Lawrence et al. 2015, Udayanga et al. 2015), species identification in *Diaporthe* remains difficult.

Morphologically, *Diaporthe* is characterized by dark brown to black perithecia, often aggregated and embedded in black-lined pseudostromata composed of host and fungal tissues (Hanlin 1998). Perithecia have ostiolar necks that are erumpent through host tissue and contain asci that are unitunicate, clavate, evanescent at the base, and have a large apical ring. Asci are usually eight-spored, ascospores are hyaline, 2-celled, septate, fusoid, ellipsoid to cylindrical, straight, inequilateral or curved, and sometimes

with appendages (Wehmeyer 1933). The asexual stage of *Diaporthe*, formerly referred to as *Phomopsis*, is characterized by dark brown to black pycnidia that protrude from the substratum surface, containing cylindrical and elongated phialides, and conidia (Rehner & Uecker 1994). There are traditionally two types of conidia produced: alpha and beta (Dennis 1978). Alpha conidia are hyaline, aseptate, fusiform to fusiform-cylindrical, and with guttules typically at either end, but can be present in greater numbers or absent. Beta conidia are hyaline, aseptate, filiform, sometimes hamate and lack guttules. Alpha conidia are more commonly observed than beta, but both may be present. A third, intermediate type, gamma conidia, has been described in a limited number of species; gamma are similar to alpha conidia, but with an exaggerated fusiform-cylindrical to sub-cylindrical shape.

Endophytic *Diaporthe* species are common plant endophytes, having been isolated from numerous and diverse plant families from angiosperms, gymnosperms, bryophytes and ferns (Rehner & Uecker 1994) and are the dominant endophyte species in temperate woody angiosperms (Sieber 2007). Endophytic *Diaporthe* spp. have been isolated from diverse tissues including healthy stems, bark, leaves, seeds and pericarps (Gamboa-Gaitan et al. 2005, Gomes et al. 2013, Udayanga et al. 2011 Washington et al. 1999, Tang et al. 2003, Gure et al. 2005, Maehara et al. 2016). Many *Diaporthe* spp. appear to be generalists, with a single species inhabiting multiple host families (Suryanarayanan & Johnson 2005, Murali et al. 2006, Sun et al. 2008, Lawrence et al. 2015). It is also not uncommon for multiple species of *Diaporthe* to be reported for a particular host (Girish et al. 2012, Diogo et al. 2010).

Sometimes a single *Diaporthe* species can be pathogenic in some plant families and endophytic and asymptomatic in others. For example, *Diaporthe eres* Nitschke has been recovered from asymptomatic *Acer* (Aceraceae), *Citrus* (Rutaceae), *Fagus* (Fagaceae), and *Pinus* (Pinaceae) (Sieber 2007, Lee et al. 2014, Huang et al. 2015), but has also been associated with diseases in *Juglans* (Juglandaceae), *Prunus* and *Rubus* (Rosaceae), and *Vitis* (Vitaceae) (Anagnostakis 2007, Thomidis & Michailides 2009, Vrandecic et al. 2011, Kaliterna et al. 2012, Baumgartner et al. 2013, Lawrence et al. 2015).

The ecological role of *Diaporthe* cannot be generalized even at the species level, meaning that a single *Diaporthe* can be pathogenic in some plant families and endophytic and asymptomatic in others (Udayanga et al., 2011). For example, *D. gulyae* R.G. Shivas, S.M. Thomps. & A.J. Young and *D. helianthi* Munt.-Cvetk., Mihaljc. & M. Petrov have only been isolated from *Helianthus* spp. (Asteraceae), causing stem canker disease (Muntanola-Cvetkovic et al. 1981, Thompson et al. 2015, Mathew et al. 2015). *Diaporthe helianthi* was first described by Mihaljcic and Petrov (1981) from *Helianthus* in the former Yugoslavia and it is now known to have a worldwide distribution on cultivated *Helianthus*. Mihaljcic and Petrov (1994) also examined over 50 unrelated plant species to detect *D. helianthi* and were unsuccessful. *Diaporthe vaccinii* Shear is another example of another species that shows host specificity. Widespread in United States, Canada and Chile (EPPO 2016) with isolated incidents in Europe (EFSA PLH Panel 2014), *D. vaccinii* causes twig blight, canker, fruit rot and storage rot on cultivated *Vaccinium* spp. (Ericaceae) (Weingartner & Klos, 1975, Farr et al., 2002). Reports of *D. vaccinii* on other Ericaceae hosts, such as heather and rhododendrons, are rare and have been based on

morphological characteristics not molecular (Eglitis et al. 1966, Petrini 1984). *Diaporthe vaccinii* needs to be molecularly confirmed as it is at times misidentified as *D. eres* (Lombard et al. 2014). *Diaporthe citri* (H.S. Fawc.) F.A. Wolf causes melanose and stem end rot diseases on *Citrus* spp. (Rutaceae). Reported in all the major citrus producing countries (EPPO 2016), *D. citri* has not been isolated on non-*Citrus* spp. (Udayanga et al. 2014b). These examples of host specificity in *Diaporthe* are all on cultivated crop species where disease management is a necessity. Further sampling of endophytes may find additional hosts for *D. helianthi*, *D. citri* and *D. vaccinii*. There may be additional examples of host specificity in the many plant species that are not commercially important and not typically studied. *Diaporthe* species have also been associated with seed-borne diseases such as damping off, seedling mortality and seed rots in nursery and agronomic crops (Bienapfl & Balci 2013, Girish et al. 2012, Kita & Ohya 2005). On the other hand, host-specific relationships of non-pathogenic or endophytic *Diaporthe* have not been reported.

During a larger endophyte discovery project in Peru, a great number of *Diaporthe* isolates were recovered from asymptomatic leaves and seedlings of wild and planted *Hevea* spp. and *Micrandra* spp. (Euphorbiaceae). These isolates were used in the present study to (1) resolve the identity of the endophytic *Diaporthe* of *Hevea* and *Micrandra*, (2) place these isolates in a phylogenetic context with known pathogenic and non-pathogenic *Diaporthe* spp., and (3) determine if endophytic *Diaporthe* lineages group based on host identity. Knowledge generated from this research will aid in monitoring the geographical range and hosts of known pathogenic *Diaporthe* spp. and will contribute to the knowledge of the poorly studied mycoflora from the Amazonian Peru.

Materials and Methods:

Collection sites:

Wild plants (adults and seedlings) of *Hevea brasiliensis*, *H. guianensis*, *H. nitida*, *H. pauciflora*, *Micrandra spruceana* and *M. elata* were sampled within five Peruvian localities: ACTS Biological Station (3°14'57.20"S, 72°54'33.60"W), Allpahuayo-Mishana National Reserve (3°58'1.16"S, 73°25'8.11"W), Jenaro Herrera Research Center (4°53'54.29"S, 73°38'59.80"W), Los Amigos Biological Station (3°14'52.3"S, 72°54'53.8"W), and Madre Selva Biological Station (3°37'14.90"S, 72°14'48.33"W). Samples were also collected from planted *H. brasiliensis* in Tabasco, Mexico (17°58'32.53"N, 93°23'13.65"W); Tocache, Peru (8°11'33.69"S, 76°32'35.86"W), and Ekonna, Cameroon (4°9'18.61"N, 9°13'53.00"E). A summary of the locations, habitat, number of trees and tissues sampled, and number of recovered *Diaporthe* isolates for each location is provided in Table 2.1.

Endophyte isolation:

Sapwood samples from adult trees were collected by shaving the outer tree bark and using a flame-sterilized knife to expose 10 cm² of sapwood at 1.5 m height. Using a smaller flame-sterilized knife, three pieces of sapwood (~5 mm length) were excised and transferred to nine individual Petri plates containing BBL™ cornmeal-agar (Sigma-Aldrich, St Louis, Missouri) with 2% dextrose and 2 mL of 1% neomycin-penicillin-streptomycin solution to suppress bacterial growth (CMD+). Adult leaf samples from wild and cultivated *H. brasiliensis* were sampled as described by Gazis and Chaverri (2010, 2011). Three leaflets were collected per adult-tree sampled. Three segments from

each leaflet (lamina tip, midrib, and lamina base were surface-sterilized through sequential immersion and transferred onto CMD+.

Three seedlings were collected per adult-tree sampled. Each seedling was selected randomly from those within approximately 3 m of the parent tree, and ranged between 20 to 30 cm in height. From each seedling stem, 3 segments (~ 5mm long) that included the entire stem with all the inner primary tissues (cortex and vascular, both phloem and xylem), were excised in the field station using sterile surgical blades and surface-sterilized through sequential immersion in 2 % sodium hypochlorite solution (2 min), 70 % ethanol (2 min) and sterilize water (Gazis and Chaverri 2010). Each segment was transferred to an individual Petri dish containing CMD+.

All cultures emerging from plant tissues were incubated at room temperature in the field and later the lab, and emerging colonies were sub-cultured onto BBL™ potato-dextrose-agar (PDA) to obtain pure cultures. Cultures are stored at University of Maryland (College Park, Maryland, U.S.A.) in 20% glycerol cryovials at -80° C and in CMD test tubes at 4° C. Ex-type and ex-epitype isolates designated in this study were deposited in CBS-KNAW Fungal Biodiversity Centre (Utrecht, Netherlands) and U.S. National Fungus Collections (Maryland, USA).

Morphology characterization

Specimens were grown on 1% water agar (WA) with alfalfa stems to induce sporulation and pycnidia formation. All illustrations of type and epitype specimens and documented morphological characteristics were observed as described by Udayanga et al. (2014a). Observations of conidiomata were made with a Discovery V20 stereo microscope and

Axioplan2 compound light microscope, each mounted with an AxioCam digital camera (Carl Zeiss Microscopy, Thornwood, NY, USA) imaging system. Twenty to 30 measurements of each structure were made using 40x or 100x objectives. Mean and standard deviations were calculated and are presented with extreme measurements in parenthesis.

DNA extraction, PCR and sequencing

Isolates were sub-cultured onto PDA and incubated at 25° C for 4 days. Mycelia harvested directly from PDA plates was suspended in a microcentrifuge tube containing 60 µL of PrepMan® Ultra Reagent (Applied Biosystems, California, U.S.A). DNA was extracted following the manufacturer's protocol. PCR conditions used were previously described by Gomes et al. (2013) and were performed on a Bio-Rad Dyad Peltier thermal cycler (Bio-Rad, Hercules, CA). PCR products were sequenced at the Systematic Mycology and Microbiology Laboratory (USDA, Beltsville, Maryland, U.S.A.) as outlined by Udayanga et al. (2014a).

The following loci were sequenced and used in the phylogenetic analyses: (1) the internal transcribed spacer regions (ITS) 1 and 2 of the nuclear ribosomal DNA, including the 5.8S, primers ITS5 and ITS4 (White et al. 1990); (2) a region of the β -tubulin gene (TUB), primers T1 (O'Donnell & Cigelnik 1997) and BT-2b (Glass & Donaldson 1995); (3) an intron-containing region of the translation elongation factor 1- α gene (TEF1), primers EF1-728F and EF1-986R (Carbone & Kohn 1999); (4) a region of the histone H3 gene (HIS), primers CYLH3F (Crous et al. 2004); and H3-1b (Glass & Donaldson 1995); and (5) the partial mini-chromosome maintenance protein (MCM7)

(primers designed here Dia-MCM7F2: GACTGCAAGGCCAACCAGA; and Dia-MCM7R3: GACTGCAAGGCCAACCAGA). All sequences newly generated in this study were deposited in GenBank (Table 2.2).

New primer design and PCR optimization

Frequent failures of sequencing and non-specific priming in the sequences of MCM7 were observed when using primer pairs MCM7-1348r and MCM7-709f, and MCM7-1447 and MCM7-709f (Schmitt et al. 2009). New primers (Dia-MCM7F2 and Dia-MCM7R3) were designed by aligning successfully amplified MCM7. OligoCalc (<http://www.basic.northwestern.edu/biotools/oligocalc.html>) was used to check for self-complementarities and hairpin formations. Standard PCR protocol from Schmitt et al. (2009) was followed.

Species delimitation and phylogenetic analyses

To reduce costs, a two-step strategy was chosen to narrow down the set of isolates multiple locus sequencing. First ITS sequences were clustered into operational taxonomic units (OTUs) and then one to four representatives from each putative species were chosen for further sequencing. The ITS region is the recommended DNA barcode marker for fungi and is commonly used to cluster sequences into OTUs (Schoch et al. 2014). Advantages to ITS include that it is a multi-copy region, its amplification is feasible even with low concentrations of DNA and a large reference database exists for comparison (Nilsson et al. 2008, Kõljalg et al. 2013). Clusters were created using the furthest neighbor algorithm implemented in MOTHUR (Schloss et al. 2009) with a 1% dissimilarity criterion, meaning all sequences within each OTU were not more than 1%

different from one another. Due to the large number of sequences, the initial alignment was done using the MAFFT aligner (Katoh & Toh 2008) within SATé suite (Liu et al. 2009). Choosing up to four representatives from each OTU reduced the number of isolates for further analysis from 970 to 200 (91 OTUs). Sequence alignments were submitted to TreeBase (www.treebase.org) as study ID pending.

To further reduce the representative numbers, TEF1 was amplified for each of the representative isolates. TEF1 was chosen due to its species level resolution in *Diaporthe* (Gomes et al. 2013, Udayanga et al. 2015), its ease of amplification, and short amplicon products (~300 bp). A maximum likelihood gene tree was used to further reduce the representative numbers. A total of 71 representatives were used for further study.

To place the chosen representative isolates associated with *Hevea* and *Micrandra* in a phylogenetic context, 149 sequences were retrieved from GenBank; 97 of which were derived from ex-type specimens (Supp. Table 1). To evaluate the utility of each locus in assigning sequences to a known taxon through a cluster algorithm, clusters were created using the same parameters for each of the five loci (ITS, TUB, TEF1, HIS and MCM7). Clusters or OTUs for each locus were then compared to the groups obtained through phylogenetic reconstruction using the four loci. The analyses included the 97 type-derived sequences and the 71 endophytic representative sequences. To explore congruence among single gene trees (ITS, TUB, TEF1, HIS and MCM7) a 70% reciprocal bootstrap threshold (Gueidan et al. 2007) was implemented. All trees were analyzed using both maximum likelihood (ML), estimated by RAxML 8.0.0 (Stamatakis 2014), and Bayesian inference (BI), performed using MrBayes 3.2 (Huelsenbeck &

Ronquist 2001). Substitution models for each gene were determined using the Akaike Information Criterion (AIC) as implemented in PartitionFinder (Lanfear et al. 2012).

A large tree based on four loci (ITS, TUB, TEF1, HIS) was constructed for the chosen representative isolates, along with sequences obtained from GenBank.

Diaporthella corylina (CBS 121124), a genus within Valsaceae (sister family to Diaporthaceae), was selected as the outgroup. Additionally, smaller clade trees were constructed. *Diaporthe* species, distantly related to each clade, were chosen as outgroups. Alignments were done using the MAFFT aligner (Katoh & Toh 2008). The ITS dataset was complete. TEF1 dataset had one missing sequence, and TUB had 2 missing sequences. There were 15 missing sequences from the HIS dataset, nine of which were from GenBank representative taxa. Each locus within the concatenated dataset was partitioned and substitution models were applied for maximum likelihood (ML) and Bayesian inference (BI) analyses. In MrBayes v 3.2, four Markov chains ran simultaneously for 10,000,000 generations. The initial 25% of the trees sampled were discarded. Trees were saved every 100th generation after the initial burn-in trees were discarded. In total, 10,000 trees were generated. The resulting consensus tree was visualized using Geneious 6.0.6 software. Maximum likelihood was conducted with RAxML v 8.2.10 in CIPRES (Miller et al. 2015) and using 10,000 replicates were used to calculate bootstrap support. A smaller tree was constructed excluding GenBank species that were distantly related to the species of interest, using the same parameters described above (Table 2.2).

Species Recognition

The genealogical concordance and genealogical non-discordance criteria of the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) (Taylor et al. 2000, Dettman et al. 2003) were applied to delimit species. A clade was considered genealogically concordant if it was present in at least three of the single gene trees. Those clades were then considered genealogical non-discordant if they were well supported (ML BP $\geq 70\%$) and not contradicted in another single gene tree by similar or greater support. A multilocus phylogeny was constructed to further refine species delimitation.

Results

Isolates

A total of 970 *Diaporthe* isolates were recovered from 317 adult trees and 390 seedling stems. Of the 1440 leaf subsamples from adult trees, only 46 *Diaporthe* isolates were recovered (3.19%) and 17 *Diaporthe* isolates were recovered from 2178 adult sapwood subsamples (1.01%). Of the 1170 seedling subsamples, 907 *Diaporthe* were recovered (77.52%). There was no apparent host preference among the isolates collected in Peru, being that they each were recovered from several different hosts.

Phylogenetic analyses

From the 71 representative isolates, 362 sequences were generated. Additional sequences were obtained from GenBank. Each gene region was analyzed individually and in combination. Maximum likelihood and Bayesian tree topologies were similar except that MrBayes generally had higher support values. Individual gene tree topologies of ITS,

TUB, TEF1, HIS and MCM7 were similar and did not show supported conflicts (Supplementary Figure 2.1, 2.2, 2.3, 2.4). Twenty-one distinct lineages of endophytic *Diaporthe* in *Hevea* spp. and *Micrandra* spp. were recognized, 15 of which are novel. Seven are described as new species; the others were left as *Diaporthe* sp. until more data is gathered (Fig. 2.1)

The multilocus alignment consisted of 175 strains with 1,967 characters including gaps (Supplementary Table 2.1). For the Bayesian analysis, the GTR+G+I nucleotide substitution model was applied to ITS, whereas HKY+I+G was applied to TEF, TUB1 and HIS. The Bayesian tree was used to represent the multilocus phylogeny with bootstrap and Bayesian posterior probability values at the nodes. For the maximum likelihood analysis, the model of nucleotide substitution applied to the partitioned dataset was general time reversal (GTR) with gamma distribution (G), and a proportion of invariable sites (I).

Of the 71 chosen representative isolates, four seedling endophytes formed a clade with *D. ueckerae* a muskmelon pathogen from Oklahoma, USA. Six seedling endophytes formed a monophyletic group with *Diaporthe hongkongensis* (CBS 115448), a strain recovered from *Dichroa febrifuga* in Hong Kong. Eight endophytes recovered from seedling stems formed a clade with *Diaporthe inconspicua* (CBS 133813), a leaf endophyte strain from *Maytenus ilicifolia* (espinheira-santa) in Brazil; and with *D. pterocarpi* (CBS 135768), a strain recovered from *Pterocarpus indicus* (New Guinea Rosewood) in Thailand. However, *D. pterocarpi* (CBS 135768) had only three of the four genes in GenBank used in this study and resolution was lacking. Isolate GPB18_1A, an endophyte collected from ACTS biological station in Peru, was monophyletic with *D. cf.*

hevea 1 (CBS 852.97, sensu Gomes et al. 2013) an isolate collected from *H. brasiliensis* in Brazil. CM15, collected from a plantation in Cameroon, was sister species to *Diaporthe* cf. *hevea* 2 (CBS 681.84, sensu Gomes et al. 2013), a strain isolated from *H. brasiliensis* leaves in India. Of the four representative isolates collected from a rubber plantation in Tabasco, Mexico, three formed a clade with *D. pseudomangiferae* (CBS 101339), a strain recovered from *Mangifera indica* (mango) in the Dominican Republic and one formed a clade with *D. mayteni* (CBS 133185), a petiole endophyte strain from Brazil. Of the three representative isolates collected from a rubber plantation in Tocache, Peru, one was sister species to *D. schini* (CBS 133181), a leaf endophyte recovered from *Schinus terebinthifolius* in Brazil. TC239 formed a monophyletic group with *Diaporthe heveicola* and TC78 formed a monophyletic group with *Diaporthe umbrina* sp. nov., both novel species.

Clustering with MOTHUR

The number of species used in the analysis was 110. TEF1 was the most efficient gene for initial clustering of sequences into OTUs. It overestimated the number of putative species by 18, but did not incorrectly group different species into a single OTU as did the other loci used in this analysis. BTUB performed similarly to TEF1, it overestimated by 19 OTUs, unlike TEF1 one OTU comprised sister species. While the OTUs generated with HIS more closely reflected the true species diversity (overestimated by 7), successful amplification and sequencing proved to be inconsistent. ITS1, ITS2 and the entire ITS, including 5.8S, performed the poorest (Table 2.3).

ITS tended to split members of a single species into several smaller groups. 36% of the OTUs generated by ITS were problematic, meaning that either members of the same species were split out into separate putative species or that they were incorrectly grouped with more distance relatives. ITS1 had similar results, 44 of the 133 OTUs generated by ITS1 were comprised of split species (members of the same species split into different OTUs). The most severe instance being *Diaporthe ubiqueta*, which had its 13 representative isolates split into six separate OTUs. ITS1 also had eight OTUs which were comprised of sister species or species from neighboring clades grouped together. Three OTUs had both types of grouping errors.

Clustering with ITS2 yielded the poorest results. 40% of the OTUs generated were problematic. Several OTUs comprised distantly related members, while at the same time they excluded members of a species. The most severe instance being OTU 1 which grouped together members from 8 different species.

For MCM7 tended to split species into several groups. Clustering using the furthest neighbor algorithm in MOTHUR with a 1% dissimilarity criterion resulted in 38 OTUs. Increasing the similarity criteria to 2% reduced the number of OTUs to 33. With 3% similarity, splitting still occurred and lumping of sister species was introduced.

Taxonomy

Of the 15 novel *Diaporthe* species, seven species are described and illustrated as new species based on morphological and molecular phylogenetic evidence. Two species were described solely based on molecular data, as they did not sporulate in culture. Eight putative species were left as *Diaporthe* sp. until more data is gathered

Diaporthe amazonica D. Skaltsas, P. Chaverri & Castl., sp. nov. (Fig. 2.2)

Mycobank TBD.

Holotype: Peru: ACTS Biological Station, endophyte from *Hevea guianensis* seedling stem, D. Skaltsas, July 2012 (ex-type culture GPB18-1a = CBS TBD)

Etymology: Named after the South American Amazon where the endophytes were sampled.

Pycnidia on alfalfa twigs on WA, globose, ostiolate, occurring as clusters, 80–100 µm diam., embedded in tissue, erumpent at maturity, with reduced black neck, often with a yellowish, conidial cirrus extruding from ostiole. Conidiophores hyaline, smooth, unbranched, ampulliform, long, slender, (14–)15–21(–30) × 1.4–2 µm. Paraphyses absent. Alpha conidia abundant in culture and on alfalfa twigs, aseptate, hyaline, smooth, ellipsoidal, multiguttulate, base subtruncate, (4–)5–6(–6.8) × 1.5–2.3 µm ($x \pm SD = 5.5 \pm 0.7 \times 2 \pm 0.2$, $n = 30$). Beta conidia not seen.

Additional specimens: Brazil: São Paulo, CBS 852.97 from *Hevea brasiliensis*, D.S. Attili, April 1997 (Gomes et al.).

Habitat and distribution: Endophyte from *Hevea guianensis* seedling stems.

Known from Brazil and Peru.

Notes: *Diaporthe* cf. *hevea* 1 was the working name given by Gomes (2012) to CBS 852.97, which had originally been deposited in CBS-KNAW as *Phomopsis hevea*. *D.* cf. *hevea* 1 was collected from leaves of *Hevea brasiliensis* in Brazil, and thus far has only been reported from the Amazon. There is also an isolate in CBS-KNAW deposited as *Diaporthe heveae* (CBS 681.24) from India, which

Gomes (2012) temporarily named *D. cf. hevea* 2. *Diaporthe heveae* and *Phomopsis hevea* were both described from *Hevea brasiliensis* in Sri Lanka and have also been reported in Brazil, China, India, Indonesia, Malaysia, and Thailand (Gomes et al. 2012). Being that *Diaporthe cf. hevea* 1 CBS 852.97 has only been reported from the Amazon and *D. cf. hevea* 2 has been reported in southeast Asia, it is most likely that *Diaporthe cf. hevea* 2 CBS 852.97 is *Diaporthe hevea*.

Diaporthe heveicola D. Skaltsas, R. Gazis, P. Chaverri & Castl., sp. nov. (Fig. 2.3)

Mycobank TBD.

Holotype: Peru: Allpahuayo-Mishana National Reserve, endophyte from *Hevea pauciflora* seedling stem, D. Skaltsas, July 2013 (ex-type culture AHGB25-8b= CBS TBD).

Etymology: Refers to the occurrence of species on *Hevea*.

Pycnidia on alfalfa twigs on WA, globose, ostiolate, scattered, 70–100 mm diam., superficial on tissue, erumpent at maturity, with short, black neck 40–80 mm high, often with a yellowish, conidial cirrus extruding from ostiole.

Conidiophores hyaline, smooth, branched, ampulliform, long, slender, (15–)17–22(–26) \times 1.5–2.5 μ m. Paraphyses absent. Alpha conidia abundant in culture and on alfalfa twigs, aseptate, hyaline, smooth, ellipsoidal to ovoid, biguttulate or multi-guttulate, base subtruncate, (5–)5.6–6.7(–7) \times (2–)2.3–3 μ m ($x \pm SD = 6.1 \pm 0.4 \times 2.4 \pm 0.3$, $n = 40$). Beta conidia not seen.

Additional specimens examined: Peru: Tocache, living culture TC239.

Habitat and distribution: Endophyte from *Hevea pauciflora* seedling stem.

Known from Peru.

Notes: This species represents two isolates including one collected from cultivated *Hevea brasiliensis* and one from wild *Hevea pauciflora* in Allpahuayo-Mishana National Reserve, Peru. It is closely related to *Diaporthe ancardii* a fungal pathogen on cashew, *Anacardium occidentale*, and originally reported from South Africa.

Diaporthe napoensis D. Skaltsas, P. Chaverri & Castl., sp. nov. (Fig. 2.3)

Mycobank TBD.

Etymology: Named after the river “Napo” in Peru located near the collection site Pycnidia on alfalfa twigs on WA, globose, ostiolate, scattered, 140–160 µm diam., embedded in tissue, erumpent at maturity, with an elongated, black branched or unbranched necks 100–130 mm high, conidial cirrus extruding from ostiole. Conidiophores hyaline, smooth, unbranched, ampulliform, short and cylindrical, wider at the base $(11-12-19(-22) \times 1.5-2.5 \mu\text{m})$. Paraphyses absent. Alpha conidia abundant in culture and on alfalfa twigs, aseptate, hyaline, smooth, globose, aguttulate, base subtruncate, $(3-3.3-4(-4.7) \times (2-)1.5-2.0 \mu\text{m})$ ($x \pm \text{SD} = 3.7 \pm 0.4 \times 1.7 \pm 0.2$, $n = 30$). Beta conidia not seen.

Holotype: Peru: ACTS Biological Station, endophyte from *Micrandra spruceana* seedling stem, D. Skaltsas, July 2012 (ex-type culture GXB11-4b2 = CBS TBD).

Additional specimens examined: Peru: ACTS Biological Station, living culture GPB13-9a.

Habitat and distribution: Endophyte from *Micrandra spruceana* and *Hevea guianensis* seedling stems. Known from Peru.

Notes: *Diaporthe napoensis* is closely related to *D. batatas* within the *D. sojae* species complex (sensu Udayanga et al. 2014). This species was recovered solely in ACTS Biological Station from both *Micrandra spruceana* and *Hevea guianensis* seedlings.

Diaporthe neotropica D. Skaltsas, P. Chaverri & Castl., sp. nov. (Fig. 2.5)

Mycobank TBD.

Holotype: Peru: Jenaro Herrera Research Center, endophyte from *Micrandra spruceana* seedling stem, D. Skaltsas, July 2013 (ex-type culture JMGB04-6b = CBS TBD).

Etymology: Named after the geographic location of the collection sites.

Pycnidia on alfalfa twigs on WA, globose, ostiolate, scattered, 40–70 µm diam., embedded in tissue, erumpent at maturity, with a slightly elongated, black neck 30–50 µm high, often with a yellowish, conidial cirrus extruding from ostiole.

Conidiophores hyaline, smooth, unbranched, ampulliform (14–)16–21 (–28) × 1.5–3 µm. Paraphyses absent. Alpha conidia abundant in culture and on alfalfa twigs, aseptate, hyaline, smooth, ellipsoidal, biguttulate, base subtruncate 6–8 × (2–) 2–3 µm ($\bar{x} \pm \text{SD} = 7.2 \pm 0.4 \times 2.4 \pm 0.2$, $n = 30$). Beta conidia not seen.

Additional specimens examined: Peru: Jenaro Herrera Research Center, living cultures JHGB04-7a, JHGB20-5a, JMGB10-2b2, JMGB13-9b.

Habitat and distribution: Endophyte from *Micrandra spruceana* seedling stem.

Known from Peru.

Notes: This is the sister species for *D. amazonica*, also known to occur as endophytic species on *Hevea* from the same region. However, it is phylogenetically distinct with all four genes analyzed. *Diaporthe neotropica* has larger conidial measurements on alfalfa twigs in WA ($6\text{--}8 \times (2\text{--})2\text{--}3 \mu\text{m}$) compared to *D. amazonica*.

Diaporthe peruviansis D. Skaltsas, R. Gazis, P. Chaverri & Castl., sp. nov. (Fig. 2.6)

Mycobank TBD.

Etymology: Named after the country (Peru) from which the species was originally isolated as an endophyte from *Micrandra spruceana*.

Pycnidia on alfalfa twigs on WA, globose, ostiolate, scattered, $100\text{--}110 \mu\text{m}$ diam., embedded in tissue, erumpent at maturity, with slightly elongated black neck $80\text{--}140 \mu\text{m}$ high, often with a yellowish, conidial cirrus extruding from ostiole. Conidiophores hyaline, smooth, unbranched, cylindrical, short $(3\text{--})7\text{--}12$ $(\text{--}13) \times 1.5\text{--}2.5(\text{--}3.7) \mu\text{m}$. Paraphyses, smooth, unbranched, cylindrical, long, slender, arranged within conidiophores $(24)37\text{--}44$ $(\text{--}60) \times 1.5\text{--}2.5 \mu\text{m}$ $(x \pm \text{SD} = 41 \pm 9 \times 2.4 \pm 0.3, n = 20)$. Alpha conidia abundant in culture and on alfalfa twigs, aseptate, hyaline, smooth, ellipsoidal, biguttulate, base subtruncate, $6\text{--}8 \times (2\text{--})2.2\text{--}3.3 \mu\text{m}$ $(x \pm \text{SD} = 7 \pm 0.6 \times 2.8 \pm 0.2, n = 30)$. Beta conidia not seen.

Holotype: Peru: Jenaro Herrera Research Center, endophyte from *Micrandra spruceana* seedling stem, D. Skaltsas, July 2013 (ex-type culture JMGB13-6a = CBS TBD).

Additional specimens examined: Peru: ACTS Biological Station, living cultures GPB06-8b, GXB18-7. Peru: Jenaro Herrera Research Center, living culture JHGB21-5a.

Habitat and distribution: Endophyte from *Micrandra spruceana* seedling stem. Known from Peru.

Notes: Few species of *Diaporthe* have been reported bearing paraphyses among conidiophores such as *Diaporthe ceratozamia*, *D. longiparaphysata*, *D. siamensis* and *D. theae* (Uecker 1989, Udayanga et al. 2011, Udayanga et al. 2012a, Udayanga et al. 2012b, Crous et al. 2011).

Diaporthe ubiqueta D. Skaltsas, R. Gazis, P. Chaverri & Castl., sp. nov. (Fig 2.7)

Mycobank TBD.

Holotype: Peru: Allpahuayo-Mishana National Reserve, endophyte from *Micrandra spruceana* seedling stem, D. Skaltsas, July 2013 (ex-type culture AHGB7-9a1 = CBS TBD).

Etymology: Refers to its abundance (refer to notes).

Culture sterile. Culture characteristics on PDA after 7 days at 25°C, white with patches of iron grey, reverse pale olivaceous grey with patches of iron grey to olivaceous grey, abundant aerial mycelium, irregular form with filiform margins and raised elevation.

Additional specimens examined: Peru: Allpahuayo-Mishana National Reserve, living cultures AMGB15-1a, AHGB2-3a. Peru: Jenaro Herrera Research Center, living culture JHGB10-6a.

Habitat and distribution: Endophyte from *Micrandra spruceana* seedling stem. Known from Peru.

Notes: This is the dominant species among endophytic isolates obtained from sapwood and seedling stems of *Hevea* and *Micrandra* in this study, which represents 41% of total *Diaporthe*. All isolates examined remained sterile in culture. May represent an exclusively endophytic species. *Diaporthe ubiqueta* is not closely related to any known species presently in GenBank.

Diaporthe umbrina D. Skaltsas, R. Gazis, P. Chaverri & Castl., sp. nov. (Fig 2.8)

Mycobank TBD.

Holotype: Peru: Jenaro Herrera Research Center endophyte from *Micrandra spruceana* seedling stem, D. Skaltsas, July 2013 (ex-type culture JHGB2-8a = CBS TBD).

Etymology: Refers to the umber (dark reddish brown) appearance of the culture. Culture sterile. Culture characteristics on PDA after 7 days at 25°C, white with patches of umber, reverse umber with patches of white and sepia, moderate aerial mycelium, circular form with undulate margins and crateriform elevation.

Additional specimens examined: Peru: ACTS Biological Station, living culture IQ286. Peru: Jenaro Herrera Research Center, living cultures JMGB10-5b1, JMGB11-3a. Peru: Tocache, living culture TC78.

Habitat and distribution: Endophyte from *Micrandra spruceana* seedling stem.
Known from Peru.

Notes: Falls in the *Diaporthe sojae* complex. The closest relatives are *D. schini*, *D. terebinthifolii* and *D. tecomae*, three endophytes from medicinal plants in Brazil.

Discussion

The overall purpose of this study was to identify and determine the *Diaporthe* species associated with *Hevea* and *Micrandra* trees in Peru, as opposed to a phylogenetic treatment of the entire genus *Diaporthe*. Another objective was to evaluate the utility of commonly used fungal markers in diversity estimation of common tropical endophytes. Molecular analysis strongly supports 21 distinct lineages, 15 of which are novel, seven of which are described here. Eight potential new species were left undescribed until additional data is gathered to better understand their phylogenetic placement. Recently, there have been isolated reports of endophytic *Diaporthe* recovered from *H. brasiliensis* (Rocha et al. 2011, Gomes et al. 2013), but little is currently known about the distribution of *Diaporthe* spp. on *Hevea*. Reports of *Diaporthe* spp. in Peru are lacking in a number of databases, including EPPO (European and Mediterranean Plant Protection Organization), USDA (United States Department of Agriculture), CBS-KNAW Fungal Biodiversity Centre (Utrecht, Netherlands), APS (American Phytopathological Society), MINAG (Ministry of Agriculture and Irrigation of Peru, <http://www.minag.gob.pe/portal/>) and UNALM (Universidad Nacional Agraria La Molina, <http://www.lamolina.edu.pe/portada/>). This study expands the host and geographical

range of known-and potentially pathogenic- *Diaporthe* species and introduce novel species associated to leaf and sapwood tissue of two Amazonian hardwood genera.

In South America, only a few studies on fungal endophytes have been published (Gazis & Chaverri 2010, Gazis et al. 2012, Smith et al. 2008, Unterseher et al. 2013), with Brazil being the most prolific (Rodrigues & Samuels 1999, Hilarino et al. 2011, Abreu et al. 2012, Garcia et al. 2012, Vieira et al. 2014, dos Santos Reis et al. 2015). More commonly, but still sparse, are reports of pathogenic *Diaporthe* species. *Diaporthe* species have been associated with diseases on multiple crops in South America such as *D. australafricana* on *Vaccinium* spp., *D. ambigua* on *Actinidia* spp. and *D. caulivora* on *Glycine max*, (Auger et al. 2013, Grijalba & Ridao 2012, Elfar et al. 2013, Díaz et al. 2014, Latorre et al. 2013). Outside of these agronomic important instances, *Diaporthe* species are not well documented. In this study, we placed isolates recovered as endophytes from *Hevea* and *Micrandra* into a phylogenetic context, using known and well characterized pathogenic and non-pathogenic *Diaporthe* species as reference. In both the phylogenetic trees and MOTHUR clustering analysis, isolates from Peru clustered with many endophytic species from Brazil, but surprisingly many clustered with other, more distant geographical locations and with isolates with various ecological roles. Of the 970 isolates examined, 97 isolates formed a monophyletic group with *D. ueckerae* Udayanga & Castl., 2014 USA, a muskmelon pathogen from Oklahoma, USA. 51 isolates grouped with *D. hongkongensis* R.R. Gomes, C. Glienke & Crous, 2013, a strain originally recovered from symptomatic fruit of *Dichroa febrifuga* (Hydrangeaceae) in Hong Kong and 43 grouped with *D. pterocarpi* (S. Hughes) Udayanga, X.Z. Liu & K.D. Hyde, 2012 an isolate recovered from *Pterocarpus indicus* (Fabaceae) in Thailand.

Wild *Hevea* spp. were targeted for comparisons with previous studies on plantation-grown trees (Gazis & Chaverri 2010, Gazis & Chaverri 2015) due to their economic significance in natural rubber production, and *Micrandra* spp. were sampled as the closest known relative of *Hevea*. The sample sizes here are significantly larger than in prior studies, such that any conclusions drawn from comparisons with plantation trees are tentative. Pathogenic and endophytic *Diaporthe* species have been reported on *H. brasiliensis* previously. *Diaporthe heveae* was first observed in Sri Lanka by Petch (1905) on stems of *H. brasiliensis*. Since then there have been reports of severe dieback in seedlings caused by *D. heveae* in rubber producing regions (Singh & Mathur, 2004).

Gazis & Chaverri (2015) found that rubber plantation trees harbored fewer of the beneficial endophytes that can protect them from infection by pathogenic microbiota. All 17 *Diaporthe* isolates collected from the rubber plantation in Tocache, Peru, formed monophyletic groups with Brazilian and Peruvian endophytes. Of the eight isolates collected from the rubber plantations in Tabasco, Mexico, half formed monophyletic groups with endophytes, while the other half formed a monophyletic group with *D. pseudomangiferae*, a species associated with mild mango diseases in Mexico, Dominican Republic and Puerto Rico (Gomes et al. 2013, Serrato-Diaz et al. 2014). One of the isolates collected from the rubber plantation in Cameroon was sister species to *D. ueckerae*, while the other was sister species to *Diaporthe* cf. *hevea* 2. The *Diaporthe* isolated from the plantations were no more or less potentially pathogenic than the ones obtained from the wild. However, most isolates in this study were recovered from wild seedling rather than adult tissues and the endophytic fungal community of seedlings were mainly comprised of potentially pathogenic genera.

Plant hosts in the tropics generally obtain their endophytes horizontally, meaning from the surrounding environment (e.g., soil, rain, air, other plants) (Clay 1993). Seedlings may be more susceptible to colonization by pathogenic fungi or there may be forces such as Negative Density Dependence (NDD) due to higher inoculation levels of *Diaporthe* surrounding the parent trees (Bagchi et al. 2014, Connell 1971, Janzen 1970), or a combination of those. Observed host preference of *Diaporthe* on seedlings may also be due to insufficient time for the diversity of fungi to accumulate, as are seen on adults (Guo et al. 2008). Adult trees had almost no *Diaporthe*, and other species that were found in adult trees were not found in seedlings, indicates that at some point during the maturation of the trees *Diaporthe* species were replaced by other fungal endophytes.

This study evaluated the utility of commonly used fungal markers in diversity estimation of common tropical endophytes by comparing the resulting number of species estimated through clustering analyses to the that of species delimited through multilocus phylogenetic analyses

Four or more loci are commonly used to identify *Diaporthe* to species, however in many diversity studies the cost and time to amplify and sequence multiple loci for all isolates is not feasible, as the case was in this study. This study evaluated the utility of commonly used fungal markers in assigning sequences to a known taxon through a cluster algorithm; the resulting number of species estimated through clustering analyses were compared to those species delimited through multilocus phylogenetic analyses using known and well-characterized pathogenic and non-pathogenic *Diaporthe* species. The results of this study suggest that using ITS to cluster *Diaporthe* into OTUs is problematic. When applying the 1% dissimilarity criterion ITS tended to split individuals from the

same species into separate OTUs (putative species) while also grouping together sister species or species from neighboring clades into a single OTU. Although the OTUs generated with HIS were more concordant to the number of species inferred through multilocus analysis, successful amplification and sequencing proved to be inconsistent. TEF1 was the only locus that did not incorrectly group sister species or sister clades into a single OTU, thus insuring that any potentially new species are not overlooked for further study. Coupled with the ease of amplification and sequencing, TEF1 proved to be the best choice of barcode when amplification of several markers is not feasible. Since most endophyte studies begin with amplifying ITS, another approach would be to choose representative isolates from the OTUs generated using the UNIQUE criteria, in which all the OTUs are comprised of identical sequences.

The choice of barcode locus has major implications for ecological hypotheses since the number of OTUs affects diversity estimates (Gotelli & Colwell 2001, Agapow et al. 2004, Magurran 2008, Gazis et al. 2011). This is especially problematic for endophyte studies where *Diaporthe* is common. Initially clustering with TEF1 or HIS would reduce the number of sequence efforts in large scale ecological studies, and assure that any potential species are not incorrectly grouped and underestimate the diversity.

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TABLE 2.1. Summary of the locations, habitat, number of trees and tissues sampled, and number of recovered *Diaporthe* isolates for each location.

Locality	Country	Habitat	No. of Trees Sampled	Total number of subsamples (Sapwood/Leaves/Seedling Stems)	No. of <i>Diaporthe</i> Isolates (Sapwood/Leaves/Seedling Stems)
Ekonna	Cameroon	Plantation	15	270 (135/135/NA)	2 (1/1/NA)
Tabasco	Mexico	Plantation	53	585 (135/450/NA)	9 (9/0/NA)
Tocache	Peru	Plantation	15	270 (135/135/NA)	18 (0/18/NA)
Los Amigos	Peru	Wild	16	270 (135/135/NA)	2 (0/2/NA)
Madre Selva	Peru	Wild	50	585 (135/450/NA)	5 (0/5/NA)
ACTS	Peru	Wild	68	1,116 (603/135/378)	388 (5/20/363)
Allpahuayo	Peru	Wild	59	963 (531/0/432)	322 (1/0/321)
Jenaro Herrera	Peru	Wild	41	729 (369/0/360)	224 (1/0/223)
Totals			317	4788 (2178/1440/1170)	970 (17/46/907)

TABLE 2.2. Species and sequences used in this study, including GenBank accession number, isolation source, substrate and country of isolation.

Species name	Strain	ITS	TEF1	TUB	HIS	Country	Substrate	Host species
<i>D. alleghaniensis</i>	CBS 495.72	KC343007	KC343733	KC34397	KC343491	Canada	Branch	<i>Betula alleghaniensis</i>
<i>D. amazonica</i>	pending, GPB18-1a	pending	pending	pending	pending	Peru	Stem	<i>Hevea guanensis</i>
<i>D. anacardii</i>	CBS 720.97	KC343024	KC343750	KC343992	KC343508	Africa	-	<i>Anacardium occidentale</i>
<i>D. arecae</i>	CBS 161.64	KC343032	KC343758	KC344000	KC343516	India	Fruit	<i>Areca catechu</i>
<i>D. asheicola</i>	CBS 136967	KJ160562	KJ160594	KJ160518	-	Chile	-	<i>Vaccinium ashei</i>
<i>D. australafricana</i>	CBS 111886	KC343038	KC343764	KC344006	KC343522	Australia	-	<i>Vitis vinifera</i>
<i>D. batatas</i>	CBS 122.21	KC343040	KC343766	KC344008	KC343524	USA	-	<i>Ipomoea batatas</i>
<i>D. biguttulata</i>	ICMP20657	KJ490582	KJ490461	KJ490403	KJ490524	China	Branch	<i>Citrus limon</i>
<i>D. brasiliensis</i>	CBS 133183	KC343042	KC343768	KC344010	KC343526	Brazil	Leaf	<i>Aspidosperma tomentosum</i>
<i>D. cf. heveae 1</i>	CBS 852.97	KC343116	KC343842	KC344084	KC343600	Brazil	-	<i>Hevea brasiliensis</i>
<i>D. cf. heveae 2</i>	CBS 681.84	KC343117	KC343843	KC344085	KC343601	India	Leaf	<i>Hevea brasiliensis</i>
<i>D. citri</i>	AR3405	KC843311	KC843071	KC843187	-	USA	Stem	<i>Citrus sp.</i>

Species name	Strain	ITS	TEF1	TUB	HIS	Country	Substrate	Host species
<i>D. convolvuli</i>	CBS 124654	KC343054	KC343780	KC344022	KC343538	Turkey	Leaf	<i>Convolvulus arvensis</i>
<i>D. cynaroidis</i>	CBS 122676	NR_111846	KC343784	KC344026	KC343542	South Africa	L. litter	<i>Protea cynaroides</i>
<i>D. discoidispora</i>	ZJUD89	KJ490624	KJ490503	KJ490445	KJ490566	China	-	<i>Citrus unshiu</i>
<i>D. eres</i>	AR5193	KJ210529	KJ210550	KJ420799	KJ420850	Germany	Twig	<i>Ulmus</i> sp.
<i>D. heveicola</i>	AHGB25-8b	pending	pending	pending	pending	Peru	Stem	<i>Hevea pauciflora</i>
	TC239	pending	pending	pending	pending	Peru	Leaf	<i>Hevea brasiliensis</i>
<i>D. hongkongensis</i>	CBS 115448	KC343119	KC343845	KC344087	KC343603	Hong Kong	Fruit	<i>Dichroa febrifuga</i>
<i>D. inconspicua</i>	CBS 133813	KC343123	KC343849	KC344091	KC343607	Brazil	Petiole	<i>Maytenus ilicifolia</i>
<i>D. kongii</i>	BRIP 54031	JF431301	JN645797	KJ197272	-	Australia	-	<i>Helianthus annuus</i>
<i>D. lithocarpus</i>	CGMCC 3.15175	KC153104	KC153095	-	-	China	Leaf	<i>Lithocarpus glabra</i>
<i>D. longicolla</i>	FAU599	KJ590728	KJ590767	KJ610883	KJ659188	USA	-	<i>Glycine max</i>
<i>D. masirevicii</i>	BRIP 57892a	KJ197276	KJ197239	KJ197257	-	Australia	-	<i>Helianthus annuus</i>
<i>D. mayteni</i>	CBS 133185	KC343139	KC343865	KC344107	KC343623	Brazil	Petiole	<i>Maytenus ilicifolia</i>
<i>D. melonis</i>	CBS 507.78	KC343142	KC343868	KC344110	KC343626	USA	-	<i>Cucumis melo</i>
<i>D. napoensis</i>	pending, GXB11-4b2	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>

Species name	Strain	ITS	TEF1	TUB	HIS	Country	Substrate	Host species
	GPB13-9a	pending	pending	pending	pending	Peru	Stem	<i>Hevea guianensis</i>
<i>D. neotropica</i>	pending, JMGB04-6b	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
	JHGB04-7a	pending	pending	pending	pending	Peru	Stem	<i>Hevea brasiliensis</i>
	JHGB20-5a	pending	pending	pending	pending	Peru	Stem	<i>Hevea nitida</i>
	JMGB10-2b2	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
	JMGB13-9b	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
<i>D. ovalispora</i>	ICMP20659	KJ490628	KJ490507	KJ490449	KJ490570	China	Twig	<i>Citrus limon</i>
<i>D. oxe</i>	CBS 133186	KC343164	KC343890	KC344132	KC343648	Brazil	Petiole	<i>Maytenus ilicifolia</i>
<i>D. paranensis</i>	CBS 133184	KC343171	KC343897	KC344139	KC343655	Brazil	Petiole	<i>Maytenus ilicifolia</i>
<i>D. perseae</i>	CBS 151.73	KC343173	KC343899	KC344141	KC343657	Netherlands	Fruit	<i>Persea americana</i>
<i>D. peruviana</i>	pending, JMGB13-6a	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
	GPB06-8b	pending	pending	pending	pending	Peru	Stem	<i>Hevea guianensis</i>
	GXB18-7	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
	JHGB21-5a	pending	pending	pending	pending	Peru	Stem	<i>Hevea nitida</i>
<i>D. pseudomangiferae</i>	CBS 101339	KC343181	KC343907	KC344149	KC343665	Dominican Republic	-	<i>Mangifera indica</i>
<i>D. pseudophoenicicola</i>	CBS 462.69	KC343184	KC343910	KC344152	KC343668	Spain	Leaf	<i>Phoenix dactylifera</i>
<i>D. psoraleae-pinnatae</i>	CPC 21638	KF777159	-	KF777252	-	South Africa	Stem	<i>Psoralea pinnata</i>

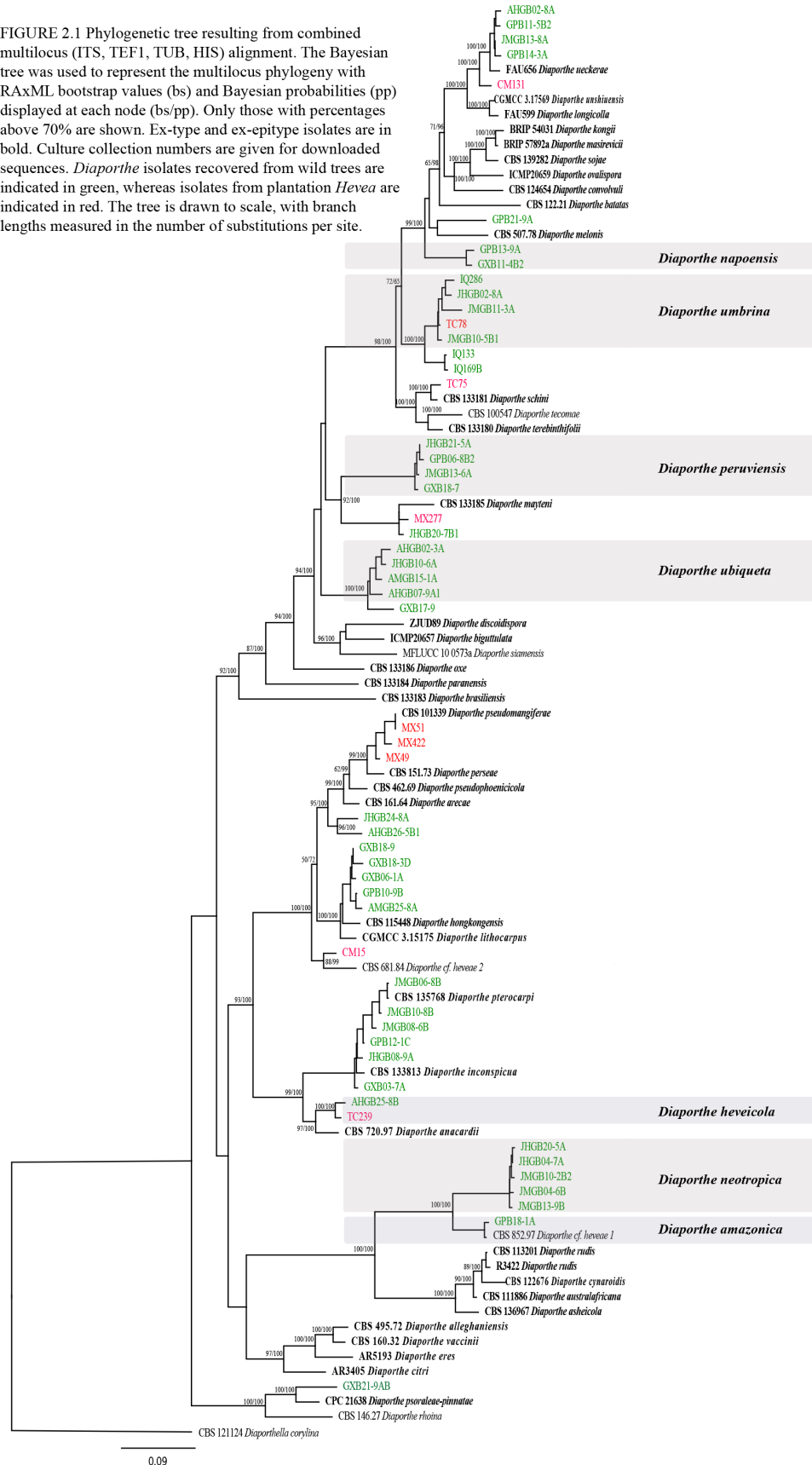
Species name	Strain	ITS	TEF1	TUB	HIS	Country	Substrate	Host species
<i>D. pterocarpi</i>	CBS 135768	JQ619899	JX275416	JX275460	-	Thailand	-	<i>Pterocarpus brenanii</i>
<i>D. rhoina</i>	CBS 146.27	KC343189	KC343915	KC344157	KC343673	-	-	<i>Toxicodendron pubescens</i>
<i>D. rudis</i>	CBS 113201	KC343234	KC343960	KC344202	KC343718	Portugal	-	<i>Vitis vinifera</i>
	AR3422	KC843331	KC843090	KC843177	-	Austria	Stem	<i>Laburnum anagyroides</i>
<i>D. schini</i>	CBS 133181	KC343191	KC343917	KC344159	KC343675	Brazil	Leaf	<i>Schinus terebinthifolius</i>
<i>D. siamensis</i>	MFLUCC 10 0573a	JQ619879	JX275393	JX275429	-	Thailand	-	<i>Pterocarpus brenanii</i>
<i>D. sojae</i>	CBS 139282	KJ590719	KJ590762	KJ610875	KJ659208	USA	-	<i>Glycine max</i>
<i>D. tecomae</i>	CBS 100547	KC343215	KC343941	KC344183	KC343699	Brail	-	<i>Tabebuia sp.</i>
<i>D. terebinthifolii</i>	CBS 133180	KC343216	KC343942	KC344184	KC343700	Brail	Leaf	<i>Schinus terebinthifolius</i>
<i>D. ubiqueta</i>	pending, AHGB7-9a1	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
	AMGB15-1a	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
	AHGB2-3a,	pending	pending	pending	pending	Peru	Stem	<i>Hevea pauciflora</i>
	JHGB10-6a	pending	pending	pending	pending	Peru	Stem	<i>Hevea nitida</i>
<i>D. ueckerae</i>	FAU656	KJ590726	KJ590747	KJ610881	KJ659215	USA	-	<i>Cucumis melo</i>
<i>D. umbrina</i>	pending, JHGB2-8a	pending	pending	pending	pending	Peru	Stem	<i>Hevea brasiliensis</i>
	IQ286	pending	pending	pending	pending	Peru	Leaf	<i>Hevea brasiliensis</i>
	JMGB10-5b1	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>

Species name	Strain	ITS	TEF1	TUB	HIS	Country	Substrate	Host species
	JMGB11-3	pending	pending	pending	pending	Peru	Stem	<i>Micrandra spruceana</i>
	TC78	pending	pending	pending	pending	Peru	Leaf	<i>Hevea brasiliensis</i>
<i>D. unshiuensis</i>	CGMCC 3.17569	KJ490587	KJ490466	KJ490408	KJ490529	China	Fruit	<i>Citrus unshiu</i>
<i>D. vaccinii</i>	CBS 160.32	KC343228	KC343954	KC344196	KC343712	USA	-	<i>Oxycoccus macrocarpos</i>
<i>Diaporthella corylina</i>	CBS 121124	KC343004	KC343730	KC343972	KC343488	China	Stem	<i>Corylus sp.</i>

TABLE 2.3. MOTHUR results. Operational taxonomic units (OTUs) were generated using the furthest neighbor method in MOTHUR with a 1% dissimilarity criterion. No. OTUs w/split sp = Members of the same species split into different OTUs, No. OTUs w/grouped Spp = Members of different species grouped into an OTU.

Locus	No. Species in analysis	No. OTUs (MOTHUR)	Difference	% Problematic OTU's	No. OTUs w/split species	No. OTUs w/grouped Spp	% Total OTUs w/ grouping	No. OTUs w/ both split & group
HIS	110	117	7	18.80%	21	1	0.008%	0
TUB	110	129	19	26.40%	32	1	0.007%	0
TEF1	110	128	18	26.60%	34	0	0.00%	0
ITS Entire	110	131	21	35.90%	41	6	4.60%	6
ITS1	110	133	23	35.30%	44	8	6.00%	3
ITS2	110	107	-3	40.20%	28	15	14.00%	10

FIGURE 2.1 Phylogenetic tree resulting from combined multilocus (ITS, TEF1, TUB, HIS) alignment. The Bayesian tree was used to represent the multilocus phylogeny with RAxML bootstrap values (bs) and Bayesian probabilities (pp) displayed at each node (bs/pp). Only those with percentages above 70% are shown. Ex-type and ex-epitype isolates are in bold. Culture collection numbers are given for downloaded sequences. *Diaporthe* isolates recovered from wild trees are indicated in green, whereas isolates from plantation *Hevea* are indicated in red. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.



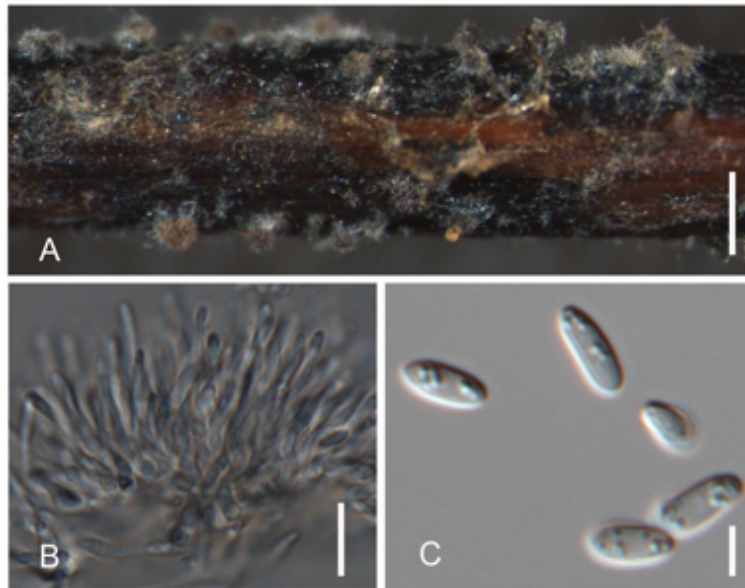


FIGURE 2.2. *Diaporthe amazonica* (GPB18-1a). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 10 μm , C = 5 μm .

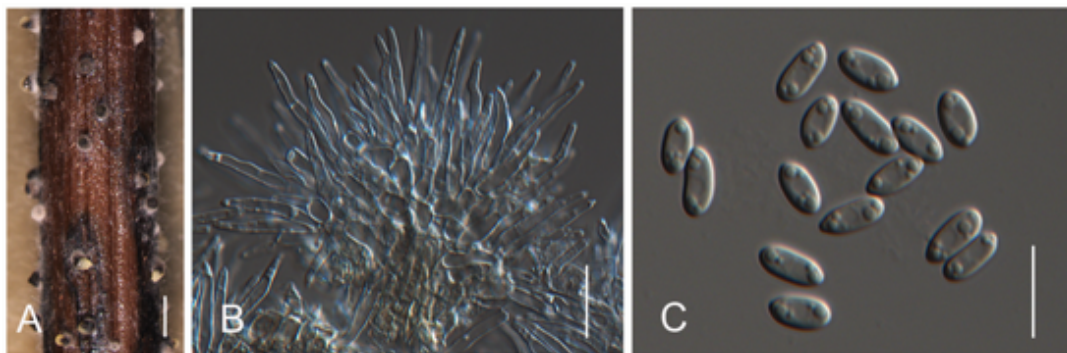


FIGURE 2.3. *Diaporthe heveicola* (AHGB25-8b). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 20 μm , C = 10 μm .

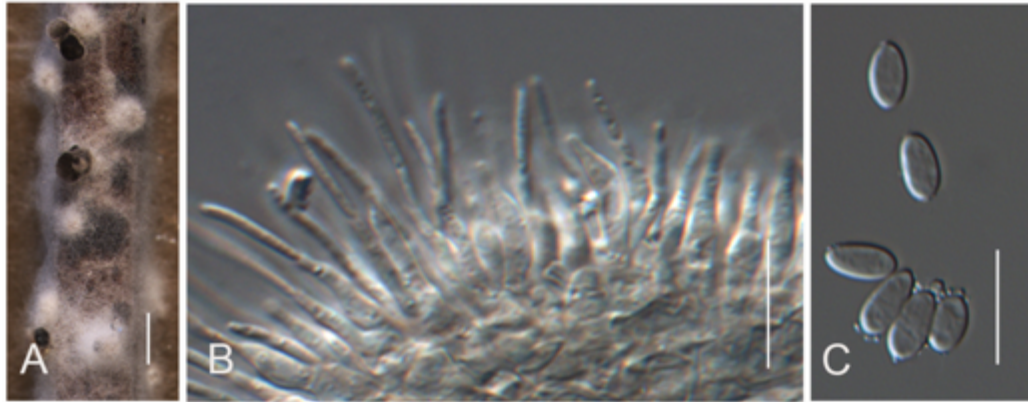


FIGURE 2.4. *Diaporthe napoensis* (GXB11-4b2). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 10 μm , C = 10 μm .

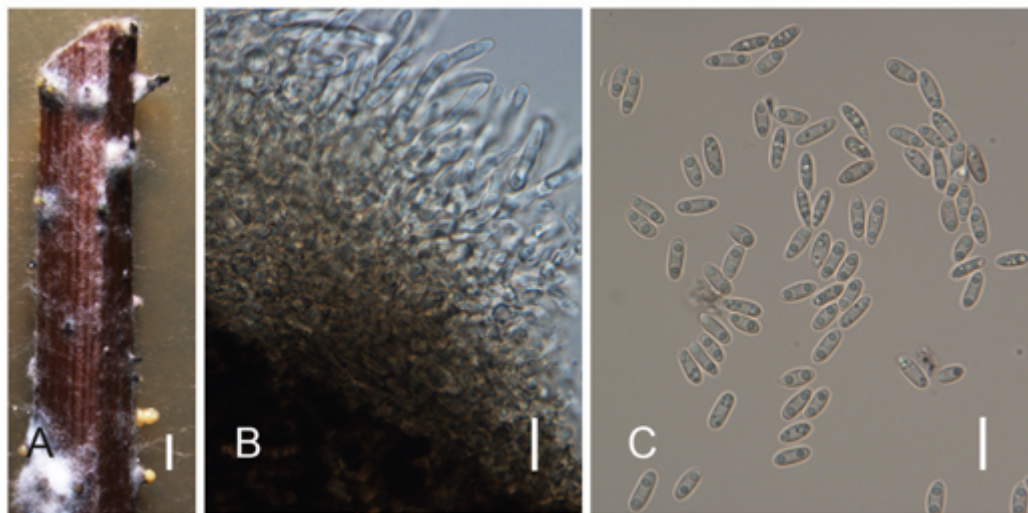


FIGURE 2.5. *Diaporthe neotropica* (JMGB04-6b). A) Sporulation on alfalfa stem in Wag, B) conidiophores, C) alpha conidia. — Scale bars: A = 2,000 μm , B = 10 μm , C = 10 μm .

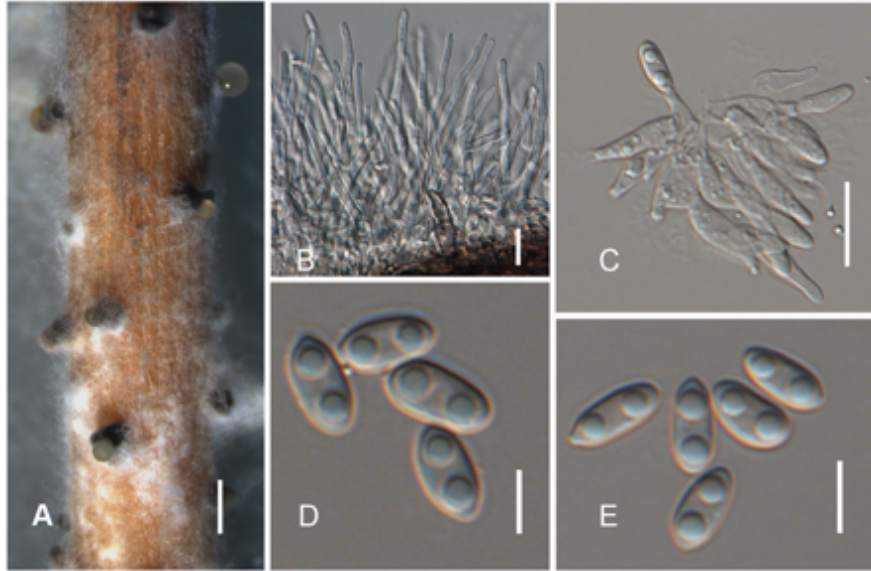


FIGURE 2.6. *Diaporthe peruviensis* (JMGB13-6a). A) Sporulation on alfalfa stem in Wag, B) pycnidial wall lined with paraphyses, C) conidiophores, D) alpha conidia, E) alpha conidia — Scale bars: A = 2,000 μm , B = 10 μm , C = 20 μm , D) 5 μm , E) 5 μm .

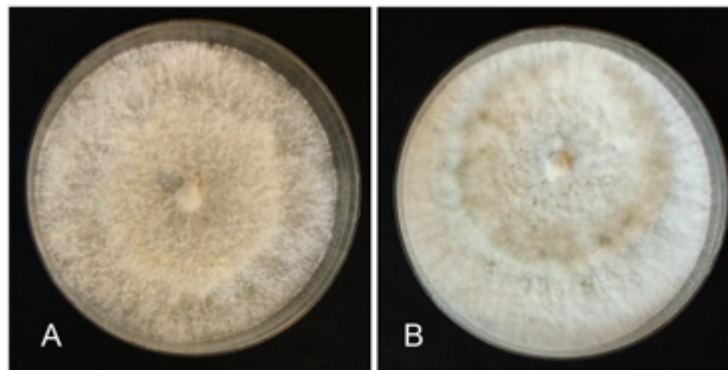


FIGURE 2.7. A) *Diaporthe ubiqueta* (AHGB7-9a1), and B) *Diaporthe umbrina* (JHGB2-8a) on potato-dextrose-agar (PDA) after seven days incubation at room temperature.

Chapter 3: Impact of manual and automated OTU curation of metabarcoding datasets

Abstract

Metabarcoding has become an important tool for exploring fungal communities across multiple systems ranging from plants and animals to water, soil and even the atmosphere. Unfortunately, there are several inherent issues with next generation sequencing that may lead to incorrect inferences. In this study, four different methods were used to classify OTUs in a sample dataset of endophytes collected from rubber trees in three locations in Peru. The effect of those different methods on endophyte distribution, endophyte diversity estimates, and endophyte ecological function roles were examined. When partitioning the data at the genus level, three of the four datasets had the same ranking for the four most dominant genera, but rankings from five and beyond were inconsistent across datasets, especially when partitioned by location. The number of core species detected by the different classification methods varied. A higher proportion of Basidiomycota and Chytridiomycota were retained using the manually curated datasets. One of the manually curated datasets (CLU REP) had two unique core species, while one of the automated datasets (PIPE OTU) was missing a common core species. When the distribution of fungal function guilds was analyzed using both OTU incidence frequency and number of OTU sequence reads across locations and tree hosts, the results varied between methods. One of the more interesting results was the difference between OTU incidence frequency results and sequence reads

abundance results, regardless of classification method. The two manually curated datasets were less error prone; however, automated classification methods were less time consuming to perform. For that reason, automated methods will likely remain the dominant for OTU classification; however, algorithm adjustments will be needed to reduce errors.

Keywords: Ascomycota, Basidiomycota, chimeras, endophytes, *Hevea*, *Micrandra*, Next Generation Sequencing (NGS), Operational Taxonomic Units (OTUs).

Introduction

Metabarcoding has become an important tool for exploring microbial communities across multiple systems ranging from plants and animals to water, soil and even the atmosphere (Gao et al. 2008, Bellemain et al. 2013, Cox et al. 2016, Miller et al. 2016, Núñez et al. 2016, Durand et al. 2017). Unfortunately, there are many inherent errors when using next generation sequencing that may lead to incorrect inferences regarding community composition and diversity, beginning with the initial amplicon library preparation. Protocols for preparing amplicon libraries for metabarcoding environmental samples vary but always involve polymerase chain reaction (PCR). Perfect amplification would mean that every DNA molecule would be fully replicated during each cycle but due to stochastic events, perfect amplification does not occur. Kebschull and Zador (2015) observed this phenomenon while investigating the effects of PCR bias on a pool of DNA amplicons they designed. The authors found that even though each

DNA sequence was present only once before amplification, the abundances after amplification were greatly uneven. Additionally, they found that stochastic events during the first few cycles of PCR greatly skewed sequence abundances, especially when amplifying low copy number sequences.

Another error that occurs when building amplicon libraries for metabarcoding is DNA template switching during PCR and sequencing. Template switching occurs in the presence of highly conserved regions within the barcode marker region, or if the marker is GC rich (Dighton and White 2017). In such conserved or GC environments, an incomplete amplicon can act as a primer and, as a consequence, chimeric sequences (sequences composed of DNA fragments from multiple taxa) are synthesized and amplified (Nilsson et al. 2010). Template switching is exacerbated in high diversity of the communities (Fonseca et al. 2012, Bjørnsgaard Aas et al. 2017). The universal barcode for fungi is the nuclear ribosomal internal transcribed spacer region (ITS1, 5.8S, ITS2) (Schoch et al. 2012). For sequencing fungi directly from environmental samples, only a portion of ITS is targeted, either ITS1 or ITS2. The 5.8S ribosomal RNA gene situated between ITS1 and ITS2 is highly conserved and prone to template switching when ITS is targeted in its entirety (Nilsson et al. 2015). Although ITS1 and ITS2 are highly variable regions, they are not immune to template switching. Discovery and exclusion of chimeric reads is necessary, otherwise diversity estimates are inflated (Jumpponen 2007, Fonseca et al. 2012, Dighton and White 2017). A common practice to avoid inadvertently inflating diversity through the inclusion of chimeric sequences is to remove operational taxonomic units (OTUs) that are

rare or with less than five sequences, since they are most likely PCR artifacts (Brown et al. 2015). Algorithms such as UCHIME (Edgar et al. 2011) have been developed for chimera detection. Additionally, reference databases for algorithms to align sequences against such as UNITE and MaarJAM are utilized (Kõljalg et al. 2005, Öpik et al. 2010, Nilsson et al. 2015). However, these tools are not infallible and it is possible for chimeric sequences to pass through a bioinformatics pipeline undetected (Bjørnsgaard Aas et al. 2017).

Other sources of errors occur during clustering and classifying sequences (Gazis et al. 2011, Nguyen et al. 2015, Yahr et al. 2016, Raja et al. 2017a). The clustering algorithm one uses may have great impact on diversity estimates, since different clustering algorithms can generate different number of OTUs (Schloss et al. 2011, Nguyen et al. 2015). Furthermore, there is no universal similarity percentage that delimits fungal species or any species in any group. For instance, clustering ITS (entire) sequences at 99% is insufficient to delimit species within the *Colletotrichum gloeosporioides* species complex (most of which are common endophytes), due to low variability within the ITS region (Crouch et al. 2009, Gazis et al. 2011). Nevertheless, for the purpose of making comparisons across studies, many researchers opt for a 98% similarity cutoff based on Nilsson et al. (2008) findings that the Ascomycota interspecific variation averages 1.96%. One way to minimize clustering errors is to sequence a defined mock community to calibrate both the clustering algorithms and the percent similarity (Nguyen et al. 2015).

There is a wide-range of strategies employed by researchers to classify fungal OTUs obtained from environmental samples. Some researchers choose a single percent similarity cutoff to assign species level names, generally 97% or 98% (Eusemann et al. 2016, Vaz et al. 2017), while others select a range of percentages to assign an identity to OTUs at different taxonomic ranks (Millberg et al. 2015, Ottosson et al. 2015). For example, if the percent similarity of a BLAST match is between 90% to 97%, then the OTU is assigned a generic name such as *Trichoderma* species 3. If the closest BLAST match is between 89% to 80% similarity, then the OTU is assigned to an order level such as *Hypocreales* species 3; and so on. There are also researchers who choose to manually curate their OTUs and/or implement phylogenetic approaches (Bonito et al. 2016). More recently fungal metabarcoding studies have begun using the RdP classifier (Dawkins and Esiobu 2017, Khomich et al. 2017, Zhang et al. 2017). The Rdp classifier was initially developed to help classify bacterial rRNA deposited in the Ribosomal Database (RDP), but training sets were later developed for both fungal large-subunit rRNA (LSU) and ITS (Kõljalg et al. 2013, Porras-Alfaro et al. 2014, Deshpande et al. 2016). The classifier does not use a phylogenetic approach, but instead uses naïve Bayesian probabilities to compare “words” of a given length. The words are the query sequences compared against a “training set” (composed of reference sequences, along with their taxonomical hierarchy) (Werner et al. 2012). Some of the advantages to using the RdP classifier are that it is fast, does not require long sequences for accuracy, and does not need to align sequences. The latter feature is important when working with fungal ITS as it does not align

well across the fungal kingdom (Wang et al. 2007, Bjørnsgaard Aas et al. 2017). More importantly it provides confidence estimates for each taxonomic assignment from domain to species level (Wang et al. 2007, Deshpande et al. 2016). Despite all the advantages of the RdP classifier, it is only as reliable as the training set used, which in turn requires well-curated reference sequences.

Accurate OTU classification is needed for making ecological inferences about the sampled endophytic community and requires well-curated reference sequences (i.e., sequences from published studies, with voucher/culture collection numbers, with minimal ambiguities and covering the entire ITS region) against which to compare (Nagy et al. 2011, Kõljalg et al. 2013, Yahr et al. 2016).

UNITE (Kõljalg et al. 2005) and The National Center for Biotechnology Information (NCBI, RefSeq) have made great strides in creating and maintaining databases with well-curated reference sequences (Pruitt et al. 2006, Kõljalg et al. 2013, O'Leary et al. 2015), but many obstacles still hinder proper identification of environmental sequences. For instance, many type specimens do not have DNA sequences in a repository and, due to the age of some of the samples, it may not be possible to extract quality DNA, thereby necessitating the epitypification of names (Hibbett et al. 2011, Nagy et al. 2011). On the other hand, many deposited sequences are either lacking species names or are misidentified (Smith et al. 2016, Jargalmaa et al. 2017, Raja et al. 2017b). Even with well-curated reference sequences, there still remains the issue of no universal similarity percentages for fungal species delimitation.

In this study, four different methods were used to classify OTUs in a sample dataset of endophytes collected from multiple hosts in multiple locations: 1) Pipeline automated NCBI BLASTn, 2) RdP classifier with Warcup Fungal training set, 3) Manual BLAST and Percent Based, and 4) Manual clustering with GenBank Representatives. The effect of these methods on endophyte distribution, endophyte diversity estimates, and endophyte ecological function roles were examined.

Materials and Methods

Collection sites and study system

Samples were collected from three Amazon localities within the Loreto Region of Peru: Amazon Conservatory for Tropical Studies (ACTS) Biological Station (NAPO; 3°14'57.20"S, 72°54'33.60"W), Allpahuayo-Mishana National Reserve (ALPE; 3°58'1.16"S, 73°25'8.11"W), and Jenaro Herrera Research Center (JEHE; 4°53'54.29"S, 73°38'59.80"W). Diversity and distribution of tropical fungal endophytes of wild individuals of *Hevea* and its sister genus *Micrandra* were investigated as part of a larger study. *Hevea brasiliensis* is the primary species for tapped natural rubber and plantation grown trees suffer from a variety of diseases that reduce production or destroy entire plantation areas.

Sample collection

The number of individual trees sampled, per species and site, varied due to their low abundance and scattered distribution (Table 3.1). Sapwood samples were

collected from 136 adult trees. Four species of *Hevea* (*H. brasiliensis*, *H. guianensis*, *H. nitida*, *H. pauciflora*) and two species of *Micrandra* (*M. elata*, *M. spruceana*) were opportunistically sampled. Geographical coordinates were recorded for each sample using a handheld GPS unit (GPSmap 62sc, Garmin Inc. Schaffhausen, Switzerland). Trunk diameter (dbh) was measured at 1.4 meters above the ground (*Hevea* spp.) or 1.4 meters above the swell of buttressed roots (*Micrandra* spp.) and dbh 23–100 cm were targeted. Inner bark tissue (wood containing functioning vascular tissue) samples were collected by shaving the outer tree bark and exposing a 10-cm² area. Using a smaller flame-sterilized knife, three pieces of wood (~4x5 mm) were excised and then transferred into a single cryovial containing 500 µL of MoBio Bead Solution Buffer (MoBio Laboratories, Carlsbad, California, USA). Each adult tree had this procedure replicated three times, yielding a total of three cryovials (each containing 3 sapwood pieces) for direct sequencing of a total of 408 samples.

DNA extraction, PCR and sequencing

Excised plant tissues were placed into tubes prefilled with 500 µm garnet beads and a 6-mm zirconium grinding satellite bead (OPS Diagnostics LLC, New Jersey, USA). The tubes were homogenized using a FastPrep® instrument (Zymo Research, Irvine, California, USA). Each tube was treated to three rounds of homogenization (speed: 5.0 m/s time: 43 seconds) or until no visually recognizable fragments remained. Total DNA was extracted using the Qiagen® DNeasy Plant Mini Kit according to manufacturer's instructions (Qiagen, Hilden,

Germany). Fungal ITS 2 was amplified with fITS7 (Ihrmark et al. 2012) and ITS4 (White et al. 1990) primers containing a unique additional 6-bp barcode to tag each PCR sample according to the individual tree sample. PCR amplification was performed using HotStarTaq Plus Master Mix Kit (Qiagen®, Hilden, Germany). PCR products were then pooled together in equal proportions based on molecular weight and concentration and purified using AMPure® XP beads (Agencourt Bioscience, Massachusetts, USA). Sequencing was performed on the Illumina MiSeq platform at MR DNA (www.mrdnalab.com, Shallowater, TX, USA).

Forward and reverse sequences of each sample were merged into contigs with VSEARCH. For quality control and optimization of downstream analyses, sequences with length smaller than 300 bp were removed and sequences larger than 300 bp were truncated to 300 bp (Puente-Sánchez et al. 2015). Sequences with less than 90% of quality score (Q) 30 were removed (Cox et al. 2010). Singletons, sequences with abundance equal to one, were removed from the dataset and UCHIME and the UCHIME database were used to retrieve and remove chimeras from the dataset (Edgar et al. 2011). The sequences were clustered with VSEARCH, using a threshold of 98% of similarity. Centroid sequences from each pipeline generated cluster were subsequently classified taxonomically using four methods: Pipeline automated NCBI BLASTn (PIPE OTU), Rdp classifier with Warcup Fungal training set (RDP WAR), Manual BLAST and Percent Based (MAN PER), 4) Manual cluster with GenBank Representatives (CLU REP).

Pipeline automated NCBI BLASTn OTU dataset (PIPE OTU)

Centroid sequences were classified via a bioinformatics pipeline implementing the NCBI database BLASTn program option NCBI using 80% similarity and 90% coverage cutoffs, any OTUs below the cutoff were removed from the dataset. OTUs classified as “unassigned” or “leaf litter” were removed. Hereafter, OTUs will be considered as the species level. For analyses at the generic level all non-informative names (uncultured, fungal, fungi, fungus, isolate, *aceae, *ales, *mycota, *mycetidae) were excluded and OTUs were assigned corresponding generic names (Vaz et al. 2017).

RdP classifier dataset with Warcup Fungal training set (RDP WAR)

The taxonomy of each centroid sequence was assigned using UNITE with a cutoff similarity of 97% and a minimum cover of 90% (Millberg et al. 2015). For OTUs below the 97% similarity threshold, or that were not assigned a genus level name, the RdP classifier (Wang et al. 2007) was used against the Warcup Fungal ITS training set with a confidence threshold of 95% (Deshpande et al. 2016). OTUs with phylum confidences below 90% were removed from the dataset. Hereafter, OTUs will be considered as the species level. For analyses at the generic level all non-informative names (uncultured, fungal, fungi, fungus, isolate, *aceae, *ales, *mycota, *mycetidae) were excluded and OTUs were assigned corresponding generic names.

Manual BLAST and Percent-Based OTU dataset (MAN PER)

A comparative sequence analysis was conducted manually through BLAST

(Madden 2002) using the nucleotide database

(<https://www.ncbi.nlm.nih.gov/nucleotide>) excluding uncultured/environmental sample sequences. Classification was based according to the consensus taxonomic rank of top 10 BLAST matches. In this method, the taxonomic rank of the sequences with the highest percent similarity values were favored. Criteria for OTU classification were based on identity percentages: 1) 100-97% species; 2) 95-100% genus; 3) 90-94% family; 4) 85-89% order; 5) 80-84% class; and 6) <80% phylum.

Clustered GenBank Representatives OTU dataset (CLU REP)

To deal with the challenge of no universal similarity percentage that delimits fungal species when assigning OTUs, the following was performed: 1) preliminary BLAST search and collected representative sequences of the matched taxa, when possible, well-curated sequences (sequences from published studies, with voucher/culture collection numbers) were included ; 2) compiled a database that contained 1,400 species (not including sequences from this study); 3) aligned sequences from this study with representative database using the MAFFT aligner with the default parameters (Kato and Toh 2008) in CIPRES (Miller et al. 2015); 4) clustered sequences into OTUs using the furthest neighbor method in MOTHUR (Schloss et al. 2009). The percent similarity at which all the GenBank representative sequences clustered together exclusively, meaning no other representative sequences outside of the desired taxonomic level were clustered with them, was considered the taxonomic limit for the OTU.

Ecological analyses

Proportional read abundance is customarily correlated to the proportional abundance of an organism within a sample, however this assumption is often incorrect due to variation of gene copy number among fungal taxa, PCR biases, and/or stochastic PCR amplification (Amend et al. 2010, Kebschull and Zador 2015). Therefore, both sequence reads (number of reads per OTU) and species incidence frequency (number of samples from which an OTU was captured) were analyzed.

The distribution of fungal OTUs for each dataset was visualized as a Venn diagram using the VIB-UGENT Venn Diagram Tool

(<http://bioinformatics.psb.ugent.be/webtools/Venn/>) (Chen and Boutros 2011).

Fungal taxa were considered core (abundant) species if they occurred in more than 50% of the individuals within a tree genus within a site (Unterseher et al. 2011). Fungus genus level abundances were ranked for each site and tree genus using the *Rankabundance* function in BiodiversityR package version 2.8-0.

Richness and diversity were examined at the fungus species level using full datasets, as well as reduced datasets in which OTUs with non-informative names were excluded (fungal, fungi, fungus, isolate, *aceae, *ales, *mycota, *mycetidae). Customarily, OTUs with non-informative names have been excluded from datasets to reduce uncertainty in OTU classification. Three orders of Hill numbers (HN) were used to interpolate and extrapolate species richness and diversity at tree host level within each locality (species richness, $q=0$), common species (Shannon's entropy, $q=1$) and dominant species (inverse

Simpson's, $q=2$), decreasingly sensitive to rare species (Jost 2006, Chao et al. 2014). Chao2 was calculated to extrapolate asymptotic richness using iNext package version 2.0.14. Hill numbers are expressed as the number of equally abundant species that would be needed to return the same value given by a diversity measure (Jost 2016, Chao et al. 2014). Accumulation and diversity curves were built using iNext package version 2.0.14. A 95 % confidence interval was obtained by applying 1,000 bootstrap iterations. Non-overlapping confidence intervals denote a significant difference between samples.

confidence intervals denote a significant difference between samples.

OTUs were parsed into six ecological guilds using the FunGuild database (Nguyen et al. 2016): entomopathogenic (parasitic or causes disease in insects), fungicolous (parasitic or grows on other fungi), plant pathogen (causes disease in plants), saprotroph (rots plant litter), wood decay (rots wood). OTUs with genera with no known ecological guild, or OTUs with non-informative names were categorized as “undetermined.” Rankings were assigned to each guild according to incidence frequencies, with RANK 1 assigned to the guild with the highest incidence frequency and RANK 6 assigned to the guild with the least incidence frequency. Rankings were assigned per tree host genus within each location. Similar ranking method was applied using sequence reads with RANK 1 assigned to the guild with the most abundant sequence reads and RANK 6 assigned to the guild with the least abundant sequence reads.

Results

OTU delimitation and classification

Initial pipeline clustering and classification generated 1,075 species level OTUs (4,329,064 sequence reads). After curation, the four methods generated different number of OTUs with 651 centroid sequences shared among the datasets (Fig. 3.1, Table 3.2).

PIPE OTU method generated 733 OTU (3,222,923 sequence reads), and retained 55 chimeric OTUs (8%) after curation (Supplementary Table 3.1). This method resulted in 227 OTUs unresolved at the genus level (31% of total OTUs), which was the smallest number of unresolved OTUs among the methods. Of the 333 OTUs excluded for not meeting the 80% BLAST similarity cutoff, 103 OTUs (104,103 sequence reads) were verified as fungal (63% were Basidiomycota), 18 OTUs (8,093 sequence reads) were bacterial, 27 OTUs (3,879 sequence reads) were chimeric, and 180 OTUs (696,356 sequence reads) were plant sequences (Table 3.3.A, Table 3.3.B). A common practice to avoid inadvertently inflating diversity through the inclusion of chimeric sequences is to remove OTUs that are rare or with less than five sequences, since they are most likely PCR artifacts (Brown et al. 2015). Excluding OTUs with five or less sequence reads would have eliminated only half of the chimeras in this dataset (Table 3.4). The majority of OTUs that had five or less sequences were real (85%) and comprised 30% of the total dataset, while the chimeric OTUs with five or less sequences were 5% of the total dataset.

RDP WAR method generated 765 OTUs (6,888,097), and retained the most non-fungal centroid sequences (71 chimeric OTUs, 1 plant OTU) (Supplementary Table 3.2). The Rdp classifier assigned all of the plant and bacterial sequences, with 100% confidence, to the fungal kingdom. RDP WAR had the highest number of OTUs unresolved at the genus level (364 OTUs, 48% of total OTUs) (Table 3.5). Of the 301 OTUs excluded for falling below the 95% phylum confidence level, 88 OTUs (36,139 sequence reads) were fungal (68% were Basidiomycota), 18 OTUs (8,093 sequence reads) were bacterial, 11 OTUs (3,879 sequence reads) were chimeric, and 179 OTUs (692,727 sequence reads) were plant sequences (Table 3.3.A, Table 3.3.B). Excluding OTUs with five or less sequence reads would have eliminated half of the chimeras in the RDP WAR datasets, similar to PIPE OTU (Table 3.4). The majority of OTUs that had five or less sequences were real 89% and comprised 29% of the total dataset, while the chimeric OTUs with five or less sequences were 4% of the total dataset.

The two manually curated methods (CLU REP, MAN PER) retained the same number of centroid sequences (782) and sequence reads (3,326,685); however, the number of OTUs generated differed between the two methods. After CLU REP curation, some centroid sequences clustered with species representatives at 97% similarity and were grouped into a single OTU (Supplementary Table 3.3). Thus, the CLU REP method generated the fewest OTUs (700 OTUs, 3,326,685 sequence reads), whereas the MAN PER method generated the most OTUs, as it was unable to infer relationships (782 OTUs, 3,326,685 sequence reads) (Supplementary Table 3.4). In the CLU REP dataset,

33% of the OTUs (231 OTUs) were not resolved at the genus level, and in the MAN PER dataset 43% of the OTUs (338 OTUs) were not resolved at the genus level. In the CLU REP dataset, 33% of the OTUs (231 OTUs) were not resolved at the genus level, and in the MAN PER dataset 43% of the OTUs (338 OTUs) were not resolved at the genus level. All of the 401 non-fungal OTUs that passed through the bioinformatics pipeline were detected using the two manually curated methods (CLU REP and MAN PER) and were excluded from those datasets (28 bacterial, 100 chimeric, 266 plant, 7 other).

Sampling effort and diversity

Species accumulation curves increased steeply and did not reach asymptote for tree fungal communities regardless of dataset or location (Fig. 3.2). For host fungal endophyte communities, Simpson diversity curves reached or neared asymptote at all three locations. Shannon diversity curves, however, did not reach or near asymptote at any location, despite the slopes being less steep than the species accumulation curves.

Based on projected diversity, some samples were nearly complete while others were insufficiently recovered (Table 3.6). For all datasets, the difference between the estimated number of species (Chao and Jost 2015) and observed richness suggests a large number of species still missing from NAPO, and the smallest number of species still missing from ALPE. While the four classification methods returned different estimates of missing species for each diversity measure, location, and host genus, there was no discernable pattern. No method

consistently estimated greater or lower estimates for number of missing species.

Richness and diversity (estimated using Shannon and Simpson indices) for endophytic communities of *Hevea* and *Micrandra* trees were significantly different within each location regardless of dataset used (Table 3.6). In ALPE, richness and diversity of fungal communities from *Micrandra* hosts were greater than those from *Hevea* hosts for all datasets. In NAPO, the opposite was observed; richness and diversity of fungal communities from *Hevea* hosts were greater than those from *Micrandra* hosts for all datasets. In JEHE, richness and diversity of fungal communities from *Micrandra* hosts and *Hevea* hosts were not significantly different for CLU REP and MAN PER datasets; however, richness and diversity of fungal communities from *Hevea* hosts were greater than those from *Micrandra* hosts for both PIPE OTU and RDP WAR datasets (Table 3.6) .

These analyses, thus far, have considered the ‘full’ dataset, which included those OTUs with non-informative names. To compare the effect of ‘full’ and ‘reduced’ datasets on diversity measures, OTUs with non-informative names were removed from the ‘full’ CLU REP, MAN PER, PIPE OTU and MAN WAR datasets to create the ‘reduced’ dataset. Generally, a significant amount of fungal diversity and richness was lost in the reduced datasets compared to the full datasets. For fungal communities from ALPE hosts in the CLU REP dataset, and from JEHE *Micrandra* hosts in the PIPE OTU dataset, richness and diversity were not significantly less than the full datasets (Table 3.7). Despite the loss of richness and diversity, the reduced datasets came to the same inferences as the full datasets in both ALPE and NAPO. In ALPE, the fungal community from *Micrandra* hosts

had a greater richness and diversity than that of *Hevea* hosts, and in NAPO the fungal community from *Hevea* hosts had greater richness and diversity than that of *Micrandra* hosts.

Inferences drawn for JEHE using the reduced datasets were different than those from the full datasets. Using the entire CLU REP and MAN PER datasets, the fungal community from *Hevea* hosts in JEHE had greater richness than that of *Micrandra* hosts, but were not significantly different. Using the entire PIPE OTU and RDP WAR datasets, fungal communities from *Hevea* hosts had greater richness and diversity than those from *Micrandra* hosts in JEHE. In the reduced datasets, endophytes captured from *Hevea* hosts had greater richness and diversity than those captured from *Micrandra* for both CLU REP and MAN PER datasets while there were no significant differences in richness and diversity for either PIPE OTU or RDP WAR.

Distribution of taxa

Ascomycota was the dominant phylum for all four datasets (Fig. 3.3). A higher proportion of Basidiomycota were detected using CLU REP and MAN PER methods (206 OTUs, 16% incidence frequency, 6% sequence reads) than PIPE OTU (123 OTUs, 10% incidence frequency, 2% sequence reads), and RDP WAR (146 OTUs, 11% incidence frequency, 2% sequence reads) methods (Table 3.8). Likewise, CLU REP and MAN PER datasets had more Chytridiomycota (7 OTUs) than PIPE OTU (2 OTUs) or RDP WAR (1 OTU). All methods detected the presence of a single OTU belonging to the Zoopagomycotina. PIPE OTU

method generated 132 OTUs that were unresolved at the phylum level and were classified as “fungus”. These “fungus” OTUs were classified as Basidiomycota (14 OTUs), Ascomycota (103 OTUs), and chimeric (15 OTUs) using the CLU REP and MAN PER methods.

When partitioning the data by location and tree host, there were differences in frequency and abundance across the datasets. Generally, PIPE OTU and RDP WAR datasets had lower incidence of Basidiomycota OTUs than CLU REP or MAN PER datasets (Table 3.9). There were also within dataset differences when comparing incidence frequency to sequence reads abundance. In JEHE, the proportion of Basidiomycota sequence reads ranged between 1% (PIPE OTU, RDP WAR) and 12% (CLU REP, MAN PER), but Basidiomycota accounted for 24% (RDP WAR) to 32% (CLU REP) of incidence frequencies.

Fungal genera abundances were dataset and location dependent. For all datasets, except PIPE OTU, *Sarocladium* was the most abundant genus, followed by *Tolypocladium*, *Debaryomyces*, and *Acremonium*. The PIPE OTU method ranked *Sarocladium* first, *Debaryomyces* second, *Tolypocladium* third, *Pochonia* fourth, and *Acremonium* 15th. Across all three locations, three OTUs within the top ten most abundant genera were unique to the CLU REP dataset (*Hypocreales* 3, *Clavicipitaceae* 1.1 and *Clavicipitaceae* 1) (Table 3.10).

CLU REP and MAN PER datasets had similar top ten fungal genera rankings across all three locations, while the PIPE OTU dataset was the most disparate (Table 3.11). For tree hosts in ALPE, the ten most abundant fungal genera for the CLU REP dataset also ranked among the top ten genera in the

MAN PER dataset and in the RDP WAR dataset, except for Hypocreales 3 and *Penicillium. Acremonium*, the third most abundant genus for the CLU REP dataset, ranked 19th using the PIPE OTU method.

For tree hosts in JEHE, seven of the ten most abundant fungal genera for the CLU REP dataset were also among the top ten genera in the MAN PER dataset and the RDP WAR dataset. Three genera were unique to the CLU REP dataset (Hypocreales 3, Clavicipitaceae 1 and Clavicipitaceae 1). Only four of the ten most abundant fungal genera for the CLU REP dataset were ranked as part of the top ten for the PIPE OTU. The third, sixth and ninth ranked genera in CLU REP (*Tolypocladium*, *Acremonium*, *Peniophora*) were ranked 13th, 21st, and 30th using the PIPE OTU method.

For tree hosts in NAPO, seven of ten most abundant fungal genera for the CLU REP genera also ranked among the top ten genera in the MAN PER dataset. Two genera were unique to the CLU REP dataset (Hypocreales 3 and Clavicipitaceae 1). *Fusicola* ranked eighth for the CLU REP dataset; using the MAN PER method, these sequences were classified as *Fusarium*, Hypocreales sp. and Nectriaceae sp.), while the PIPE OTU method classified them as two different taxa (*Fusarium* and *Gliocephalotrichum*). *Fusarium* was ranked twelfth for CLU REP, fifth for MAN PER and fourth for PIPE OTU datasets, while *Gliocephalotrichum* was unique to PIPE OTU dataset and ranked 52nd.

Distribution of core species varied across locations, tree hosts and datasets (Table 3.12). Nine core species were shared across all four datasets, however, all four datasets had a different number of total core species (CLU REP 10, MAN

PER 11, PIPE OTU 12, RDP WAR 13). The CLU REP dataset had fewer core species due to multiple centroid sequences clustering into two species after CLU REP curation (*Tolypocladium* sp. 2 and *Acremonium* sp. 3). The RDP WAR and PIPE OTU datasets each had two core species that were chimeric OTUs. OTU 7 was a core species for all datasets except for PIPE OTU because it did not meet the 80% BLAST similarity and was therefore excluded from the dataset.

Ecological function guilds

When analyzing OTUs, rankings were similar for all four methods with one exception, although the number of OTUs differed. For the CLU REP dataset, the guild with the most members was the saprophyte guild (Fig. 3.4). For MAN PER, PIPE OTU, and RDP WAR datasets, the undetermined guild (OTUs with unknown functions) had the most members followed by the saprophyte guild. The entomopathogenic guild had the third most members for all datasets, followed by the plant pathogen guild, the wood decay guild, and fungicolous guild. The exception was RDP WAR, which had more fungicolous members than plant pathogenic and wood decay. CLU REP had the smallest proportion of OTUs with unknown functions (26%), while RDP WAR had the largest (45%) (Table 3.13).

When analyzing incidence frequencies and sequence reads across locations and tree hosts, the distribution of fungal function guilds varied between datasets (Table 3.14). Rankings of CLU REP and MAN PER datasets were the most similar (64% similarity of incidence frequency, 89% similarity of sequence read), while CLU REP and PIPE OTU rankings were most dissimilar (42%

similarity of incidence frequency, 47% similarity of sequence read). PIPE OTU and RDP WAR were most similar to each other (67% similarity of incidence frequency, 58% similarity of sequence reads). PIPE OTU was the only dataset that found no members in the fungicolous guild from *Micrandra* hosts in NAPO and ALPE (Table 3.15).

Additionally, rankings for a particular location and host were different within datasets when comparing incidence frequency to sequence reads abundance (Table 3.16). CLU REP, MAN PER and RDP WAR methods had the same average, 44% congruence, between incidence frequency and sequence read rankings and similar median congruence (between 33% and 50%). There are several location-host-dataset combinations that were notably different from the average congruence. For fungal endophytes captured from *Hevea* hosts in NAPO, CLU REP resulted in 83% congruence between incidence frequency and sequence read rankings. For endophytes taken from *Micrandra* hosts in NAPO, PIPE OTU resulted in 67% congruence. For fungal endophytes obtained from *Hevea* hosts in all three locations, PIPE OTU resulted in 17% congruence.

Discussion

Methods for classifying OTUs differ based on cutoff criteria, which then determine which OTUs are excluded or retained. Cutoff criteria are derived from various methods of gauging similarity between samples. Before the advent of next generation sequencing technologies, classifying OTUs was historically done manually on small data sets, but more recently bioinformatics pipelines utilizing

algorithms that reduce analysis time have been developed. The resulting downstream effect of these different cutoff criteria and methods varies, which is exactly what this study found.

Distribution of taxa

In this study, a higher proportion of Basidiomycota and Chytridiomycota were retained using the CLU REP and MAN PER method. Of the fungal centroid sequences that did not meet the criteria for RDP WAR and PIPE OTU, 68% were members of Basidiomycota. Exclusion of Basidiomycota OTUs due to no close matches in the UNITE or NCBI databases exemplifies the dependence of environmental metabarcoding on well-curated databases (Hibbett et al. 2011, Nagy et al. 2011).

When partitioning the data by location and tree hosts, JEHE had a much higher proportion of endophytes in the phylum Basidiomycota from both host genera when using CLU REP and MAN PER datasets. This was not reflected for *Micrandra* hosts when PIPE OTU and RDP WAR were used; proportion of Basidiomycota endophytes were at a similar level to what was found in *Micrandra* hosts from ALPE. A change in the proportion of Ascomycota and Basidiomycota OTUs can indicate host decline, as many Basidiomycota are pioneer wood decay pathogens (Ochimaru and Fukuda 2007, Parfitt et al. 2010, Robles et al. 2015). The differing results in this study regarding the shift of phylum proportions highlight the importance of understanding how data pre-processing filters can alter conclusions drawn from a given study.

When examining OTUs at the genus level, three of the four datasets had the same ranking for the four most dominant fungal genera, but rankings from five and beyond were inconsistent across datasets, especially when the data were partitioned by location. In some instances, the rankings were extremely different, as was the case with *Peniophora*, one of the ten most abundant genera in JEHE using the CLU REP and MAN PER methods. For the PIPE OTU dataset, *Peniophora* was ranked 30th in JEHE. *Peniophora* contains many plant pathogenic members, and some are parasitized by other fungi (Cannon and Kirk 2007, Overall 2017). *Peniophora* was abundant in JEHE only, and of the three locations, JEHE had the most anthropogenic pressures. Increase in abundance of *Peniophora* may be an indicator of forest health, as it was not found in high abundances in the other two locations. Presence of this key genus may have been overlooked if the analysis relied on PIPE OTU or RDP WAR method.

Differences in ranked abundances among the four methods were mainly due to the inclusion of chimeric reads, exclusion of real fungal sequences, and inability to infer relationships among OTUs using the MAN PER, PIPE OTU, and RDP WAR methods. By clustering OTUs in the CLU REP method using representative sequences, more biologically relevant species and genus limits were used to delimit OTUs. Using the CLU REP method of classification, three unique endophytes, Hypocreales 3, Clavicipitaceae 1.1 and Clavicipitaceae 1, were detected. Clavicipitaceae 1 representative sequence was a rare and novel endophyte isolated from *Hevea* and *Micrandra* cultures. Using next generation sequencing, we were able to see that this member of the entomopathogenic guild

occurs more frequently in *Hevea* and *Micrandra* and perhaps should be investigated further.

Likewise, with core species, the CLU REP dataset had two unique core species (*Acremonium* species 3 and *Tolypocladium* species 2) owing to clustering with representative sequences and customizing taxonomic limits. *Acremonium* members belong to various function guilds, including fungicolous, wood decay and plant pathogenic guilds, while *Tolypocladium* members largely belong to the entomopathogenic guild. PIPE OTU and RDP WAR had more core species; however, two of their core species were chimeric OTUs. While problematic, one would most likely perform a manual blast on core species, and subsequently extract it once the chimeric sequence is discovered. More problematic was the absence of a core species (OTU 7, Agaricales 15.2)

Diversity estimates

For endophyte diversity estimates, bias in the classification methods influenced diversity measures. For example, in JEHE, there was no significant difference between endophytic communities from different tree hosts when using CLU REP and MAN PER methods, but there was a significant difference when using the PIPE OTU and RDP method.

When reduced datasets (exclusion of OTUs with non-informative names) were compared to full datasets, generally, a significant amount of fungal diversity and richness was lost, but the reduced datasets came to the same inferences as the full datasets in both ALPE and NAPO. In the third location JEHE, the direction of

the results remained the same with *Hevea* hosts showing greater diversity than *Micrandra* hosts. However, the results of the significance testing between the full and reduced datasets were reversed. CLU REP and MAN PER datasets resulted in no significant differences in diversity for the full dataset while significant differences were found using the reduced dataset. PIPE OTU and MAN WAR were reversed: significant differences in diversity were found using the full dataset, but there were no significant differences in the reduced dataset.

Ecological function guilds

Determining the most dominant function guilds in a fungal community is vital when drawing conclusions regarding fungal-plant interactions. It helps to answer questions about community composition and interaction with the environment. For example, entomopathogenic fungi may help protect against herbivory (Ownley et al. 2004, Toledo et al. 2017), opportunistic pathogens can be informative about environmental conditions (Ochimaru and Fukuda 2007), or fungicolous species can indicate a level of host protection against other pathogenic organisms (Rocha et al. 2017).

Method of classifying OTUs did influence the ranking of guilds from most abundant members to least, but rankings were similar. When the distribution of fungal function guilds was analyzed using incidence frequencies and sequence reads across locations and tree hosts, the results varied among datasets. CLU REP was most similar to MAN PER while most dissimilar to PIPE OTU. The only notable distinction between methods was that PIPE OTU found no members in

the fungicolous guild in two host-location combinations, while all other datasets had members in that guild.

One of the more interesting results was the difference between incidence frequency results and sequence reads abundance results, regardless of dataset. The most abundant guild using sequence reads was the entomopathogenic guild; however, it was the second (CLU REP, MAN PER) and third most abundant guild (PIPE OTU, RDP WAR) when using incidence frequency. It is a common practice to use sequence reads to analyze abundance; however, this study adds to the growing body of evidence that relying solely on sequence reads can be misleading (Kebschull and Zador 2015, Taylor et al. 2016). A more prudent approach would be to use both types of data, incidence frequency and sequence reads for ecological inferences from environmental samples.

RDP WAR

One unexpected outcome of using the RDP WAR method was that the engine's classifier placed all non-fungal DNA as fungal with 100% confidence. To circumvent this problem, a filter can be set to remove OTUs that do not have a 95% confidence level at the phylum level. However, this can leave chimeras in the dataset. One method to remove the chimeras is to remove OTUs which have 5-sequence reads or less. When performed on RDP WAR or PIPE OTU this dataset, 85% or more of those OTUs were fungal sequences and only half of the chimeric reads were eliminated. This highlights the importance of exercising

caution when relying solely on pipeline methods to classify OTUs (Brown et al. 2015, Nguyen et al. 2015).

Conclusions

For studies examining community diversity with metabarcoding data, data preprocessing has important downstream effects on inferences and conclusions. When analyzing OTUs globally, differences between methods appeared less significant. However, when the data were parsed by location and host, the results from each method of OTU classification differed greatly at times. The distribution of OTUs, not just number of OTUs, is important for drawing conclusions about community composition.

Newly developed methods that streamline data processing (i.e., RDP WAR and PIPE OTU) had the advantage of saving time, and thus cost; however, even with filter adjustments, were more error prone than methods that employ some level of manual curation (i.e., CLU REP and MAN PER). CLU REP was the least error prone as it was highly curated, manually blasted, and OTUs were assigned by clustering centroid pipeline sequences with GenBank representative sequences. Constructing CLU REP was onerous, but resulted in the most robust analysis of community composition and diversity with the least bias.

This study examined four different methods of OTU classification in the context of endophyte diversity in a wild rubber tree system utilizing metabarcoding data. Metabarcoding has become an important tool for exploring fungal communities across multiple systems ranging from plants and animals, to

water, soil and even the atmosphere. While data preprocessing and analysis pipelines are gaining in popularity due to scalability, time-savings and ease of use, caution needs to be exercised when applying classification tools and filtering. For the case of fungal studies, automated pipelines could be improved by incorporating a clustering algorithm that set cutoff limits wherever representative sequences converge exclusively, meaning no other representative sequences from the desired taxonomic level were clustered with them, to define the taxonomic limit for the OTU.

TABLE 3.1. Number of trees sampled for endophytes per host tree species from Amazon Conservatory for Tropical Studies Biological Station (NAPO; 3°14'57.20"S, 72°54'33.60"W), Allpahuayo-Mishana National Reserve (ALPE; 3°58'1.16"S, 73°25'8.11"W), and Jenaro Herrera Research Center (JEHE; 4°53'54.29"S, 73°38'59.80"W).

Tree species	No. trees sampled		
	NAPO	ALPE	JEHE
<i>Hevea brasiliensis</i>	-	-	12
<i>Hevea guianensis</i>	21	14	-
<i>Hevea nitida</i>	11	1	8
<i>Hevea pauciflora</i>	-	16	-
<i>Micrandra elata</i>	-	15	-
<i>Micrandra spruceana</i>	18	8	13
Total trees (136)	49	54	33

TABLE 3.2. Number of sequence reads that remained after curation, number of operational taxonomic units (OTUs) and number and percentage of non-fungal sequences remaining within each dataset: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn OTUs (PIPE OTU), and the RdP classifier with Warcup Fungal training set (RDP WAR).

Dataset	No. Sequence reads	No. OTUs	No. Non-Fungal		% Non-Fungal	
			OTUs	Reads	OTUs	Reads
CLU REP	3,326,685	700	0	0	0	0
MAN PER	3,326,685	782	0	0	0	0
PIPE OTU	3,222,923	733	55	23,865	8%	0.70%
RDP WAR	6,888,097	765	72	23,983	9%	0.30%

TABLE 3.3.A. Number and percent of fungal operational taxonomic units (OTUs) that fell below classification criteria. For Pipeline BLASTn OTUs method (PIPE OTU), 80% BLAST similarity was the classification criteria cutoff. For RdP classifier with Warcup Fungal training set (RDP WAR) a 95% phylum confidence level was the classification criteria cutoff.

Phylum	No. fungal OTUs excluded		% fungal OTUs excluded		No. fungal reads excluded		%fungal reads excluded	
	RDP WAR	PIPE OTU	RDP WAR	PIPE OTU	RDP WAR	PIPE OTU	RDP WAR	PIPE OTU
Ascomycota	21	30	23.9%	29.1%	72,315	1,218	66.0%	1.2%
Basidiomycota	60	65	68.2%	63.1%	36,139	101,382	33.0%	97.4%
Chytridiomycota	6	5	6.8%	4.9%	1,027	1,024	0.9%	1.0%
Fungus	0	1	0.0%	1.0%	0	24	0.0%	0.0%
Mucoromycota	1	2	1.1%	1.9%	50	455	0.0%	0.4%
Fungal Totals	88	103			109,531	104,103		

TABLE 3.3.B. Number and percent of non-fungal OTUs that fell below classification criteria. For Pipeline BLASTn OTUs method (PIPE OTU), 80% BLAST similarity was the classification criteria cutoff. For RdP classifier with Warcup Fungal training set (RDP WAR), a 95% phylum confidence level was the classification criteria cutoff.

Organism	No. non-fungal OTUs excluded		% non-fungal OTUs excluded		No. non-fungal reads excluded		% non-fungal reads excluded	
	RAD WAR	PIPE OTU	RAD WAR	PIPE OTU	RAD WAR	PIPE OTU	RAD WAR	PIPE OTU
Bacteria	18	18	8.5%	7.8%	8,093	8,093	1.1%	1.1%
Chimera	11	27	5.2%	11.7%	3,767	3,879	0.5%	0.5%
Other	5	5	2.3%	2.2%	16,960	16,960	2.4%	2.3%
Planta	179	180	84.0%	78.3%	692,727	696,356	96.0%	96.0%
Non-Fungal Totals	213	230			721,547	725,288		

TABLE 3.4. Number and proportion of real and chimeric OTUs that had five sequence reads or less in the RdP classifier with Warcup Fungal training set (RDP WAR) and the Pipeline BLASTn OTUs datasets.

No. of sequence reads	Dataset	No. OTUs	Sequence type	No. of OTUs	% of OTUs with 5 or less reads	% of Total OTUs
2 reads	RDP WAR	161	Real	132	82%	17%
			Chimeric	29	18%	4%
	PIPE OTU	145	Real	126	87%	17%
			Chimeric	19	13%	3%
3 reads	RDP WAR	34	Real	29	85%	4%
			Chimeric	5	15%	1%
	PIPE OTU	32	Real	28	88%	4%
			Chimeric	4	13%	1%
4 reads	RDP WAR	45	Real	40	89%	5%
			Chimeric	5	11%	1%
	PIPE OTU	41	Real	38	93%	5%
			Chimeric	3	7%	0%
5 reads	RDP WAR	26	Real	25	96%	3%
			Chimeric	1	4%	0%
	PIPE OTU	24	Real	24	10%	3%
			Chimeric	0	0%	0%
Totals	RDP WAR	266	Real	226	85%	30%
			Chimeric	40	15%	5%
	PIPE OTU	242	Real	216	89%	29%
			Chimeric	26	11%	4%

TABLE 3.5. Number and percent of operational taxonomic units (OTUs) unresolved at the genus level partitioned by phylum level and dataset: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn OTUs, and the RdP classifier with Warcup Fungal training set (RDP WAR).

Phylum unresolved at the Genus level	CLU REP		MAN PER		PIPE OTU		RDP WAR	
	No. Unres. OTUs	% Unres. OTUs	No. OTUs	% Unres. OTUs	No. Unres. OTUs	% Unres. OTUs	No. OTUs	% Unres. OTUs
Ascomycota	143	67%	226	67%	73	32%	320	88%
Basidiomycota	82	30%	103	30%	23	10%	44	12%
Chytridiomycota	6	2%	6	2%	0	0%	0	0%
Mucoromycota	0	1%	3	1%	0	0%	0	0%
Fungus	0	0%	0	0%	131	58%	0	0%
Total unresolved OTUs	231	100%	338	100%	227	100%	364	100%
% of Total dataset OTUs	33%		43%		31%		48%	

TABLE 3.6. Observed and estimated richness (SR) and diversity (Shannon Hill numbers [SHAN] and Simpson Hill numbers [SIM]), including upper (UCL) and lower (LCL) confidence intervals, of species level operational taxonomic units (OTUs) per location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]), tree genera, and dataset (Clustered GenBank Representatives [CLU REP], Manual BLAST Percent Based [MAN PER], Pipeline BLASTn OTUs [PIPE OTU], and Rdp classifier with Warcup Fungal training set [RDP WAR]). LCL and UCL are highlighted in green. Partially overlapping confidence levels do not guarantee non-significance (Chao et al. 2014).

Site	Tree species	Dataset	Observed Richness and Diversity							Estimated Richness and Diversity								
			SR	SHAN	LCL	UCL	SIM	LCL	UCL	SR	LCL	UCL	SHAN	LCL	UCL	SIM	LCL	UCL
ALPE	<i>Hevea</i>	CLU REP	77	38	33	44	22	18	26	173	119	300	53	41	64	24	22	29
		MAN PER	85	43	37	50	24	18	29	181	128	296	60	49	71	26	24	31
		PIPE OTU	90	47	40	53	27	22	31	169	126	261	62	51	72	29	27	35
		RDP WAR	94	48	42	54	27	23	31	180	135	277	65	53	76	29	27	35
	<i>Micrandra</i>	CLU REP	154	98	81	115	55	44	65	452	323	678	195	151	239	67	55	84
		MAN PER	165	108	94	121	61	47	75	491	353	730	222	177	267	76	61	95
		PIPE OTU	144	91	79	104	54	42	65	406	289	619	171	137	205	65	54	82
		RDP WAR	146	93	79	107	54	44	65	400	287	603	174	140	208	66	54	83

Site	Tree species	Dataset	Observed Richness and Diversity							Estimated Richness and Diversity								
			SR	SHAN	LCL	UCL	SIM	LCL	UCL	SR	LCL	UCL	SHAN	LCL	UCL	SIM	LCL	UCL
JEHE	<i>Hevea</i>	CLU REP	139	83	72	94	49	40	58	478	319	776	163	124	201	58	49	72
		MAN PER	149	92	80	103	55	44	66	478	329	752	176	141	211	66	55	82
		PIPE OTU	145	88	74	103	52	42	63	511	341	830	175	137	213	63	52	79
		RDP WAR	152	92	79	106	55	46	63	569	377	926	190	149	230	66	55	79
	<i>Micrandra</i>	CLU REP	93	63	52	74	42	35	49	364	213	705	134	93	176	55	42	71
		MAN PER	101	70	58	83	49	39	58	406	237	785	150	107	194	63	49	79
		PIPE OTU	87	60	50	71	42	32	52	289	174	554	114	84	144	54	42	68
		RDP WAR	91	63	52	73	43	36	51	364	207	735	130	91	168	56	43	70
NAPO	<i>Hevea</i>	CLU REP	386	241	221	262	130	110	150	1105	884	1424	467	405	529	156	130	183
		MAN PER	444	287	261	312	161	141	181	1277	1034	1619	560	494	625	196	161	232
		PIPE OTU	454	292	271	313	165	146	184	1325	1072	1680	571	499	642	201	171	232
		RDP WAR	459	296	270	323	166	144	188	1407	1131	1795	596	528	664	203	167	238
	<i>Micrandra</i>	CLU REP	121	71	61	82	42	35	50	384	256	632	131	103	159	50	42	61
		MAN PER	143	86	74	99	52	42	61	495	331	804	168	127	209	62	52	75
		PIPE OTU	131	79	68	91	48	39	58	363	255	566	139	111	167	58	48	70
		RDP WAR	140	84	74	94	51	41	60	422	292	660	153	120	186	60	51	73

TABLE 3.7. Observed and estimated richness (SR) and diversity (Shannon Hill numbers [SHAN] and Simpson Hill numbers [SIM]), including upper (UCL) and lower (LCL) confidence intervals, of species level operational taxonomic units (OTUs) for reduced datasets (non-informative names excluded). These are presented per location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]), tree genera, and reduced dataset (Clustered GenBank Representatives [CLU REP], Manual BLAST Percent Based [MAN PER], Pipeline BLASTn OTUs [PIPE OTU], and RdP classifier with Warcup Fungal training set [RDP WAR]). LCL and UCL are highlighted in green. Partially overlapping confidence levels do not guarantee non-significance (Chao et al. 2014).

Site	Tree species	Reduced Dataset	Observed Richness and Diversity							Estimated Richness and Diversity								
			SR	SHAN	LCL	UCL	SIM	LCL	UCL	SR	LCL	UCL	SHAN	LCL	UCL	SIM	LCL	UCL
ALPE	<i>Hevea</i>	CLU REP	69	35	28	42	20	15	25	149	102	264	47	38	57	22	20	26
		MAN PER	67	35	29	41	20	15	24	116	87	188	46	37	54	21	20	27
		PIPE OTU	67	34	29	39	20	16	24	125	90	209	44	36	52	21	20	26
		RDP WAR	60	31	26	35	18	15	22	107	78	181	38	32	45	20	18	24
	<i>Micrandra</i>	CLU REP	97	59	50	68	34	24	44	224	161	352	100	79	121	40	34	52
		MAN PER	101	64	54	73	36	29	44	250	176	399	111	88	135	43	36	57
		PIPE OTU	102	63	55	71	36	27	46	271	186	442	112	86	139	43	36	56
		RDP WAR	91	56	47	66	33	24	43	206	146	331	91	73	110	39	33	50

Site	Tree species	Reduced Dataset	Observed Richness and Diversity							Estimated Richness and Diversity								
			SR	SHAN	LCL	UCL	SIM	LCL	UCL	SR	LCL	UCL	SHAN	LCL	UCL	SIM	LCL	UCL
JEHE	<i>Hevea</i>	CLU REP	108	64	50	77	36	27	46	360	233	619	123	91	156	43	36	54
		MAN PER	104	63	52	73	37	30	44	339	217	593	116	86	146	44	37	55
		PIPE OTU	97	58	48	69	33	25	41	384	229	720	124	89	158	39	33	50
		RDP WAR	96	57	47	67	33	27	40	352	213	656	110	77	142	39	33	50
	<i>Micrandra</i>	CLU REP	54	37	31	43	26	20	31	136	85	268	63	43	84	32	26	42
		MAN PER	59	42	34	50	31	23	38	131	87	242	69	49	88	39	31	50
		PIPE OTU	64	44	35	54	30	21	38	207	122	419	91	56	126	39	30	52
		RDP WAR	57	41	32	49	29	20	38	193	106	436	80	52	108	38	29	52
NAPO	<i>Hevea</i>	CLU REP	289	177	160	194	98	83	113	789	615	1055	318	271	365	116	98	136
		MAN PER	257	160	143	178	96	82	111	590	468	781	256	225	287	114	96	132
		PIPE OTU	301	193	173	214	107	87	128	885	683	1193	373	323	423	130	107	156
		RDP WAR	232	143	127	160	84	70	98	561	435	767	233	202	264	99	84	116
	<i>Micrandra</i>	CLU REP	79	47	38	55	28	21	34	224	144	402	82	61	102	32	28	41
		MAN PER	83	50	41	58	31	25	37	256	160	474	87	64	110	36	31	45
		PIPE OTU	77	46	38	54	27	21	34	199	133	346	79	58	99	32	27	41
		RDP WAR	79	46	38	54	28	22	33	252	156	470	82	57	108	32	28	40

TABLE 3.8. Distribution of phyla for each dataset generated using one of four OTU classification methods: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), and Pipeline BLASTn OTUs (PIPE OTU), Rdp classifier with Warcup Fungal training set (RDP WAR).

[illegible]

TABLE 3.9. Distribution of phyla presented by incidence frequency and sequence reads, partitioned by tree genus, location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]), and dataset (Clustered GenBank Representatives [CLU REP], Manual BLAST Percent Based [MAN PER], Pipeline BLASTn OTUs [PIPE OTU], and RdP classifier with Warcup Fungal training set [RDP WAR]). Phyla were abbreviated as follows: Ascomycota (Asco), Basidiomycota (Basidio), Chytridiomycota (Chytridio), Mucoromycotina (Mucoro), and Zoopagomycotina (Zoopago).

Site	Tree species	Dataset	Incidence Frequency					Sequence Reads				
			Asco	Basidio	Chytridio	Mucoro	Zoopago	Asco.	Basidio	Chytridio	Mucoro	Zoopago
ALPE	<i>Hevea</i>	CLU REP	93.7%	6%	0.0%	0.4%	0.0%	98.6%	1%	0.0%	0.0%	0.0%
		MAN PER	93.8%	6%	0.0%	0.4%	0.0%	98.6%	1%	0.0%	0.0%	0.0%
		PIPE OTU	94.1%	6%	0.0%	0.4%	0.0%	98.6%	1%	0.0%	0.0%	0.0%
		RDP WAR	94.9%	5%	0.0%	0.3%	0.0%	98.6%	1%	0.0%	0.0%	0.0%
	<i>Micrandra</i>	CLU REP	70.0%	27%	1.7%	1.0%	0.0%	95.8%	4%	0.1%	0.0%	0.0%
		MAN PER	71.1%	26%	1.6%	1.0%	0.0%	95.8%	4%	0.1%	0.0%	0.0%
		PIPE OTU	78.2%	20%	0.4%	1.2%	0.0%	96.5%	4%	0.0%	0.0%	0.0%
		RDP WAR	78.7%	21%	0.0%	0.7%	0.0%	96.2%	4%	0.0%	0.0%	0.0%

Site	Tree species	Dataset	Incidence Frequency					Sequence Reads				
			Asco	Basidio	Chytridio	Mucoro	Zoopago	Asco.	Basidio	Chytridio	Mucoro	Zoopago
JEHE	Hevea	CLU REP	61.5%	39%	0.0%	0.0%	0.0%	94.0%	6%	0.0%	0.0%	0.0%
		MAN PER	63.4%	37%	0.0%	0.0%	0.0%	94.0%	6%	0.0%	0.0%	0.0%
		PIPE OTU	64.9%	35%	0.0%	0.0%	0.0%	93.2%	7%	0.0%	0.0%	0.0%
		RDP WAR	67.5%	33%	0.0%	0.0%	0.0%	94.1%	6%	0.0%	0.0%	0.0%
	Micrandra	CLU REP	68%	32%	0.0%	0.0%	0.0%	88.5%	12%	0.0%	0.0%	0.0%
		MAN PER	70%	30%	0.0%	0.0%	0.0%	88.5%	12%	0.0%	0.0%	0.0%
		PIPE OTU	73%	27%	0.0%	0.0%	0.0%	97.5%	1%	1.6%	0.0%	0.0%
		RDP WAR	76%	24%	0.0%	0.0%	0.0%	99.0%	1%	0.0%	0.0%	0.0%
NAPO	Hevea	CLU REP	92.6%	7%	0.1%	0.5%	0.0%	99.5%	1%	0.0%	0.0%	0.0%
		MAN PER	93.5%	6%	0.1%	0.5%	0.0%	99.5%	1%	0.0%	0.0%	0.0%
		PIPE OTU	96.8%	3%	0.0%	0.6%	0.0%	99.8%	0%	0.0%	0.0%	0.0%
		RDP WAR	96.9%	3%	0.1%	0.4%	0.0%	99.8%	0%	0.0%	0.0%	0.0%
	Micrandra	CLU REP	83.2%	15%	0.7%	0.4%	0.4%	75.5%	24%	0.0%	0.0%	0.0%
		MAN PER	85.2%	14%	0.6%	0.3%	0.0%	75.5%	24%	0.0%	0.0%	0.0%
		PIPE OTU	91.5%	8%	0.5%	0.0%	0.0%	98.4%	2%	0.0%	0.0%	0.0%
		RDP WAR	90.2%	9%	0.3%	0.3%	0.0%	73.2%	27%	0.0%	0.0%	0.0%

TABLE 3.10. The five most abundant fungal genera, their incidence frequencies, number of sequence reads, and number of host trees each genus was captured from per dataset: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), and Pipeline BLASTn OTUs (PIPE OTU), and RdP classifier with Warcup Fungal training set (RDP WAR).

Dataset	Genus	Incidence Freq.	No. Trees	No. Reads	% Incidence Freq.	% Trees	% Reads
CLU REP	<i>Sarocladium</i>	336	129	1,839,185	15%	95%	55%
	<i>Tolypocladium</i>	272	91	182,201	12%	67%	5%
	<i>Debaryomyces</i>	169	79	296,325	8%	58%	9%
	<i>Acremonium</i>	156	59	208,583	7%	43%	6%
	<i>Hypocreales 3</i>	105	73	128,685	5%	54%	4%
MAN PER	<i>Sarocladium</i>	315	128	1,829,984	19%	94%	63%
	<i>Tolypocladium</i>	304	89	181,809	18%	65%	6%
	<i>Debaryomyces</i>	165	79	296,305	10%	58%	10%
	<i>Acremonium</i>	136	59	207,728	8%	43%	7%
	<i>Metapochonia</i>	84	46	70,393	5%	34%	2%
PIPE OTU	<i>Sarocladium</i>	392	129	1,839,381	17%	95%	57%
	<i>Debaryomyces</i>	173	66	297,045	7%	49%	9%
	<i>Tolypocladium</i>	112	79	37,221	5%	58%	1%
	<i>Pochonia</i>	104	48	135,719	4%	35%	4%
	<i>Metapochonia</i>	86	46	70,279	4%	34%	2%
RDP WAR	<i>Sarocladium</i>	611	129	1,828,353	26%	95%	56%
	<i>Tolypocladium</i>	341	93	201,037	15%	68%	6%
	<i>Debaryomyces</i>	171	79	296,329	7%	58%	9%
	<i>Acremonium</i>	91	37	58,265	4%	27%	2%
	<i>Malassezia</i>	55	38	38,647	2%	28%	1%

TABLE 3.11. The ten most abundant genera per location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]) using the Clustered GenBank Representatives (CLU REP) operational taxonomic unit (OTU) classification method, and the corresponding rankings for each genus when using Manual BLAST and Percent (MAN PER), Pipeline BLASTn OTUs (PIPE OTU), and Rdp classifier with Warcup Fungal training set (RDP WAR) OTU classification methods. Incidence frequencies and number of sequence reads are provided. The number of host trees the genera was captured from is also listed. Cells labeled with “-”, denotes datasets with no corresponding genera.

Site	Genera	CLU REP				MAN PER				PIPE OTU				RDP WAR			
		Rank	Inci Freq.	No. Seq. Reads	No. Trees	Rank	Inci Freq.	No. Seq. Reads	No. Trees	Rank	Inci Freq.	No. Seq. Reads	No. Trees	Rank	Inci Freq.	No. Seq. Reads	No. Trees
ALPE	<i>Sarocladium</i>	1	207	1,715,773	54	1	197	1,715,664	53	1	262	1,716,078	54	1	237	1,715,418	54
	<i>Tolypocladium</i>	2	43	4,898	29	2	56	4,898	28	3	24	261	17	2	55	4,922	30
	<i>Hypocreales</i> 3	3	28	2,378	28	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Acremonium</i>	4	23	10,302	15	3	24	10,302	15	19	2	4	2	7	9	3,248	8
	<i>Debaryomyces</i>	5	21	142	17	4	21	142	17	4	22	6,36	17	3	21	142	17
	<i>Malassezia</i>	6	19	23,911	14	7	17	20,665	12	9	7	1,715	7	4	19	23,911	14
	<i>Metapochonia</i>	7	17	46	17	5	18	46	17	5	18	46	17	-	-	-	-
	<i>Penicillium</i>	8	17	4,169	10	-	-	-	-	6	17	4,169	10	5	16	4,167	10
	<i>Nectria</i>	9	17	21,862	13	6	17	21,862	12	3	23	21,874	17	6	14	21,853	13

Site	Genera	CLU REP				MAN PER				PIPE OTU				RDP WAR			
		Rank	Inci Freq.	No. Seq. Reads	No. Trees	Rank	Inci Freq.	No. Seq. Reads	No. Trees	Rank	Inci Freq.	No. Seq. Reads	No. Trees	Rank	Inci Freq.	No. Seq. Reads	No. Trees
	<i>Metarhizium</i>	10	7	30	7	9	7	30	7	10	7	30	7	9	7	30	7
JEHE	<i>Sarocladium</i>	1	47	112,321	28	2	44	112,304	28	1	50	112,328	28	3	42	110,919	28
	<i>Debaryomyces</i>	2	43	174,439	27	3	42	174,437	27	2	45	174,663	27	2	43	174,439	27
	<i>Tolypocladium</i>	3	30	50,153	23	1	63	50,153	23	13	5	14	5	1	75	57,029	24
	<i>Malassezia</i>	4	24	14,617	12	4	22	14,447	12	6	13	4,945	9	4	23	14,478	12
	<i>Clavicipitaceae</i> 1	5	23	82,191	20	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Acremonium</i>	6	21	35,567	19	5	21	35,567	19	21	2	65	2	7	11	8,334	7
	<i>Metarhizium</i>	7	17	62,630	16	7	16	62,625	16	5	17	62,630	16	5	16	62,625	16
	<i>Hypocreales</i> 3	8	17	115	16	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Peniophora</i>	9	15	289	9	8	15	289	10	30	2	16	2	6	16	472	10
	<i>Clavicipitaceae</i> 1	10	14	43,102	14	-	-	-	-	-	-	-	-	-	-	-	-
NAPO	<i>Tolypocladium</i>	1	199	127,150	39	1	185	126,758	38	2	83	36,946	22	1	209	1,39,086	39
	<i>Acremonium</i>	2	112	162,714	25	3	91	161,859	25	13	18	26,844	12	4	71	46,683	22
	<i>Debaryomyces</i>	3	105	121,744	35	2	102	121,726	35	1	106	121,746	35	2	107	121,748	35
	<i>Sarocladium</i>	4	82	11,091	47	4	74	2,016	47	3	80	10,975	47	3	74	2,016	47
	<i>Hypocreales</i> 3	5	60	126,192	29	-	-	-	-	-	-	-	-	-	-	-	-
	<i>Metapochonia</i>	6	53	70,552	15	6	49	70,304	15	5	51	70,190	15	-	-	-	-

[illegible]

[illegible]

Location	Dataset	Tree genus	otu_3	otu_10	otu_2	otu_5	otu_77	otu_434	otu_6	otu_7	otu_8	otu_12	otu_40	otu_38	otu_584	multi OTUs 1	multi OTUs 2
	MAN PER	<i>Micrandra</i>	x	x	x	x	-	-	-	x	x	x	x	-	-	-	-
	PIPE OTU	<i>Hevea</i>	x	x	x	-	-	-	-	-	-	-	-	-	-		
		<i>Micrandra</i>	x	x	x	x	-	-	-	-	x	x	x	x	-		
	RDP WAR	<i>Hevea</i>	x	x	x	-	-	-	-	-	-	-	-	-	-	-	-
		<i>Micrandra</i>	x	x	x	x	-	-	-	x	x	x	x	x	-	-	-

TABLE 3.13. Number of operational taxonomic units (OTU)s and proportion of OTUs assigned to each function guild for each OTU classification method: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn OTUs (PIPE OTU), and RdP classifier with Warcup Fungal training set (RDP WAR).

Function Guild	No. of OTUs				Proportion of OTUs			
	CLU REP	MAN PER	PIPE OTU	RDP WAR	CLU REP	MAN PER	PIPE OTU	RDP WAR
Fungicolous	46	29	13	64	6%	4%	2%	8%
Wood decay	56	48	62	45	7%	6%	8%	6%
Plant pathogen	80	77	101	49	10%	10%	14%	6%
Entomopathogenic	154	156	114	71	20%	20%	16%	9%
Saprotroph	229	169	193	174	29%	22%	26%	23%
Undetermined	204	297	249	348	26%	38%	34%	45%

TABLE 3.14. Percent similarity of function guild rankings between datasets based on incidence frequencies and sequence reads generated using four operational taxonomic unit (OTU) classification methods: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn OTUs (PIPE OTU), and Rdp classifier with Warcup Fungal training set (RDP WAR).

Dataset	Incidence Frequency				Sequence reads			
	CLU REP	MAN PER	PIPE OTU	RDP WAR	CLU REP	MAN PER	PIPE OTU	RDP WAR
CLU REP	100%	64%	42%	61%	100%	89%	50%	47%
MAN PER	64%	100%	42%	64%	89%	100%	53%	47%
PIPE OTU	42%	42%	100%	67%	50%	53%	100%	58%
RDP WAR	61%	64%	67%	100%	47%	47%	58%	100%

TABLE 3.15. Function guild rankings based on incidence frequency and sequence read abundances per tree host endophytic communities, location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]), and dataset (Clustered GenBank Representatives [CLU REP], Manual BLAST Percent Based [MAN PER], Pipeline BLASTn OTUs [PIPE OTU] and Rdp classifier with Warcup Fungal training set (RDP WAR). Function guilds were abbreviated as follows: Entomopathogenic (Ento), Fungicolous (Fung), Plant pathogen (Path), Saprotroph (Sapro), Wood decay (Decay), and Undetermined (Undet).

Site	Tree genus	Dataset	Incidence Frequency						Sequence reads						Ranking
			Ento	Fung	Path	Sapro	Decay	Undet	Ento	Fung	Path	Sapro	Decay	Undet	
ALPE	<i>Hevea</i>	CLU REP	36	13	17	171	1	26	351	1,933	21,860	1,091,022	8	2,407	1
		MAN PER	40	14	18	161	1	40	351	1,933	21,862	1,090,897	8	2,571	2
		PIPE OTU	29	2	21	201	1	60	271	4	21,879	1,075,358	8	20,379	3
		RDP WAR	25	8	16	191	1	67	219	67	21,866	1,090,606	8	5,130	4
	<i>Micrandra</i>	CLU REP	49	11	15	134	19	72	5,754	8,377	4,436	657,264	5,476	8,721	5
		MAN PER	53	11	14	126	19	88	4,697	8,377	4,041	653,989	5,469	13,455	6
		PIPE OTU	40	0	15	146	16	82	263	0	3,894	650,891	5,261	24,777	
		RDP WAR	38	5	14	142	19	83	4,770	3,225	4,080	657,222	5,492	11,132	
JEHE	<i>Hevea</i>	CLU REP	56	13	14	132	37	48	49,016	35,561	1,501	244,648	1,216	1,449	

Site	Tree genus	Dataset	Incidence Frequency						Sequence reads						Ranking
			Ento	Fung	Path	Sapro	Decay	Undet	Ento	Fung	Path	Sapro	Decay	Undet	
		MAN PER	69	12	13	117	32	77	48,985	35,538	1,501	241,554	947	4,901	1
		PIPE OTU	41	2	16	111	29	111	178	84	1,555	235,159	1,512	98,860	2
		RDP WAR	55	8	12	111	30	104	52,898	40	487	239,085	1,710	43,515	3
															4
	<i>Micrandra</i>	CLU REP	48	10	4	58	19	48	189,760	52	31	72,162	398	32,604	5
		MAN PER	57	10	4	56	18	58	146,689	52	31	72,018	396	75,821	
		PIPE OTU	41	2	3	58	18	66	188,459	27	6	71,908	322	5,120	6
		RDP WAR	28	14	2	53	20	73	65,600	9,501	27	63,727	543	127,204	
NAPO	<i>Hevea</i>	CLU REP	144	86	85	307	8	129	174,009	91,223	19,993	210,898	398	98,087	
		MAN PER	238	74	99	257	6	204	171,342	90,385	21,411	198,213	109	140,084	
		PIPE OTU	160	18	124	280	11	311	124,184	26,845	21,610	232,669	771	223,914	
		RDP WAR	127	112	50	259	3	326	128,082	55,932	19,397	181,463	345	176,403	
	<i>Micrandra</i>	CLU REP	88	19	15	86	5	58	83,965	71,493	2,519	5,226	54	105,584	
		MAN PER	111	18	16	81	5	80	83,933	71,476	2,519	5,196	54	105,891	
		PIPE OTU	65	0	14	87	10	125	40,999	0	1,471	6,482	73	161,750	
		RDP WAR	69	26	12	77	2	126	50,384	987	1,467	6,166	6	184,318	

TABLE 3.16. Percent congruence of function guild assignment between incidence frequency and sequence reads per location (Amazon Conservatory for Tropical Studies Biological Station [NAPO], Allpahuayo-Mishana National Reserve [ALPE], and Jenaro Herrera Research Center [JEHE]), and dataset (Clustered GenBank Representatives [CLU REP], Manual BLAST Percent Based [MAN PER], Pipeline BLASTn OTUs [PIPE OTU] and RdP classifier with Warcup Fungal training set [RDP WAR]).

Dataset	ALPE % Congruence		JEHE % Congruence		NAPO % Congruence		Overall Congruence
	<i>Hevea</i>	<i>Micrandra</i>	<i>Hevea</i>	<i>Micrandra</i>	<i>Hevea</i>	<i>Micrandra</i>	
CLU REP	50%	33%	33%	33%	83%	33%	44%
MAN PER	50%	50%	33%	50%	50%	33%	44%
PIPE OTU	17%	50%	17%	33%	17%	67%	33%
RDP WAR	33%	67%	50%	33%	50%	33%	44%

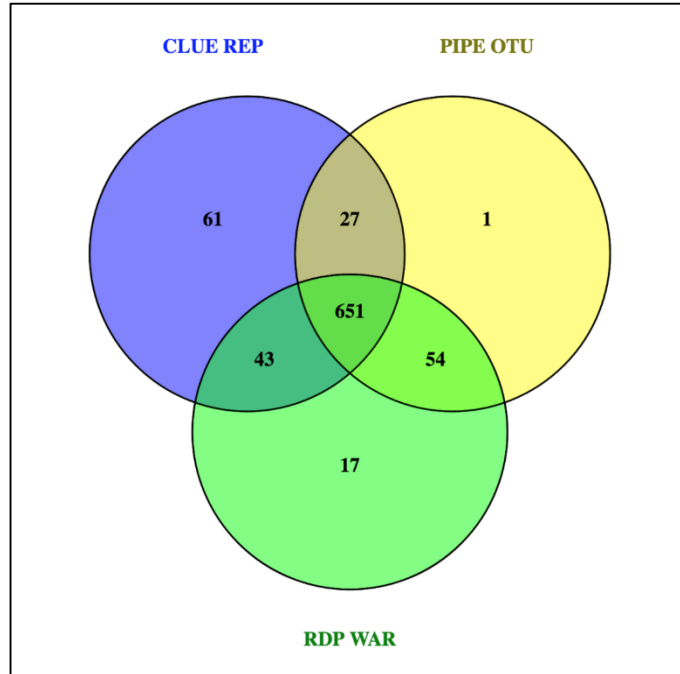


FIGURE 3.1. Venn diagram showing overlap of fungal centroid sequences among datasets curated using three different methods (CLU REP: Clustered GenBank Representatives method, PIPE OTU: Pipeline BLASTn method, RDP WAR: RdP classifier with Warcup Fungal training set method). MAN PER (Manual BLAST Percent Based method), not pictured, had the same centroid sequences as CLU REP.

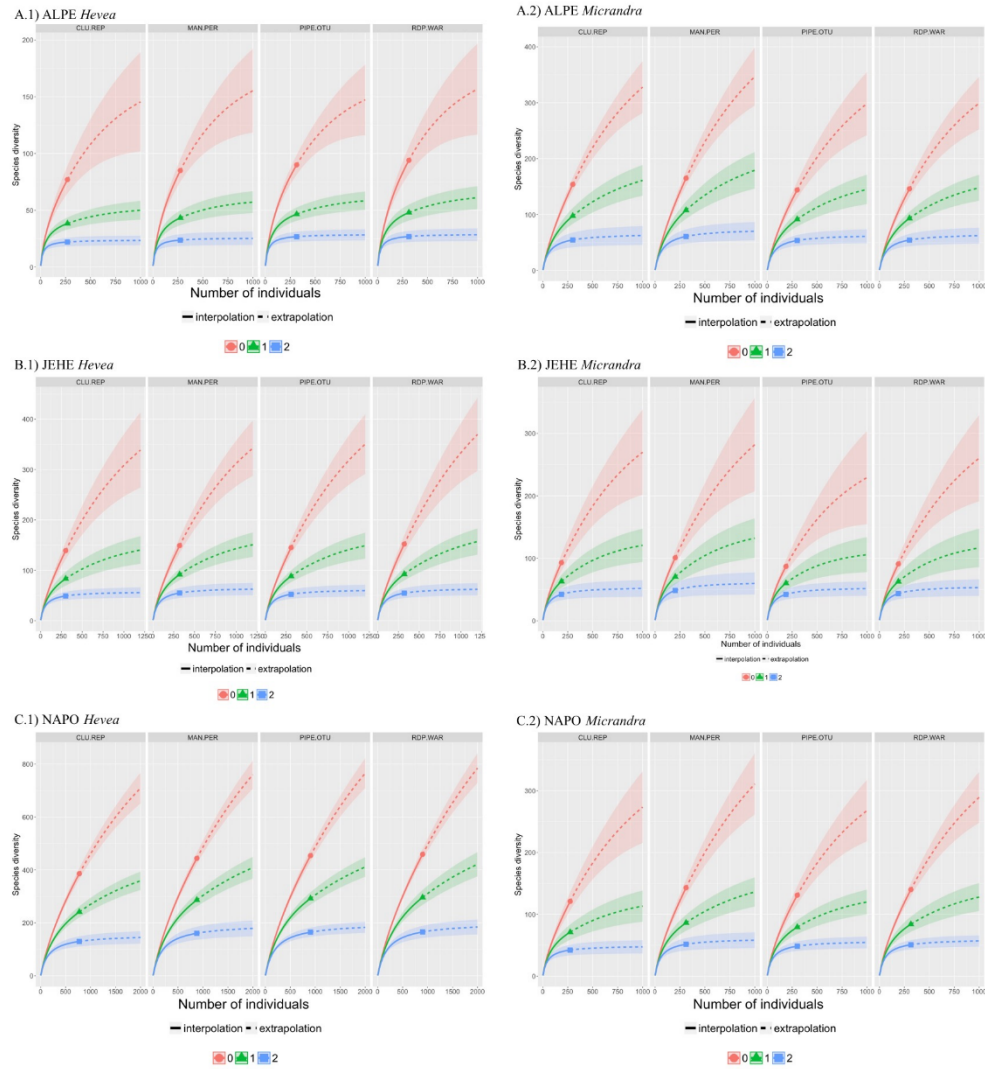


FIGURE 3.2. Species accumulation and diversity curves for fungal communities partitioned by dataset (Clustered GenBank Representatives [CLU REP], Manual BLAST Percent Based [MAN PER], Pipeline BLASTn OTUs [PIPE OTU], and the RdP classifier with Warcup Fungal training set [RDP WAR]) within location (A. Allpahuayo-Mishana National Reserve [ALPE], B. The Jenaro Herrera Research Center [JEHE], and C. the Amazon Conservatory for Tropical Studies Biological Station [NAPO], and host tree genus (1. *Hevea* and 2. *Micrandra*). Species accumulation metrics include richness ($q=0$), Shannon ($q=1$), Simpson's ($q=2$).

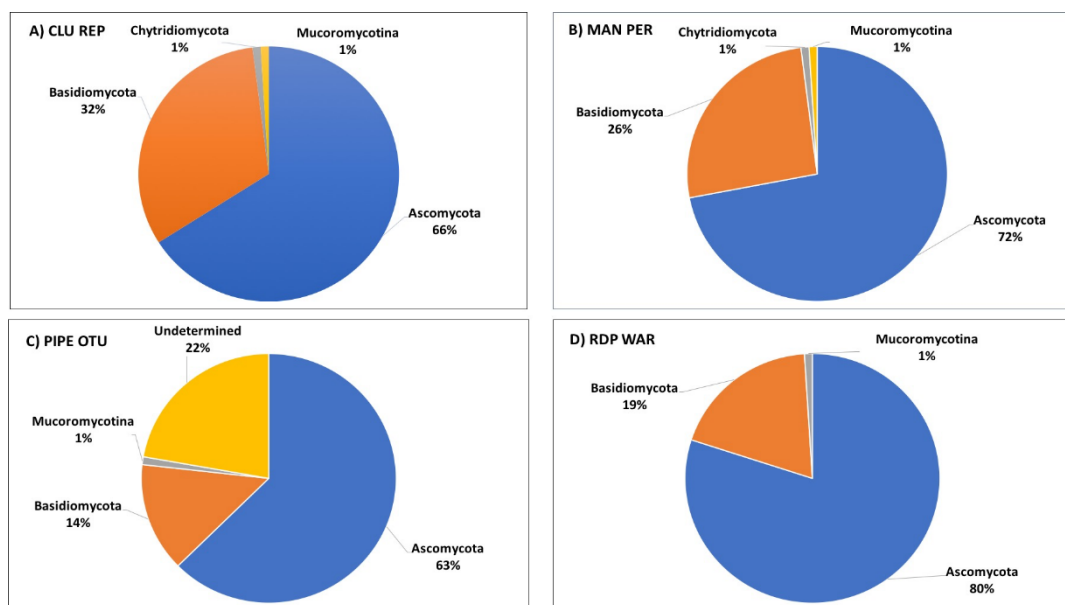


FIGURE 3.3. Distribution of operational taxonomic units (OTUs) at the phylum level for each dataset generated using one of the four OTU classification methods: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn (PIPE OTU), and the Rdp classifier with Warcup Fungal training set (RDP WAR).

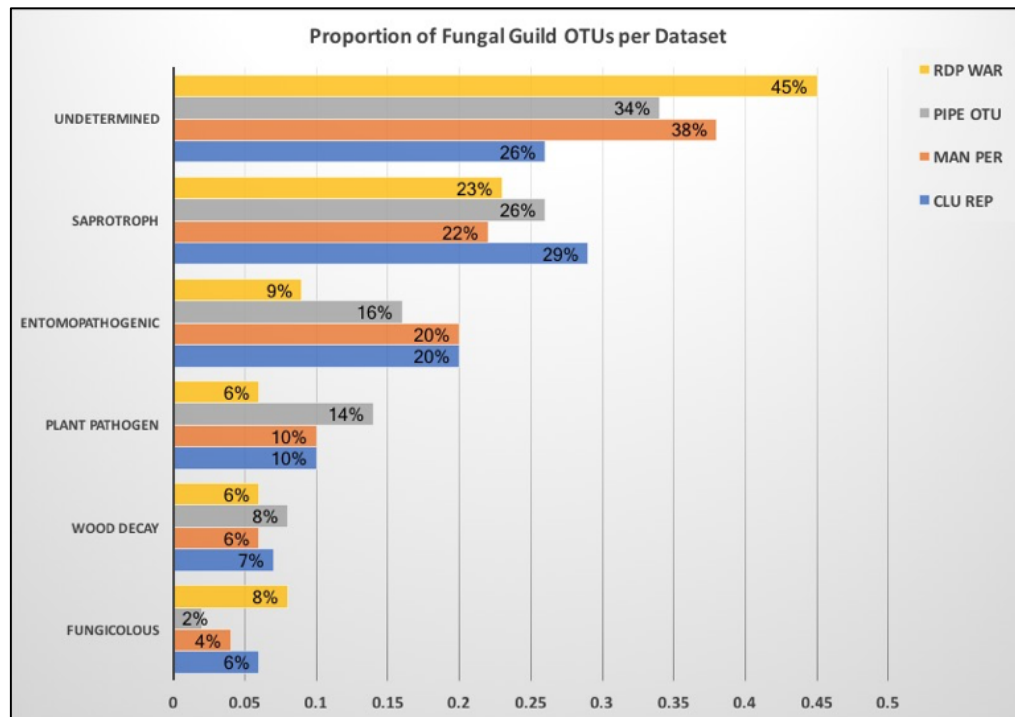


FIGURE 3.4. Proportion of operational taxonomic units (OTUs) assigned to each function guild per dataset: Clustered GenBank Representatives (CLU REP), Manual BLAST Percent Based (MAN PER), Pipeline BLASTn (PIPE OTU), and the RdP classifier with Warcup Fungal training set (RDP WAR).

Appendices

SUPPLEMENTARY TABLE 1.1. Representative isolates obtained in this study, with their corresponding GenBank accession numbers and function guild assignment.

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Absidia species 1</i>	PNB02_2A	pending	Saprotroph
<i>Absidia species 2</i>	PNB13_7C1	pending	Saprotroph
<i>Abundisporus species 1</i>	AMB17_3A	pending	Wood decay
<i>Acaromyces species 1</i>	GPB23_8B	pending	Entomopathogenic
<i>Acremoniopsis species 1</i>	PNB22_1A	pending	Saprotroph
<i>Acremonium species 1</i>	PNB07_7A3	pending	Fungicolous
<i>Acremonium species 2</i>	JMB07_1A1	pending	Fungicolous
<i>Acremonium species 3</i>	PXB21_6B	pending	Fungicolous
<i>Acrocalymma species 1</i>	AHGB04_6B	pending	Fungicolous
<i>Acrodictys species 1</i>	AHGB14_8B	pending	Saprotroph
<i>Agaricomycetes species 1</i>	PNB22_4A	pending	Undetermined
<i>Albonectria species 1</i>	PXB17_6B	pending	Plant pathogen
<i>Alloconiothyrium species 1</i>	AMB12_8A	pending	Saprotroph
<i>Alternaria species 1</i>	AHB25_4A	pending	Plant pathogen
<i>Annulohyphoxylon species 1</i>	AHB05_1B	pending	Wood decay
<i>Annulohyphoxylon species 2</i>	JMB08_7A1	pending	Wood decay
<i>Ascomycota species 1</i>	JMGB06_5A1	pending	Undetermined
<i>Ascomycota species 2</i>	PXB02_1B	pending	Undetermined
<i>Ascomycota species 3</i>	PXB20_6B	pending	Undetermined
<i>Aspergillus species 1</i>	AHB20_9B	pending	Saprotroph
<i>Aspergillus species 2</i>	JHB13_8C	pending	Saprotroph
<i>Aspergillus species 3</i>	AHB20_4B	pending	Saprotroph
<i>Aspergillus species 4</i>	JMB13_2BC	pending	Saprotroph
<i>Aspergillus species 5</i>	JHB08_1A	pending	Saprotroph
<i>Aspergillus species 6</i>	PXB15_2A	pending	Saprotroph
<i>Aspergillus species 7</i>	AHB20_3A	pending	Saprotroph
<i>Aspergillus species 8</i>	PXB18_7A	pending	Saprotroph

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Aspergillus species 9</i>	AHB10_3A	pending	Saprotroph
<i>Beltrania species 1</i>	GPB03_3B	pending	Saprotroph
<i>Beltraniella species 1</i>	AHGB21_9A1	pending	Saprotroph
<i>Beltraniella species 2</i>	JHGB09_6A	pending	Saprotroph
<i>Biatriospora species 2</i>	PXB15_7A	pending	Fungicolous
<i>Bionectriaceae species 1</i>	AHB01_5B	pending	Undetermined
<i>Bionectriaceae species 2</i>	PXB07_1A	pending	Undetermined
<i>Bjerkander species 1</i>	PXB08_5B	pending	Wood decay
<i>Boliniales species 2</i>	AMB21_6A	pending	Undetermined
<i>Botryosphaeriales species 1</i>	JHGB09_1A	pending	Undetermined
<i>Calonectria species 1</i>	JMGB02_4A	pending	Plant pathogen
<i>Castanediella species 1</i>	JHGB10_4A	pending	Saprotroph
<i>Castanediella species 2</i>	JHGB24_6A	pending	Saprotroph
<i>Ceriporia species 1</i>	JHB23_4C1	pending	Wood decay
<i>Ceriporia species 2</i>	AHB01_4A	pending	Wood decay
<i>Chaetosphaeriaceae 1</i>	AHGB16_2A	pending	Undetermined
<i>Chloridium species 1</i>	PXB03_2A	pending	Wood decay
<i>Chrysosporthe species 1</i>	JHGB18_6A	pending	Plant pathogen
<i>Cladosporium species 1</i>	JHB02_4D	pending	Plant pathogen
<i>Cladosporium species 2</i>	JHGB02_6B1A1	pending	Plant pathogen
<i>Cladosporium species 3</i>	JHGB21_1A	pending	Plant pathogen
<i>Cladosporium species 4</i>	AHB17_5A	pending	Plant pathogen
<i>Clavicipitaceae species 1</i>	PNB11_6A	pending	Entomopathogenic
<i>Clonostachys species 1</i>	JMGB02_4B	pending	Saprotroph
<i>Clonostachys species 2</i>	GPB10_3B	pending	Saprotroph
<i>Clonostachys species 3</i>	AHB27_2B	pending	Saprotroph
<i>Clonostachys species 4</i>	PNB12_2A	pending	Saprotroph
<i>Colletotrichum species 1</i>	AMGB14_1B	pending	Plant pathogen
<i>Colletotrichum species 10</i>	AHGB10_3A	pending	Plant pathogen
<i>Colletotrichum species 11</i>	GPB14_2B	pending	Plant pathogen
<i>Colletotrichum species 12</i>	GPB23_1A	pending	Plant pathogen
<i>Colletotrichum species 13</i>	AMGB09_6B	pending	Plant pathogen
<i>Colletotrichum species 14</i>	AHGB15_8A	pending	Plant pathogen
<i>Colletotrichum species 15</i>	AHGB04_2B	pending	Plant pathogen
<i>Colletotrichum species 16</i>	AHGB04_8C	pending	Plant pathogen
<i>Colletotrichum species 17</i>	PNB12_3C2	pending	Plant pathogen

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Colletotrichum species 2</i>	AMGB17_5A1	pending	Plant pathogen
<i>Colletotrichum species 3</i>	AHGB10_8A	pending	Plant pathogen
<i>Colletotrichum species 4</i>	AMGB19_6A	pending	Plant pathogen
<i>Colletotrichum species 5</i>	AHGB02_7A	pending	Plant pathogen
<i>Colletotrichum species 6</i>	AHGB10_5A	pending	Plant pathogen
<i>Colletotrichum species 7</i>	AHGB19_4B	pending	Plant pathogen
<i>Colletotrichum species 8</i>	AHGB10_5C	pending	Plant pathogen
<i>Colletotrichum species 9</i>	AHGB03_5A	pending	Plant pathogen
<i>Conferticium species 1</i>	AMB14_7B	pending	Wood decay
<i>Conoideocrella species 1</i>	AHB21_4B2	pending	Entomopathogenic
<i>Cophinforma species 1</i>	JHGB09_5A	pending	Saprotroph
<i>Coprinellus species 1</i>	PXB01_5B	pending	Saprotroph
<i>Cordyceps species 1</i>	AHB01_1A	pending	Entomopathogenic
<i>Coriolopsis species 1</i>	AHB04_2A	pending	Saprotroph
<i>Corticiales species 1</i>	JHGB12_7B	pending	Undetermined
<i>Corynespora species 1</i>	AHGB22_6A2	pending	Plant pathogen
<i>Cosmospora species 1</i>	AMB03_3A	pending	Fungicolous
<i>Cryphonectriaceae species</i>	JHGB17_5B	pending	Plant pathogen
<i>Curvularia species 1</i>	GPB32_9B	pending	Plant pathogen
<i>Cylindrium species 1</i>	PNB29_2B	pending	Saprotroph
<i>Cyphellophora species 1</i>	AHGB32_3B	pending	Saprotroph
<i>Daedalea species 1</i>	JHGB24_6B	pending	Plant pathogen
<i>Daldinia species 1</i>	PXB05_4A	pending	Saprotroph
<i>Debaryomyces species 1</i>	AHB19_9A	pending	Saprotroph
<i>Dentocorticium species 1</i>	JHGB17_2A	pending	Saprotroph
<i>Diaporthales species 1</i>	PXB20_7A	pending	Undetermined
<i>Diaporthales species 2</i>	JHGB13_7A	pending	Undetermined
<i>Diaporthe species 1</i>	JMGB10_5B1	pending	Plant pathogen
<i>Diaporthe species 10</i>	AHGB26_4A	pending	Plant pathogen
<i>Diaporthe species 11</i>	AHGB02_2A	pending	Plant pathogen
<i>Diaporthe species 12</i>	AHGB02_1A	pending	Plant pathogen
<i>Diaporthe species 13</i>	AHGB25_8B	pending	Plant pathogen
<i>Diaporthe species 14</i>	AHGB04_3A	pending	Plant pathogen
<i>Diaporthe species 15</i>	AHB22_6B	pending	Plant pathogen
<i>Diaporthe species 16</i>	AHGB05_1B	pending	Plant pathogen
<i>Diaporthe species 17</i>	GXB18_7A	pending	Plant pathogen

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Diaporthe species 18</i>	JHGB06_5A1	pending	Plant pathogen
<i>Diaporthe species 2</i>	GXB11_4A	pending	Plant pathogen
<i>Diaporthe species 3</i>	GPB21_9A	pending	Plant pathogen
<i>Diaporthe species 4</i>	AHGB01_1B	pending	Plant pathogen
<i>Diaporthe species 5</i>	JMGB13_6A	pending	Plant pathogen
<i>Diaporthe species 6</i>	GXB21_9A	pending	Plant pathogen
<i>Diaporthe species 7</i>	JMGB14_3A2	pending	Plant pathogen
<i>Diaporthe species 8</i>	GPB18_1A	pending	Plant pathogen
<i>Diaporthe species 9</i>	JMGB04_6B	pending	Plant pathogen
<i>Dothideomycetes species 1</i>	AHGB13_8A	pending	Undetermined
<i>Dothideomycetes species 2</i>	AHB03_4A	pending	Undetermined
<i>Dothideomycetes species 3</i>	JMB08_8A	pending	Undetermined
<i>Dothideomycetes species 4</i>	PNB05_9B	pending	Undetermined
<i>Dothideomycetes species 5</i>	AMB12_5B	pending	Undetermined
<i>Dothideomycetes species 6</i>	AMB23_9B	pending	Undetermined
<i>Dothideomycetes species 7</i>	JHGB05_3A	pending	Undetermined
<i>Dothideomycetes species 8</i>	AHGB03_6B	pending	Undetermined
<i>Endomelanconiopsis</i>	PXB02_3B	pending	Saprotroph
<i>Endomelanconiopsis</i>	JHGB09_1B	pending	Saprotroph
<i>Endomelanconiopsis</i>	AMB09_5A	pending	Saprotroph
<i>Engyodontium species 1</i>	AMB04_2B2	pending	Entomopathogenic
<i>Entonaema species 1</i>	AHB18_5B	pending	Saprotroph
<i>Entonaema species 2</i>	JHGB08_1A	pending	Saprotroph
<i>Eucasphaeria species 1</i>	AHB04_5B	pending	Saprotroph
<i>Eutypella species 1</i>	AHGB29_3B	pending	Plant pathogen
<i>Eutypella species 2</i>	JHGB22_6A2	pending	Plant pathogen
<i>Eutypella species 3</i>	PNB18_5A	pending	Plant pathogen
<i>Exophiala species 1</i>	JHB07_7C	pending	Saprotroph
<i>Fellomyces species 1</i>	PNB12_6A	pending	Fungicolous
<i>Fusarium species 2</i>	GPB13_6A2	pending	Plant pathogen
<i>Fusarium species 3</i>	PNB33_2B	pending	Plant pathogen
<i>Fusarium species 4</i>	JMGB04_3A	pending	Plant pathogen
<i>Fusarium species 5</i>	JMGB14_7B	pending	Plant pathogen
<i>Fusarium species 6</i>	GPB25_1B	pending	Plant pathogen
<i>Fusarium species 7</i>	AMB05_2A	pending	Plant pathogen
<i>Fusicolla species 1</i>	PNB01_2A	pending	Saprotroph

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Ganoderma species 1</i>	PNB15_5B1	pending	Plant pathogen
<i>Ganoderma species 2</i>	PNB22_7	pending	Plant pathogen
<i>Gliomastix species 1</i>	PXB15_8A	pending	Saprotroph
<i>Gliomastix species 2</i>	AMB07_3A	pending	Saprotroph
<i>Gliomastix species 3</i>	AHB04_1B	pending	Saprotroph
<i>Gloeophyllum species 1</i>	AHGB09_1B1	pending	Wood decay
<i>Gongronella species 1</i>	AMB06_6A	pending	Saprotroph
<i>Graphium species 1</i>	PNB14_9B	pending	Saprotroph
<i>Graphium species 2</i>	AHB20_2A	pending	Saprotroph
<i>Gymnopilus species 1</i>	JHGB16_6A	pending	Wood decay
<i>Helotiales species 1</i>	AHGB12_4B2	pending	Undetermined
<i>Helotiales species 2</i>	JMB06_2C	pending	Undetermined
<i>Helotiales species 3</i>	JMB02_5B	pending	Undetermined
<i>Helotiales species 4</i>	PXB21_8A	pending	Undetermined
<i>Herpotrichiellaceae species</i>	AMB17_2A	pending	Undetermined
<i>Herpotrichiellaceae species</i>	JHB02_9B2	pending	Saprotroph
<i>Hortaea species 1</i>	AHB01_2A3	pending	Undetermined
<i>Hyalocladosporiella</i>	AMB23_2A	pending	Plant pathogen
<i>Hyaloscypha species 1</i>	JHB05_5B	pending	Wood decay
<i>Hymenochaete species 1</i>	PXB08_5A	pending	Wood decay
<i>Hyphodontia species 1</i>	PNB27_5A	pending	Wood decay
<i>Hypocreaceae species 1</i>	AMB03_4A	pending	Undetermined
<i>Hypocreales species 1</i>	PXB10_3B	pending	Undetermined
<i>Hypocreales species 2</i>	JHB13_6B	pending	Undetermined
<i>Hypocreales species 4</i>	AHB02_1A	pending	Undetermined
<i>Hypocreales species 5</i>	PXB19_7B	pending	Undetermined
<i>Hypoxyton species 1</i>	PNB11_8C	pending	Saprotroph
<i>Infundibulomyces species 1</i>	JHGB24_7A	pending	Saprotroph
<i>Irpex species 1</i>	JMGB02_5A	pending	Wood decay
<i>Isaria species 1</i>	PXB03_9A	pending	Entomopathogenic
<i>Jattaia species 1</i>	AMB05_9A2A	pending	Wood decay
<i>Kirschsteiniothelia species</i>	AHGB13_8B	pending	Saprotroph
<i>Kirschsteiniothelia species</i>	PNB24_8B	pending	Saprotroph
<i>Kretzschmaria species 1</i>	PNB08_9C1	pending	Wood decay
<i>Lachnum species 1</i>	JHB02_3A2	pending	Saprotroph
<i>Lasiodiplodia species 1</i>	PXB05_3A	pending	Plant pathogen

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Lasiodiplodia species 2</i>	AMB14_1A	pending	Plant pathogen
<i>Lecanicillium species 1</i>	JMB06_8B	pending	Entomopathogenic
<i>Leptodiscella species 1</i>	PNB23_8C	pending	Saprotroph
<i>Letendraea species 1</i>	PNB05_3A	pending	Saprotroph
<i>Lophiostoma species 1</i>	PNB31_2A	pending	Saprotroph
<i>Lophiostoma species 2</i>	PXB22_4C2	pending	Saprotroph
<i>Magnaporthaceae species 1</i>	AHGB19_4BC	pending	Undetermined
<i>Magnaporthaceae species 2</i>	AHGB25_2A	pending	Undetermined
<i>Marasmiellus species 1</i>	JHGB06_2A	pending	Plant pathogen
<i>Metapochonia species 1</i>	JHB10_4A	pending	Entomopathogenic
<i>Metapochonia species 2</i>	AHB21_6A	pending	Entomopathogenic
<i>Mucorales species 1</i>	PXB11_6A	pending	Undetermined
<i>Mucorales species 2</i>	PNB07_6A	pending	Undetermined
<i>Muscodor species 1</i>	JMGB05_7B	pending	Fungicolous
<i>Muscodor species 2</i>	AMGB23_6A	pending	Fungicolous
<i>Muscodor species 3</i>	AHGB10_2B	pending	Fungicolous
<i>Mycena species 1</i>	AHB15_9A1	pending	Saprotroph
<i>Mycoleptodiscus species 1</i>	JHGB12_8A	pending	Plant pathogen
<i>Myrothecium species 1</i>	AHGB03_4A	pending	Plant pathogen
<i>Nectria species 1</i>	AHB02_4A	pending	Plant pathogen
<i>Nectriaceae species 1</i>	AHB12_1C	pending	Undetermined
<i>Nemania species 1</i>	PXB16_9B	pending	Saprotroph
<i>Nemania species 2</i>	JHGB07_5B	pending	Saprotroph
<i>Nemania species 3</i>	JMGB03_2A	pending	Saprotroph
<i>Nemania species 5</i>	AMGB24_8A	pending	Saprotroph
<i>Nemania species 6</i>	AHGB23_4A	pending	Saprotroph
<i>Neocosmospora species 1</i>	AMB09_3B	pending	Fungicolous
<i>Neopestalotiopsis species 1</i>	PNB24_5A	pending	Plant pathogen
<i>Neopestalotiopsis species 2</i>	JHB09_8A	pending	Plant pathogen
<i>Neopestalotiopsis species 3</i>	AHB12_8B	pending	Plant pathogen
<i>Oidiodendron species 1</i>	JMB08_5A	pending	Saprotroph
<i>Oxydothis species 1</i>	JHGB17_3A	pending	Saprotroph
<i>Paecilomyces species 1</i>	PNB19_2A1	pending	Entomopathogenic
<i>Paraconiothyrium species 1</i>	PXB09_4A	pending	Fungicolous
<i>Paraconiothyrium species 2</i>	JMB01_2B	pending	Fungicolous
<i>Paraconiothyrium species 3</i>	PNB10_6A	pending	Fungicolous

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Paraconiothyrium species 4</i>	PNB15_1B1	pending	Fungicolous
<i>Paramyrothecium species 1</i>	AHGB09_6A1	pending	Plant pathogen
<i>Paraphaeosphaeria species</i>	AHB05_2A	pending	Saprotroph
<i>Penicillium species 1</i>	PNB11_7A	pending	Saprotroph
<i>Penicillium species 10</i>	AMB16_2A	pending	Saprotroph
<i>Penicillium species 11</i>	AHB02_6B	pending	Saprotroph
<i>Penicillium species 12</i>	JHB22_8A	pending	Saprotroph
<i>Penicillium species 13</i>	PNB19_6A1	pending	Saprotroph
<i>Penicillium species 14</i>	PNB05_1B	pending	Saprotroph
<i>Penicillium species 15</i>	PNB11_5B	pending	Saprotroph
<i>Penicillium species 16</i>	JHB06_3D1	pending	Saprotroph
<i>Penicillium species 17</i>	PNB13_9A	pending	Saprotroph
<i>Penicillium species 18</i>	PNB01_1B	pending	Saprotroph
<i>Penicillium species 2</i>	PNB18_6A1	pending	Saprotroph
<i>Penicillium species 3</i>	PNB11_4A	pending	Saprotroph
<i>Penicillium species 4</i>	PNB24_1B	pending	Saprotroph
<i>Penicillium species 5</i>	AMB04_1A	pending	Saprotroph
<i>Penicillium species 6</i>	PXB17_9B	pending	Saprotroph
<i>Penicillium species 7</i>	AHB27_1AB	pending	Saprotroph
<i>Penicillium species 8</i>	PXB06_8A	pending	Saprotroph
<i>Penicillium species 9</i>	PXB13_3A	pending	Saprotroph
<i>Peniophora species 1</i>	AMB03_1A	pending	Wood decay
<i>Peniophora species 2</i>	GPB11_7D	pending	Wood decay
<i>Pestalotiopsis species 1</i>	JMB08_3B2	pending	Plant pathogen
<i>Pezicula species 1</i>	PXB14_1B	pending	Plant pathogen
<i>Pezicula species 2</i>	AHGB23_2A2	pending	Plant pathogen
<i>Pezicula species 3</i>	AMGB06_5B	pending	Plant pathogen
<i>Phaeoacremonium species</i>	AMB18_8B2	pending	Plant pathogen
<i>Phaeoacremonium species</i>	AHB24_3A	pending	Plant pathogen
<i>Phaeophlebiopsis species 1</i>	JHGB25_4A	pending	Saprotroph
<i>Phanerochaete species 1</i>	PXB08_9B	pending	Wood decay
<i>Phanerochaete species 2</i>	AMB21_5A	pending	Wood decay
<i>Phialea species 1</i>	AMB18_3A	pending	Saprotroph
<i>Phialemoniopsis species 1</i>	PNB33_3A	pending	Saprotroph
<i>Phialemoniopsis species 2</i>	PXB05_5A	pending	Saprotroph
<i>Phialocephala species 1</i>	AHB14_9A1A	pending	Saprotroph

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Phialocephala species 2</i>	AMB14_7A	pending	Saprotroph
<i>Phlebia species 1</i>	AMB20_4A	pending	Wood decay
<i>Phlebiopsis species 1</i>	JHGB12_6B	pending	Saprotroph
<i>Phlebiopsis species 2</i>	JHB09_6B	pending	Saprotroph
<i>Phyllosticta species 1</i>	AHGB01_6A	pending	Plant pathogen
<i>Phyllosticta species 2</i>	AHGB12_5A	pending	Plant pathogen
<i>Phyllosticta species 3</i>	JHGB13_8A	pending	Plant pathogen
<i>Physisporinus species 1</i>	AHB01_7B	pending	Wood decay
<i>Pleosporales species 1</i>	JMGB08_3A1	pending	Undetermined
<i>Pleosporales species 2</i>	JMB15_9B	pending	Undetermined
<i>Pleosporales species 3</i>	AMB08_2B	pending	Undetermined
<i>Pleosporales species 4</i>	AHB18_9B	pending	Undetermined
<i>Pleosporales species 5</i>	AHB11_2A1A	pending	Undetermined
<i>Pleurostoma species 1</i>	AMB01_6A	pending	Saprotroph
<i>Polyporales species 1</i>	PXB17_2A	pending	Undetermined
<i>Polyporales species 2</i>	PNB28_5A	pending	Undetermined
<i>Pseudallescheria species 1</i>	JMB10_5B	pending	Saprotroph
<i>Pseudofusicoccum species</i>	AHGB12_2B	pending	Plant pathogen
<i>Pseudopezalotiopsis</i>	GPB03_6B	pending	Plant pathogen
<i>Psilocybe species 1</i>	AHB13_3A1	pending	Saprotroph
<i>Purpureocillium species 1</i>	PXB04_1B	pending	Entomopathogenic
<i>Purpureocillium species 2</i>	AHB10_9A	pending	Entomopathogenic
<i>Pyrenochaetopsis species 1</i>	AHB10_7A	pending	Saprotroph
<i>Rigidoporus species 1</i>	AHGB17_3B	pending	Wood decay
<i>Roussoella species 1</i>	PNB08_6A	pending	Saprotroph
<i>Thyridariaceae species 1</i>	PNB16_5A1	pending	Saprotroph
<i>Thyridariaceae species 2</i>	PXB15_4B	pending	Saprotroph
<i>Thyridariaceae species 3</i>	AHB24_2B	pending	Saprotroph
<i>Sarocladium species 1</i>	AHB01_8B	pending	Saprotroph
<i>Schizophyllum species 1</i>	AHGB05_6A	pending	Wood decay
<i>Scopuloides species 1</i>	PNB08_8A2	pending	Wood decay
<i>Scytalidium species 1</i>	PXB08_9A	pending	Fungicolous
<i>Scytalidium species 2</i>	AMB15_1A	pending	Fungicolous
<i>Scytalidium species 3</i>	JHB14_8A	pending	Fungicolous
<i>Scytalidium species 4</i>	PNB27_4C_1	pending	Fungicolous
<i>Septobasidium species 1</i>	PNB30_8B	pending	Entomopathogenic

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Sistotrema species 1</i>	AHGB05_5B	pending	Mycorrhizal
<i>Sistotrema species 2</i>	PNB21_8	pending	Mycorrhizal
<i>Sistotremastrum species 1</i>	AHB20_7A2	pending	Saprotroph
<i>Sordariales species 1</i>	JHGB25_5B	pending	Undetermined
<i>Sordariales species 2</i>	JMGB03_6B1	pending	Undetermined
<i>Sordariomycetes species 1</i>	JHGB15_7B	pending	Undetermined
<i>Sordariomycetes species 10</i>	JHB04_2A	pending	Undetermined
<i>Sordariomycetes species 2</i>	JHGB16_1A	pending	Undetermined
<i>Sordariomycetes species 3</i>	JHGB02_5B	pending	Undetermined
<i>Sordariomycetes species 5</i>	JHGB10_2A	pending	Undetermined
<i>Sordariomycetes species 6</i>	JHGB06_3B	pending	Undetermined
<i>Sphaeronaemella species 1</i>	PXB04_2B	pending	Saprotroph
<i>Stachybotryaceae species 1</i>	AHB27_4F	pending	Undetermined
<i>Stereum species 1</i>	AMB05_6B	pending	Saprotroph
<i>Stereum species 2</i>	JHGB02_3A	pending	Saprotroph
<i>Talaromyces species 1</i>	PNB11_5A1	pending	Saprotroph
<i>Talaromyces species 2</i>	PNB17_5A2	pending	Saprotroph
<i>Talaromyces species 3</i>	PXB20_3A	pending	Saprotroph
<i>Talaromyces species 4</i>	AHB30_8A	pending	Saprotroph
<i>Talaromyces species 5</i>	JHB10_8A	pending	Saprotroph
<i>Talaromyces species 6</i>	PXB08_8A	pending	Saprotroph
<i>Talaromyces species 7</i>	AHB27_4G	pending	Saprotroph
<i>Thozetella species 1</i>	JMGB15_5A	pending	Saprotroph
<i>Thozetella species 2</i>	JMGB06_7A1	pending	Saprotroph
<i>Tinctoporellus species 1</i>	PNB27_6A	pending	Wood decay
<i>Tinctoporellus species 2</i>	JHGB01_1A	pending	Wood decay
<i>Tolypocladium species 1</i>	PNB01_1A1	pending	Entomopathogenic
<i>Tolypocladium species 2</i>	AHB21_5B	pending	Entomopathogenic
<i>Tolypocladium species 3</i>	PNB17_7A1	pending	Entomopathogenic
<i>Tolypocladium species 4</i>	AHB13_7A	pending	Entomopathogenic
<i>Tolypocladium species 5</i>	JHB08_3B	pending	Entomopathogenic
<i>Trametes species 1</i>	AHB23_1A	pending	Wood decay
<i>Trematosphaeriaceae</i>	AHGB26_2B	pending	Undetermined
<i>Tremellales species 1</i>	PNB09_9A	pending	Undetermined
<i>Trichocomaceae species 1</i>	PNB28_4A	pending	Saprotroph
<i>Trichoderma species 1</i>	AMB08_8B	pending	Fungicolous

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Trichoderma species 10</i>	PXB02_8B	pending	Fungicolous
<i>Trichoderma species 11</i>	AHB02_2A	pending	Fungicolous
<i>Trichoderma species 12</i>	AHB14_3B	pending	Fungicolous
<i>Trichoderma species 13</i>	PNB09_5A	pending	Fungicolous
<i>Trichoderma species 15</i>	PXB01_8B	pending	Fungicolous
<i>Trichoderma species 16</i>	PNB03_2A	pending	Fungicolous
<i>Trichoderma species 17</i>	PXB09_9B	pending	Fungicolous
<i>Trichoderma species 18</i>	AMB08_2A	pending	Fungicolous
<i>Trichoderma species 19</i>	PNB14_8A	pending	Fungicolous
<i>Trichoderma species 2</i>	AHB15_1A	pending	Fungicolous
<i>Trichoderma species 20</i>	AMB22_3A1A	pending	Fungicolous
<i>Trichoderma species 21</i>	AHB03_3A	pending	Fungicolous
<i>Trichoderma species 22</i>	PXB06_1A	pending	Fungicolous
<i>Trichoderma species 23</i>	AHB05_3B2	pending	Fungicolous
<i>Trichoderma species 24</i>	AMB11_7A	pending	Fungicolous
<i>Trichoderma species 3</i>	PNB10_7A2	pending	Fungicolous
<i>Trichoderma species 4</i>	PNB15_6B	pending	Fungicolous
<i>Trichoderma species 5</i>	JHB08_2A	pending	Fungicolous
<i>Trichoderma species 6</i>	PNB12_1A1	pending	Fungicolous
<i>Trichoderma species 7</i>	AMB17_6A	pending	Fungicolous
<i>Trichoderma species 8</i>	JMB03_8B	pending	Fungicolous
<i>Trichoderma species 9</i>	AHB24_4B	pending	Fungicolous
<i>Umbelopsis species 1</i>	AHB27_3F2	pending	Saprotroph
<i>Verticillium species 1</i>	PXB21_4A	pending	Nematicidal
<i>Virgaria species 1</i>	PNB13_4A1	pending	Saprotroph
<i>Wardomyces species 1</i>	AHB16_5A	pending	Saprotroph
<i>Xenoacremonium species 1</i>	AHB27_3B	pending	Saprotroph
<i>Xylaria species 1</i>	JMGB05_9B	pending	Saprotroph
<i>Xylaria species 4</i>	GPB18_4A	pending	Saprotroph
<i>Xylaria species 5</i>	PXB08_4A	pending	Saprotroph
<i>Xylaria species 6</i>	JHGB20_9	pending	Saprotroph
<i>Xylaria species 7</i>	AHGB04_1A	pending	Saprotroph
<i>Xylaria species 8</i>	GPB06_4C	pending	Saprotroph
<i>Xylariaceae species 1</i>	PXB19_5A	pending	Saprotroph
<i>Anungitea species 1</i>	JHGB05_3B	pending	Undetermined
<i>Xylariales species 2</i>	PNB02_6D	pending	Undetermined

Taxonomic assignment	Representative isolate	GenBank no.	Function guild assignment
<i>Sordariomycetes species 4</i>	PNB10_2A	pending	Undetermined
<i>Sordariomycetes species 7</i>	JHGB23_7B	pending	Undetermined
<i>Xylomelasma species 1</i>	AMB02_6A	pending	Undetermined
<i>Xylona species 1</i>	PNB16_8B	pending	Undetermined
<i>Zasmidium species 1</i>	AHB32_8A	pending	Saprotroph

SUPPLEMENTARY TABLE 2.1. The number of characters per locus, as well as the nucleotide substitution models used in this study.

Alignment properties such as percent gaps, number of missing data, number of conserved or variable characters, number of parsimony informative or singleton characters, are also provided.

Genes/loci	ITS	TEF	TUB	HIS
Characters included in analysis (with gaps)	507	396	538	526
Conserved characters	303	79	183	279
Variable characters	193	300	196	209
Parsimony informative (PI)	142	252	166	168
Singleton (non PI)	51	42	30	39
Percent gaps in analysis	13%	29%	12%	19%
Number of missing data	0	1	2	15
Nucleotide substitution models	GTR+G+I	HKY+I+G	HKY+I+G	HKY+I+G

SUPPLEMENTARY TABLE 3.1. Operational taxonomic unit (OTU) taxonomic and function guild assignments using Pipeline BLASTn OTUs (PIPE OTU) method.

OTU	PIPE OTU Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment	Chimeric sequence (x) or real (-)
otu_389	<i>Absidia</i>	1	50	Saprotroph	-
otu_248	<i>Acremonium antarcticum</i>	3	95	Fungicolous	-
otu_27	<i>Acremonium antarcticum</i>	8	26649	Fungicolous	-
otu_468	<i>Acremonium citrinum</i>	1	15	Fungicolous	-
otu_384	<i>Acremonium persicinum</i>	1	18	Fungicolous	-
otu_607	<i>Acremonium persicinum</i>	2	17	Fungicolous	-
otu_204	<i>Acremonium polychromum</i>	2	4	Saprotroph	-
otu_284	<i>Acremonium polychromum</i>	1	61	Fungicolous	-
otu_447	<i>Acremonium polychromum</i>	1	16	Fungicolous	-
otu_716	<i>Acremonium psammosporum</i>	1	4	Fungicolous	-
otu_722	<i>Acremonium varicolor</i>	1	32	Fungicolous	-
otu_431	<i>Agaricales species 1</i>	1	37	Undetermined	-
otu_640	<i>Agrocybe erebia</i>	1	8	Saprotroph	-
otu_789	<i>Alternaria alternata</i>	1	5	Plant pathogen	-
otu_484	<i>Antrodia alpina</i>	1	15	Wood decay	-
otu_337	<i>Ascomycota species 1</i>	1	52	Undetermined	-
otu_695	<i>Ascomycota species 2</i>	1	8	Undetermined	-
otu_853	<i>Ascomycota species 3</i>	1	5	Undetermined	-
otu_340	<i>Aspergillus penicillioides</i>	1	29	Saprotroph	-
otu_211	<i>Athelia decipiens</i>	1	94	Plant pathogen	-
otu_305	<i>Basidiobolus species 1</i>	1	91	Saprotroph	-
otu_167	<i>Basidiomycete species 1</i>	8	445	Undetermined	-
otu_1028	<i>Basidiomycota species 1</i>	3	14	Undetermined	-
otu_329	<i>Basidiomycota species 2</i>	9	243	Undetermined	-
otu_130	<i>Basidiomycota species 3</i>	1	582	Undetermined	-
otu_400	<i>Beltrania species 1</i>	1	23	Saprotroph	-
otu_809	<i>Beltrania pseudorhombica</i>	1	5	Saprotroph	-
otu_540	<i>Betamyces species</i>	1	13	Plant pathogen	-
otu_726	<i>Blastobotrys nivea</i>	1	13	Saprotroph	-
otu_61	<i>Buckleyzyma armeniaca</i>	1	1136	Undetermined	-
otu_453	<i>Bullera alba</i>	1	18	Saprotroph	-
otu_1122	<i>Campylocarpon fasciculare</i>	1	2	Plant pathogen	-

otu_429	<i>Campylocarpon fasciculare</i>	1	12	Plant pathogen	-
otu_57	<i>Campylocarpon fasciculare</i>	4	1744	Plant pathogen	-
otu_671	<i>Campylocarpon fasciculare</i>	1	8	Plant pathogen	-
otu_1206	<i>Candida ascalaphidarum</i>	1	2	Saprotroph	x
otu_1079	<i>Candida mucifera</i>	1	2	Saprotroph	-
otu_44	<i>Candida mucifera</i>	1	2366	Saprotroph	-
otu_436	<i>Candida oceani</i>	1	13	Saprotroph	-
otu_4	<i>Candida temnochilae</i>	20	106	Saprotroph	-
otu_693	<i>Candida zeylanoides</i>	1	6	Saprotroph	-
otu_596	<i>Ceriporia species 1</i>	1	10	Wood decay	-
otu_302	<i>Ceriporia spissa</i>	4	66	Wood decay	-
otu_467	<i>Chaetothyriales species 1</i>	1	20	Undetermined	-
otu_966	<i>Chaetothyriales species 2</i>	1	2	Undetermined	-
otu_703	<i>Cladophialophora species 1</i>	1	4	Saprotroph	-
otu_704	<i>Cladophialophora species 2</i>	1	4	Saprotroph	-
otu_54	<i>Clonostachys species 1</i>	3	1507	Saprotroph	-
otu_1101	<i>Clonostachys byssicola</i>	1	2	Saprotroph	-
otu_111	<i>Clonostachys byssicola</i>	9	1480	Saprotroph	-
otu_1159	<i>Clonostachys byssicola</i>	1	4	Saprotroph	-
otu_561	<i>Clonostachys byssicola</i>	2	24	Saprotroph	-
otu_672	<i>Clonostachys byssicola</i>	1	7	Saprotroph	-
otu_891	<i>Clonostachys byssicola</i>	1	11	Saprotroph	-
otu_301	<i>Clonostachys divergens</i>	2	50	Saprotroph	-
otu_1160	<i>Clonostachys phyllophila</i>	1	2	Saprotroph	-
otu_1171	<i>Clonostachys phyllophila</i>	1	2	Saprotroph	-
otu_1158	<i>Clonostachys pityrodes</i>	1	8	Saprotroph	-
otu_1233	<i>Clonostachys pityrodes</i>	1	2	Saprotroph	-
otu_1234	<i>Clonostachys pityrodes</i>	1	2	Saprotroph	-
otu_581	<i>Clonostachys pityrodes</i>	1	22	Saprotroph	-
otu_1199	<i>Clonostachys rosea</i>	1	2	Saprotroph	-
otu_1200	<i>Clonostachys rosea</i>	1	2	Saprotroph	x
otu_1204	<i>Clonostachys rosea</i>	1	2	Saprotroph	-
otu_1207	<i>Clonostachys rosea</i>	1	2	Saprotroph	x
otu_1208	<i>Clonostachys rosea</i>	1	2	Saprotroph	-
otu_129	<i>Clonostachys rosea</i>	2	658	Saprotroph	-
otu_432	<i>Clonostachys rosea</i>	1	21	Saprotroph	-
otu_567	<i>Clonostachys rosea</i>	1	12	Saprotroph	x
otu_617	<i>Clonostachys rosea</i>	2	15	Saprotroph	-
otu_621	<i>Clonostachys rosea</i>	5	19	Saprotroph	-

otu_887	<i>Clonostachys rosea</i>	1	3	Saprotroph	-
otu_894	<i>Clonostachys rosea</i>	1	3	Saprotroph	x
otu_895	<i>Clonostachys rosea</i>	1	6	Saprotroph	-
otu_913	<i>Clonostachys rosea</i>	4	40	Saprotroph	x
otu_1244	<i>Coralloidiomyces digitatus</i>	1	2	Undetermined	-
otu_735	<i>Corallomycetella repens</i>	1	9	Plant pathogen	-
otu_1149	<i>Cordyceps pseudomilitaris</i>	1	2	Entomopathogenic	-
otu_877	<i>Cordyceps pseudomilitaris</i>	1	6	Entomopathogenic	-
otu_1245	<i>Crepidotus epibryus</i>	1	2	Wood decay	-
otu_404	<i>Cylindrobasidium laeve</i>	1	17	Undetermined	-
otu_788	<i>Cyphellophora europaea</i>	1	10	Saprotroph	-
otu_702	<i>Cyphellophora olivacea</i>	1	7	Undetermined	-
otu_1198	<i>Debaryomyces species 1</i>	1	18	Saprotroph	-
otu_208	<i>Debaryomyces species 2</i>	4	235	Saprotroph	-
otu_160	<i>Debaryomyces species 3</i>	2	224	Saprotroph	-
otu_108	<i>Debaryomyces hansenii</i>	1	494	Saprotroph	-
otu_1118	<i>Debaryomyces hansenii</i>	1	4	Saprotroph	-
otu_120	<i>Debaryomyces hansenii</i>	10	1662	Saprotroph	-
otu_1212	<i>Debaryomyces hansenii</i>	1	2	Saprotroph	-
otu_2	<i>Debaryomyces hansenii</i>	72	255672	Saprotroph	-
otu_405	<i>Debaryomyces hansenii</i>	5	111	Saprotroph	-
otu_530	<i>Debaryomyces hansenii</i>	3	60	Saprotroph	-
otu_659	<i>Debaryomyces hansenii</i>	2	11	Saprotroph	-
otu_669	<i>Debaryomyces hansenii</i>	3	16	Saprotroph	-
otu_751	<i>Debaryomyces hansenii</i>	1	11	Saprotroph	-
otu_18	<i>Debaryomyces nepalensis</i>	28	36255	Saprotroph	-
otu_668	<i>Debaryomyces nepalensis</i>	6	113	Saprotroph	-
otu_862	<i>Debaryomyces nepalensis</i>	30	2147	Saprotroph	-
otu_905	<i>Debaryomyces nepalensis</i>	3	10	Saprotroph	-
otu_715	<i>Deconica species 1</i>	1	6	Saprotroph	-
otu_154	<i>Dendrophora albobadia</i>	2	196	Saprotroph	-
otu_970	<i>Dothideomycetes species 1</i>	1	2	Undetermined	x
otu_485	<i>Endophytic basidiomycete</i>	1	23	Undetermined	-
otu_308	<i>Entomocorticium species 1</i>	1	46	Entomopathogenic	-
otu_175	<i>Exophiala species 1</i>	3	215	Saprotroph	-
otu_1162	<i>Fibroporia gossypium</i>	1	2	Wood decay	-
otu_161	<i>Filobasidium magnum</i>	1	296	Saprotroph	-
otu_910	<i>Fomitiporia species 1</i>	1	3	Plant pathogen	-
otu_1036	<i>Fungal species 1</i>	1	2	Undetermined	-

otu_1067	<i>Fungal species 2</i>	1	4	Undetermined	-
otu_1105	<i>Fungal species 3</i>	1	2	Undetermined	-
otu_1120	<i>Fungal species 4</i>	1	2	Undetermined	-
otu_1126	<i>Fungal species 5</i>	1	4	Undetermined	-
otu_1167	<i>Fungal species 6</i>	1	4	Undetermined	-
otu_1228	<i>Fungal species 7</i>	1	4	Undetermined	-
otu_168	<i>Fungal species 8</i>	1	351	Undetermined	-
otu_178	<i>Fungal species 9</i>	1	345	Undetermined	-
otu_195	<i>Fungal species 10</i>	1	112	Undetermined	-
otu_23	<i>Fungal species 11</i>	12	22585	Undetermined	-
otu_288	<i>Fungal species 12</i>	1	13	Undetermined	-
otu_410	<i>Fungal species 13</i>	2	74	Undetermined	-
otu_534	<i>Fungal species 14</i>	1	27	Undetermined	-
otu_604	<i>Fungal species 15</i>	1	9	Undetermined	-
otu_657	<i>Fungal species 16</i>	1	21	Undetermined	-
otu_661	<i>Fungal species 17</i>	1	10	Undetermined	x
otu_72	<i>Fungal species 18</i>	2	208	Undetermined	-
otu_731	<i>Fungal species 19</i>	2	204	Undetermined	-
otu_733	<i>Fungal species 20</i>	2	25	Undetermined	-
otu_906	<i>Fungal species 21</i>	1	5	Undetermined	-
otu_742	<i>Fungal endophyte species 1</i>	1	14	Undetermined	-
otu_258	<i>Fusarium species 1</i>	4	205	Plant pathogen	-
otu_748	<i>Fusarium ambrosium</i>	1	9	Plant pathogen	-
otu_417	<i>Fusarium species 2</i>	1	28	Plant pathogen	-
otu_1128	<i>Fusarium decemcellulare</i>	1	2	Plant pathogen	-
otu_1143	<i>Fusarium decemcellulare</i>	1	2	Plant pathogen	-
otu_1121	<i>Fusarium nematophilum</i>	1	2	Plant pathogen	-
otu_864	<i>Fusarium nematophilum</i>	1	7	Plant pathogen	-
otu_1057	<i>Fusarium solani</i>	1	2	Plant pathogen	-
otu_1097	<i>Fusarium solani</i>	1	2	Plant pathogen	-
otu_1102	<i>Fusarium solani</i>	1	2	Plant pathogen	-
otu_1178	<i>Fusarium solani</i>	1	8	Plant pathogen	-
otu_1194	<i>Fusarium solani</i>	1	4	Plant pathogen	-
otu_188	<i>Fusarium solani</i>	3	151	Plant pathogen	-
otu_26	<i>Fusarium solani</i>	12	9913	Plant pathogen	-
otu_359	<i>Fusarium solani</i>	1	23	Plant pathogen	-
otu_523	<i>Fusarium solani</i>	1	10	Plant pathogen	-
otu_564	<i>Fusarium solani</i>	1	9	Plant pathogen	-
otu_886	<i>Fusarium solani</i>	1	3	Plant pathogen	-

otu_908	<i>Fuscoporia species 1</i>	1	5	Saprotroph	-
otu_294	<i>Fuscoporia ferruginosa</i>	1	49	Saprotroph	-
otu_320	<i>Fuscoporia gilva</i>	1	44	Saprotroph	-
otu_1072	<i>Fusicolla acetilerea</i>	3	6	Plant pathogen	x
otu_1081	<i>Fusicolla acetilerea</i>	1	2	Plant pathogen	-
otu_1094	<i>Fusicolla acetilerea</i>	1	2	Plant pathogen	-
otu_1156	<i>Fusicolla acetilerea</i>	1	2	Plant pathogen	-
otu_1181	<i>Fusicolla acetilerea</i>	1	4	Plant pathogen	-
otu_213	<i>Fusicolla acetilerea</i>	3	79	Plant pathogen	-
otu_368	<i>Fusicolla acetilerea</i>	5	78	Plant pathogen	-
otu_411	<i>Fusicolla acetilerea</i>	4	112	Plant pathogen	-
otu_522	<i>Fusicolla acetilerea</i>	5	38	Plant pathogen	-
otu_611	<i>Fusicolla acetilerea</i>	1	13	Plant pathogen	-
otu_67	<i>Fusicolla acetilerea</i>	11	1325	Plant pathogen	-
otu_737	<i>Fusicolla acetilerea</i>	1	6	Plant pathogen	-
otu_854	<i>Fusicolla acetilerea</i>	2	9	Plant pathogen	-
otu_855	<i>Fusicolla acetilerea</i>	1	6	Plant pathogen	-
otu_874	<i>Fusicolla acetilerea</i>	1	3	Plant pathogen	-
otu_939	<i>Fusicolla acetilerea</i>	1	2	Plant pathogen	-
otu_944	<i>Ganoderma applanatum</i>	1	2	Plant pathogen	-
otu_269	<i>Gelatoporia pannocincta</i>	1	62	Wood decay	-
otu_1076	<i>Geosmithia species 1</i>	1	2	Saprotroph	-
otu_1189	<i>Geosmithia species 2</i>	1	2	Saprotroph	-
otu_758	<i>Geosmithia species 3</i>	4	18	Saprotroph	-
otu_1148	<i>Gliocephalotrichum species 1</i>	1	2	Saprotroph	-
otu_670	<i>Gliomastix murorum</i>	1	7	Saprotroph	-
otu_965	<i>Gliomastix murorum</i>	1	2	Saprotroph	-
otu_1027	<i>Gliomastix polychroma</i>	2	22	Saprotroph	-
otu_153	<i>Gliomastix polychroma</i>	6	3216	Saprotroph	-
otu_212	<i>Gliomastix polychroma</i>	4	134	Saprotroph	-
otu_214	<i>Gliomastix polychroma</i>	1	193	Saprotroph	-
otu_226	<i>Gliomastix polychroma</i>	1	96	Saprotroph	-
otu_28	<i>Gliomastix polychroma</i>	20	26018	Saprotroph	-
otu_300	<i>Gliomastix polychroma</i>	1	50	Saprotroph	-
otu_562	<i>Gliomastix polychroma</i>	1	12	Saprotroph	-
otu_713	<i>Gliomastix polychroma</i>	2	12	Saprotroph	-
otu_734	<i>Gliomastix polychroma</i>	1	7	Saprotroph	-
otu_850	<i>Gliomastix polychroma</i>	1	7	Saprotroph	-
otu_872	<i>Gliomastix polychroma</i>	1	3	Saprotroph	-

otu_907	<i>Gliomastix polychroma</i>	1	3	Saprotroph	-
otu_1139	<i>Gloeotinia temulenta</i>	1	2	Saprotroph	-
otu_1141	<i>Gloeotinia temulenta</i>	1	2	Saprotroph	-
otu_1175	<i>Gloeotinia temulenta</i>	1	2	Saprotroph	-
otu_118	<i>Gloeotinia temulenta</i>	2	775	Saprotroph	-
otu_1230	<i>Gloeotinia temulenta</i>	1	2	Saprotroph	-
otu_31	<i>Gloeotinia temulenta</i>	11	25806	Saprotroph	-
otu_498	<i>Gloeotinia temulenta</i>	1	37	Saprotroph	-
otu_740	<i>Gloeotinia temulenta</i>	1	6	Saprotroph	-
otu_367	<i>Gongronella butleri</i>	3	100	Saprotroph	-
otu_975	<i>Gongronella butleri</i>	1	2	Saprotroph	-
otu_705	<i>Grandinia species 1</i>	2	9	Plant Pathogen	-
otu_375	<i>Granulobasidium vellereum</i>	1	19	Wood decay	-
otu_1080	<i>Graphium penicillioides</i>	1	4	Saprotroph	-
otu_1082	<i>Graphium penicillioides</i>	1	2	Saprotroph	-
otu_192	<i>Graphium penicillioides</i>	2	133	Saprotroph	-
otu_326	<i>Graphium penicillioides</i>	2	49	Saprotroph	-
otu_614	<i>Graphium penicillioides</i>	1	6	Saprotroph	-
otu_552	<i>Gymnopilus species 1</i>	2	15	Wood decay	-
otu_310	<i>Gymnopilus picreus</i>	1	42	Wood decay	-
otu_964	<i>Gymnopus species 1</i>	1	2	Saprotroph	-
otu_943	<i>Gymnopus dichrous</i>	1	2	Saprotroph	-
otu_927	<i>Gymnopus melanopus</i>	1	2	Saprotroph	-
otu_312	<i>Hirsutella species 1</i>	1	48	Entomopathogenic	-
otu_786	<i>Hirsutella species 2</i>	1	3	Entomopathogenic	-
otu_712	<i>Hymenochaete corrugata</i>	1	7	Wood decay	-
otu_1031	<i>Hymenochaete senatoumbrina</i>	1	2	Wood decay	-
otu_268	<i>Hyphodermella rosae</i>	3	82	Saprotroph	-
otu_666	<i>Hyphodontia crustosa</i>	1	12	Saprotroph	-
otu_278	<i>Hyphodontia flavipora</i>	5	87	Saprotroph	-
otu_163	<i>Hyphodontia nespori</i>	5	253	Saprotroph	-
otu_590	<i>Hyphodontia rimosissima</i>	1	9	Saprotroph	-
otu_1010	<i>Hypholoma capnoides</i>	1	4	Wood decay	-
otu_1022	<i>Hypocreales species 1</i>	3	20	Undetermined	x
otu_1071	<i>Hypocreales species 2</i>	1	2	Undetermined	-
otu_1087	<i>Hypocreales species 3</i>	2	4	Undetermined	-
otu_1111	<i>Hypocreales species 4</i>	1	2	Undetermined	-
otu_1151	<i>Hypocreales species 5</i>	1	2	Undetermined	-
otu_116	<i>Hypocreales species 6</i>	9	3752	Undetermined	-

otu_1163	<i>Hypocreales species 7</i>	1	2	Undetermined	-
otu_1169	<i>Hypocreales species 8</i>	1	2	Undetermined	-
otu_1176	<i>Hypocreales species 9</i>	1	2	Undetermined	-
otu_1197	<i>Hypocreales species 10</i>	1	4	Undetermined	x
otu_1201	<i>Hypocreales species 11</i>	2	8	Undetermined	x
otu_128	<i>Hypocreales species 12</i>	3	542	Undetermined	-
otu_150	<i>Hypocreales species 13</i>	4	296	Undetermined	-
otu_186	<i>Hypocreales species 14</i>	1	127	Undetermined	-
otu_236	<i>Hypocreales species 15</i>	9	632	Undetermined	-
otu_304	<i>Hypocreales species 16</i>	1	74	Undetermined	-
otu_371	<i>Hypocreales species 17</i>	9	164	Undetermined	-
otu_50	<i>Hypocreales species 18</i>	3	1936	Undetermined	-
otu_529	<i>Hypocreales species 19</i>	1	8	Undetermined	-
otu_578	<i>Hypocreales species 20</i>	3	19	Undetermined	-
otu_645	<i>Hypocreales species 21</i>	3	11	Undetermined	-
otu_665	<i>Hypocreales species 22</i>	1	10	Undetermined	-
otu_675	<i>Hypocreales species 23</i>	1	17	Undetermined	-
otu_682	<i>Hypocreales species 24</i>	4	31	Undetermined	x
otu_725	<i>Hypocreales species 25</i>	1	6	Undetermined	x
otu_744	<i>Hypocreales species 26</i>	1	17	Undetermined	-
otu_750	<i>Hypocreales species 27</i>	2	20	Undetermined	x
otu_755	<i>Hypocreales species 28</i>	1	8	Undetermined	-
otu_8	<i>Hypocreales species 29</i>	51	150142	Undetermined	-
otu_837	<i>Hypocreales species 30</i>	1	3	Undetermined	-
otu_896	<i>Hypocreales species 31</i>	2	13	Undetermined	-
otu_976	<i>Hypocreales species 32</i>	1	2	Undetermined	-
otu_183	<i>Irpex lacteus</i>	2	166	Wood decay	-
otu_629	<i>Jattaea prunicola</i>	1	11	Wood decay	-
otu_972	<i>Junghuhnia nitida</i>	1	2	Wood decay	-
otu_1218	<i>Lasiodiplodia theobromae</i>	1	2	Plant pathogen	-
otu_971	<i>Lecanicillium Hypocreales</i>	1	2	Entomopathogenic	-
otu_554	<i>Lecanicillium kalimantanense</i>	1	9	Entomopathogenic	-
otu_97	<i>Lecanicillium kalimantanense</i>	2	631	Entomopathogenic	-
otu_206	<i>Lentinellus castoreus</i>	1	92	Saprotroph	-
otu_41	<i>Lenzites betulinus</i>	2	3309	Wood decay	-
otu_1017	<i>Leptosphaeria microscopica</i>	1	2	Plant pathogen	x
otu_808	<i>Malassezia globosa</i>	4	43	Saprotroph	-
otu_92	<i>Malassezia japonica</i>	10	878	Saprotroph	-
otu_53	<i>Malassezia restricta</i>	18	5987	Saprotroph	-

otu_585	<i>Marasmiellus species 1</i>	1	13	Plant pathogen	-
otu_24	<i>Marasmiellus candidus</i>	3	3507	Plant pathogen	-
otu_94	<i>Marasmius rotula</i>	1	1046	Saprotroph	-
otu_532	<i>Memnoniella echinata</i>	1	13	Wood decay	-
otu_6	<i>Metarhizium anisopliae</i>	32	62691	Entomopathogenic	-
otu_820	<i>Metarhizium anisopliae</i>	1	5	Entomopathogenic	-
otu_158	<i>Metschnikowia species 1</i>	3	252	Undetermined	-
otu_1236	<i>Meyerozyma guilliermondii</i>	1	2	Saprotroph	-
otu_277	<i>Mycena species 1</i>	1	51	Saprotroph	-
otu_574	<i>Myxarium nucleatum</i>	1	18	Wood decay	-
otu_1170	<i>Myxospora musae</i>	1	2	Undetermined	-
otu_1177	<i>Myxospora musae</i>	2	4	Undetermined	-
otu_239	<i>Myxospora musae</i>	1	125	Undetermined	-
otu_286	<i>Myxospora musae</i>	1	63	Undetermined	-
otu_35	<i>Myxospora musae</i>	7	7925	Undetermined	-
otu_395	<i>Myxospora musae</i>	1	25	Undetermined	-
otu_746	<i>Myxospora musae</i>	1	8	Undetermined	-
otu_882	<i>Myxospora musae</i>	1	3	Undetermined	-
otu_32	<i>Naganishia albida</i>	2	8	Undetermined	-
otu_935	<i>Nectria species 1</i>	1	2	Plant pathogen	-
otu_961	<i>Nectria bactridioides</i>	1	2	Plant pathogen	-
otu_1165	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_1180	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_1188	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_1190	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_1192	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_1195	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_1196	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_1219	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_13	<i>Nectria pseudotrichia</i>	25	25796	Plant pathogen	-
otu_197	<i>Nectria pseudotrichia</i>	1	107	Plant pathogen	-
otu_289	<i>Nectria pseudotrichia</i>	2	69	Plant pathogen	-
otu_324	<i>Nectria pseudotrichia</i>	1	51	Plant pathogen	-
otu_37	<i>Nectria pseudotrichia</i>	1	3703	Plant pathogen	-
otu_571	<i>Nectria pseudotrichia</i>	1	12	Plant pathogen	-
otu_749	<i>Nectria pseudotrichia</i>	1	13	Plant pathogen	-
otu_766	<i>Nectria pseudotrichia</i>	1	5	Plant pathogen	-
otu_829	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_884	<i>Nectria pseudotrichia</i>	1	3	Plant pathogen	-

otu_901	<i>Nectria pseudotrichia</i>	1	6	Plant pathogen	-
otu_933	<i>Nectria pseudotrichia</i>	1	2	Plant pathogen	-
otu_781	<i>Ocellularia perforata</i>	1	5	Lichenized	-
otu_470	<i>Ophiocordyceps species 1</i>	1	14	Entomopathogenic	-
otu_174	<i>Ophiocordyceps arbuscula</i>	1	233	Entomopathogenic	-
otu_133	<i>Ophiostoma flexuosum</i>	2	323	Plant pathogen	-
otu_296	<i>Ophiostoma perfectum</i>	1	30	Plant pathogen	-
otu_822	<i>Panus species 1</i>	1	5	Undetermined	-
otu_477	<i>Paracremonium inflatum</i>	1	12	Undetermined	-
otu_576	<i>Penicillium citrinum</i>	2	17	Saprotroph	-
otu_977	<i>Penicillium lineolatum</i>	1	2	Saprotroph	-
otu_1117	<i>Penicillium meleagrimum</i>	2	8	Saprotroph	-
otu_1210	<i>Penicillium meleagrimum</i>	1	2	Saprotroph	-
otu_15	<i>Penicillium meleagrimum</i>	19	53002	Saprotroph	-
otu_200	<i>Penicillium meleagrimum</i>	4	365	Saprotroph	-
otu_393	<i>Penicillium meleagrimum</i>	3	26	Saprotroph	-
otu_433	<i>Penicillium meleagrimum</i>	12	1038	Saprotroph	-
otu_754	<i>Penicillium meleagrimum</i>	1	6	Saprotroph	-
otu_974	<i>Penicillium meleagrimum</i>	1	4	Saprotroph	-
otu_1172	<i>Penicillium roseopurpureum</i>	1	2	Saprotroph	-
otu_146	<i>Penicillium steckii</i>	1	292	Saprotroph	-
otu_550	<i>Peniophora species 1</i>	1	13	Wood decay	-
otu_627	<i>Peniophora species 1</i>	2	11	Wood decay	-
otu_223	<i>Peniophorella guttuliferum</i>	1	119	Saprotroph	-
otu_1231	<i>Perenniporia species 1</i>	1	2	Wood decay	-
otu_339	<i>Perenniporia corticola</i>	1	40	Wood decay	-
otu_597	<i>Perenniporia vanhullii</i>	1	6	Wood decay	-
otu_1191	<i>Phaeoacremonium parasiticum</i>	1	4	Plant pathogen	-
otu_969	<i>Phaeoacremonium viticola</i>	1	2	Plant pathogen	-
otu_219	<i>Phanerochaete sordida</i>	1	23	Wood decay	-
otu_1182	<i>Phialemoniopsis curvata</i>	1	2	Saprotroph	-
otu_171	<i>Phialemoniopsis curvata</i>	4	327	Saprotroph	-
otu_496	<i>Phialemoniopsis curvata</i>	1	14	Saprotroph	-
otu_662	<i>Phialemoniopsis curvata</i>	1	5	Saprotroph	-
otu_338	<i>Phialemonium dimorphosporum</i>	1	34	Saprotroph	-
otu_1187	<i>Phialophora geniculata</i>	1	2	Undetermined	-
otu_392	<i>Phlebia acanthocystis</i>	2	39	Wood decay	-
otu_441	<i>Phlebia acerina</i>	1	16	Wood decay	-

otu_806	<i>Phlebia chrysocreas</i>	1	3	Wood decay	-
otu_514	<i>Phlebia tremellosa</i>	1	12	Wood decay	-
otu_812	<i>Phlebia uda</i>	1	3	Wood decay	-
otu_978	<i>Pholiota species 1</i>	1	2	Saprotroph	-
otu_979	<i>Physisporinus vitreus</i>	1	4	Wood decay	-
otu_711	<i>Plectosphaerella species 1</i>	1	26	Plant pathogen	-
otu_33	<i>Plectosphaerella citrullae</i>	8	1114	Plant pathogen	-
otu_646	<i>Plectosphaerella citrullae</i>	2	22	Plant pathogen	-
otu_1125	<i>Plectosphaerella cucumerina</i>	1	2	Plant pathogen	-
otu_124	<i>Plectosphaerella cucumerina</i>	1	270	Plant pathogen	-
otu_647	<i>Plectosphaerella cucumerina</i>	1	8	Plant pathogen	-
otu_680	<i>Plectosphaerellaceae species 1</i>	1	12	Undetermined	-
otu_1085	<i>Plectosporium alismatis</i>	1	2	Plant Pathogen	x
otu_1068	<i>Pleosporales species 1</i>	1	2	Undetermined	-
otu_1069	<i>Pleosporales species 2</i>	1	2	Undetermined	-
otu_143	<i>Pleosporales species 3</i>	2	442	Undetermined	-
otu_492	<i>Pleosporales species 4</i>	1	82	Undetermined	-
otu_557	<i>Pleosporales species 5</i>	1	23	Undetermined	-
otu_603	<i>Pleosporales species 6</i>	1	13	Undetermined	-
otu_723	<i>Pleosporales species 7</i>	1	4	Undetermined	-
otu_842	<i>Pleosporales species 8</i>	1	23	Undetermined	-
otu_262	<i>Pluteus variabilicolor</i>	1	67	Wood decay	-
otu_1140	<i>Pochonia species 1</i>	1	8	Entomopathogenic	-
otu_224	<i>Pochonia species 2</i>	3	148	Entomopathogenic	-
otu_58	<i>Pochonia bulbillosa</i>	1	1630	Entomopathogenic	-
otu_580	<i>Pochonia bulbillosa</i>	1	19	Entomopathogenic	-
otu_1032	<i>Pochonia chlamydosporia</i>	1	2	Entomopathogenic	-
otu_1033	<i>Pochonia chlamydosporia</i>	1	2	Entomopathogenic	-
otu_11	<i>Pochonia chlamydosporia</i>	30	47429	Entomopathogenic	-
otu_1119	<i>Pochonia chlamydosporia</i>	1	4	Entomopathogenic	-
otu_1123	<i>Pochonia chlamydosporia</i>	1	2	Entomopathogenic	-
otu_1127	<i>Pochonia chlamydosporia</i>	1	2	Entomopathogenic	-
otu_1129	<i>Pochonia chlamydosporia</i>	1	2	Entomopathogenic	-
otu_1225	<i>Pochonia chlamydosporia</i>	2	6	Entomopathogenic	-
otu_1237	<i>Pochonia chlamydosporia</i>	1	2	Entomopathogenic	-
otu_140	<i>Pochonia chlamydosporia</i>	2	288	Entomopathogenic	-
otu_196	<i>Pochonia chlamydosporia</i>	2	142	Entomopathogenic	-
otu_412	<i>Pochonia chlamydosporia</i>	1	30	Entomopathogenic	-
otu_451	<i>Pochonia chlamydosporia</i>	1	42	Entomopathogenic	-

otu_488	<i>Pochonia chlamydosporia</i>	1	13	Entomopathogenic	-
otu_5	<i>Pochonia chlamydosporia</i>	41	87459	Entomopathogenic	-
otu_525	<i>Pochonia chlamydosporia</i>	1	16	Entomopathogenic	-
otu_565	<i>Pochonia chlamydosporia</i>	4	45	Entomopathogenic	-
otu_577	<i>Pochonia chlamydosporia</i>	2	17	Entomopathogenic	-
otu_608	<i>Pochonia chlamydosporia</i>	1	13	Entomopathogenic	-
otu_667	<i>Pochonia chlamydosporia</i>	1	25	Entomopathogenic	-
otu_863	<i>Pochonia chlamydosporia</i>	1	5	Entomopathogenic	-
otu_865	<i>Pochonia chlamydosporia</i>	1	7	Entomopathogenic	-
otu_866	<i>Pochonia chlamydosporia</i>	1	3	Entomopathogenic	-
otu_911	<i>Pochonia chlamydosporia</i>	1	7	Entomopathogenic	-
otu_1131	<i>Pochonia rubescens</i>	2	4	Entomopathogenic	-
otu_1152	<i>Pochonia rubescens</i>	1	2	Entomopathogenic	-
otu_122	<i>Pochonia rubescens</i>	21	1783	Entomopathogenic	-
otu_1224	<i>Pochonia rubescens</i>	1	2	Entomopathogenic	-
otu_14	<i>Pochonia rubescens</i>	35	65889	Entomopathogenic	-
otu_207	<i>Pochonia rubescens</i>	2	272	Entomopathogenic	-
otu_273	<i>Pochonia rubescens</i>	1	118	Entomopathogenic	-
otu_299	<i>Pochonia rubescens</i>	2	34	Entomopathogenic	-
otu_334	<i>Pochonia rubescens</i>	6	385	Entomopathogenic	-
otu_414	<i>Pochonia rubescens</i>	2	29	Entomopathogenic	-
otu_495	<i>Pochonia rubescens</i>	1	23	Entomopathogenic	-
otu_533	<i>Pochonia rubescens</i>	1	16	Entomopathogenic	-
otu_610	<i>Pochonia rubescens</i>	2	23	Entomopathogenic	-
otu_612	<i>Pochonia rubescens</i>	2	10	Entomopathogenic	-
otu_729	<i>Pochonia rubescens</i>	1	10	Entomopathogenic	-
otu_868	<i>Pochonia rubescens</i>	1	5	Entomopathogenic	-
otu_869	<i>Pochonia rubescens</i>	1	11	Entomopathogenic	-
otu_870	<i>Pochonia rubescens</i>	1	5	Entomopathogenic	-
otu_902	<i>Pochonia rubescens</i>	1	9	Entomopathogenic	-
otu_136	<i>Polyporales species 1</i>	1	310	Undetermined	-
otu_265	<i>Polyporales species 2</i>	5	144	Undetermined	-
otu_440	<i>Polyporales species 3</i>	2	26	Undetermined	-
otu_1030	<i>Polypore species 1</i>	1	6	Wood decay	-
otu_271	<i>Postia fragilis</i>	1	74	Wood decay	-
otu_548	<i>Postia stiptica</i>	1	13	Wood decay	-
otu_137	<i>Puccinia coronata</i>	1	260	Plant pathogen	-
otu_841	<i>Purpureocillium species 1</i>	1	8	Entomopathogenic	-
otu_1070	<i>Purpureocillium lavendulum</i>	1	2	Entomopathogenic	-

otu_1084	<i>Purpureocillium lavendulum</i>	1	4	Entomopathogenic	x
otu_519	<i>Purpureocillium lavendulum</i>	1	19	Entomopathogenic	-
otu_520	<i>Purpureocillium lavendulum</i>	1	28	Entomopathogenic	-
otu_836	<i>Purpureocillium lavendulum</i>	1	5	Entomopathogenic	-
otu_840	<i>Purpureocillium lavendulum</i>	1	13	Entomopathogenic	x
otu_90	<i>Purpureocillium lavendulum</i>	7	1844	Entomopathogenic	x
otu_555	<i>Purpureocillium lilacinum</i>	1	2	Entomopathogenic	-
otu_382	<i>Resupinatus species 1</i>	1	26	Wood decay	-
otu_95	<i>Resupinatus alboniger</i>	2	838	Wood decay	-
otu_222	<i>Rhizoctonia bataticola</i>	1	123	Plant pathogen	-
otu_493	<i>Rhizomucor variabilis</i>	1	12	Saprotroph	-
otu_263	<i>Rigidoporus crocatus</i>	1	76	Wood decay	-
otu_210	<i>Rigidoporus vinctus</i>	1	96	Wood decay	-
otu_1023	<i>Roussoellaceae species 1</i>	2	4	Undetermined	-
otu_1024	<i>Roussoellaceae species 2</i>	1	2	Undetermined	-
otu_1066	<i>Roussoellaceae species 3</i>	1	4	Undetermined	-
otu_235	<i>Roussoellaceae species 4</i>	1	481	Undetermined	-
otu_843	<i>Roussoellaceae species 5</i>	1	5	Undetermined	-
otu_138	<i>Saccharomyces cerevisiae</i>	1	460	Wood decay	x
otu_458	<i>Sakaguchia dacryoidea</i>	1	17	Undetermined	-
otu_45	<i>Sampaiozyma ingeniosa</i>	1	2020	Undetermined	-
otu_1098	<i>Sarcopodium araliae</i>	1	2	Saprotroph	-
otu_295	<i>Sarcopodium araliae</i>	2	60	Saprotroph	-
otu_155	<i>Sarocladium gamsii</i>	1	198	Saprotroph	-
otu_20	<i>Sarocladium gamsii</i>	4	10	Saprotroph	-
otu_232	<i>Sarocladium gamsii</i>	1	210	Saprotroph	-
otu_34	<i>Sarocladium gamsii</i>	3	8534	Saprotroph	-
otu_736	<i>Sarocladium gamsii</i>	1	11	Saprotroph	-
otu_1124	<i>Sarocladium hominis</i>	1	2	Saprotroph	-
otu_1136	<i>Sarocladium strictum</i>	1	8	Saprotroph	-
otu_114	<i>Sarocladium strictum</i>	4	463	Saprotroph	-
otu_250	<i>Sarocladium strictum</i>	32	656	Saprotroph	-
otu_3	<i>Sarocladium strictum</i>	129	1823481	Saprotroph	-
otu_306	<i>Sarocladium strictum</i>	9	121	Saprotroph	x
otu_319	<i>Sarocladium strictum</i>	3	93	Saprotroph	-
otu_388	<i>Sarocladium strictum</i>	2	84	Saprotroph	-
otu_391	<i>Sarocladium strictum</i>	6	39	Saprotroph	-
otu_418	<i>Sarocladium strictum</i>	4	74	Saprotroph	-
otu_419	<i>Sarocladium strictum</i>	2	36	Saprotroph	-

otu_434	<i>Sarocladium strictum</i>	31	284	Saprotroph	-
otu_435	<i>Sarocladium strictum</i>	8	107	Saprotroph	-
otu_452	<i>Sarocladium strictum</i>	1	22	Saprotroph	-
otu_475	<i>Sarocladium strictum</i>	6	34	Saprotroph	-
otu_510	<i>Sarocladium strictum</i>	2	25	Saprotroph	-
otu_56	<i>Sarocladium strictum</i>	5	1372	Saprotroph	-
otu_584	<i>Sarocladium strictum</i>	28	113	Saprotroph	x
otu_622	<i>Sarocladium strictum</i>	3	17	Saprotroph	-
otu_641	<i>Sarocladium strictum</i>	2	14	Saprotroph	-
otu_764	<i>Sarocladium strictum</i>	3	31	Saprotroph	x
otu_765	<i>Sarocladium strictum</i>	19	50	Saprotroph	x
otu_767	<i>Sarocladium strictum</i>	11	42	Saprotroph	-
otu_77	<i>Sarocladium strictum</i>	42	3103	Saprotroph	-
otu_776	<i>Sarocladium strictum</i>	16	121	Saprotroph	-
otu_924	<i>Sarocladium strictum</i>	5	10	Saprotroph	-
otu_928	<i>Sarocladium strictum</i>	3	8	Saprotroph	-
otu_940	<i>Sarocladium strictum</i>	1	2	Saprotroph	-
otu_953	<i>Sarocladium strictum</i>	1	2	Saprotroph	x
otu_957	<i>Sarocladium strictum</i>	1	2	Saprotroph	-
otu_958	<i>Sarocladium strictum</i>	1	2	Saprotroph	-
otu_228	<i>Schizophyllum commune</i>	1	84	Wood decay	-
otu_448	<i>Schizopora radula</i>	1	66	Wood decay	-
otu_1209	<i>Simplicillium species 1</i>	1	2	Entomopathogenic	-
otu_335	<i>Simplicillium species 2</i>	1	52	Entomopathogenic	-
otu_454	<i>Simplicillium species 3</i>	1	17	Entomopathogenic	-
otu_753	<i>Simplicillium species 4</i>	1	13	Entomopathogenic	-
otu_9	<i>Simplicillium species 5</i>	9	42624	Entomopathogenic	-
otu_1238	<i>Simplicillium cylindrosporum</i>	1	2	Entomopathogenic	-
otu_42	<i>Simplicillium minatense</i>	1	2811	Entomopathogenic	-
otu_649	<i>Sistotremastrum guttuliferum</i>	1	8	Saprotroph	-
otu_1203	<i>Sordariomycetes species 1</i>	1	2	Undetermined	x
otu_1205	<i>Sordariomycetes species 2</i>	2	148	Undetermined	-
otu_142	<i>Sordariomycetes species 3</i>	6	1905	Undetermined	-
otu_249	<i>Sordariomycetes species 4</i>	2	245	Undetermined	-
otu_358	<i>Sordariomycetes species 5</i>	2	89	Undetermined	-
otu_752	<i>Sordariomycetes species 6</i>	1	8	Undetermined	-
otu_846	<i>Sordariomycetes species 7</i>	4	86	Undetermined	-
otu_847	<i>Sordariomycetes species 8</i>	1	3	Undetermined	-
otu_890	<i>Sordariomycetes species 9</i>	1	3	Undetermined	-

otu_390	<i>Sporobolomyces species 10</i>	1	23	Fungicolous	-
otu_30	<i>Stachybotrys species 1</i>	8	17	Wood decay	-
otu_663	<i>Stachybotrys longispora</i>	1	5	Wood decay	-
otu_79	<i>Stachybotrys longispora</i>	2	643	Wood decay	-
otu_1183	<i>Stachybotrys parvispora</i>	1	8	Wood decay	-
otu_1186	<i>Stachybotrys parvispora</i>	1	4	Wood decay	-
otu_1193	<i>Stachybotrys parvispora</i>	1	4	Wood decay	-
otu_499	<i>Stachybotrys parvispora</i>	1	33	Wood decay	-
otu_885	<i>Stachybotrys parvispora</i>	1	3	Wood decay	-
otu_889	<i>Stachybotrys parvispora</i>	1	3	Wood decay	-
otu_346	<i>Steccherinum ochraceum</i>	1	33	Saprotroph	-
otu_272	<i>Stephanonectria species 1</i>	4	57	Saprotroph	-
otu_63	<i>Stephanonectria species 2</i>	1	1071	Saprotroph	-
otu_732	<i>Stephanonectria species 3</i>	2	10	Saprotroph	-
otu_459	<i>Stephanonectria keithii</i>	1	22	Saprotroph	-
otu_743	<i>Stephanonectria keithii</i>	1	4	Saprotroph	-
otu_676	<i>Stereum species 1</i>	1	5	Saprotroph	-
otu_923	<i>Talaromyces atricola</i>	1	2	Saprotroph	-
otu_267	<i>Thanatephorus cucumeris</i>	1	47	Plant pathogen	-
otu_1086	<i>Tolypocladium species 1</i>	1	4	Entomopathogenic	-
otu_1088	<i>Tolypocladium species 2</i>	1	2	Entomopathogenic	-
otu_1104	<i>Tolypocladium species 3</i>	1	2	Entomopathogenic	x
otu_1107	<i>Tolypocladium species 4</i>	1	2	Entomopathogenic	x
otu_1108	<i>Tolypocladium species 5</i>	1	4	Entomopathogenic	-
otu_1109	<i>Tolypocladium species 6</i>	1	2	Entomopathogenic	x
otu_1110	<i>Tolypocladium species 7</i>	1	4	Entomopathogenic	-
otu_1135	<i>Tolypocladium species 8</i>	1	2	Entomopathogenic	-
otu_1155	<i>Tolypocladium species 9</i>	1	2	Entomopathogenic	-
otu_1211	<i>Tolypocladium species 10</i>	1	2	Entomopathogenic	x
otu_201	<i>Tolypocladium species 11</i>	5	139	Entomopathogenic	-
otu_21	<i>Tolypocladium species 12</i>	23	35337	Entomopathogenic	-
otu_257	<i>Tolypocladium species 13</i>	6	157	Entomopathogenic	-
otu_348	<i>Tolypocladium species 14</i>	1	41	Entomopathogenic	x
otu_387	<i>Tolypocladium species 15</i>	2	38	Entomopathogenic	-
otu_528	<i>Tolypocladium species 16</i>	1	17	Entomopathogenic	-
otu_559	<i>Tolypocladium species 17</i>	3	16	Entomopathogenic	x
otu_560	<i>Tolypocladium species 18</i>	2	15	Entomopathogenic	x
otu_606	<i>Tolypocladium species 19</i>	2	8	Entomopathogenic	-
otu_686	<i>Tolypocladium species 20</i>	2	9	Entomopathogenic	x

otu_688	<i>Tolypocladium species 21</i>	24	994	Entomopathogenic	-
otu_720	<i>Tolypocladium species 22</i>	1	2	Entomopathogenic	-
otu_730	<i>Tolypocladium species 23</i>	1	10	Entomopathogenic	-
otu_777	<i>Tolypocladium species 24</i>	2	8	Entomopathogenic	-
otu_858	<i>Tolypocladium species 25</i>	1	3	Entomopathogenic	-
otu_859	<i>Tolypocladium species 26</i>	1	3	Entomopathogenic	x
otu_941	<i>Tolypocladium species 27</i>	3	8	Entomopathogenic	-
otu_1154	<i>Tolypocladium album</i>	3	8	Entomopathogenic	-
otu_266	<i>Tolypocladium album</i>	2	109	Entomopathogenic	-
otu_413	<i>Tolypocladium album</i>	1	46	Entomopathogenic	-
otu_428	<i>Tolypocladium album</i>	1	41	Entomopathogenic	-
otu_449	<i>Tolypocladium album</i>	6	89	Entomopathogenic	-
otu_857	<i>Tolypocladium album</i>	1	7	Entomopathogenic	-
otu_950	<i>Tolypocladium album</i>	1	2	Entomopathogenic	x
otu_1239	<i>Tolypocladium inegoensis</i>	1	6	Entomopathogenic	x
otu_502	<i>Tolypocladium inegoensis</i>	1	35	Entomopathogenic	x
otu_526	<i>Tolypocladium pustulatum</i>	3	36	Entomopathogenic	-
otu_527	<i>Tolypocladium pustulatum</i>	1	8	Entomopathogenic	-
otu_892	<i>Tolypocladium pustulatum</i>	1	3	Fungicolous	x
otu_314	<i>Trametes species 1</i>	1	56	Wood decay	-
otu_544	<i>Trametes gibbosa</i>	1	13	Wood decay	-
otu_182	<i>Trechispora regularis</i>	2	164	Wood decay	-
otu_242	<i>Trechispora regularis</i>	1	63	Wood decay	-
otu_407	<i>Trechispora regularis</i>	1	24	Wood decay	-
otu_121	<i>Trichaptum abietinum</i>	5	942	Wood decay	-
otu_462	<i>Trichoderma koningiopsis</i>	2	25	Fungicolous	-
otu_460	<i>Tyromyces species 1</i>	1	25	Wood decay	-
otu_253	<i>Tyromyces chioneus</i>	1	60	Wood decay	-
otu_316	<i>Tyromyces fissilis</i>	2	79	Wood decay	-
otu_372	<i>Umbelopsis isabellina</i>	2	34	Saprotroph	-
otu_921	Uncultured acremonium	1	2	Fungicolous	-
otu_521	Uncultured ascomycota	1	13	Undetermined	-
otu_558	Uncultured ascomycota	1	9	Undetermined	-
otu_658	Uncultured ascomycota	1	7	Undetermined	-
otu_839	Uncultured ascomycota	1	7	Undetermined	-
otu_86	Uncultured ascomycota	1	728	Undetermined	-
otu_956	Uncultured ascomycota	1	2	Undetermined	x
otu_1026	Uncultured basidiomycete	1	2	Basidiomycete	-
otu_1029	Uncultured basidiomycete	1	2	Undetermined	-

otu_135	Uncultured basidiomycete	3	16	Undetermined	-
otu_152	Uncultured basidiomycete	1	224	Undetermined	-
otu_25	Uncultured basidiomycete	12	28413	Undetermined	-
otu_43	Uncultured basidiomycete	3	3277	Undetermined	-
otu_504	Uncultured basidiomycete	3	28	Undetermined	-
otu_785	Uncultured basidiomycete	1	3	Undetermined	-
otu_871	Uncultured basidiomycete	1	5	Undetermined	-
otu_967	Uncultured basidiomycete	1	2	Undetermined	-
otu_1007	Uncultured basidiomycota	1	4	Undetermined	-
otu_246	Uncultured basidiomycota	1	108	Undetermined	-
otu_632	Uncultured basidiomycota	1	7	Undetermined	-
otu_354	Uncultured calyptella	1	22	Saprotroph	-
otu_1004	Uncultured chaetothyriales	1	2	Undetermined	-
otu_461	Uncultured corticiaceae	1	31	Undetermined	-
otu_59	Uncultured eurotiales	5	1627	Undetermined	-
otu_760	Uncultured eurotiales	1	6	Undetermined	-
otu_10	Uncultured fungus	73	128406	Undetermined	-
otu_1000	Uncultured fungus	9	20	Undetermined	-
otu_1011	Uncultured fungus	1	2	Undetermined	-
otu_1015	Uncultured fungus	1	4	Undetermined	-
otu_106	Uncultured fungus	13	1403	Undetermined	-
otu_1073	Uncultured fungus	1	4	Undetermined	x
otu_1077	Uncultured fungus	1	2	Undetermined	-
otu_1078	Uncultured fungus	1	2	Undetermined	x
otu_1093	Uncultured fungus	1	2	Undetermined	x
otu_1106	Uncultured fungus	1	2	Undetermined	-
otu_1112	Uncultured fungus	1	2	Undetermined	-
otu_1113	Uncultured fungus	1	4	Undetermined	-
otu_1114	Uncultured fungus	1	2	Undetermined	-
otu_1115	Uncultured fungus	1	2	Undetermined	x
otu_1134	Uncultured fungus	1	2	Undetermined	-
otu_1137	Uncultured fungus	1	6	Undetermined	-
otu_1147	Uncultured fungus	1	2	Undetermined	x
otu_1150	Uncultured fungus	1	2	Undetermined	-
otu_1153	Uncultured fungus	3	12	Undetermined	-
otu_1157	Uncultured fungus	1	2	Undetermined	-
otu_1166	Uncultured fungus	3	18	Undetermined	-
otu_1173	Uncultured fungus	1	2	Undetermined	-
otu_1179	Uncultured fungus	1	2	Undetermined	-

otu_1185	Uncultured fungus	2	4	Undetermined	-
otu_12	Uncultured fungus	52	78889	Undetermined	-
otu_1213	Uncultured fungus	1	2	Undetermined	-
otu_1214	Uncultured fungus	1	2	Undetermined	-
otu_1215	Uncultured fungus	1	24	Undetermined	-
otu_1220	Uncultured fungus	1	8	Undetermined	-
otu_1223	Uncultured fungus	1	4	Undetermined	-
otu_1226	Uncultured fungus	1	4	Undetermined	-
otu_1241	Uncultured fungus	1	2	Undetermined	x
otu_148	Uncultured fungus	7	1477	Undetermined	-
otu_151	Uncultured fungus	5	150	Undetermined	-
otu_157	Uncultured fungus	1	456	Undetermined	-
otu_165	Uncultured fungus	1	339	Undetermined	-
otu_17	Uncultured fungus	23	27062	Undetermined	-
otu_189	Uncultured fungus	3	288	Undetermined	-
otu_198	Uncultured fungus	1	209	Undetermined	-
otu_22	Uncultured fungus	19	24464	Undetermined	-
otu_221	Uncultured fungus	1	175	Undetermined	-
otu_238	Uncultured fungus	1	107	Undetermined	-
otu_251	Uncultured fungus	1	65	Undetermined	-
otu_280	Uncultured fungus	1	267	Undetermined	-
otu_281	Uncultured fungus	5	104	Undetermined	-
otu_292	Uncultured fungus	1	45	Undetermined	-
otu_328	Uncultured fungus	3	130	Undetermined	-
otu_350	Uncultured fungus	1	29	Undetermined	-
otu_353	Uncultured fungus	2	53	Undetermined	-
otu_364	Uncultured fungus	1	35	Undetermined	-
otu_366	Uncultured fungus	1	25	Undetermined	-
otu_38	Uncultured fungus	38	19402	Undetermined	x
otu_381	Uncultured fungus	4	110	Undetermined	x
otu_396	Uncultured fungus	2	16	Undetermined	-
otu_40	Uncultured fungus	31	10597	Undetermined	-
otu_408	Uncultured fungus	7	102	Undetermined	-
otu_415	Uncultured fungus	3	42	Undetermined	-
otu_416	Uncultured fungus	1	20	Undetermined	-
otu_425	Uncultured fungus	3	33	Undetermined	-
otu_427	Uncultured fungus	1	14	Undetermined	-
otu_430	Uncultured fungus	2	39	Undetermined	-
otu_443	Uncultured fungus	2	42	Undetermined	x

otu_444	Uncultured fungus	1	20	Undetermined	-
otu_450	Uncultured fungus	6	119	Undetermined	-
otu_466	Uncultured fungus	12	1288	Undetermined	x
otu_469	Uncultured fungus	2	52	Undetermined	-
otu_472	Uncultured fungus	1	2	Undetermined	-
otu_48	Uncultured fungus	2	2494	Undetermined	-
otu_501	Uncultured fungus	1	13	Undetermined	x
otu_505	Uncultured fungus	1	46	Undetermined	-
otu_524	Uncultured fungus	1	18	Undetermined	-
otu_531	Uncultured fungus	1	17	Undetermined	-
otu_536	Uncultured fungus	3	43	Undetermined	-
otu_549	Uncultured fungus	2	15	Undetermined	-
otu_563	Uncultured fungus	1	13	Undetermined	-
otu_568	Uncultured fungus	2	17	Undetermined	-
otu_572	Uncultured fungus	1	15	Undetermined	-
otu_609	Uncultured fungus	1	14	Undetermined	-
otu_616	Uncultured fungus	2	25	Undetermined	-
otu_619	Uncultured fungus	2	17	Undetermined	-
otu_620	Uncultured fungus	2	13	Undetermined	-
otu_653	Uncultured fungus	3	7	Undetermined	-
otu_673	Uncultured fungus	1	8	Undetermined	-
otu_679	Uncultured fungus	6	20	Undetermined	-
otu_697	Uncultured fungus	1	18	Undetermined	-
otu_710	Uncultured fungus	3	15	Undetermined	-
otu_738	Uncultured fungus	1	8	Undetermined	-
otu_739	Uncultured fungus	1	6	Undetermined	-
otu_74	Uncultured fungus	1	1036	Undetermined	-
otu_741	Uncultured fungus	1	11	Undetermined	-
otu_745	Uncultured fungus	2	868	Undetermined	-
otu_747	Uncultured fungus	1	10	Undetermined	-
otu_769	Uncultured fungus	1	3	Undetermined	-
otu_774	Uncultured fungus	1	5	Undetermined	-
otu_775	Uncultured fungus	1	3	Undetermined	-
otu_778	Uncultured fungus	1	5	Undetermined	-
otu_817	Uncultured fungus	1	3	Undetermined	x
otu_821	Uncultured fungus	1	33	Undetermined	x
otu_823	Uncultured fungus	1	3	Undetermined	-
otu_852	Uncultured fungus	1	3	Undetermined	-
otu_856	Uncultured fungus	1	3	Undetermined	-

otu_875	Uncultured fungus	1	3	Undetermined	-
otu_880	Uncultured fungus	1	11	Undetermined	-
otu_883	Uncultured fungus	1	3	Undetermined	-
otu_888	Uncultured fungus	1	3	Undetermined	-
otu_893	Uncultured fungus	2	11	Undetermined	-
otu_912	Uncultured fungus	2	8	Undetermined	x
otu_963	Uncultured fungus	1	2	Undetermined	-
otu_973	Uncultured fungus	2	4	Undetermined	-
otu_879	Uncultured helotiales	1	3	Undetermined	-
otu_954	Uncultured helotiales	1	2	Undetermined	-
otu_385	Uncultured marasmiaceae	2	66	Undetermined	-
otu_47	Uncultured <i>mycena</i>	2	2859	Saprotroph	-
otu_343	Uncultured <i>tilletiopsis</i>	1	37	Undetermined	-
otu_1096	<i>Verticillium insectorum</i>	1	2	Entomopathogenic	-
otu_1100	<i>Volutella species 1</i>	1	2	Plant pathogen	-
otu_1103	<i>Volutella species 2</i>	1	2	Plant pathogen	-
otu_1138	<i>Volutella species 3</i>	3	22	Plant pathogen	-
otu_1168	<i>Volutella species 4</i>	1	2	Plant pathogen	-
otu_147	<i>Volutella species 5</i>	2	252	Plant pathogen	-
otu_227	<i>Volutella species 6</i>	4	301	Plant pathogen	-
otu_287	<i>Volutella species 7</i>	2	66	Plant pathogen	-
otu_327	<i>Volutella species 8</i>	1	96	Plant pathogen	-
otu_370	<i>Volutella species 9</i>	3	98	Plant pathogen	-
otu_494	<i>Volutella species 10</i>	1	11	Plant pathogen	-
otu_570	<i>Volutella species 11</i>	2	21	Plant pathogen	-
otu_692	<i>Volutella species 12</i>	1	4	Plant pathogen	-
otu_873	<i>Volutella species 13</i>	1	5	Plant pathogen	-
otu_881	<i>Volutella species 14</i>	1	5	Plant pathogen	-
otu_660	<i>Volutella consors</i>	1	5	Plant pathogen	-
otu_844	<i>Volutella consors</i>	1	7	Plant pathogen	-
otu_115	<i>Wallemia mellicola</i>	1	416	Saprotroph	-
otu_46	<i>Wallemia mellicola</i>	3	3303	Saprotroph	-
otu_849	<i>Wallrothiella subiculosa</i>	1	5	Undetermined	-
otu_547	<i>Wolfiporia dilatohypha</i>	1	10	Wood decay	-
otu_455	<i>Xenasmata aff</i>	1	20	Wood decay	-
otu_573	<i>Xenasmata aff</i>	1	28	Wood decay	-
otu_365	<i>Xylariales species 1</i>	2	30	Undetermined	-
otu_323	<i>Xylobolus frustulatus</i>	1	41	Saprotroph	-
otu_303	<i>Yuchengia narymica</i>	1	56	Saprotroph	-

SUPPLEMENTARY TABLE 3.2. Operational taxonomic unit (OTU) taxonomic and function guild assignments using RdP classifier with Warcup Fungal training set (RDP WAR) method.

OTU	RDP WAR Taxonomic assignment	Incidence frequency	No. Sequence reads	Function guild assignment	Chimeric seq (x) or real (-)
otu_558	<i>Acremonium</i>	1	9	Fungicolous	-
otu_86	<i>Acremonium</i>	1	728	Fungicolous	-
otu_1067	<i>Acremonium asperulatum</i>	1	4	Fungicolous	-
otu_168	<i>Acremonium asperulatum</i>	1	351	Fungicolous	-
otu_657	<i>Acremonium asperulatum</i>	1	21	Fungicolous	-
otu_722	<i>Acremonium asperulatum</i>	1	32	Fungicolous	-
otu_1120	<i>Acremonium furcatum</i>	1	2	Fungicolous	-
otu_23	<i>Acremonium furcatum</i>	12	22585	Fungicolous	-
otu_410	<i>Acremonium furcatum</i>	2	74	Fungicolous	-
otu_661	<i>Acremonium furcatum</i>	1	10	Fungicolous	x
otu_731	<i>Acremonium furcatum</i>	2	204	Fungicolous	-
otu_733	<i>Acremonium furcatum</i>	2	25	Fungicolous	-
otu_214	<i>Acremonium polychromum</i>	1	193	Fungicolous	-
otu_562	<i>Acremonium polychromum</i>	1	12	Fungicolous	-
otu_713	<i>Acremonium polychromum</i>	2	12	Fungicolous	-
otu_848	<i>Acremonium polychromum</i>	1	5	Fungicolous	-
otu_872	<i>Acremonium polychromum</i>	1	3	Fungicolous	-
otu_907	<i>Acremonium polychromum</i>	1	3	Fungicolous	-
otu_1071	<i>Acremonium stromaticum</i>	1	2	Fungicolous	-
otu_116	<i>Acremonium stromaticum</i>	9	3752	Fungicolous	-
otu_128	<i>Acremonium stromaticum</i>	3	542	Fungicolous	-
otu_304	<i>Acremonium stromaticum</i>	1	74	Fungicolous	-
otu_725	<i>Acremonium stromaticum</i>	1	6	Fungicolous	x
otu_607	<i>Acremonium persicinum</i>	2	17	Fungicolous	-
otu_1027	<i>Acremonium polychromum</i>	2	22	Fungicolous	-
otu_153	<i>Acremonium polychromum</i>	6	3216	Fungicolous	-
otu_204	<i>Acremonium polychromum</i>	2	4	Fungicolous	-
otu_226	<i>Acremonium polychromum</i>	1	96	Fungicolous	-
otu_28	<i>Acremonium polychromum</i>	20	26018	Fungicolous	-
otu_447	<i>Acremonium polychromum</i>	1	16	Fungicolous	-

otu_850	<i>Acremonium polychromum</i>	1	7	Fungicolous	-
otu_186	<i>Acremonium species 1</i>	1	127	Fungicolous	-
otu_837	<i>Acremonium species 2</i>	1	3	Fungicolous	-
otu_846	<i>Acremonium species 3</i>	4	86	Fungicolous	-
otu_1087	<i>Acremonium species 4</i>	2	4	Fungicolous	-
otu_7	<i>Agaricales species 1</i>	24	63494	Undetermined	-
otu_139	<i>Agaricales species 2</i>	2	303	Undetermined	-
otu_310	<i>Agaricales species 3</i>	1	42	Undetermined	-
otu_431	<i>Agaricales species 4</i>	1	37	Undetermined	-
otu_385	<i>Agaricales species 5</i>	2	66	Undetermined	-
otu_666	<i>Agaricomycetes species 10</i>	1	12	Undetermined	-
otu_392	<i>Agaricomycetes species 11</i>	2	39	Undetermined	-
otu_1021	<i>Agaricomycetes species 12</i>	1	2	Undetermined	-
otu_509	<i>Agaricomycetes species 13</i>	2	17	Undetermined	-
otu_448	<i>Agaricomycetes species 14</i>	1	66	Undetermined	-
otu_598	<i>Agaricomycetes species 2</i>	1	10	Undetermined	-
otu_302	<i>Agaricomycetes species 3</i>	4	66	Undetermined	-
otu_223	<i>Agaricomycetes species 4</i>	1	119	Undetermined	-
otu_1231	<i>Agaricomycetes species 5</i>	1	2	Undetermined	-
otu_1245	<i>Agaricomycetes species 6</i>	1	2	Undetermined	-
otu_136	<i>Agaricomycetes species 7</i>	1	310	Undetermined	-
otu_710	<i>Agaricomycetes species 8</i>	3	15	Undetermined	-
otu_944	<i>Agaricomycetes species 9</i>	1	2	Undetermined	-
otu_640	<i>Agrocybe erebia</i>	1	8	Saprotroph	-
otu_789	<i>Alternaria alternata</i>	1	5	Plant pathogen	-
otu_484	<i>Amyloporia xantha</i>	1	15	Saprotroph	-
otu_485	<i>Amyloxenasma</i>	1	23	Saprotroph	-
otu_486	<i>Ascomycota species 10</i>	1	13	Undetermined	-
otu_240	<i>Ascomycota species 11</i>	1	82	Undetermined	-
otu_1004	<i>Ascomycota species 12</i>	1	2	Undetermined	-
otu_1112	<i>Ascomycota species 13</i>	1	2	Undetermined	-
otu_119	<i>Ascomycota species 14</i>	1	432	Undetermined	-
otu_1079	<i>Ascomycota species 15</i>	1	2	Undetermined	-
otu_235	<i>Ascomycota species 16</i>	1	481	Undetermined	-
otu_575	<i>Ascomycota species 17</i>	1	11	Undetermined	-
otu_695	<i>Ascomycota species 18</i>	1	8	Undetermined	-
otu_1023	<i>Ascomycota species 19</i>	2	4	Undetermined	-
otu_1228	<i>Ascomycota species 20</i>	1	4	Undetermined	-
otu_557	<i>Ascomycota species 21</i>	1	23	Undetermined	-

otu_906	<i>Ascomycota species 22</i>	1	5	Undetermined	-
otu_59	<i>Ascomycota species 23</i>	5	1627	Undetermined	-
otu_524	<i>Ascomycota species 24</i>	1	18	Undetermined	-
otu_865	<i>Ascomycota species 25</i>	1	7	Undetermined	-
otu_760	<i>Ascomycota species 26</i>	1	6	Undetermined	-
otu_1066	<i>Ascomycota species 27</i>	1	4	Undetermined	-
otu_1165	<i>Ascomycota species 28</i>	1	2	Undetermined	-
otu_966	<i>Ascomycota species 29</i>	1	2	Undetermined	-
otu_1081	<i>Ascomycota species 30</i>	1	2	Undetermined	-
otu_1069	<i>Ascomycota species 31</i>	1	2	Undetermined	-
otu_681	<i>Ascomycota species 32</i>	1	8	Undetermined	-
otu_522	<i>Ascomycota species 33</i>	5	38	Undetermined	-
otu_322	<i>Ascomycota species 34</i>	1	34	Undetermined	x
otu_1181	<i>Ascomycota species 35</i>	1	4	Undetermined	-
otu_939	<i>Ascomycota species 36</i>	1	2	Undetermined	-
otu_173	<i>Ascomycota species 37</i>	1	158	Undetermined	-
otu_368	<i>Ascomycota species 38</i>	5	78	Undetermined	-
otu_1083	<i>Ascomycota species 39</i>	1	2	Undetermined	-
otu_970	<i>Ascomycota species 4</i>	1	2	Undetermined	x
otu_411	<i>Ascomycota species 40</i>	4	112	Undetermined	-
otu_1156	<i>Ascomycota species 41</i>	1	2	Undetermined	-
otu_737	<i>Ascomycota species 42</i>	1	6	Undetermined	-
otu_874	<i>Ascomycota species 43</i>	1	3	Undetermined	-
otu_611	<i>Ascomycota species 44</i>	1	13	Undetermined	-
otu_1148	<i>Ascomycota species 45</i>	1	2	Undetermined	-
otu_502	<i>Ascomycota species 46</i>	1	35	Undetermined	x
otu_1094	<i>Ascomycota species 47</i>	1	2	Undetermined	-
otu_1068	<i>Ascomycota species 48</i>	1	2	Undetermined	-
otu_1024	<i>Ascomycota species 49</i>	1	2	Undetermined	-
otu_819	<i>Ascomycota species 5</i>	1	6	Undetermined	-
otu_898	<i>Ascomycota species 50</i>	1	3	Undetermined	-
otu_723	<i>Ascomycota species 51</i>	1	4	Undetermined	-
otu_1130	<i>Ascomycota species 52</i>	1	2	Undetermined	x
otu_609	<i>Ascomycota species 53</i>	1	14	Undetermined	-
otu_854	<i>Ascomycota species 54</i>	2	9	Undetermined	-
otu_714	<i>Ascomycota species 55</i>	1	8	Undetermined	-
otu_855	<i>Ascomycota species 56</i>	1	6	Undetermined	-
otu_647	<i>Ascomycota species 57</i>	1	8	Undetermined	-
otu_703	<i>Ascomycota species 58</i>	1	4	Undetermined	-

otu_1096	<i>Ascomycota species 59</i>	1	2	Undetermined	-
otu_853	<i>Ascomycota species 6</i>	1	5	Undetermined	-
otu_413	<i>Ascomycota species 60</i>	1	46	Undetermined	-
otu_459	<i>Ascomycota species 61</i>	1	22	Undetermined	-
otu_1070	<i>Ascomycota species 62</i>	1	2	Undetermined	-
otu_744	<i>Ascomycota species 63</i>	1	17	Undetermined	-
otu_1216	<i>Ascomycota species 64</i>	1	2	Undetermined	-
otu_338	<i>Ascomycota species 65</i>	1	34	Undetermined	-
otu_174	<i>Ascomycota species 66</i>	1	233	Undetermined	-
otu_519	<i>Ascomycota species 67</i>	1	19	Undetermined	-
otu_730	<i>Ascomycota species 68</i>	1	10	Undetermined	-
otu_841	<i>Ascomycota species 69</i>	1	8	Undetermined	-
otu_704	<i>Ascomycota species 7</i>	1	4	Undetermined	-
otu_876	<i>Ascomycota species 70</i>	1	3	Undetermined	-
otu_568	<i>Ascomycota species 71</i>	2	17	Undetermined	-
otu_425	<i>Ascomycota species 72</i>	3	33	Undetermined	-
otu_178	<i>Ascomycota species 73</i>	1	345	Undetermined	-
otu_494	<i>Ascomycota species 74</i>	1	11	Undetermined	-
otu_736	<i>Ascomycota species 75</i>	1	11	Undetermined	-
otu_373	<i>Ascomycota species 76</i>	1	44	Undetermined	-
otu_957	<i>Ascomycota species 77</i>	1	2	Undetermined	-
otu_836	<i>Ascomycota species 78</i>	1	5	Undetermined	-
otu_274	<i>Ascomycota species 79</i>	1	68	Undetermined	-
otu_631	<i>Ascomycota species 8</i>	3	12	Undetermined	-
otu_842	<i>Ascomycota species 80</i>	1	23	Undetermined	-
otu_954	<i>Ascomycota species 9</i>	1	2	Undetermined	-
otu_340	<i>Aspergillus penicillioides</i>	1	29	Saprotroph	-
otu_211	<i>Athelia decipiens</i>	1	94	Plant pathogen	-
otu_198	<i>Auriculariales Incertae sedis</i>	1	209	Undetermined	-
otu_305	<i>Basidiobolus ranarum</i>	1	91	Saprotroph	-
otu_127	<i>Basidiomycota speccies 1</i>	1	325	Undetermined	-
otu_503	<i>Basidiomycota speccies 2</i>	1	4	Undetermined	-
otu_455	<i>Basidiomycota speccies 3</i>	1	20	Undetermined	-
otu_76	<i>Basidiomycota speccies 4</i>	2	1483	Undetermined	-
otu_618	<i>Basidiomycota speccies 5</i>	1	8	Undetermined	-
otu_573	<i>Basidiomycota speccies 6</i>	1	28	Undetermined	-
otu_152	<i>Basidiomycota speccies 7</i>	1	224	Undetermined	-
otu_260	<i>Basidiomycota speccies 8</i>	1	85	Undetermined	-
otu_809	<i>Beltrania rhombica</i>	1	5	Saprotroph	-

otu_20	<i>Bionectriaceae species 1</i>	4	10	Saprotroph	-
otu_1199	<i>Bionectriaceae species 2</i>	1	2	Saprotroph	-
otu_1158	<i>Bionectriaceae species 3</i>	1	8	Saprotroph	-
otu_432	<i>Bionectriaceae species 4</i>	1	21	Saprotroph	-
otu_267	<i>Bjerkandera species 1</i>	1	47	Saprotroph	-
otu_726	<i>Blastobotrys nivea</i>	1	13	Saprotroph	-
otu_453	<i>Bullera alba</i>	1	18	Saprotroph	-
otu_354	<i>Calyprella capula</i>	1	22	Saprotroph	-
otu_1122	<i>Campylocarpon fasciculare</i>	1	2	Plant pathogen	-
otu_1140	<i>Campylocarpon fasciculare</i>	1	8	Plant pathogen	-
otu_224	<i>Campylocarpon fasciculare</i>	3	148	Plant pathogen	-
otu_57	<i>Campylocarpon fasciculare</i>	4	1744	Plant pathogen	-
otu_671	<i>Campylocarpon species 1</i>	1	8	Plant pathogen	-
otu_429	<i>Campylocarpon species 2</i>	1	12	Plant pathogen	-
otu_922	<i>Candida duobushaemulonii</i>	1	2	Saprotroph	x
otu_108	<i>Candida glabrosa</i>	1	494	Saprotroph	-
otu_1132	<i>Candida pseudohaemulonii</i>	1	2	Saprotroph	x
otu_436	<i>Candida oceani</i>	1	13	Saprotroph	-
otu_693	<i>Candida santamariae</i>	1	6	Saprotroph	-
otu_623	<i>Candida species 3</i>	1	40	Saprotroph	x
otu_4	<i>Candida temnochilae</i>	20	106	Saprotroph	-
otu_467	<i>Chaetothyriales species 1</i>	1	20	Undetermined	-
otu_702	<i>Chaetothyriales species 2</i>	1	7	Undetermined	-
otu_788	<i>Chaetothyriales species 3</i>	1	10	Undetermined	-
otu_72	<i>Clavicipitaceae species 1</i>	2	208	Entomopathogenic	-
otu_869	<i>Clavicipitaceae species 3</i>	1	11	Entomopathogenic	-
otu_451	<i>Clavicipitaceae species 4</i>	1	42	Entomopathogenic	-
otu_870	<i>Clavicipitaceae species 5</i>	1	5	Entomopathogenic	-
otu_288	<i>Clavicipitaceae species 6</i>	1	13	Entomopathogenic	-
otu_902	<i>Clavicipitaceae species 7</i>	1	9	Entomopathogenic	-
otu_820	<i>Clavicipitaceae species 8</i>	1	5	Entomopathogenic	-
otu_1233	<i>Clonostachys pityrodes</i>	1	2	Saprotroph	-
otu_1234	<i>Clonostachys pityrodes</i>	1	2	Saprotroph	-
otu_301	<i>Clonostachys divergens</i>	2	50	Saprotroph	-
otu_1171	<i>Clonostachys phyllophila</i>	1	2	Saprotroph	-
otu_1077	<i>Clonostachys rosea</i>	1	2	Saprotroph	-
otu_111	<i>Clonostachys rosea</i>	9	1480	Saprotroph	-
otu_1200	<i>Clonostachys rosea</i>	1	2	Saprotroph	x
otu_1207	<i>Clonostachys rosea</i>	1	2	Saprotroph	x

otu_129	<i>Clonostachys rosea</i>	2	658	Saprotroph	-
otu_561	<i>Clonostachys rosea</i>	2	24	Saprotroph	-
otu_567	<i>Clonostachys rosea</i>	1	12	Saprotroph	x
otu_894	<i>Clonostachys rosea</i>	1	3	Saprotroph	x
otu_913	<i>Clonostachys rosea</i>	4	40	Saprotroph	x
otu_1208	<i>Clonostachys species 1</i>	1	2	Saprotroph	-
otu_581	<i>Clonostachys species 10</i>	1	22	Saprotroph	-
otu_887	<i>Clonostachys species 11</i>	1	3	Saprotroph	-
otu_891	<i>Clonostachys species 2</i>	1	11	Saprotroph	-
otu_617	<i>Clonostachys species 3</i>	2	15	Saprotroph	-
otu_1101	<i>Clonostachys species 4</i>	1	2	Saprotroph	-
otu_621	<i>Clonostachys species 5</i>	5	19	Saprotroph	-
otu_1159	<i>Clonostachys species 6</i>	1	4	Saprotroph	-
otu_895	<i>Clonostachys species 7</i>	1	6	Saprotroph	-
otu_935	<i>Clonostachys species 8</i>	1	2	Saprotroph	-
otu_672	<i>Clonostachys species 9</i>	1	7	Saprotroph	-
otu_871	<i>Cutaneotrichosporon jirovecii</i>	1	5	Saprotroph	-
otu_404	<i>Cylindrobasidium evolvens</i>	1	17	Undetermined	-
otu_375	<i>Cyphellaceae species 1</i>	1	19	Undetermined	-
otu_251	<i>Cystofilobasidium macerans</i>	1	65	Saprotroph	-
otu_811	<i>Dacryobolus sudans</i>	1	5	Plant pathogen	-
otu_1198	<i>Debaryomyces nepalensis</i>	1	18	Saprotroph	-
otu_18	<i>Debaryomyces nepalensis</i>	28	36255	Saprotroph	-
otu_862	<i>Debaryomyces nepalensis</i>	30	2147	Saprotroph	-
otu_1212	<i>Debaryomyces species 1</i>	1	2	Saprotroph	-
otu_751	<i>Debaryomyces species 2</i>	1	11	Saprotroph	-
otu_1206	<i>Debaryomyces species 3</i>	1	2	Saprotroph	x
otu_669	<i>Debaryomyces species 4</i>	3	16	Saprotroph	-
otu_530	<i>Debaryomyces species 5</i>	3	60	Saprotroph	-
otu_208	<i>Debaryomyces species 6</i>	4	235	Saprotroph	-
otu_1118	<i>Debaryomyces species 7</i>	1	4	Saprotroph	-
otu_120	<i>Debaryomyces vindobonensis</i>	10	1662	Saprotroph	-
otu_2	<i>Debaryomyces vindobonensis</i>	72	255672	Saprotroph	-
otu_405	<i>Debaryomyces vindobonensis</i>	5	111	Saprotroph	-
otu_659	<i>Debaryomyces vindobonensis</i>	2	11	Saprotroph	-
otu_668	<i>Debaryomyces vindobonensis</i>	6	113	Saprotroph	-
otu_905	<i>Debaryomyces vindobonensis</i>	3	10	Saprotroph	-
otu_1030	<i>Erythromyces crocicreas</i>	1	6	Saprotroph	-
otu_175	<i>Exophiala equina</i>	3	215	Saprotroph	-

otu_161	<i>Filobasidium magnum</i>	1	296	Saprotroph	-
otu_910	<i>Fomitiporia</i>	1	3	Plant pathogen	-
otu_1178	<i>Fusarium keratoplasticum</i>	1	8	Plant pathogen	-
otu_258	<i>Fusarium keratoplasticum</i>	4	205	Plant pathogen	-
otu_26	<i>Fusarium neocosmosporiellum</i>	12	9913	Plant pathogen	-
otu_523	<i>Fusarium neocosmosporiellum</i>	1	10	Plant pathogen	-
otu_748	<i>Fusarium neocosmosporiellum</i>	1	9	Plant pathogen	-
otu_359	<i>Fusarium solani</i>	1	23	Plant pathogen	-
otu_417	<i>Fusarium solani</i>	1	28	Plant pathogen	-
otu_908	<i>Fuscoporia</i>	1	5	Saprotroph	-
otu_320	<i>Fuscoporia gilva</i>	1	44	Wood decay	-
otu_294	<i>Fuscoporia ferruginosa</i>	1	49	Saprotroph	-
otu_1072	<i>Fusicolla acetilerea</i>	3	6	Saprotroph	x
otu_213	<i>Fusicolla acetilerea</i>	3	79	Saprotroph	-
otu_67	<i>Fusicolla acetilerea</i>	11	1325	Saprotroph	-
otu_734	<i>Gliomastix species 1</i>	1	7	Saprotroph	-
otu_300	<i>Gliomastix species 2</i>	1	50	Saprotroph	-
otu_212	<i>Gliomastix species 3</i>	4	134	Saprotroph	-
otu_269	<i>Gloeoporus pannocinctus</i>	1	62	Wood decay	-
otu_343	<i>Golubevia pallescens</i>	1	37	Undetermined	-
otu_367	<i>Gongronella butleri</i>	3	100	Saprotroph	-
otu_975	<i>Gongronella butleri</i>	1	2	Saprotroph	-
otu_192	<i>Graphium jumulu</i>	2	133	Saprotroph	-
otu_614	<i>Graphium jumulu</i>	1	6	Saprotroph	-
otu_1082	<i>Graphium species 1</i>	1	2	Saprotroph	-
otu_1080	<i>Graphium species 2</i>	1	4	Saprotroph	-
otu_326	<i>Graphium species 3</i>	2	49	Saprotroph	-
otu_552	<i>Gymnopilus</i>	2	15	Wood decay	-
otu_927	<i>Gymnopus melanopus</i>	1	2	Saprotroph	-
otu_497	<i>Halomyces littoreus</i>	1	12	Plant Pathogen	-
otu_249	<i>Halosphaeriaceae species 1</i>	2	245	Undetermined	-
otu_1031	<i>Hymenochaetaceae species 1</i>	1	2	Undetermined	-
otu_712	<i>Hymenochaetopsis rigidula</i>	1	7	Saprotroph	-
otu_268	<i>Hyphodermella rosae</i>	3	82	Saprotroph	-
otu_278	<i>Hyphodontia flavipora</i>	5	87	Wood decay	-
otu_705	<i>Hyphodontia arguta</i>	2	9	Saprotroph	-
otu_442	<i>Hyphodontia microspora</i>	1	16	Saprotroph	-
otu_1010	<i>Hypholoma capnoides</i>	1	4	Wood decay	-
otu_926	<i>Hypocreales Incertae sedis</i>	1	2	Undetermined	x

otu_976	<i>Hypocreales species 1</i>	1	2	Undetermined	-
otu_1182	<i>Hypocreales species 10</i>	1	2	Undetermined	-
otu_11	<i>Hypocreales species 100</i>	30	47429	Undetermined	-
otu_475	<i>Hypocreales species 101</i>	6	34	Undetermined	-
otu_821	<i>Hypocreales species 102</i>	1	33	Undetermined	x
otu_608	<i>Hypocreales species 103</i>	1	13	Undetermined	-
otu_727	<i>Hypocreales species 104</i>	1	4	Undetermined	-
otu_1205	<i>Hypocreales species 105</i>	2	148	Undetermined	-
otu_675	<i>Hypocreales species 106</i>	1	17	Undetermined	-
otu_1246	<i>Hypocreales species 107</i>	1	2	Undetermined	x
otu_858	<i>Hypocreales species 108</i>	1	3	Undetermined	-
otu_774	<i>Hypocreales species 109</i>	1	5	Undetermined	-
otu_466	<i>Hypocreales species 11</i>	12	1288	Undetermined	x
otu_1111	<i>Hypocreales species 110</i>	1	2	Undetermined	-
otu_114	<i>Hypocreales species 111</i>	4	463	Undetermined	-
otu_1126	<i>Hypocreales species 112</i>	1	4	Undetermined	-
otu_358	<i>Hypocreales species 113</i>	2	89	Undetermined	-
otu_890	<i>Hypocreales species 114</i>	1	3	Undetermined	-
otu_884	<i>Hypocreales species 115</i>	1	3	Undetermined	-
otu_414	<i>Hypocreales species 116</i>	2	29	Undetermined	-
otu_1194	<i>Hypocreales species 117</i>	1	4	Undetermined	-
otu_679	<i>Hypocreales species 118</i>	6	20	Undetermined	-
otu_468	<i>Hypocreales species 119</i>	1	15	Undetermined	-
otu_845	<i>Hypocreales species 12</i>	1	3	Undetermined	x
otu_201	<i>Hypocreales species 120</i>	5	139	Undetermined	-
otu_327	<i>Hypocreales species 121</i>	1	96	Undetermined	-
otu_750	<i>Hypocreales species 122</i>	2	20	Undetermined	x
otu_1227	<i>Hypocreales species 123</i>	1	2	Undetermined	x
otu_775	<i>Hypocreales species 124</i>	1	3	Undetermined	-
otu_54	<i>Hypocreales species 125</i>	3	1507	Undetermined	-
otu_873	<i>Hypocreales species 126</i>	1	5	Undetermined	-
otu_653	<i>Hypocreales species 127</i>	3	7	Undetermined	-
otu_1151	<i>Hypocreales species 128</i>	1	2	Undetermined	-
otu_1155	<i>Hypocreales species 129</i>	1	2	Undetermined	-
otu_729	<i>Hypocreales species 13</i>	1	10	Undetermined	-
otu_1203	<i>Hypocreales species 130</i>	1	2	Undetermined	x
otu_150	<i>Hypocreales species 131</i>	4	296	Undetermined	-
otu_520	<i>Hypocreales species 132</i>	1	28	Undetermined	-
otu_1224	<i>Hypocreales species 133</i>	1	2	Undetermined	-

otu_1091	<i>Hypocreales species 134</i>	1	4	Undetermined	x
otu_122	<i>Hypocreales species 136</i>	21	1783	Undetermined	-
otu_273	<i>Hypocreales species 137</i>	1	118	Undetermined	-
otu_856	<i>Hypocreales species 138</i>	1	3	Undetermined	-
otu_868	<i>Hypocreales species 139</i>	1	5	Undetermined	-
otu_1179	<i>Hypocreales species 14</i>	1	2	Undetermined	-
otu_207	<i>Hypocreales species 140</i>	2	272	Undetermined	-
otu_610	<i>Hypocreales species 141</i>	2	23	Undetermined	-
otu_570	<i>Hypocreales species 15</i>	2	21	Undetermined	-
otu_395	<i>Hypocreales species 16</i>	1	25	Undetermined	-
otu_353	<i>Hypocreales species 17</i>	2	53	Undetermined	-
otu_189	<i>Hypocreales species 18</i>	3	288	Undetermined	-
otu_1116	<i>Hypocreales species 19</i>	1	2	Undetermined	x
otu_1187	<i>Hypocreales species 2</i>	1	2	Undetermined	-
otu_881	<i>Hypocreales species 20</i>	1	5	Undetermined	-
otu_866	<i>Hypocreales species 21</i>	1	3	Undetermined	-
otu_921	<i>Hypocreales species 22</i>	1	2	Undetermined	-
otu_1136	<i>Hypocreales species 23</i>	1	8	Undetermined	-
otu_371	<i>Hypocreales species 24</i>	9	164	Undetermined	-
otu_1086	<i>Hypocreales species 25</i>	1	4	Undetermined	-
otu_34	<i>Hypocreales species 26</i>	3	8534	Undetermined	-
otu_1015	<i>Hypocreales species 27</i>	1	4	Undetermined	-
otu_384	<i>Hypocreales species 28</i>	1	18	Undetermined	-
otu_1127	<i>Hypocreales species 29</i>	1	2	Undetermined	-
otu_786	<i>Hypocreales species 3</i>	1	3	Undetermined	-
otu_1152	<i>Hypocreales species 30</i>	1	2	Undetermined	-
otu_1085	<i>Hypocreales species 31</i>	1	2	Undetermined	x
otu_334	<i>Hypocreales species 32</i>	6	385	Undetermined	-
otu_56	<i>Hypocreales species 33</i>	5	1372	Undetermined	-
otu_97	<i>Hypocreales species 34</i>	2	631	Undetermined	-
otu_554	<i>Hypocreales species 35</i>	1	9	Undetermined	-
otu_155	<i>Hypocreales species 36</i>	1	198	Undetermined	-
otu_50	<i>Hypocreales species 37</i>	3	1936	Undetermined	-
otu_670	<i>Hypocreales species 38</i>	1	7	Undetermined	-
otu_889	<i>Hypocreales species 39</i>	1	3	Undetermined	-
otu_312	<i>Hypocreales species 4</i>	1	48	Undetermined	-
otu_1193	<i>Hypocreales species 40</i>	1	4	Undetermined	-
otu_885	<i>Hypocreales species 41</i>	1	3	Undetermined	-
otu_606	<i>Hypocreales species 42</i>	2	8	Undetermined	-

otu_257	<i>Hypocreales species 43</i>	6	157	Undetermined	-
otu_1168	<i>Hypocreales species 44</i>	1	2	Undetermined	-
otu_559	<i>Hypocreales species 45</i>	3	16	Undetermined	x
otu_622	<i>Hypocreales species 46</i>	3	17	Undetermined	-
otu_839	<i>Hypocreales species 47</i>	1	7	Undetermined	-
otu_488	<i>Hypocreales species 48</i>	1	13	Undetermined	-
otu_1078	<i>Hypocreales species 49</i>	1	2	Undetermined	x
otu_529	<i>Hypocreales species 5</i>	1	8	Undetermined	-
otu_667	<i>Hypocreales species 50</i>	1	25	Undetermined	-
otu_1149	<i>Hypocreales species 51</i>	1	2	Undetermined	-
otu_743	<i>Hypocreales species 52</i>	1	4	Undetermined	-
otu_1115	<i>Hypocreales species 53</i>	1	2	Undetermined	x
otu_941	<i>Hypocreales species 54</i>	3	8	Undetermined	-
otu_1032	<i>Hypocreales species 55</i>	1	2	Undetermined	-
otu_965	<i>Hypocreales species 56</i>	1	2	Undetermined	-
otu_1110	<i>Hypocreales species 57</i>	1	4	Undetermined	-
otu_1135	<i>Hypocreales species 58</i>	1	2	Undetermined	-
otu_510	<i>Hypocreales species 59</i>	2	25	Undetermined	-
otu_1057	<i>Hypocreales species 6</i>	1	2	Undetermined	-
otu_1129	<i>Hypocreales species 60</i>	1	2	Undetermined	-
otu_735	<i>Hypocreales species 61</i>	1	9	Undetermined	-
otu_641	<i>Hypocreales species 62</i>	2	14	Undetermined	-
otu_1088	<i>Hypocreales species 63</i>	1	2	Undetermined	-
otu_1167	<i>Hypocreales species 64</i>	1	4	Undetermined	-
otu_572	<i>Hypocreales species 65</i>	1	15	Undetermined	-
otu_1183	<i>Hypocreales species 66</i>	1	8	Undetermined	-
otu_1036	<i>Hypocreales species 67</i>	1	2	Undetermined	-
otu_1188	<i>Hypocreales species 68</i>	1	2	Undetermined	-
otu_1074	<i>Hypocreales species 69</i>	1	2	Undetermined	x
otu_604	<i>Hypocreales species 7</i>	1	9	Undetermined	-
otu_1022	<i>Hypocreales species 70</i>	3	20	Undetermined	x
otu_1197	<i>Hypocreales species 71</i>	1	4	Undetermined	x
otu_1033	<i>Hypocreales species 72</i>	1	2	Undetermined	-
otu_1201	<i>Hypocreales species 73</i>	2	8	Undetermined	x
otu_682	<i>Hypocreales species 74</i>	4	31	Undetermined	x
otu_8	<i>Hypocreales species 75</i>	50	150140	Undetermined	-
otu_289	<i>Hypocreales species 76</i>	2	69	Undetermined	-
otu_1102	<i>Hypocreales species 77</i>	1	2	Undetermined	-
otu_1076	<i>Hypocreales species 78</i>	1	2	Undetermined	-

otu_419	<i>Hypocreales species 79</i>	2	36	Undetermined	-
otu_911	<i>Hypocreales species 8</i>	1	7	Undetermined	-
otu_971	<i>Hypocreales species 80</i>	1	2	Undetermined	-
otu_563	<i>Hypocreales species 81</i>	1	13	Undetermined	-
otu_620	<i>Hypocreales species 82</i>	2	13	Undetermined	-
otu_525	<i>Hypocreales species 83</i>	1	16	Undetermined	-
otu_844	<i>Hypocreales species 84</i>	1	7	Undetermined	-
otu_1214	<i>Hypocreales species 85</i>	1	2	Undetermined	-
otu_549	<i>Hypocreales species 86</i>	2	15	Undetermined	-
otu_387	<i>Hypocreales species 87</i>	2	38	Undetermined	-
otu_1131	<i>Hypocreales species 88</i>	2	4	Undetermined	-
otu_928	<i>Hypocreales species 89</i>	3	8	Undetermined	-
otu_284	<i>Hypocreales species 9</i>	1	61	Undetermined	-
otu_940	<i>Hypocreales species 90</i>	1	2	Undetermined	-
otu_1176	<i>Hypocreales species 91</i>	1	2	Undetermined	-
otu_528	<i>Hypocreales species 92</i>	1	17	Undetermined	-
otu_720	<i>Hypocreales species 93</i>	1	2	Undetermined	-
otu_196	<i>Hypocreales species 94</i>	2	142	Undetermined	-
otu_1123	<i>Hypocreales species 95</i>	1	2	Undetermined	-
otu_777	<i>Hypocreales species 96</i>	2	8	Undetermined	-
otu_1119	<i>Hypocreales species 97</i>	1	4	Undetermined	-
otu_749	<i>Hypocreales species 98</i>	1	13	Undetermined	-
otu_5	<i>Hypocreales species 99</i>	41	87459	Undetermined	-
otu_183	<i>Irpex lacteus</i>	2	166	Wood decay	-
otu_590	<i>Isodon ramosissimus</i>	1	9	Saprotroph	-
otu_629	<i>Jattaea prunicola</i>	1	11	Wood decay	-
otu_972	<i>Junghuhnia nitida</i>	1	2	Wood decay	-
otu_1218	<i>Lasiodiplodia theobromae</i>	1	2	Plant pathogen	-
otu_222	<i>Lasiodiplodia theobromae</i>	1	123	Plant pathogen	-
otu_206	<i>Lentinellus castoreus</i>	1	92	Saprotroph	-
otu_41	<i>Lenzites betulina</i>	2	3309	Wood decay	-
otu_1017	<i>Leptosphaeria</i>	1	2	Plant pathogen	x
otu_569	<i>Leptosporomyces</i>	1	17	Saprotroph	-
otu_1026	<i>Lyomyces erastii</i>	1	2	Saprotroph	-
otu_1029	<i>Malassezia globosa</i>	1	2	Saprotroph	-
otu_135	<i>Malassezia globosa</i>	3	16	Saprotroph	-
otu_25	<i>Malassezia globosa</i>	12	28413	Saprotroph	-
otu_504	<i>Malassezia globosa</i>	3	28	Saprotroph	-
otu_53	<i>Malassezia globosa</i>	18	5987	Saprotroph	-

otu_785	<i>Malassezia globosa</i>	1	3	Saprotroph	-
otu_808	<i>Malassezia globosa</i>	4	43	Saprotroph	-
otu_92	<i>Malassezia globosa</i>	10	878	Saprotroph	-
otu_43	<i>Malassezia species 1</i>	3	3277	Saprotroph	-
otu_943	<i>Marasmiaceae species 1</i>	1	2	Plant pathogen	-
otu_585	<i>Marasmiaceae species 2</i>	1	13	Plant pathogen	-
otu_1014	<i>Marasmiaceae species 3</i>	1	2	Plant pathogen	-
otu_24	<i>Marasmiaceae species 4</i>	3	3507	Plant pathogen	-
otu_964	<i>Marasmiaceae species 5</i>	1	2	Plant pathogen	-
otu_1217	<i>Marasmiaceae species 6</i>	1	2	Plant pathogen	-
otu_94	<i>Marasmius species 1</i>	1	1046	Saprotroph	-
otu_596	<i>Meruliaceae species 1</i>	1	10	Undetermined	-
otu_6	<i>Metarhizium species 1</i>	32	62691	Entomopathogenic	-
otu_1236	<i>Meyerozyma caribbica</i>	1	2	Saprotroph	-
otu_1232	<i>Mortierella species 1</i>	1	2	Saprotroph	-
otu_493	<i>Mucor</i>	1	12	Saprotroph	-
otu_632	<i>Mycena galericulata</i>	1	7	Saprotroph	-
otu_277	<i>Mycena species 1</i>	1	51	Saprotroph	-
otu_47	<i>Mycenaceae species 1</i>	2	2859	Undetermined	-
otu_440	<i>Mycoacia fuscoatra</i>	2	26	Saprotroph	-
otu_812	<i>Mycoacia uda</i>	1	3	Saprotroph	-
otu_35	<i>Myrothecium species 1</i>	7	7925	Saprotroph	-
otu_1170	<i>Myrothecium species 2</i>	1	2	Saprotroph	-
otu_32	<i>Naganishia diffluens</i>	2	8	Undetermined	-
otu_13	<i>Nectria pseudotrichia</i>	25	25796	Plant pathogen	-
otu_37	<i>Nectria pseudotrichia</i>	1	3703	Plant pathogen	-
otu_766	<i>Nectria pseudotrichia</i>	1	5	Plant pathogen	-
otu_901	<i>Nectria pseudotrichia</i>	1	6	Plant pathogen	-
otu_1121	<i>Nectria setofusarii</i>	1	2	Plant pathogen	-
otu_1180	<i>Nectriaceae species 1</i>	1	2	Undetermined	-
otu_1143	<i>Nectriaceae species 2</i>	1	2	Undetermined	-
otu_1128	<i>Nectriaceae species 3</i>	1	2	Undetermined	-
otu_886	<i>Nectriaceae species 4</i>	1	3	Undetermined	-
otu_1097	<i>Nectriaceae species 5</i>	1	2	Undetermined	-
otu_564	<i>Nectriaceae species 6</i>	1	9	Undetermined	-
otu_864	<i>Nectriaceae species 7</i>	1	7	Undetermined	-
otu_1073	<i>Ophiocordycipitaceae species 1</i>	1	4	Entomopathogenic	x
otu_1134	<i>Ophiocordycipitaceae species 2</i>	1	2	Entomopathogenic	-
otu_852	<i>Ophiocordycipitaceae species 3</i>	1	3	Entomopathogenic	-

otu_1092	<i>Ophiocordycipitaceae species 4</i>	1	2	Entomopathogenic	x
otu_888	<i>Ophiocordycipitaceae species 5</i>	1	3	Entomopathogenic	-
otu_1239	<i>Ophiocordycipitaceae species 6</i>	1	6	Entomopathogenic	x
otu_296	<i>Ophiostoma perfectum</i>	1	30	Plant pathogen	-
otu_133	<i>Ophiostoma rachisporum</i>	2	323	Plant pathogen	-
otu_576	<i>Penicillium citrinum</i>	2	17	Saprotroph	-
otu_1172	<i>Penicillium copticola</i>	1	2	Saprotroph	-
otu_1105	<i>Penicillium daleae</i>	1	2	Saprotroph	-
otu_754	<i>Penicillium species 1</i>	1	6	Saprotroph	-
otu_974	<i>Penicillium species 2</i>	1	4	Saprotroph	-
otu_393	<i>Penicillium species 3</i>	3	26	Saprotroph	-
otu_200	<i>Penicillium species 4</i>	4	365	Saprotroph	-
otu_146	<i>Penicillium steckii</i>	1	292	Saprotroph	-
otu_1117	<i>Penicillium sumatraense</i>	2	8	Saprotroph	-
otu_1210	<i>Penicillium sumatraense</i>	1	2	Saprotroph	-
otu_15	<i>Penicillium sumatraense</i>	19	53002	Saprotroph	-
otu_433	<i>Penicillium sumatraense</i>	12	1038	Saprotroph	-
otu_308	<i>Peniophora</i>	1	46	Wood decay	-
otu_154	<i>Peniophora albobadia</i>	2	196	Wood decay	-
otu_265	<i>Peniophora laxitexta</i>	5	144	Wood decay	-
otu_329	<i>Peniophora species 1</i>	9	243	Wood decay	-
otu_1028	<i>Peniophora species 2</i>	3	14	Wood decay	-
otu_627	<i>Peniophora species 3</i>	2	11	Wood decay	-
otu_550	<i>Peniophoraceae species 1</i>	1	13	Undetermined	-
otu_339	<i>Perenniporia vanhullii</i>	1	40	Wood decay	-
otu_969	<i>Phaeoacremonium</i>	1	2	Plant pathogen	-
otu_1162	<i>Phaeophlebiopsis caribbeana</i>	1	2	Saprotroph	-
otu_219	<i>Phanerochaete sordida</i>	1	23	Wood decay	-
otu_806	<i>Phlebia chrysocreas</i>	1	3	Wood decay	-
otu_441	<i>Phlebia rufa</i>	1	16	Wood decay	-
otu_514	<i>Phlebia tremellosa</i>	1	12	Wood decay	-
otu_978	<i>Pholiota adiposa</i>	1	2	Saprotroph	-
otu_979	<i>Physisporinus vitreus</i>	1	4	Wood decay	-
otu_124	<i>Plectosphaerella cucumerina</i>	1	270	Plant pathogen	-
otu_711	<i>Plectosphaerella cucumerina</i>	1	26	Plant pathogen	-
otu_783	<i>Plectosphaerella species 1</i>	1	5	Plant pathogen	-
otu_603	<i>Pleosporales species 1</i>	1	13	Undetermined	-
otu_143	<i>Pleosporales species 3</i>	2	442	Undetermined	-
otu_531	<i>Pleurotus pulmonarius</i>	1	17	Entomopathogenic	-

otu_262	<i>Pluteus leoninus</i>	1	67	Wood decay	-
otu_195	<i>Pochonia bulbillosa</i>	1	112	Entomopathogenic	-
otu_534	<i>Pochonia bulbillosa</i>	1	27	Entomopathogenic	-
otu_58	<i>Pochonia bulbillosa</i>	1	1630	Entomopathogenic	-
otu_580	<i>Pochonia bulbillosa</i>	1	19	Entomopathogenic	-
otu_612	<i>Pochonia species 1</i>	2	10	Entomopathogenic	-
otu_533	<i>Pochonia species 2</i>	1	16	Entomopathogenic	-
otu_822	<i>Polyporaceae species 1</i>	1	5	Undetermined	-
otu_597	<i>Polyporales species 1</i>	1	6	Undetermined	-
otu_130	<i>Polyporales species 2</i>	1	582	Undetermined	-
otu_271	<i>Postia species 1</i>	1	74	Wood decay	-
otu_548	<i>Postia stiptica</i>	1	13	Wood decay	-
otu_715	<i>Psilocybe</i>	1	6	Saprotroph	-
otu_137	<i>Puccinia coronata</i>	1	260	Plant pathogen	-
otu_1045	<i>Purpureocillium lilacinum</i>	1	2	Entomopathogenic	-
otu_1084	<i>Purpureocillium lilacinum</i>	1	4	Entomopathogenic	x
otu_555	<i>Purpureocillium lilacinum</i>	1	2	Entomopathogenic	-
otu_840	<i>Purpureocillium lilacinum</i>	1	13	Entomopathogenic	x
otu_90	<i>Purpureocillium lilacinum</i>	7	1844	Entomopathogenic	x
otu_1007	<i>Resinicium furfuraceum</i>	1	4	Saprotroph	-
otu_382	<i>Resupinatus</i>	1	26	Wood decay	-
otu_95	<i>Resupinatus alboniger</i>	2	838	Wood decay	-
otu_210	<i>Rigidoporus</i>	1	96	Wood decay	-
otu_263	<i>Rigidoporus crocatus</i>	1	76	Wood decay	-
otu_337	<i>Roussoella solani</i>	1	52	Saprotroph	-
otu_324	<i>Rubrinectria species 1</i>	1	51	Saprotroph	-
otu_1195	<i>Rubrinectria species 2</i>	1	2	Saprotroph	-
otu_933	<i>Rubrinectria species 3</i>	1	2	Saprotroph	-
otu_571	<i>Rubrinectria species 4</i>	1	12	Saprotroph	-
otu_829	<i>Rubrinectria species 5</i>	1	2	Saprotroph	-
otu_1219	<i>Rubrinectria species 6</i>	1	2	Saprotroph	-
otu_197	<i>Rubrinectria species 7</i>	1	107	Saprotroph	-
otu_1196	<i>Rubrinectria species 8</i>	1	2	Saprotroph	-
otu_1192	<i>Rubrinectria species 9</i>	1	2	Saprotroph	-
otu_323	<i>Russulales species 1</i>	1	41	Undetermined	-
otu_1240	<i>Saccharomyces species 1</i>	1	4	Wood decay	-
otu_138	<i>Saccharomyces species 2</i>	1	460	Wood decay	x
otu_458	<i>Sakaguchia dacryoidea</i>	1	17	Undetermined	-
otu_45	<i>Sampaiozyma ingeniosa</i>	1	2020	Undetermined	-

otu_1098	<i>Sarcopodium araliae</i>	1	2	Saprotroph	-
otu_295	<i>Sarcopodium araliae</i>	2	60	Saprotroph	-
otu_920	<i>Sarocladium oryzae</i>	1	2	Saprotroph	x
otu_1124	<i>Sarocladium hominis</i>	1	2	Saprotroph	-
otu_950	<i>Sarocladium species 3</i>	1	2	Saprotroph	x
otu_768	<i>Sarocladium species 4</i>	2	5	Saprotroph	x
otu_250	<i>Sarocladium strictum</i>	32	656	Saprotroph	-
otu_3	<i>Sarocladium strictum</i>	129	1823481	Saprotroph	-
otu_3	<i>Sarocladium strictum</i>	129	1823481	Saprotroph	-
otu_3	<i>Sarocladium strictum</i>	129	1823481	Saprotroph	-
otu_306	<i>Sarocladium strictum</i>	9	121	Saprotroph	x
otu_388	<i>Sarocladium strictum</i>	2	84	Saprotroph	-
otu_391	<i>Sarocladium strictum</i>	6	39	Saprotroph	-
otu_418	<i>Sarocladium strictum</i>	4	74	Saprotroph	-
otu_434	<i>Sarocladium strictum</i>	31	284	Saprotroph	-
otu_435	<i>Sarocladium strictum</i>	8	107	Saprotroph	-
otu_452	<i>Sarocladium strictum</i>	1	22	Saprotroph	-
otu_584	<i>Sarocladium strictum</i>	28	113	Saprotroph	x
otu_764	<i>Sarocladium strictum</i>	3	31	Saprotroph	x
otu_765	<i>Sarocladium strictum</i>	19	50	Saprotroph	x
otu_767	<i>Sarocladium strictum</i>	11	42	Saprotroph	-
otu_77	<i>Sarocladium strictum</i>	42	3103	Saprotroph	-
otu_776	<i>Sarocladium strictum</i>	16	121	Saprotroph	-
otu_924	<i>Sarocladium strictum</i>	5	10	Saprotroph	-
otu_953	<i>Sarocladium strictum</i>	1	2	Saprotroph	x
otu_958	<i>Sarocladium strictum</i>	1	2	Saprotroph	-
otu_228	<i>Schizophyllum commune</i>	1	84	Wood decay	-
otu_160	<i>Schwanniomyces vanrijiae</i>	2	224	Undetermined	-
otu_1209	<i>Simplicillium</i>	1	2	Entomopathogenic	-
otu_335	<i>Simplicillium</i>	1	52	Entomopathogenic	-
otu_753	<i>Simplicillium</i>	1	13	Entomopathogenic	-
otu_9	<i>Simplicillium</i>	9	42624	Entomopathogenic	-
otu_42	<i>Simplicillium minatense</i>	1	2811	Entomopathogenic	-
otu_1238	<i>Simplicillium species 2</i>	1	2	Entomopathogenic	-
otu_649	<i>Sistotremastrum guttuliferum</i>	1	8	Saprotroph	-
otu_460	<i>Skeletocutis odora</i>	1	25	Wood decay	-
otu_245	<i>Sordariomycetes species 1</i>	1	72	Undetermined	-
otu_1173	<i>Sordariomycetes species 10</i>	1	2	Undetermined	-
otu_1191	<i>Sordariomycetes species 11</i>	1	4	Undetermined	-

otu_63	<i>Sordariomycetes species 12</i>	1	1071	Undetermined	-
otu_496	<i>Sordariomycetes species 13</i>	1	14	Undetermined	-
otu_30	<i>Sordariomycetes species 14</i>	8	17	Undetermined	-
otu_1189	<i>Sordariomycetes species 15</i>	1	2	Undetermined	-
otu_79	<i>Sordariomycetes species 16</i>	2	643	Undetermined	-
otu_1237	<i>Sordariomycetes species 17</i>	1	2	Undetermined	-
otu_281	<i>Sordariomycetes species 18</i>	5	104	Undetermined	-
otu_10	<i>Sordariomycetes species 19</i>	73	128406	Undetermined	-
otu_536	<i>Sordariomycetes species 2</i>	3	43	Undetermined	-
otu_1223	<i>Sordariomycetes species 20</i>	1	4	Undetermined	-
otu_823	<i>Sordariomycetes species 21</i>	1	3	Undetermined	-
otu_716	<i>Sordariomycetes species 22</i>	1	4	Undetermined	-
otu_663	<i>Sordariomycetes species 23</i>	1	5	Undetermined	-
otu_1225	<i>Sordariomycetes species 24</i>	2	6	Undetermined	-
otu_1204	<i>Sordariomycetes species 25</i>	1	2	Undetermined	-
otu_532	<i>Sordariomycetes species 26</i>	1	13	Undetermined	-
otu_248	<i>Sordariomycetes species 27</i>	3	95	Undetermined	-
otu_758	<i>Sordariomycetes species 28</i>	4	18	Undetermined	-
otu_961	<i>Sordariomycetes species 29</i>	1	2	Undetermined	-
otu_399	<i>Sordariomycetes species 3</i>	2	25	Undetermined	-
otu_1160	<i>Sordariomycetes species 30</i>	1	2	Undetermined	-
otu_877	<i>Sordariomycetes species 31</i>	1	6	Undetermined	-
otu_140	<i>Sordariomycetes species 32</i>	2	288	Undetermined	-
otu_232	<i>Sordariomycetes species 33</i>	1	210	Undetermined	-
otu_658	<i>Sordariomycetes species 34</i>	1	7	Undetermined	-
otu_521	<i>Sordariomycetes species 35</i>	1	13	Undetermined	-
otu_1114	<i>Sordariomycetes species 36</i>	1	2	Undetermined	-
otu_662	<i>Sordariomycetes species 37</i>	1	5	Undetermined	-
otu_1125	<i>Sordariomycetes species 38</i>	1	2	Undetermined	-
otu_578	<i>Sordariomycetes species 39</i>	3	19	Undetermined	-
otu_1009	<i>Sordariomycetes species 4</i>	1	2	Undetermined	-
otu_645	<i>Sordariomycetes species 40</i>	3	11	Undetermined	-
otu_1190	<i>Sordariomycetes species 41</i>	1	2	Undetermined	-
otu_454	<i>Sordariomycetes species 42</i>	1	17	Undetermined	-
otu_646	<i>Sordariomycetes species 43</i>	2	22	Undetermined	-
otu_577	<i>Sordariomycetes species 44</i>	2	17	Undetermined	-
otu_680	<i>Sordariomycetes species 45</i>	1	12	Undetermined	-
otu_477	<i>Sordariomycetes species 46</i>	1	12	Undetermined	-
otu_1163	<i>Sordariomycetes species 47</i>	1	2	Undetermined	-

otu_752	<i>Sordariomycetes species 48</i>	1	8	Undetermined	-
otu_847	<i>Sordariomycetes species 49</i>	1	3	Undetermined	-
otu_286	<i>Sordariomycetes species 5</i>	1	63	Undetermined	-
otu_171	<i>Sordariomycetes species 50</i>	4	327	Undetermined	-
otu_896	<i>Sordariomycetes species 51</i>	2	13	Undetermined	-
otu_1169	<i>Sordariomycetes species 52</i>	1	2	Undetermined	-
otu_1108	<i>Sordariomycetes species 53</i>	1	4	Undetermined	-
otu_236	<i>Sordariomycetes species 54</i>	9	632	Undetermined	-
otu_142	<i>Sordariomycetes species 55</i>	6	1905	Undetermined	-
otu_863	<i>Sordariomycetes species 56</i>	1	5	Undetermined	-
otu_33	<i>Sordariomycetes species 57</i>	8	1114	Undetermined	-
otu_27	<i>Sordariomycetes species 58</i>	8	26649	Undetermined	-
otu_755	<i>Sordariomycetes species 59</i>	1	8	Undetermined	-
otu_319	<i>Sordariomycetes species 6</i>	3	93	Undetermined	-
otu_427	<i>Sordariomycetes species 60</i>	1	14	Undetermined	-
otu_366	<i>Sordariomycetes species 61</i>	1	25	Undetermined	-
otu_238	<i>Sordariomycetes species 62</i>	1	107	Undetermined	-
otu_665	<i>Sordariomycetes species 7</i>	1	10	Undetermined	-
otu_1113	<i>Sordariomycetes species 8</i>	1	4	Undetermined	-
otu_778	<i>Sordariomycetes species 9</i>	1	5	Undetermined	-
otu_61	<i>Sporidiobolales Incertae sedis</i>	1	1136	Undetermined	-
otu_390	<i>Sporobolomyces phaffii</i>	1	23	Fungicolous	-
otu_882	<i>Stachybotryaceae species 1</i>	1	3	Undetermined	-
otu_1186	<i>Stachybotryaceae species 2</i>	1	4	Undetermined	-
otu_746	<i>Stachybotryaceae species 3</i>	1	8	Undetermined	-
otu_239	<i>Stachybotryaceae species 4</i>	1	125	Undetermined	-
otu_1177	<i>Stachybotryaceae species 5</i>	2	4	Undetermined	-
otu_499	<i>Stachybotryaceae species 6</i>	1	33	Undetermined	-
otu_346	<i>Steccherinum ochraceum</i>	1	33	Saprotroph	-
otu_272	<i>Stephanonectria keithii</i>	4	57	Saprotroph	-
otu_732	<i>Stephanonectria keithii</i>	2	10	Saprotroph	-
otu_676	<i>Stereum</i>	1	5	Saprotroph	-
otu_167	<i>Stereum sanguinolentum</i>	8	445	Saprotroph	-
otu_923	<i>Talaromyces</i>	1	2	Saprotroph	-
otu_1104	<i>Tolypocladium</i>	1	2	Entomopathogenic	x
otu_1107	<i>Tolypocladium</i>	1	2	Entomopathogenic	x
otu_1109	<i>Tolypocladium</i>	1	2	Entomopathogenic	x
otu_1157	<i>Tolypocladium</i>	1	2	Entomopathogenic	-
otu_1211	<i>Tolypocladium</i>	1	2	Entomopathogenic	x

otu_1213	<i>Tolypocladium</i>	1	2	Entomopathogenic	-
otu_21	<i>Tolypocladium</i>	23	35337	Entomopathogenic	-
otu_38	<i>Tolypocladium</i>	38	19402	Entomopathogenic	x
otu_526	<i>Tolypocladium</i>	3	36	Entomopathogenic	-
otu_686	<i>Tolypocladium</i>	2	9	Entomopathogenic	x
otu_688	<i>Tolypocladium</i>	24	994	Entomopathogenic	-
otu_859	<i>Tolypocladium</i>	1	3	Entomopathogenic	x
otu_501	<i>Tolypocladium</i>	1	13	Fungicolous	x
otu_1093	<i>Tolypocladium album</i>	1	2	Fungicolous	x
otu_1164	<i>Tolypocladium album</i>	1	4	Fungicolous	x
otu_1174	<i>Tolypocladium album</i>	1	2	Fungicolous	x
otu_1226	<i>Tolypocladium album</i>	1	4	Fungicolous	-
otu_266	<i>Tolypocladium album</i>	2	109	Fungicolous	-
otu_328	<i>Tolypocladium album</i>	3	130	Fungicolous	-
otu_40	<i>Tolypocladium album</i>	31	10597	Fungicolous	-
otu_408	<i>Tolypocladium album</i>	7	102	Fungicolous	-
otu_415	<i>Tolypocladium album</i>	3	42	Fungicolous	-
otu_428	<i>Tolypocladium album</i>	1	41	Fungicolous	-
otu_449	<i>Tolypocladium album</i>	6	89	Fungicolous	-
otu_469	<i>Tolypocladium album</i>	2	52	Fungicolous	-
otu_472	<i>Tolypocladium album</i>	1	2	Fungicolous	-
otu_527	<i>Tolypocladium album</i>	1	8	Fungicolous	-
otu_616	<i>Tolypocladium album</i>	2	25	Fungicolous	-
otu_619	<i>Tolypocladium album</i>	2	17	Fungicolous	-
otu_738	<i>Tolypocladium album</i>	1	8	Fungicolous	-
otu_739	<i>Tolypocladium album</i>	1	6	Fungicolous	-
otu_769	<i>Tolypocladium album</i>	1	3	Fungicolous	-
otu_857	<i>Tolypocladium album</i>	1	7	Fungicolous	-
otu_892	<i>Tolypocladium album</i>	1	3	Fungicolous	x
otu_893	<i>Tolypocladium album</i>	2	11	Fungicolous	-
otu_912	<i>Tolypocladium album</i>	2	8	Fungicolous	x
otu_912	<i>Tolypocladium album</i>	2	8	Fungicolous	x
otu_1000	<i>Tolypocladium album</i>	9	20	Entomopathogenic	-
otu_106	<i>Tolypocladium album</i>	13	1403	Entomopathogenic	-
otu_1137	<i>Tolypocladium album</i>	1	6	Entomopathogenic	-
otu_1147	<i>Tolypocladium album</i>	1	2	Entomopathogenic	x
otu_1150	<i>Tolypocladium album</i>	1	2	Entomopathogenic	-
otu_1153	<i>Tolypocladium album</i>	3	12	Entomopathogenic	-
otu_1154	<i>Tolypocladium album</i>	3	8	Entomopathogenic	-

otu_1166	<i>Tolypocladium album</i>	3	18	Entomopathogenic	-
otu_1185	<i>Tolypocladium album</i>	2	4	Entomopathogenic	-
otu_12	<i>Tolypocladium album</i>	52	78889	Entomopathogenic	-
otu_1215	<i>Tolypocladium album</i>	1	24	Entomopathogenic	-
otu_1220	<i>Tolypocladium album</i>	1	8	Entomopathogenic	-
otu_1241	<i>Tolypocladium album</i>	1	2	Entomopathogenic	x
otu_148	<i>Tolypocladium album</i>	7	1477	Entomopathogenic	-
otu_151	<i>Tolypocladium album</i>	5	150	Entomopathogenic	-
otu_17	<i>Tolypocladium album</i>	23	27062	Entomopathogenic	-
otu_22	<i>Tolypocladium album</i>	19	24464	Entomopathogenic	-
otu_381	<i>Tolypocladium album</i>	4	110	Entomopathogenic	x
otu_396	<i>Tolypocladium album</i>	2	16	Entomopathogenic	-
otu_443	<i>Tolypocladium album</i>	2	42	Entomopathogenic	x
otu_450	<i>Tolypocladium album</i>	6	119	Entomopathogenic	-
otu_505	<i>Tolypocladium album</i>	1	46	Entomopathogenic	-
otu_560	<i>Tolypocladium album</i>	2	15	Entomopathogenic	x
otu_741	<i>Tolypocladium album</i>	1	11	Entomopathogenic	-
otu_817	<i>Tolypocladium album</i>	1	3	Entomopathogenic	x
otu_963	<i>Tolypocladium album</i>	1	2	Entomopathogenic	-
otu_348	<i>Tolypocladium paradoxum</i>	1	41	Entomopathogenic	x
otu_875	<i>Tolypocladium species 1</i>	1	3	Fungicolous	-
otu_544	<i>Trametes gibbosa</i>	1	13	Wood decay	-
otu_314	<i>Trametes hirsuta</i>	1	56	Wood decay	-
otu_165	<i>Trechispora</i>	1	339	Wood decay	-
otu_407	<i>Trechispora species 1</i>	1	24	Wood decay	-
otu_182	<i>Trechispora species 2</i>	2	164	Wood decay	-
otu_242	<i>Trechispora species 3</i>	1	63	Wood decay	-
otu_246	<i>Trechispora species 4</i>	1	108	Wood decay	-
otu_1184	<i>Trechispora species 5</i>	1	2	Wood decay	-
otu_350	<i>Trechispora species 6</i>	1	29	Wood decay	-
otu_967	<i>Tremellales species 1</i>	1	2	Undetermined	-
otu_121	<i>Trichaptum bifforme</i>	5	942	Wood decay	-
otu_977	<i>Trichocomaceae species 1</i>	1	2	Undetermined	-
otu_188	<i>Trichoderma</i>	3	151	Fungicolous	-
otu_462	<i>Trichoderma koningiopsis</i>	2	25	Fungicolous	-
otu_253	<i>Tyromyces chioneus</i>	1	60	Wood decay	-
otu_316	<i>Tyromyces fissilis</i>	2	79	Wood decay	-
otu_372	<i>Umbelopsis isabellina</i>	2	34	Saprotroph	-
otu_158	<i>Ustilago</i>	3	252	Plant pathogen	-

otu_430	<i>Verticillium leptobactrum</i>	2	39	Nematicidal	-
otu_879	<i>Verticillium leptobactrum</i>	1	3	Nematicidal	-
otu_1230	<i>Verticillium leptobactrum</i>	1	2	Nematicidal	-
otu_221	<i>Verticillium leptobactrum</i>	1	175	Nematicidal	-
otu_280	<i>Verticillium leptobactrum</i>	1	267	Nematicidal	-
otu_31	<i>Verticillium leptobactrum</i>	11	25806	Nematicidal	-
otu_673	<i>Verticillium leptobactrum</i>	1	8	Nematicidal	-
otu_740	<i>Verticillium leptobactrum</i>	1	6	Nematicidal	-
otu_742	<i>Verticillium leptobactrum</i>	1	14	Nematicidal	-
otu_745	<i>Verticillium leptobactrum</i>	2	868	Nematicidal	-
otu_880	<i>Verticillium leptobactrum</i>	1	11	Nematicidal	-
otu_1175	<i>Verticillium species 1</i>	1	2	Nematicidal	-
otu_498	<i>Verticillium species 2</i>	1	37	Nematicidal	-
otu_118	<i>Verticillium species 3</i>	2	775	Nematicidal	-
otu_1141	<i>Verticillium species 4</i>	1	2	Nematicidal	-
otu_747	<i>Verticillium species 5</i>	1	10	Nematicidal	-
otu_1139	<i>Verticillium species 6</i>	1	2	Nematicidal	-
otu_1100	<i>Volutella</i>	1	2	Plant pathogen	-
otu_1103	<i>Volutella</i>	1	2	Plant pathogen	-
otu_1138	<i>Volutella</i>	3	22	Plant pathogen	-
otu_227	<i>Volutella</i>	4	301	Plant pathogen	-
otu_287	<i>Volutella</i>	2	66	Plant pathogen	-
otu_370	<i>Volutella</i>	3	98	Plant pathogen	-
otu_692	<i>Volutella consors</i>	1	4	Plant pathogen	-
otu_660	<i>Volutella consors</i>	1	5	Plant pathogen	-
otu_147	<i>Volutella species 1</i>	2	252	Plant pathogen	-
otu_291	<i>Volvariella bombycina</i>	1	47	Saprotroph	-
otu_46	<i>Wallemia canadensis</i>	3	3303	Saprotroph	-
otu_115	<i>Wallemia mellicola</i>	1	416	Saprotroph	-
otu_849	<i>Wallrothiella subiculosa</i>	1	5	Undetermined	-
otu_547	<i>Wolfiporia dilatohypha</i>	1	10	Wood decay	-
otu_365	<i>Xylariales species 1</i>	2	30	Undetermined	-
otu_400	<i>Xylariales species 2</i>	1	23	Undetermined	-
otu_706	<i>Xylariales species 3</i>	1	8	Undetermined	-
otu_163	<i>Xylodon nespori</i>	5	253	Saprotroph	-
otu_303	<i>Yuchengia narymica</i>	1	56	Saprotroph	-

SUPPLEMENTARY TABLE 3.3. Operational taxonomic unit (OTU) taxonomic and function guild assignments using Clustered GenBank Representatives (CLU REP) method.

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_389	<i>Absidia species 1</i>	1	50	Saprotroph
otu_168	<i>Acremonium species 1</i>	1	351	Fungicolous
otu_521	<i>Acremonium species 1.1</i>	1	13	Fungicolous
otu_755	<i>Acremonium species 10</i>	1	8	Fungicolous
otu_837	<i>Acremonium species 12</i>	1	3	Fungicolous
otu_846	<i>Acremonium species 13</i>	4	86	Fungicolous
otu_847	<i>Acremonium species 14</i>	1	3	Fungicolous
otu_890	<i>Acremonium species 15</i>	1	3	Fungicolous
otu_896	<i>Acremonium species 16</i>	2	13	Fungicolous
otu_1071	<i>Acremonium species 17</i>	1	2	Fungicolous
otu_1087	<i>Acremonium species 18</i>	2	4	Fungicolous
otu_558	<i>Acremonium species 2.1</i>	1	9	Fungicolous
otu_1151	<i>Acremonium species 20</i>	1	2	Fungicolous
otu_1169	<i>Acremonium species 22</i>	1	2	Fungicolous
otu_1176	<i>Acremonium species 23</i>	1	2	Fungicolous
otu_1205	<i>Acremonium species 24</i>	2	148	Fungicolous
otu_128	<i>Acremonium species 25</i>	3	542	Fungicolous
otu_142	<i>Acremonium species 26</i>	6	1905	Fungicolous
otu_186	<i>Acremonium species 27</i>	1	127	Fungicolous
otu_23	<i>Acremonium species 28</i>	12	22585	Fungicolous
otu_236	<i>Acremonium species 29</i>	9	632	Fungicolous
otu_116	<i>Acremonium species 3</i>	9	3752	Fungicolous
otu_8	<i>Acremonium species 3</i>	50	150140	Fungicolous
otu_658	<i>Acremonium species 3.1</i>	1	7	Fungicolous
otu_248	<i>Acremonium species 30</i>	3	95	Fungicolous
otu_27	<i>Acremonium species 31</i>	8	26649	Fungicolous
otu_304	<i>Acremonium species 32</i>	1	74	Fungicolous
otu_358	<i>Acremonium species 33</i>	2	89	Fungicolous
otu_371	<i>Acremonium species 34</i>	9	164	Fungicolous
otu_410	<i>Acremonium species 35</i>	2	74	Fungicolous
otu_578	<i>Acremonium species 36</i>	3	19	Fungicolous
otu_604	<i>Acremonium species 37</i>	1	9	Fungicolous

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_675	<i>Acremonium species 38</i>	1	17	Fungicolous
otu_1067	<i>Acremonium species 39</i>	1	4	Fungicolous
otu_727	<i>Acremonium species 4</i>	1	4	Fungicolous
otu_657	<i>Acremonium species 40</i>	1	21	Fungicolous
otu_722	<i>Acremonium species 41</i>	1	32	Fungicolous
otu_607	<i>Acremonium species 43</i>	2	17	Fungicolous
otu_839	<i>Acremonium species 5</i>	1	7	Fungicolous
otu_86	<i>Acremonium species 6</i>	1	728	Fungicolous
otu_731	<i>Acremonium species 7</i>	2	204	Fungicolous
otu_1120	<i>Acremonium species 8</i>	1	2	Fungicolous
otu_733	<i>Acremonium species 8</i>	2	25	Fungicolous
otu_752	<i>Acremonium species 9</i>	1	8	Fungicolous
otu_1163	<i>Acrostalagmus species 1</i>	1	2	Saprotroph
otu_50	<i>Acrostalagmus species 2</i>	3	1936	Saprotroph
otu_744	<i>Acrostalagmus species 3</i>	1	17	Saprotroph
otu_139	<i>Agaricales species 14.1</i>	2	303	Undetermined
otu_1229	<i>Agaricales species 15.1</i>	1	2	Undetermined
otu_1202	<i>Agaricales species 16.1</i>	1	4	Undetermined
otu_431	<i>Agaricales species 6.1</i>	1	37	Undetermined
otu_598	<i>Agaricales species 7</i>	1	10	Undetermined
otu_7	<i>Agaricales species ecies 15.2</i>	24	63494	Undetermined
otu_694	<i>Agaricomycetes species 10.1</i>	1	4	Undetermined
otu_960	<i>Agaricomycetes species 10.2</i>	1	2	Undetermined
otu_76	<i>Agaricomycetes species 12</i>	2	1483	Undetermined
otu_962	<i>Agaricomycetes species 14</i>	1	2	Undetermined
otu_16	<i>Agaricomycetes species 15.1</i>	12	30634	Undetermined
otu_900	<i>Agaricomycetes species 16.1</i>	1	9	Undetermined
otu_1243	<i>Agaricomycetes species 17.1</i>	1	2	Undetermined
otu_485	<i>Agaricomycetes species 18</i>	1	23	Undetermined
otu_553	<i>Agaricomycetes species 2</i>	1	12	Undetermined
otu_260	<i>Agaricomycetes species 20</i>	1	85	Undetermined
otu_666	<i>Agaricomycetes species 21.1</i>	1	12	Undetermined
otu_185	<i>Agaricomycetes species 23</i>	1	151	Undetermined
otu_461	<i>Agaricomycetes species 25</i>	1	31	Undetermined
otu_375	<i>Agaricomycetes species 28</i>	1	19	Undetermined
otu_198	<i>Agaricomycetes species 29</i>	1	209	Undetermined
otu_509	<i>Agaricomycetes species 3</i>	2	17	Undetermined

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_407	<i>Agaricomycetes species 30</i>	1	24	Undetermined
otu_246	<i>Agaricomycetes species 31</i>	1	108	Undetermined
otu_182	<i>Agaricomycetes species 32</i>	2	164	Undetermined
otu_104	<i>Agaricomycetes species 5.1</i>	3	766	Undetermined
otu_1075	<i>Agaricomycetes species 5.2</i>	3	8	Undetermined
otu_952	<i>Agaricomycetes species 5.3</i>	4	10	Undetermined
otu_98	<i>Agaricomycetes species 5.4</i>	3	860	Undetermined
otu_252	<i>Agaricomycetes species 6</i>	1	75	Undetermined
otu_959	<i>Agaricomycetes species 7</i>	1	4	Undetermined
otu_903	<i>Agaricomycetes species 8.1</i>	1	7	Undetermined
otu_640	<i>Agrocybe species 1</i>	1	8	Saprotroph
otu_789	<i>Alternaria species 1</i>	1	5	Plant pathogen
otu_365	<i>Amphispecies haeriaceae species</i>	2	30	Saprotroph
otu_706	<i>Amphispecies haeriaceae species</i>	1	8	Saprotroph
otu_484	<i>Amyloporia species 1</i>	1	15	Saprotroph
otu_254	<i>Ascomycota species 17</i>	1	69	Undetermined
otu_647	<i>Ascomycota species 23</i>	1	8	Undetermined
otu_644	<i>Ascomycota species 6</i>	1	5	Undetermined
otu_340	<i>Aspecies ergillus species 1</i>	1	29	Saprotroph
otu_211	<i>Athelia species 1</i>	1	94	Plant pathogen
otu_316	<i>Aurantiporus species 1</i>	2	79	Wood decay
otu_157	<i>Auriculariales species 1.1</i>	1	456	Undetermined
otu_364	<i>Auriculariales species 1.2</i>	1	35	Undetermined
otu_416	<i>Auriculariales species 1.3</i>	1	20	Undetermined
otu_615	<i>Auriculariales species 1.4</i>	1	16	Undetermined
otu_883	<i>Auriculariales species 1.5</i>	1	3	Undetermined
otu_643	<i>Auriculariales species 2</i>	1	7	Undetermined
otu_305	<i>Basidiobolus species 1</i>	1	91	Saprotroph
otu_1011	<i>Basidiodendron species 1</i>	1	2	Saprotroph
otu_362	<i>Basidiodendron species 3</i>	1	28	Saprotroph
otu_1142	<i>Basidiomycota species 1.1</i>	1	2	Undetermined
otu_625	<i>Basidiomycota species 1.2</i>	2	25	Undetermined
otu_618	<i>Basidiomycota species 10.1</i>	1	8	Undetermined
otu_824	<i>Basidiomycota species 10.2</i>	1	5	Undetermined
otu_503	<i>Basidiomycota species 13.2</i>	1	4	Undetermined
otu_444	<i>Basidiomycota species 14.1</i>	1	20	Undetermined
otu_1106	<i>Basidiomycota species 14.2</i>	1	2	Undetermined

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_311	<i>Basidiomycota species 17</i>	1	47	Undetermined
otu_199	<i>Basidiomycota species 19.1</i>	2	275	Undetermined
otu_66	<i>Basidiomycota species 19.2</i>	5	1788	Undetermined
otu_1099	<i>Basidiomycota species 22.1</i>	1	2	Undetermined
otu_386	<i>Basidiomycota species 22.2</i>	1	30	Undetermined
otu_566	<i>Basidiomycota species 22.3</i>	1	19	Undetermined
otu_677	<i>Basidiomycota species 23.1</i>	1	5	Undetermined
otu_202	<i>Basidiomycota species 23.2</i>	1	105	Undetermined
otu_867	<i>Basidiomycota species 26.1</i>	1	3	Undetermined
otu_1006	<i>Basidiomycota species 28.1</i>	1	2	Undetermined
otu_968	<i>Basidiomycota species 28.2</i>	1	2	Undetermined
otu_225	<i>Basidiomycota species 35</i>	3	127	Undetermined
otu_878	<i>Basidiomycota species 36.1</i>	1	5	Undetermined
otu_318	<i>Basidiomycota species 38.1</i>	1	48	Undetermined
otu_369	<i>Basidiomycota species 38.2</i>	1	35	Undetermined
otu_321	<i>Basidiomycota species 39</i>	1	43	Undetermined
otu_678	<i>Basidiomycota species 4.1</i>	1	8	Undetermined
otu_383	<i>Basidiomycota species 5.1</i>	1	61	Undetermined
otu_650	<i>Basidiomycota species 6</i>	1	5	Undetermined
otu_809	<i>Beltrania species 1</i>	1	5	Saprotroph
otu_540	<i>Betamyces species 1</i>	1	13	Plant pathogen
otu_695	<i>Biatriospecies ora species 1</i>	1	8	Fungicolous
otu_670	<i>Bionectriaceae species 2.1</i>	1	7	Saprotroph
otu_267	<i>Bjerkander species 1</i>	1	47	Wood decay
otu_726	<i>Blastobotrys species 1.1</i>	1	13	Saprotroph
otu_500	<i>Brevicellicium species 2</i>	1	16	Saprotroph
otu_613	<i>Brevicellicium species 5</i>	1	11	Saprotroph
otu_61	<i>Buckleyzyma species 2</i>	1	1136	Undetermined
otu_453	<i>Bullera species 1</i>	1	18	Saprotroph
otu_354	<i>Calyprella species 1</i>	1	22	Saprotroph
otu_1122	<i>Campylocarpon species 1</i>	1	2	Plant pathogen
otu_1140	<i>Campylocarpon species 2</i>	1	8	Plant pathogen
otu_224	<i>Campylocarpon species 3</i>	3	148	Plant pathogen
otu_429	<i>Campylocarpon species 4</i>	1	12	Plant pathogen
otu_57	<i>Campylocarpon species 5</i>	4	1744	Plant pathogen
otu_671	<i>Campylocarpon species 6</i>	1	8	Plant pathogen
otu_1079	<i>Candida species 1</i>	1	2	Saprotroph

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_44	<i>Candida species 1</i>	1	2366	Saprotroph
otu_436	<i>Candida species 1</i>	1	13	Saprotroph
otu_108	<i>Candida species 1</i>	1	494	Saprotroph
otu_4	<i>Candida species 1</i>	20	106	Saprotroph
otu_693	<i>Candida species 1</i>	1	6	Saprotroph
otu_302	<i>Ceriporia species 2</i>	4	66	Wood decay
otu_1021	<i>Ceriporiopsis species 1</i>	1	2	Wood decay
otu_966	<i>Chaetothyriales species 13</i>	1	2	Undetermined
otu_788	<i>Chaetothyriales species 14</i>	1	10	Undetermined
otu_1187	<i>Chaetothyriales species 15.1</i>	1	2	Undetermined
otu_680	<i>Chaetothyriales species 15.2</i>	1	12	Undetermined
otu_467	<i>Chaetothyriales species 17.1</i>	1	20	Undetermined
otu_702	<i>Chaetothyriales species 25</i>	1	7	Undetermined
otu_703	<i>Chaetothyriales species 4</i>	1	4	Undetermined
otu_497	<i>Chytridiomycota species 10.1</i>	1	12	Undetermined
otu_1242	<i>Chytridiomycota species 2.1</i>	1	2	Undetermined
otu_184	<i>Chytridiomycota species 2.2</i>	2	159	Undetermined
otu_307	<i>Chytridiomycota species 4</i>	1	42	Undetermined
otu_84	<i>Chytridiomycota species 5</i>	1	809	Undetermined
otu_11	<i>Clavicipitaceae species 1.1</i>	30	47429	Entomopathogenic
otu_1237	<i>Clavicipitaceae species 1.10</i>	1	2	Entomopathogenic
otu_140	<i>Clavicipitaceae species 1.11</i>	2	288	Entomopathogenic
otu_5	<i>Clavicipitaceae species 1.12</i>	41	87459	Entomopathogenic
otu_866	<i>Clavicipitaceae species 1.13</i>	1	3	Entomopathogenic
otu_1127	<i>Clavicipitaceae species 1.2</i>	1	2	Entomopathogenic
otu_863	<i>Clavicipitaceae species 1.3</i>	1	5	Entomopathogenic
otu_1119	<i>Clavicipitaceae species 1.4</i>	1	4	Entomopathogenic
otu_1129	<i>Clavicipitaceae species 1.5</i>	1	2	Entomopathogenic
otu_196	<i>Clavicipitaceae species 1.6</i>	2	142	Entomopathogenic
otu_565	<i>Clavicipitaceae species 1.7</i>	4	45	Entomopathogenic
otu_667	<i>Clavicipitaceae species 1.8</i>	1	25	Entomopathogenic
otu_1225	<i>Clavicipitaceae species 1.9</i>	2	6	Entomopathogenic
otu_1033	<i>Clavicipitaceae species 3.1</i>	1	2	Entomopathogenic
otu_525	<i>Clavicipitaceae species 3.1</i>	1	16	Entomopathogenic
otu_865	<i>Clavicipitaceae species 3.1</i>	1	7	Entomopathogenic
otu_470	<i>Clavicipitaceae species 4.1</i>	1	14	Entomopathogenic
otu_451	<i>Clavicipitaceae species 4.2</i>	1	42	Entomopathogenic

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_911	<i>Clavicipitaceae species 4.3</i>	1	7	Entomopathogenic
otu_577	<i>Clavicipitaceae species 4.4</i>	2	17	Entomopathogenic
otu_1032	<i>Clavicipitaceae species 4.5</i>	1	2	Entomopathogenic
otu_412	<i>Clavicipitaceae species 5.1</i>	1	30	Entomopathogenic
otu_729	<i>Clavicipitaceae species 5.2</i>	1	10	Entomopathogenic
otu_488	<i>Clavicipitaceae species 6</i>	1	13	Entomopathogenic
otu_608	<i>Clavicipitaceae species 7.1</i>	1	13	Entomopathogenic
otu_864	<i>Clavicipitaceae species 7.2</i>	1	7	Entomopathogenic
otu_1123	<i>Clavicipitaceae species 7.3</i>	1	2	Entomopathogenic
otu_697	<i>Clavicipitaceae species 9.1</i>	1	18	Entomopathogenic
otu_74	<i>Clavicipitaceae species 9.2</i>	1	1036	Entomopathogenic
otu_973	<i>Clavicipitaceae species 9.3</i>	2	4	Entomopathogenic
otu_1112	<i>Clavicipitaceae species 9.4</i>	1	2	Entomopathogenic
otu_48	<i>Clavicipitaceae species 9.5</i>	2	2494	Entomopathogenic
otu_524	<i>Clavicipitaceae species 9.6</i>	1	18	Entomopathogenic
otu_1077	<i>Clonostachys species 1</i>	1	2	Saprotroph
otu_129	<i>Clonostachys species 10</i>	2	658	Saprotroph
otu_301	<i>Clonostachys species 11</i>	2	50	Saprotroph
otu_432	<i>Clonostachys species 12</i>	1	21	Saprotroph
otu_581	<i>Clonostachys species 13</i>	1	22	Saprotroph
otu_617	<i>Clonostachys species 14</i>	2	15	Saprotroph
otu_621	<i>Clonostachys species 15</i>	5	19	Saprotroph
otu_672	<i>Clonostachys species 16</i>	1	7	Saprotroph
otu_887	<i>Clonostachys species 17</i>	1	3	Saprotroph
otu_891	<i>Clonostachys species 18</i>	1	11	Saprotroph
otu_895	<i>Clonostachys species 19</i>	1	6	Saprotroph
otu_1158	<i>Clonostachys species 2</i>	1	8	Saprotroph
otu_935	<i>Clonostachys species 20</i>	1	2	Saprotroph
otu_1171	<i>Clonostachys species 21</i>	1	2	Saprotroph
otu_1160	<i>Clonostachys species 22</i>	1	2	Saprotroph
otu_459	<i>Clonostachys species 24</i>	1	22	Saprotroph
otu_54	<i>Clonostachys species 25</i>	3	1507	Saprotroph
otu_63	<i>Clonostachys species 26</i>	1	1071	Saprotroph
otu_743	<i>Clonostachys species 27</i>	1	4	Saprotroph
otu_111	<i>Clonostachys species 28</i>	9	1480	Saprotroph
otu_1101	<i>Clonostachys species 29</i>	1	2	Saprotroph
otu_561	<i>Clonostachys species 3</i>	2	24	Saprotroph

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_1159	<i>Clonostachys species 3</i>	1	4	Saprotroph
otu_1199	<i>Clonostachys species 4</i>	1	2	Saprotroph
otu_1204	<i>Clonostachys species 5</i>	1	2	Saprotroph
otu_1208	<i>Clonostachys species 6</i>	1	2	Saprotroph
otu_1233	<i>Clonostachys species 7</i>	1	2	Saprotroph
otu_1234	<i>Clonostachys species 8</i>	1	2	Saprotroph
otu_1149	<i>Cordycipitaceae species 1.1</i>	1	2	Entomopathogenic
otu_877	<i>Cordycipitaceae species 1.2</i>	1	6	Entomopathogenic
otu_454	<i>Cordycipitaceae species 5</i>	1	17	Entomopathogenic
otu_944	<i>Corticiales species 1</i>	1	2	Undetermined
otu_223	<i>Corticiales species 1.2</i>	1	119	Undetermined
otu_1245	<i>Crepidotus species 1</i>	1	2	Wood decay
otu_251	<i>Cryptococcus species 1</i>	1	65	Saprotroph
otu_871	<i>Cutaneotrichospecies oron</i>	1	5	Saprotroph
otu_404	<i>Cylindrobasidium species 1</i>	1	17	Undetermined
otu_811	<i>Dacryobolus species 1</i>	1	5	Plant pathogen
otu_18	<i>Debaryomyces species 1</i>	28	36255	Saprotroph
otu_659	<i>Debaryomyces species 10</i>	2	11	Saprotroph
otu_668	<i>Debaryomyces species 11</i>	6	113	Saprotroph
otu_669	<i>Debaryomyces species 12</i>	3	16	Saprotroph
otu_751	<i>Debaryomyces species 13</i>	1	11	Saprotroph
otu_862	<i>Debaryomyces species 14</i>	30	2147	Saprotroph
otu_905	<i>Debaryomyces species 15</i>	3	10	Saprotroph
otu_1118	<i>Debaryomyces species 2</i>	1	4	Saprotroph
otu_1198	<i>Debaryomyces species 3</i>	1	18	Saprotroph
otu_120	<i>Debaryomyces species 4</i>	10	1662	Saprotroph
otu_2	<i>Debaryomyces species 6</i>	72	255672	Saprotroph
otu_208	<i>Debaryomyces species 7</i>	4	235	Saprotroph
otu_405	<i>Debaryomyces species 8</i>	5	111	Saprotroph
otu_530	<i>Debaryomyces species 9</i>	3	60	Saprotroph
otu_1083	<i>Dothideomycetes species 1</i>	1	2	Undetermined
otu_575	<i>Dothideomycetes species 1.1</i>	1	11	Undetermined
otu_954	<i>Eurotiomycetes species 2</i>	1	2	Undetermined
otu_127	<i>Exobasidiomycetes species 2.1</i>	1	325	Undetermined
otu_175	<i>Exophiala species 1</i>	3	215	Saprotroph
otu_161	<i>Filobasidium species 1</i>	1	296	Saprotroph
otu_910	<i>Fomitiporia species 1</i>	1	3	Plant pathogen

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_26	<i>Fusarium species 1</i>	12	9913	Plant pathogen
otu_1194	<i>Fusarium species 10</i>	1	4	Plant pathogen
otu_188	<i>Fusarium species 11</i>	3	151	Plant pathogen
otu_359	<i>Fusarium species 15</i>	1	23	Plant pathogen
otu_417	<i>Fusarium species 16</i>	1	28	Plant pathogen
otu_1057	<i>Fusarium species 2</i>	1	2	Plant pathogen
otu_258	<i>Fusarium species 2</i>	4	205	Plant pathogen
otu_523	<i>Fusarium species 20</i>	1	10	Plant pathogen
otu_564	<i>Fusarium species 22</i>	1	9	Plant pathogen
otu_748	<i>Fusarium species 23</i>	1	9	Plant pathogen
otu_886	<i>Fusarium species 25</i>	1	3	Plant pathogen
otu_855	<i>Fusarium species 26</i>	1	6	Plant pathogen
otu_1081	<i>Fusarium species 27</i>	1	2	Plant pathogen
otu_1097	<i>Fusarium species 4.1</i>	1	2	Plant pathogen
otu_1102	<i>Fusarium species 5.1</i>	1	2	Plant pathogen
otu_1121	<i>Fusarium species 6.1</i>	1	2	Plant pathogen
otu_1128	<i>Fusarium species 7.1</i>	1	2	Plant pathogen
otu_1143	<i>Fusarium species 8</i>	1	2	Plant pathogen
otu_1178	<i>Fusarium species 9</i>	1	8	Plant pathogen
otu_294	<i>Fuscoporia species 1</i>	1	49	Saprotroph
otu_320	<i>Fuscoporia species 2</i>	1	44	Saprotroph
otu_908	<i>Fuscoporia species 2</i>	1	5	Saprotroph
otu_1148	<i>Fusicolla species 1</i>	1	2	Saprotroph
otu_213	<i>Fusicolla species 1</i>	3	79	Saprotroph
otu_67	<i>Fusicolla species 1</i>	11	1325	Saprotroph
otu_611	<i>Fusicolla species 10</i>	1	13	Saprotroph
otu_737	<i>Fusicolla species 11</i>	1	6	Saprotroph
otu_854	<i>Fusicolla species 12</i>	2	9	Saprotroph
otu_874	<i>Fusicolla species 13</i>	1	3	Saprotroph
otu_939	<i>Fusicolla species 14</i>	1	2	Saprotroph
otu_1094	<i>Fusicolla species 2</i>	1	2	Saprotroph
otu_1156	<i>Fusicolla species 4</i>	1	2	Saprotroph
otu_1181	<i>Fusicolla species 5</i>	1	4	Saprotroph
otu_368	<i>Fusicolla species 7</i>	5	78	Saprotroph
otu_411	<i>Fusicolla species 8</i>	4	112	Saprotroph
otu_522	<i>Fusicolla species 9</i>	5	38	Saprotroph
otu_28	<i>Gliomastix species 1</i>	20	26018	Saprotroph

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_204	<i>Gliomastix species 1.1</i>	2	4	Saprotroph
otu_848	<i>Gliomastix species 10</i>	1	5	Saprotroph
otu_850	<i>Gliomastix species 11</i>	1	7	Saprotroph
otu_872	<i>Gliomastix species 12</i>	1	3	Saprotroph
otu_907	<i>Gliomastix species 13</i>	1	3	Saprotroph
otu_212	<i>Gliomastix species 2.1</i>	4	134	Saprotroph
otu_1027	<i>Gliomastix species 3</i>	2	22	Saprotroph
otu_153	<i>Gliomastix species 3</i>	6	3216	Saprotroph
otu_214	<i>Gliomastix species 3.1</i>	1	193	Saprotroph
otu_226	<i>Gliomastix species 4</i>	1	96	Saprotroph
otu_300	<i>Gliomastix species 5</i>	1	50	Saprotroph
otu_562	<i>Gliomastix species 7</i>	1	12	Saprotroph
otu_713	<i>Gliomastix species 8</i>	2	12	Saprotroph
otu_734	<i>Gliomastix species 9</i>	1	7	Saprotroph
otu_269	<i>Gloeoporus species 1</i>	1	62	Wood decay
otu_596	<i>Gloeoporus species 2</i>	1	10	Wood decay
otu_367	<i>Gongronella species 1</i>	3	100	Saprotroph
otu_975	<i>Gongronella species 2</i>	1	2	Saprotroph
otu_274	<i>Graphidaceae species 1.1</i>	1	68	Undetermined
otu_876	<i>Graphidaceae species 1.2</i>	1	3	Undetermined
otu_255	<i>Graphidaceae species 3</i>	1	64	Undetermined
otu_591	<i>Graphidaceae species 7</i>	2	12	Undetermined
otu_781	<i>Graphidaceae species 8</i>	1	5	Undetermined
otu_298	<i>Graphidaceae species 9</i>	2	67	Undetermined
otu_1080	<i>Graphium species 1.1</i>	1	4	Saprotroph
otu_326	<i>Graphium species 2</i>	2	49	Saprotroph
otu_1082	<i>Graphium species 2.1</i>	1	2	Saprotroph
otu_192	<i>Graphium species 3</i>	2	133	Saprotroph
otu_614	<i>Graphium species 5</i>	1	6	Saprotroph
otu_310	<i>Gymnopilus species 1</i>	1	42	Wood decay
otu_552	<i>Gymnopilus species 2</i>	2	15	Wood decay
otu_1014	<i>Gymnopus species 1</i>	1	2	Saprotroph
otu_964	<i>Gymnopus species 2</i>	1	2	Saprotroph
otu_385	<i>Gymnopus species 4</i>	2	66	Saprotroph
otu_585	<i>Gymnopus species 5</i>	1	13	Saprotroph
otu_927	<i>Gymnopus species 6</i>	1	2	Saprotroph
otu_943	<i>Gymnopus species 7</i>	1	2	Saprotroph

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_1217	<i>Gymnopus species 9</i>	1	2	Saprotroph
otu_1247	<i>Helicogloea species 1</i>	1	2	Saprotroph
otu_704	<i>Herpotrichiellaceae species 1</i>	1	4	Saprotroph
otu_231	<i>Hydnodontaceae species 11</i>	1	65	Undetermined
otu_242	<i>Hydnodontaceae species 8</i>	1	63	Undetermined
otu_1184	<i>Hydnodontaceae species 9.1</i>	1	2	Undetermined
otu_331	<i>Hymenochaetales species 2.1</i>	1	38	Undetermined
otu_1031	<i>Hymenochaete species 1</i>	1	2	Wood decay
otu_268	<i>Hyphodermella species 1</i>	3	82	Saprotroph
otu_442	<i>Hyphodontia species 1</i>	1	16	Saprotroph
otu_705	<i>Hyphodontia species 2.1</i>	2	9	Saprotroph
otu_1010	<i>Hypholoma species 1</i>	1	4	Wood decay
otu_536	<i>Hypocreales Incertae sedis</i>	3	43	Undetermined
otu_774	<i>Hypocreales Incertae sedis</i>	1	5	Undetermined
otu_1113	<i>Hypocreales incertae sedis</i>	1	4	Undetermined
otu_775	<i>Hypocreales Incertae sedis</i>	1	3	Undetermined
otu_778	<i>Hypocreales Incertae sedis</i>	1	5	Undetermined
otu_1096	<i>Hypocreales incertae sedis</i>	1	2	Undetermined
otu_1076	<i>Hypocreales incertae sedis</i>	1	2	Undetermined
otu_965	<i>Hypocreales Incertae sedis</i>	1	2	Undetermined
otu_384	<i>Hypocreales incertae sedis</i>	1	18	Undetermined
otu_477	<i>Hypocreales species 1</i>	1	12	Undetermined
otu_1086	<i>Hypocreales species 1.1</i>	1	4	Undetermined
otu_663	<i>Hypocreales species 1.2</i>	1	5	Undetermined
otu_79	<i>Hypocreales species 1.3</i>	2	643	Undetermined
otu_173	<i>Hypocreales species 10.1</i>	1	158	Undetermined
otu_961	<i>Hypocreales species 11</i>	1	2	Undetermined
otu_486	<i>Hypocreales species 18</i>	1	13	Undetermined
otu_30	<i>Hypocreales species 2.3</i>	8	17	Undetermined
otu_1135	<i>Hypocreales species 21.1</i>	1	2	Undetermined
otu_1223	<i>Hypocreales species 3</i>	1	4	Undetermined
otu_10	<i>Hypocreales species 3</i>	73	128406	Undetermined
otu_653	<i>Hypocreales species 3.1</i>	3	7	Undetermined
otu_1111	<i>Hypocreales species 3.1</i>	1	2	Undetermined
otu_425	<i>Hypocreales species 3.10</i>	3	33	Undetermined
otu_427	<i>Hypocreales species 3.11</i>	1	14	Undetermined
otu_468	<i>Hypocreales species 3.12</i>	1	15	Undetermined

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_568	<i>Hypocreales species 3.13</i>	2	17	Undetermined
otu_609	<i>Hypocreales species 3.14</i>	1	14	Undetermined
otu_679	<i>Hypocreales species 3.2</i>	6	20	Undetermined
otu_150	<i>Hypocreales species 3.2</i>	4	296	Undetermined
otu_312	<i>Hypocreales species 3.3</i>	1	48	Undetermined
otu_758	<i>Hypocreales species 3.3</i>	4	18	Undetermined
otu_1114	<i>Hypocreales species 3.4</i>	1	2	Undetermined
otu_665	<i>Hypocreales species 3.4</i>	1	10	Undetermined
otu_1173	<i>Hypocreales species 3.5</i>	1	2	Undetermined
otu_786	<i>Hypocreales species 3.5</i>	1	3	Undetermined
otu_1179	<i>Hypocreales species 3.6</i>	1	2	Undetermined
otu_856	<i>Hypocreales species 3.6</i>	1	3	Undetermined
otu_1189	<i>Hypocreales species 3.7</i>	1	2	Undetermined
otu_976	<i>Hypocreales species 3.7</i>	1	2	Undetermined
otu_281	<i>Hypocreales species 3.8</i>	5	104	Undetermined
otu_366	<i>Hypocreales species 3.9</i>	1	25	Undetermined
otu_716	<i>Hypocreales species 5</i>	1	4	Undetermined
otu_1036	<i>Hypocreales species 5.1</i>	1	2	Undetermined
otu_532	<i>Hypocreales species 7.1</i>	1	13	Undetermined
otu_249	<i>Hypocreales species 7.2</i>	2	245	Undetermined
otu_971	<i>Hypocreales species 8</i>	1	2	Undetermined
otu_183	<i>Irpex species 1</i>	2	166	Wood decay
otu_629	<i>Jattaia species 1</i>	1	11	Wood decay
otu_972	<i>Junghuhnia species 1</i>	1	2	Wood decay
otu_278	<i>Kneiffiella species 1</i>	5	87	Wood decay
otu_178	<i>Knufia species 1</i>	1	345	Plant pathogen
otu_1218	<i>Lasiodiplodia species 2</i>	1	2	Plant pathogen
otu_222	<i>Lasiodiplodia species 2</i>	1	123	Plant pathogen
otu_554	<i>Lecanicillium species 1</i>	1	9	Entomopathogenic
otu_97	<i>Lecanicillium species 2</i>	2	631	Entomopathogenic
otu_819	<i>Lecanoromycetes species 2.1</i>	1	6	Undetermined
otu_206	<i>Lentinellus species 1</i>	1	92	Saprotroph
otu_41	<i>Lenzites species 1</i>	2	3309	Wood decay
otu_569	<i>Leptosporangium oromyces species 1</i>	1	17	Saprotroph
otu_1029	<i>Malassezia species 1</i>	1	2	Saprotroph
otu_135	<i>Malassezia species 2</i>	3	16	Saprotroph
otu_193	<i>Malassezia species 3</i>	2	141	Saprotroph

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_25	<i>Malassezia species 4</i>	12	28413	Saprotroph
otu_43	<i>Malassezia species 5</i>	3	3277	Saprotroph
otu_504	<i>Malassezia species 6</i>	3	28	Saprotroph
otu_53	<i>Malassezia species 7</i>	18	5987	Saprotroph
otu_785	<i>Malassezia species 8</i>	1	3	Saprotroph
otu_808	<i>Malassezia species 8</i>	4	43	Saprotroph
otu_92	<i>Malassezia species 9</i>	10	878	Saprotroph
otu_94	<i>Marasmiaceae species 1.1</i>	1	1046	Plant pathogen
otu_24	<i>Marasmiellus species 3</i>	3	3507	Plant pathogen
otu_195	<i>Metapochonia species 1</i>	1	112	Entomopathogenic
otu_58	<i>Metapochonia species 1</i>	1	1630	Entomopathogenic
otu_273	<i>Metapochonia species 10</i>	1	118	Entomopathogenic
otu_299	<i>Metapochonia species 11</i>	2	34	Entomopathogenic
otu_414	<i>Metapochonia species 13</i>	2	29	Entomopathogenic
otu_495	<i>Metapochonia species 15</i>	1	23	Entomopathogenic
otu_533	<i>Metapochonia species 16</i>	1	16	Entomopathogenic
otu_534	<i>Metapochonia species 17</i>	1	27	Entomopathogenic
otu_580	<i>Metapochonia species 18</i>	1	19	Entomopathogenic
otu_610	<i>Metapochonia species 19</i>	2	23	Entomopathogenic
otu_122	<i>Metapochonia species 2</i>	21	1783	Entomopathogenic
otu_14	<i>Metapochonia species 2</i>	35	65889	Entomopathogenic
otu_174	<i>Metapochonia species 2</i>	1	233	Entomopathogenic
otu_334	<i>Metapochonia species 2</i>	6	385	Entomopathogenic
otu_612	<i>Metapochonia species 20</i>	2	10	Entomopathogenic
otu_868	<i>Metapochonia species 22</i>	1	5	Entomopathogenic
otu_869	<i>Metapochonia species 23</i>	1	11	Entomopathogenic
otu_870	<i>Metapochonia species 24</i>	1	5	Entomopathogenic
otu_902	<i>Metapochonia species 25</i>	1	9	Entomopathogenic
otu_1131	<i>Metapochonia species 3</i>	2	4	Entomopathogenic
otu_1152	<i>Metapochonia species 4</i>	1	2	Entomopathogenic
otu_1224	<i>Metapochonia species 5</i>	1	2	Entomopathogenic
otu_207	<i>Metapochonia species 9</i>	2	272	Entomopathogenic
otu_760	<i>Metarhizium species 10</i>	1	6	Entomopathogenic
otu_820	<i>Metarhizium species 11</i>	1	5	Entomopathogenic
otu_906	<i>Metarhizium species 12</i>	1	5	Entomopathogenic
otu_1228	<i>Metarhizium species 2</i>	1	4	Entomopathogenic
otu_59	<i>Metarhizium species 5</i>	5	1627	Entomopathogenic

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_6	<i>Metarhizium species 6</i>	32	62691	Entomopathogenic
otu_1236	<i>Meyerozyma species 1</i>	1	2	Saprotroph
otu_1232	<i>Mortierellales species 1.1</i>	1	2	Undetermined
otu_493	<i>Mucor species 1</i>	1	12	Saprotroph
otu_47	<i>Mycena species 2</i>	2	2859	Saprotroph
otu_277	<i>Mycena species 7</i>	1	51	Saprotroph
otu_632	<i>Mycena species 8</i>	1	7	Saprotroph
otu_574	<i>Myxarium species 1</i>	1	18	Wood decay
otu_746	<i>Myxospecies ora species 1</i>	1	8	Undetermined
otu_1167	<i>Myxospecies ora species 2</i>	1	4	Undetermined
otu_1170	<i>Myxospecies ora species 3</i>	1	2	Undetermined
otu_1177	<i>Myxospecies ora species 4</i>	2	4	Undetermined
otu_239	<i>Myxospecies ora species 5</i>	1	125	Undetermined
otu_35	<i>Myxospecies ora species 6</i>	7	7925	Undetermined
otu_286	<i>Myxospecies ora species 7</i>	1	63	Undetermined
otu_882	<i>Myxospecies ora species 8</i>	1	3	Undetermined
otu_32	<i>Naganishia species 1</i>	2	8	Undetermined
otu_13	<i>Nectria species 1</i>	25	25796	Plant pathogen
otu_1219	<i>Nectria species 10</i>	1	2	Plant pathogen
otu_197	<i>Nectria species 11</i>	1	107	Plant pathogen
otu_289	<i>Nectria species 12</i>	2	69	Plant pathogen
otu_324	<i>Nectria species 13</i>	1	51	Plant pathogen
otu_37	<i>Nectria species 14</i>	1	3703	Plant pathogen
otu_571	<i>Nectria species 15</i>	1	12	Plant pathogen
otu_749	<i>Nectria species 16</i>	1	13	Plant pathogen
otu_766	<i>Nectria species 17</i>	1	5	Plant pathogen
otu_829	<i>Nectria species 18</i>	1	2	Plant pathogen
otu_884	<i>Nectria species 19</i>	1	3	Plant pathogen
otu_901	<i>Nectria species 20</i>	1	6	Plant pathogen
otu_933	<i>Nectria species 21</i>	1	2	Plant pathogen
otu_1165	<i>Nectria species 3</i>	1	2	Plant pathogen
otu_1180	<i>Nectria species 4</i>	1	2	Plant pathogen
otu_1188	<i>Nectria species 5</i>	1	2	Plant pathogen
otu_1190	<i>Nectria species 6</i>	1	2	Plant pathogen
otu_1192	<i>Nectria species 7</i>	1	2	Plant pathogen
otu_1195	<i>Nectria species 8</i>	1	2	Plant pathogen
otu_1196	<i>Nectria species 9</i>	1	2	Plant pathogen

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_447	<i>Nectriaceae species 1.1</i>	1	16	Undetermined
otu_284	<i>Nectriaceae species 1.2</i>	1	61	Undetermined
otu_494	<i>Nectriaceae species 5.1</i>	1	11	Undetermined
otu_563	<i>Ophiocordycipitaceae species 1.1</i>	1	13	Entomopathogenic
otu_572	<i>Ophiocordycipitaceae species 2.1</i>	1	15	Entomopathogenic
otu_133	<i>Ophiostoma species 1</i>	2	323	Plant pathogen
otu_296	<i>Ophiostoma species 2</i>	1	30	Plant pathogen
otu_292	<i>Orbiliaceae species 1.1</i>	1	45	Undetermined
otu_822	<i>Panus species 1</i>	1	5	Undetermined
otu_1105	<i>Penicillium species 1.1</i>	1	2	Saprotroph
otu_754	<i>Penicillium species 10.1</i>	1	6	Saprotroph
otu_974	<i>Penicillium species 11</i>	1	4	Saprotroph
otu_977	<i>Penicillium species 12</i>	1	2	Saprotroph
otu_15	<i>Penicillium species 13.1</i>	19	53002	Saprotroph
otu_1172	<i>Penicillium species 2.1</i>	1	2	Saprotroph
otu_146	<i>Penicillium species 4</i>	1	292	Saprotroph
otu_576	<i>Penicillium species 5</i>	2	17	Saprotroph
otu_200	<i>Penicillium species 5.1</i>	4	365	Saprotroph
otu_433	<i>Penicillium species 6</i>	12	1038	Saprotroph
otu_1210	<i>Penicillium species 6</i>	1	2	Saprotroph
otu_1117	<i>Penicillium species 6</i>	2	8	Saprotroph
otu_393	<i>Penicillium species 6.1</i>	3	26	Saprotroph
otu_1028	<i>Peniophora species 1</i>	3	14	Wood decay
otu_154	<i>Peniophora species 2</i>	2	196	Wood decay
otu_265	<i>Peniophora species 3</i>	5	144	Wood decay
otu_308	<i>Peniophora species 4</i>	1	46	Wood decay
otu_329	<i>Peniophora species 5</i>	9	243	Wood decay
otu_550	<i>Peniophora species 6</i>	1	13	Wood decay
otu_627	<i>Peniophora species 8</i>	2	11	Wood decay
otu_339	<i>Perenniporia species 1</i>	1	40	Wood decay
otu_1004	<i>Phaeomoniella species 1</i>	1	2	Saprotroph
otu_1162	<i>Phaeophlebiopsis species 1.1</i>	1	2	Saprotroph
otu_710	<i>Phallaceae species 1.1</i>	3	15	Saprotroph
otu_130	<i>Phanerochaete species 1.1</i>	1	582	Undetermined
otu_219	<i>Phanerochaete species 1</i>	1	23	Wood decay
otu_440	<i>Phlebia species 1</i>	2	26	Wood decay
otu_441	<i>Phlebia species 2</i>	1	16	Wood decay

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_514	<i>Phlebia species 3</i>	1	12	Wood decay
otu_806	<i>Phlebia species 4</i>	1	3	Wood decay
otu_812	<i>Phlebia species 5</i>	1	3	Wood decay
otu_978	<i>Pholiota species 1</i>	1	2	Saprotroph
otu_1125	<i>Plectospecies haerella species 1</i>	1	2	Plant pathogen
otu_646	<i>Plectospecies haerella species 10</i>	2	22	Plant pathogen
otu_33	<i>Plectospecies haerella species 2</i>	8	1114	Plant pathogen
otu_711	<i>Plectospecies haerella species 6</i>	1	26	Plant pathogen
otu_124	<i>Plectospecies haerella species 7</i>	1	270	Plant pathogen
otu_783	<i>Plectospecies haerella species</i>	1	5	Plant pathogen
otu_645	<i>Plectospecies haerella species 9</i>	3	11	Plant pathogen
otu_1126	<i>Plectospecies haerellaceae</i>	1	4	Undetermined
otu_498	<i>Plectospecies haerellaceae</i>	1	37	Undetermined
otu_118	<i>Plectospecies haerellaceae</i>	2	775	Undetermined
otu_747	<i>Plectospecies haerellaceae</i>	1	10	Undetermined
otu_1141	<i>Plectospecies haerellaceae</i>	1	2	Undetermined
otu_1175	<i>Plectospecies haerellaceae</i>	1	2	Undetermined
otu_531	<i>Pleurotus species 2</i>	1	17	Entomopathogenic
otu_262	<i>Pluteus species 1</i>	1	67	Wood decay
otu_460	<i>Polyporaceae species 2.1</i>	1	25	Undetermined
otu_597	<i>Polyporales species 1.1</i>	1	6	Undetermined
otu_1231	<i>Polyporales species 2.1</i>	1	2	Undetermined
otu_392	<i>Polyporales species 3.1</i>	2	39	Undetermined
otu_136	<i>Polyporales species 4.1</i>	1	310	Undetermined
otu_979	<i>Polyporales species 6.1</i>	1	4	Undetermined
otu_271	<i>Postia species 1</i>	1	74	Wood decay
otu_548	<i>Postia species 2</i>	1	13	Wood decay
otu_712	<i>Pseudochaete species 1</i>	1	7	Saprotroph
otu_715	<i>Psilocybe species 1.1</i>	1	6	Saprotroph
otu_137	<i>Puccinia species 1</i>	1	260	Plant pathogen
otu_1045	<i>Purpureocillium species 2</i>	1	2	Entomopathogenic
otu_841	<i>Purpureocillium species 2</i>	1	8	Entomopathogenic
otu_520	<i>Purpureocillium species 2.1</i>	1	28	Entomopathogenic
otu_555	<i>Purpureocillium species 3</i>	1	2	Entomopathogenic
otu_1070	<i>Purpureocillium species 6</i>	1	2	Entomopathogenic
otu_519	<i>Purpureocillium species 6</i>	1	19	Entomopathogenic
otu_1007	<i>Resinicium species 1</i>	1	4	Saprotroph

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_382	<i>Resupinatus species 1</i>	1	26	Wood decay
otu_95	<i>Resupinatus species 2</i>	2	838	Wood decay
otu_1244	<i>Rhizophydiales species 1.1</i>	1	2	Undetermined
otu_210	<i>Rigidoporus species 1</i>	1	96	Wood decay
otu_263	<i>Rigidoporus species 2</i>	1	76	Wood decay
otu_1023	<i>Roussoella species 1.1</i>	2	4	Saprotroph
otu_557	<i>Roussoella species 10</i>	1	23	Saprotroph
otu_603	<i>Roussoella species 11</i>	1	13	Saprotroph
otu_723	<i>Roussoella species 12</i>	1	4	Saprotroph
otu_842	<i>Roussoella species 15</i>	1	23	Saprotroph
otu_843	<i>Roussoella species 16</i>	1	5	Saprotroph
otu_853	<i>Roussoella species 17</i>	1	5	Saprotroph
otu_1024	<i>Roussoella species 2</i>	1	2	Saprotroph
otu_1066	<i>Roussoella species 3</i>	1	4	Saprotroph
otu_1068	<i>Roussoella species 4</i>	1	2	Saprotroph
otu_1069	<i>Roussoella species 5</i>	1	2	Saprotroph
otu_235	<i>Roussoella species 7</i>	1	481	Saprotroph
otu_337	<i>Roussoella species 8</i>	1	52	Saprotroph
otu_492	<i>Roussoella species 9</i>	1	82	Saprotroph
otu_143	<i>Roussoellaceae species 2.1</i>	2	442	Saprotroph
otu_1240	<i>Saccharomyces species 1</i>	1	4	Wood decay
otu_1212	<i>Saccharomycetales species 2.1</i>	1	2	Undetermined
otu_458	<i>Sakaguchia species 1</i>	1	17	Undetermined
otu_45	<i>Sampaiozyma species 1</i>	1	2020	Undetermined
otu_1098	<i>Sarcopodium species 1</i>	1	2	Saprotroph
otu_295	<i>Sarcopodium species 2</i>	2	60	Saprotroph
otu_3	<i>Sarocladium species 1</i>	129	1823481	Saprotroph
otu_34	<i>Sarocladium species 10</i>	3	8534	Saprotroph
otu_388	<i>Sarocladium species 11</i>	2	84	Saprotroph
otu_391	<i>Sarocladium species 12</i>	6	39	Saprotroph
otu_418	<i>Sarocladium species 14</i>	4	74	Saprotroph
otu_419	<i>Sarocladium species 15</i>	2	36	Saprotroph
otu_435	<i>Sarocladium species 17</i>	8	107	Saprotroph
otu_452	<i>Sarocladium species 18</i>	1	22	Saprotroph
otu_475	<i>Sarocladium species 19</i>	6	34	Saprotroph
otu_434	<i>Sarocladium species 2</i>	31	284	Saprotroph
otu_510	<i>Sarocladium species 21</i>	2	25	Saprotroph

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_56	<i>Sarocladium species 22</i>	5	1372	Saprotroph
otu_622	<i>Sarocladium species 24</i>	3	17	Saprotroph
otu_641	<i>Sarocladium species 25</i>	2	14	Saprotroph
otu_1124	<i>Sarocladium species 27</i>	1	2	Saprotroph
otu_735	<i>Sarocladium species 30</i>	1	9	Saprotroph
otu_736	<i>Sarocladium species 31</i>	1	11	Saprotroph
otu_767	<i>Sarocladium species 32</i>	11	42	Saprotroph
otu_77	<i>Sarocladium species 33</i>	42	3103	Saprotroph
otu_776	<i>Sarocladium species 34</i>	16	121	Saprotroph
otu_921	<i>Sarocladium species 35</i>	1	2	Saprotroph
otu_924	<i>Sarocladium species 36</i>	5	10	Saprotroph
otu_928	<i>Sarocladium species 37</i>	3	8	Saprotroph
otu_1136	<i>Sarocladium species 38</i>	1	8	Saprotroph
otu_957	<i>Sarocladium species 39</i>	1	2	Saprotroph
otu_958	<i>Sarocladium species 4</i>	1	2	Saprotroph
otu_114	<i>Sarocladium species 41</i>	4	463	Saprotroph
otu_155	<i>Sarocladium species 42</i>	1	198	Saprotroph
otu_20	<i>Sarocladium species 43</i>	4	10	Saprotroph
otu_769	<i>Sarocladium species 45</i>	1	3	Saprotroph
otu_940	<i>Sarocladium species 46</i>	1	2	Saprotroph
otu_232	<i>Sarocladium species 6</i>	1	210	Saprotroph
otu_238	<i>Sarocladium species 7</i>	1	107	Saprotroph
otu_250	<i>Sarocladium species 8</i>	32	656	Saprotroph
otu_319	<i>Sarocladium species 9</i>	3	93	Saprotroph
otu_228	<i>Schizophyllum species 1</i>	1	84	Wood decay
otu_160	<i>Schwanniomyces species 1</i>	2	224	Undetermined
otu_1222	<i>Septobasidium species 1.1</i>	2	4	Entomopathogenic
otu_674	<i>Septobasidium species 2</i>	1	9	Entomopathogenic
otu_753	<i>Simplicillium species 1</i>	1	13	Entomopathogenic
otu_1209	<i>Simplicillium species 1.1</i>	1	2	Entomopathogenic
otu_1238	<i>Simplicillium species 2</i>	1	2	Entomopathogenic
otu_335	<i>Simplicillium species 3</i>	1	52	Entomopathogenic
otu_42	<i>Simplicillium species 4</i>	1	2811	Entomopathogenic
otu_9	<i>Simplicillium species 5</i>	9	42624	Entomopathogenic
otu_152	<i>Sistotrema species 1</i>	1	224	Mycorrhizal
otu_649	<i>Sistotremastrum species 1</i>	1	8	Saprotroph
otu_1182	<i>Sordariomycetes incertae sedis</i>	1	2	Undetermined

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_171	<i>Sordariomycetes incertae sedis</i>	4	327	Undetermined
otu_496	<i>Sordariomycetes incertae sedis</i>	1	14	Undetermined
otu_529	<i>Sordariomycetes incertae sedis</i>	1	8	Undetermined
otu_662	<i>Sordariomycetes incertae sedis</i>	1	5	Undetermined
otu_399	<i>Sordariomycetes incertae sedis</i>	2	25	Undetermined
otu_969	<i>Sordariomycetes species 1.1</i>	1	2	Undetermined
otu_245	<i>Sordariomycetes species 14</i>	1	72	Undetermined
otu_631	<i>Sordariomycetes species 15.1</i>	3	12	Undetermined
otu_898	<i>Sordariomycetes species 17.1</i>	1	3	Undetermined
otu_240	<i>Sordariomycetes species 5</i>	1	82	Undetermined
otu_1216	<i>Sordariomycetes species 7.1</i>	1	2	Undetermined
otu_119	<i>Sordariomycetes species 8.1</i>	1	432	Undetermined
otu_714	<i>Sordariomycetes species 8.2</i>	1	8	Undetermined
otu_1191	<i>Sordariomycetes species 9.1</i>	1	4	Undetermined
otu_390	<i>species orobolomyces species 1</i>	1	23	Fungicolous
otu_327	<i>Stachybotryaceae species 2.1</i>	1	96	Undetermined
otu_395	<i>Stachybotryaceae species 2.2</i>	1	25	Undetermined
otu_1183	<i>Stachybotrys species 1</i>	1	8	Wood decay
otu_1186	<i>Stachybotrys species 2</i>	1	4	Wood decay
otu_1193	<i>Stachybotrys species 3</i>	1	4	Wood decay
otu_499	<i>Stachybotrys species 4</i>	1	33	Wood decay
otu_885	<i>Stachybotrys species 5</i>	1	3	Wood decay
otu_889	<i>Stachybotrys species 6</i>	1	3	Wood decay
otu_346	<i>Steccherinum species 1</i>	1	33	Saprotroph
otu_272	<i>Stephanonectria species 2</i>	4	57	Saprotroph
otu_732	<i>Stephanonectria species 3</i>	2	10	Saprotroph
otu_167	<i>Stereum species 1</i>	8	445	Saprotroph
otu_676	<i>Stereum species 2.1</i>	1	5	Saprotroph
otu_923	<i>Talaromyces species 1</i>	1	2	Saprotroph
otu_343	<i>Tilletiopsis species 1</i>	1	37	Undetermined
otu_1030	<i>Tinctoporellus species 1</i>	1	6	Wood decay
otu_257	<i>Tolypocladium species 1</i>	6	157	Entomopathogenic
otu_201	<i>Tolypocladium species 1</i>	5	139	Entomopathogenic
otu_21	<i>Tolypocladium species 1</i>	23	35337	Entomopathogenic
otu_720	<i>Tolypocladium species 1</i>	1	2	Entomopathogenic
otu_777	<i>Tolypocladium species 1</i>	2	8	Entomopathogenic
otu_1155	<i>Tolypocladium species 14</i>	1	2	Entomopathogenic

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_606	<i>Tolypocladium species 14</i>	2	8	Entomopathogenic
otu_941	<i>Tolypocladium species 14</i>	3	8	Entomopathogenic
otu_1214	<i>Tolypocladium species 15</i>	1	2	Entomopathogenic
otu_1226	<i>Tolypocladium species 18</i>	1	4	Entomopathogenic
otu_328	<i>Tolypocladium species 18</i>	3	130	Entomopathogenic
otu_469	<i>Tolypocladium species 18</i>	2	52	Entomopathogenic
otu_40	<i>Tolypocladium species 2</i>	31	10597	Entomopathogenic
otu_408	<i>Tolypocladium species 2</i>	7	102	Entomopathogenic
otu_1157	<i>Tolypocladium species 2</i>	1	2	Entomopathogenic
otu_12	<i>Tolypocladium species 2</i>	52	78889	Entomopathogenic
otu_17	<i>Tolypocladium species 2</i>	23	27062	Entomopathogenic
otu_22	<i>Tolypocladium species 2</i>	19	24464	Entomopathogenic
otu_428	<i>Tolypocladium species 2</i>	1	41	Entomopathogenic
otu_1000	<i>Tolypocladium species 2</i>	9	20	Entomopathogenic
otu_1015	<i>Tolypocladium species 2</i>	1	4	Entomopathogenic
otu_106	<i>Tolypocladium species 2</i>	13	1403	Entomopathogenic
otu_1137	<i>Tolypocladium species 2</i>	1	6	Entomopathogenic
otu_1150	<i>Tolypocladium species 2</i>	1	2	Entomopathogenic
otu_1153	<i>Tolypocladium species 2</i>	3	12	Entomopathogenic
otu_1154	<i>Tolypocladium species 2</i>	3	8	Entomopathogenic
otu_1166	<i>Tolypocladium species 2</i>	3	18	Entomopathogenic
otu_1185	<i>Tolypocladium species 2</i>	2	4	Entomopathogenic
otu_1213	<i>Tolypocladium species 2</i>	1	2	Entomopathogenic
otu_1215	<i>Tolypocladium species 2</i>	1	24	Entomopathogenic
otu_1220	<i>Tolypocladium species 2</i>	1	8	Entomopathogenic
otu_148	<i>Tolypocladium species 2</i>	7	1477	Entomopathogenic
otu_151	<i>Tolypocladium species 2</i>	5	150	Entomopathogenic
otu_266	<i>Tolypocladium species 2</i>	2	109	Entomopathogenic
otu_353	<i>Tolypocladium species 2</i>	2	53	Entomopathogenic
otu_396	<i>Tolypocladium species 2</i>	2	16	Entomopathogenic
otu_449	<i>Tolypocladium species 2</i>	6	89	Entomopathogenic
otu_505	<i>Tolypocladium species 2</i>	1	46	Entomopathogenic
otu_526	<i>Tolypocladium species 2</i>	3	36	Entomopathogenic
otu_527	<i>Tolypocladium species 2</i>	1	8	Entomopathogenic
otu_620	<i>Tolypocladium species 2</i>	2	13	Entomopathogenic
otu_739	<i>Tolypocladium species 2</i>	1	6	Entomopathogenic
otu_857	<i>Tolypocladium species 2</i>	1	7	Entomopathogenic

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_963	<i>Tolypocladium species 2</i>	1	2	Entomopathogenic
otu_189	<i>Tolypocladium species 23</i>	3	288	Entomopathogenic
otu_387	<i>Tolypocladium species 28</i>	2	38	Entomopathogenic
otu_415	<i>Tolypocladium species 32</i>	3	42	Entomopathogenic
otu_450	<i>Tolypocladium species 32</i>	6	119	Entomopathogenic
otu_893	<i>Tolypocladium species 32</i>	2	11	Entomopathogenic
otu_472	<i>Tolypocladium species 37</i>	1	2	Entomopathogenic
otu_549	<i>Tolypocladium species 41</i>	2	15	Entomopathogenic
otu_616	<i>Tolypocladium species 42</i>	2	25	Entomopathogenic
otu_875	<i>Tolypocladium species 42</i>	1	3	Entomopathogenic
otu_738	<i>Tolypocladium species 46</i>	1	8	Entomopathogenic
otu_741	<i>Tolypocladium species 48</i>	1	11	Entomopathogenic
otu_1088	<i>Tolypocladium species 5.1</i>	1	2	Entomopathogenic
otu_1134	<i>Tolypocladium species 53</i>	1	2	Entomopathogenic
otu_852	<i>Tolypocladium species 53</i>	1	3	Entomopathogenic
otu_888	<i>Tolypocladium species 53</i>	1	3	Entomopathogenic
otu_836	<i>Tolypocladium species 56</i>	1	5	Entomopathogenic
otu_688	<i>Tolypocladium species 56</i>	24	994	Entomopathogenic
otu_1108	<i>Tolypocladium species 57</i>	1	4	Entomopathogenic
otu_1110	<i>Tolypocladium species 57</i>	1	4	Entomopathogenic
otu_413	<i>Tolypocladium species 57</i>	1	46	Entomopathogenic
otu_730	<i>Tolypocladium species 57</i>	1	10	Entomopathogenic
otu_619	<i>Tolypocladium species 68</i>	2	17	Entomopathogenic
otu_528	<i>Tolypocladium species 69</i>	1	17	Entomopathogenic
otu_858	<i>Tolypocladium species 72</i>	1	3	Entomopathogenic
otu_288	<i>Torrubiella species 3</i>	1	13	Entomopathogenic
otu_72	<i>Torrubiella species 5</i>	2	208	Entomopathogenic
otu_314	<i>Trametes species 1</i>	1	56	Wood decay
otu_544	<i>Trametes species 2</i>	1	13	Wood decay
otu_165	<i>Trechispecies ora species 2</i>	1	339	Wood decay
otu_350	<i>Trechispecies ora species 7</i>	1	29	Wood decay
otu_487	<i>Trechispecies orales species 1.1</i>	1	21	Undetermined
otu_967	<i>Tremellales species 3.1</i>	1	2	Undetermined
otu_121	<i>Trichaptum species 1</i>	5	942	Wood decay
otu_462	<i>Trichoderma species 11</i>	2	25	Fungicolous
otu_373	<i>Tubeufiales species 1.1</i>	1	44	Undetermined
otu_756	<i>Tubeufiales species 1.2</i>	1	8	Undetermined

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_253	<i>Tyromyces species 1</i>	1	60	Wood decay
otu_372	<i>Umbelopsis species 1</i>	2	34	Saprotroph
otu_158	<i>Ustilago species 1</i>	3	252	Plant pathogen
otu_681	<i>Verruconis species 3</i>	1	8	Saprotroph
otu_31	<i>Verticillium species 1</i>	11	25806	Nematicidal
otu_1139	<i>Verticillium species 10</i>	1	2	Nematicidal
otu_430	<i>Verticillium species 10</i>	2	39	Nematicidal
otu_221	<i>Verticillium species 11</i>	1	175	Nematicidal
otu_879	<i>Verticillium species 12</i>	1	3	Nematicidal
otu_745	<i>Verticillium species 2</i>	2	868	Nematicidal
otu_1230	<i>Verticillium species 3</i>	1	2	Nematicidal
otu_280	<i>Verticillium species 4</i>	1	267	Nematicidal
otu_673	<i>Verticillium species 5</i>	1	8	Nematicidal
otu_742	<i>Verticillium species 6</i>	1	14	Nematicidal
otu_740	<i>Verticillium species 7</i>	1	6	Nematicidal
otu_880	<i>Verticillium species 8</i>	1	11	Nematicidal
otu_1100	<i>Volutella species 1</i>	1	2	Plant pathogen
otu_570	<i>Volutella species 10</i>	2	21	Plant pathogen
otu_660	<i>Volutella species 11</i>	1	5	Plant pathogen
otu_692	<i>Volutella species 12</i>	1	4	Plant pathogen
otu_844	<i>Volutella species 14</i>	1	7	Plant pathogen
otu_873	<i>Volutella species 15</i>	1	5	Plant pathogen
otu_881	<i>Volutella species 16</i>	1	5	Plant pathogen
otu_1103	<i>Volutella species 2</i>	1	2	Plant pathogen
otu_1138	<i>Volutella species 3</i>	3	22	Plant pathogen
otu_1168	<i>Volutella species 4</i>	1	2	Plant pathogen
otu_147	<i>Volutella species 5</i>	2	252	Plant pathogen
otu_227	<i>Volutella species 6</i>	4	301	Plant pathogen
otu_287	<i>Volutella species 7</i>	2	66	Plant pathogen
otu_370	<i>Volutella species 8</i>	3	98	Plant pathogen
otu_291	<i>Volvariella species 1</i>	1	47	Saprotroph
otu_115	<i>Wallemia species 1</i>	1	416	Saprotroph
otu_46	<i>Wallemia species 2</i>	3	3303	Saprotroph
otu_849	<i>Wallrothiella species 1</i>	1	5	Undetermined
otu_547	<i>Wolfiporia species 1</i>	1	10	Wood decay
otu_455	<i>Xenasmata species 1</i>	1	20	Wood decay
otu_573	<i>Xenasmata species 2</i>	1	28	Wood decay

OTU	Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_1009	<i>Xylariales species 18.1</i>	1	2	Undetermined
otu_400	<i>Xylariales species 18.2</i>	1	23	Undetermined
otu_823	<i>Xylariales species 4.1</i>	1	3	Undetermined
otu_338	<i>Xylariales species 8.2</i>	1	34	Undetermined
otu_323	<i>Xylobolus species 1</i>	1	41	Saprotroph
otu_1026	<i>Xylodon species 1</i>	1	2	Saprotroph
otu_163	<i>Xylodon species 2</i>	5	253	Saprotroph
otu_448	<i>Xylodon species 3</i>	1	66	Saprotroph
otu_590	<i>Xylodon species 4</i>	1	9	Saprotroph
otu_303	<i>Yuchengia species 1</i>	1	56	Saprotroph

SUPPLEMENTARY TABLE 3.4. Operational taxonomic unit (OTU) taxonomic and function guild assignments using Manual BLAST Percent Based (MAN PER) method.

OTU	MAN PER Taxonomic assignment	Incidence frequency	No. sequence reads	Function guild assignment
otu_389	<i>Absidia species 1</i>	Saprotroph	1	50
otu_1067	<i>Acremonium species 1</i>	Fungicolous	1	4
otu_248	<i>Acremonium species 10</i>	Fungicolous	3	95
otu_27	<i>Acremonium species 11</i>	Fungicolous	8	26649
otu_358	<i>Acremonium species 12</i>	Fungicolous	2	89
otu_371	<i>Acremonium species 13</i>	Fungicolous	9	164
otu_410	<i>Acremonium species 14</i>	Fungicolous	2	74
otu_607	<i>Acremonium species 15</i>	Fungicolous	2	17
otu_657	<i>Acremonium species 16</i>	Fungicolous	1	21
otu_658	<i>Acremonium species 17</i>	Fungicolous	1	7
otu_722	<i>Acremonium species 18</i>	Fungicolous	1	32
otu_727	<i>Acremonium species 19</i>	Fungicolous	1	4
otu_1087	<i>Acremonium species 2</i>	Fungicolous	2	4
otu_731	<i>Acremonium species 20</i>	Fungicolous	2	204
otu_755	<i>Acremonium species 21</i>	Fungicolous	1	8
otu_8	<i>Acremonium species 22</i>	Fungicolous	50	150140
otu_839	<i>Acremonium species 23</i>	Fungicolous	1	7
otu_846	<i>Acremonium species 24</i>	Fungicolous	4	86
otu_847	<i>Acremonium species 25</i>	Fungicolous	1	3
otu_86	<i>Acremonium species 26</i>	Fungicolous	1	728
otu_896	<i>Acremonium species 27</i>	Fungicolous	2	13
otu_1126	<i>Acremonium species 3</i>	Fungicolous	1	4
otu_116	<i>Acremonium species 4</i>	Fungicolous	9	3752
otu_1205	<i>Acremonium species 5</i>	Fungicolous	2	148
otu_142	<i>Acremonium species 6</i>	Fungicolous	6	1905
otu_168	<i>Acremonium species 7</i>	Fungicolous	1	351
otu_23	<i>Acremonium species 8</i>	Fungicolous	12	22585
otu_236	<i>Acremonium species 9</i>	Fungicolous	9	632
otu_199	<i>Agaricales species 11.1</i>	Undetermined	2	275
otu_386	<i>Agaricales species 11.2</i>	Undetermined	1	30
otu_66	<i>Agaricales species 11.3</i>	Undetermined	5	1788
otu_1099	<i>Agaricales species 11.4</i>	Undetermined	1	2

otu_310	<i>Agaricales species 5.1</i>	Undetermined	1	42
otu_1229	<i>Agaricales species 6.1</i>	Undetermined	1	2
otu_485	<i>Agaricomycetes species 1.1</i>	Undetermined	1	23
otu_98	<i>Agaricomycetes species 11.1</i>	Undetermined	3	860
otu_952	<i>Agaricomycetes species 11.3</i>	Undetermined	4	10
otu_487	<i>Agaricomycetes species 11.4</i>	Undetermined	1	21
otu_1106	<i>Agaricomycetes species 13.1</i>	Undetermined	1	2
otu_615	<i>Agaricomycetes species 13.2</i>	Undetermined	1	16
otu_157	<i>Agaricomycetes species 13.3</i>	Undetermined	1	456
otu_444	<i>Agaricomycetes species 13.4</i>	Undetermined	1	20
otu_16	<i>Agaricomycetes species 13.5</i>	Undetermined	12	30634
otu_461	<i>Agaricomycetes species 15.1</i>	Undetermined	1	31
otu_598	<i>Agaricomycetes species 20.1</i>	Undetermined	1	10
otu_553	<i>Agaricomycetes species 22.1</i>	Undetermined	1	12
otu_260	<i>Agaricomycetes species 23.2</i>	Undetermined	1	85
otu_185	<i>Agaricomycetes species 27.1</i>	Undetermined	1	151
otu_364	<i>Agaricomycetes species 3.1</i>	Undetermined	1	35
otu_416	<i>Agaricomycetes species 3.2</i>	Undetermined	1	20
otu_883	<i>Agaricomycetes species 3.3</i>	Undetermined	1	3
otu_331	<i>Agaricomycetes species 32.1</i>	Undetermined	1	38
otu_231	<i>Agaricomycetes species 34.1</i>	Undetermined	1	65
otu_76	<i>Agaricomycetes species 34.10</i>	Undetermined	2	1483
otu_960	<i>Agaricomycetes species 34.11</i>	Undetermined	1	2
otu_252	<i>Agaricomycetes species 34.6</i>	Undetermined	1	75
otu_903	<i>Agaricomycetes species 34.7</i>	Undetermined	1	7
otu_613	<i>Agaricomycetes species 34.9</i>	Undetermined	1	11
otu_509	<i>Agaricomycetes species 36.1</i>	Undetermined	2	17
otu_900	<i>Agaricomycetes species 37.1</i>	Undetermined	1	9
otu_1243	<i>Agaricomycetes species 38.1</i>	Undetermined	1	2
otu_362	<i>Agaricomycetes species 4.1</i>	Undetermined	1	28
otu_694	<i>Agaricomycetes species 5.1</i>	Undetermined	1	4
otu_962	<i>Agaricomycetes species 6.1</i>	Undetermined	1	2
otu_139	<i>Agaricomycetes species 9.1</i>	Undetermined	2	303
otu_640	<i>Agrocybe species 1</i>	Saprotroph	1	8
otu_789	<i>Alternaria species 1</i>	Plant pathogen	1	5
otu_706	<i>Amphisphaeriaceae species 1.2</i>	Saprotroph	1	8
otu_484	<i>Amyloporia species 1</i>	Saprotroph	1	15
otu_178	<i>Ascomycota incertae sedis species</i>	Undetermined	1	345
otu_254	<i>Ascomycota species 17.1</i>	Undetermined	1	69

otu_173	<i>Ascomycota species 9.1</i>	Undetermined	1	158
otu_340	<i>Aspergillus species 1</i>	Saprotroph	1	29
otu_211	<i>Atheliaceae species 1.1</i>	Undetermined	1	94
otu_1247	<i>Atractiellales species 1.1</i>	Undetermined	1	2
otu_316	<i>Aurantiporus species 1</i>	Wood decay	2	79
otu_643	<i>Auriculariales species 1</i>	Undetermined	1	7
otu_198	<i>Auriculariales species incertae</i>	Undetermined	1	209
otu_305	<i>Basidiobolus species 1</i>	Saprotroph	1	91
otu_318	<i>Basidiomycota species 13.1</i>	Undetermined	1	48
otu_369	<i>Basidiomycota species 13.2</i>	Undetermined	1	35
otu_503	<i>Basidiomycota species 13.3</i>	Undetermined	1	4
otu_878	<i>Basidiomycota species 14.1</i>	Undetermined	1	5
otu_824	<i>Basidiomycota species 15.1</i>	Undetermined	1	5
otu_618	<i>Basidiomycota species 15.2</i>	Undetermined	1	8
otu_678	<i>Basidiomycota species 18.1</i>	Undetermined	1	8
otu_650	<i>Basidiomycota species 19.1</i>	Undetermined	1	5
otu_202	<i>Basidiomycota species 23.1</i>	Undetermined	1	105
otu_1075	<i>Basidiomycota species 25.13</i>	Undetermined	3	8
otu_1184	<i>Basidiomycota species 25.14</i>	Undetermined	1	2
otu_104	<i>Basidiomycota species 25.15</i>	Undetermined	3	766
otu_500	<i>Basidiomycota species 25.5</i>	Undetermined	1	16
otu_959	<i>Basidiomycota species 25.6</i>	Undetermined	1	4
otu_566	<i>Basidiomycota species 26.1</i>	Undetermined	1	19
otu_867	<i>Basidiomycota species 27.1</i>	Undetermined	1	3
otu_677	<i>Basidiomycota species 3.1</i>	Undetermined	1	5
otu_1142	<i>Basidiomycota species 4.1</i>	Undetermined	1	2
otu_625	<i>Basidiomycota species 4.2</i>	Undetermined	2	25
otu_311	<i>Basidiomycota species 5.1</i>	Undetermined	1	47
otu_321	<i>Basidiomycota species 6.1</i>	Undetermined	1	43
otu_968	<i>Basidiomycota species 7.1</i>	Undetermined	1	2
otu_1006	<i>Basidiomycota species 7.2</i>	Undetermined	1	2
otu_809	<i>Beltrania species 1</i>	Saprotroph	1	5
otu_540	<i>Betamyces species 1</i>	Plant pathogen	1	13
otu_695	<i>Biatriospora species 1</i>	Fungicolous	1	8
otu_617	<i>Bionectriaceae species 1.1</i>	Saprotroph	2	15
otu_432	<i>Bionectriaceae species 1.10</i>	Saprotroph	1	21
otu_1204	<i>Bionectriaceae species 1.11</i>	Saprotroph	1	2
otu_1208	<i>Bionectriaceae species 1.12</i>	Saprotroph	1	2
otu_63	<i>Bionectriaceae species 1.2</i>	Saprotroph	1	1071

otu_1160	<i>Bionectriaceae species 1.3</i>	Saprotroph	1	2
otu_54	<i>Bionectriaceae species 1.4</i>	Saprotroph	3	1507
otu_743	<i>Bionectriaceae species 1.5</i>	Saprotroph	1	4
otu_1233	<i>Bionectriaceae species 1.6</i>	Saprotroph	1	2
otu_621	<i>Bionectriaceae species 1.7</i>	Saprotroph	5	19
otu_1076	<i>Bionectriaceae species 1.8</i>	Saprotroph	1	2
otu_935	<i>Bionectriaceae species 1.9</i>	Saprotroph	1	2
otu_267	<i>Bjerkandera species 2</i>	Wood decay	1	47
otu_453	<i>Bulleromyces species 1</i>	Undetermined	1	18
otu_629	<i>Calosphaeriaceae species 1.1</i>	Undetermined	1	11
otu_354	<i>Calyprella species 1</i>	Saprotroph	1	22
otu_1122	<i>Campylocarpon species 1</i>	Plant pathogen	1	2
otu_57	<i>Campylocarpon species 2</i>	Plant pathogen	4	1744
otu_44	<i>Candida species 2</i>	Saprotroph	1	2366
otu_436	<i>Candida species 3</i>	Saprotroph	1	13
otu_693	<i>Candida species 7</i>	Saprotroph	1	6
otu_108	<i>Candida species 8</i>	Saprotroph	1	494
otu_4	<i>Candida species 9</i>	Saprotroph	20	106
otu_152	<i>Cantharellales species 1.1</i>	Undetermined	1	224
otu_302	<i>Ceriporia species 4</i>	Wood decay	4	66
otu_703	<i>Chaetothyriales species 4.1</i>	Undetermined	1	4
otu_704	<i>Chaetothyriales species 5.1</i>	Undetermined	1	4
otu_702	<i>Chaetothyriales species 6.2</i>	Undetermined	1	7
otu_680	<i>Chaetothyriales species 9.2</i>	Undetermined	1	12
otu_788	<i>Chaetothyriales species 9.3</i>	Undetermined	1	10
otu_1242	<i>Chytridiomycota species 2.1</i>	Undetermined	1	2
otu_184	<i>Chytridiomycota species 2.2</i>	Undetermined	2	159
otu_84	<i>Chytridiomycota species 3.1</i>	Undetermined	1	809
otu_497	<i>Chytridiomycota species 3.3</i>	Undetermined	1	12
otu_307	<i>Chytridiomycota species 7.1</i>	Undetermined	1	42
otu_1225	<i>Clavicipitaceae species 1.1</i>	Entomopathogenic	2	6
otu_865	<i>Clavicipitaceae species 1.10</i>	Entomopathogenic	1	7
otu_1237	<i>Clavicipitaceae species 1.11</i>	Entomopathogenic	1	2
otu_451	<i>Clavicipitaceae species 1.12</i>	Entomopathogenic	1	42
otu_866	<i>Clavicipitaceae species 1.13</i>	Entomopathogenic	1	3
otu_911	<i>Clavicipitaceae species 1.14</i>	Entomopathogenic	1	7
otu_1119	<i>Clavicipitaceae species 1.15</i>	Entomopathogenic	1	4
otu_1129	<i>Clavicipitaceae species 1.16</i>	Entomopathogenic	1	2
otu_140	<i>Clavicipitaceae species 1.17</i>	Entomopathogenic	2	288

otu_196	<i>Clavicipitaceae species 1.19</i>	Entomopathogenic	2	142
otu_488	<i>Clavicipitaceae species 1.2</i>	Entomopathogenic	1	13
otu_5	<i>Clavicipitaceae species 1.20</i>	Entomopathogenic	41	87459
otu_667	<i>Clavicipitaceae species 1.21</i>	Entomopathogenic	1	25
otu_863	<i>Clavicipitaceae species 1.22</i>	Entomopathogenic	1	5
otu_577	<i>Clavicipitaceae species 1.3</i>	Entomopathogenic	2	17
otu_608	<i>Clavicipitaceae species 1.4</i>	Entomopathogenic	1	13
otu_1032	<i>Clavicipitaceae species 1.5</i>	Entomopathogenic	1	2
otu_1033	<i>Clavicipitaceae species 1.6</i>	Entomopathogenic	1	2
otu_1123	<i>Clavicipitaceae species 1.7</i>	Entomopathogenic	1	2
otu_412	<i>Clavicipitaceae species 1.8</i>	Entomopathogenic	1	30
otu_525	<i>Clavicipitaceae species 1.9</i>	Entomopathogenic	1	16
otu_1112	<i>Clavicipitaceae species 2.1</i>	Entomopathogenic	1	2
otu_48	<i>Clavicipitaceae species 2.2</i>	Entomopathogenic	2	2494
otu_524	<i>Clavicipitaceae species 2.3</i>	Entomopathogenic	1	18
otu_697	<i>Clavicipitaceae species 2.4</i>	Entomopathogenic	1	18
otu_973	<i>Clavicipitaceae species 2.5</i>	Entomopathogenic	2	4
otu_174	<i>Clavicipitaceae species 2.6</i>	Entomopathogenic	1	233
otu_612	<i>Clavicipitaceae species 2.7</i>	Entomopathogenic	2	10
otu_870	<i>Clavicipitaceae species 2.8</i>	Entomopathogenic	1	5
otu_470	<i>Clavicipitaceae species 2.9</i>	Entomopathogenic	1	14
otu_59	<i>Clavicipitaceae species 3.1</i>	Entomopathogenic	5	1627
otu_820	<i>Clavicipitaceae species 3.2</i>	Entomopathogenic	1	5
otu_1070	<i>Clavicipitaceae species 4.1</i>	Entomopathogenic	1	2
otu_561	<i>Clonostachys species 1</i>	Saprotroph	2	24
otu_887	<i>Clonostachys species 10</i>	Saprotroph	1	3
otu_1158	<i>Clonostachys species 11</i>	Saprotroph	1	8
otu_891	<i>Clonostachys species 13</i>	Saprotroph	1	11
otu_1077	<i>Clonostachys species 14</i>	Saprotroph	1	2
otu_1199	<i>Clonostachys species 15</i>	Saprotroph	1	2
otu_129	<i>Clonostachys species 16</i>	Saprotroph	2	658
otu_895	<i>Clonostachys species 17</i>	Saprotroph	1	6
otu_1159	<i>Clonostachys species 2</i>	Saprotroph	1	4
otu_672	<i>Clonostachys species 3</i>	Saprotroph	1	7
otu_111	<i>Clonostachys species 4</i>	Saprotroph	9	1480
otu_1101	<i>Clonostachys species 5</i>	Saprotroph	1	2
otu_301	<i>Clonostachys species 6</i>	Saprotroph	2	50
otu_1171	<i>Clonostachys species 7</i>	Saprotroph	1	2
otu_1234	<i>Clonostachys species 8</i>	Saprotroph	1	2

otu_581	<i>Clonostachys species 9</i>	Saprotroph	1	22
otu_1149	<i>Cordycipitaceae species 1.1</i>	Entomopathogenic	1	2
otu_877	<i>Cordycipitaceae species 1.2</i>	Entomopathogenic	1	6
otu_1175	<i>Cordycipitaceae species 2.1</i>	Entomopathogenic	1	2
otu_118	<i>Cordycipitaceae species 2.2</i>	Entomopathogenic	2	775
otu_1141	<i>Cordycipitaceae species 2.3</i>	Entomopathogenic	1	2
otu_454	<i>Cordycipitaceae species 2.4</i>	Entomopathogenic	1	17
otu_747	<i>Cordycipitaceae species 2.5</i>	Entomopathogenic	1	10
otu_879	<i>Cordycipitaceae species 2.6</i>	Entomopathogenic	1	3
otu_165	<i>Corticaceae species 1.1</i>	Undetermined	1	339
otu_223	<i>Corticaceae species 2.1</i>	Undetermined	1	119
otu_944	<i>Corticiales species 1.1</i>	Undetermined	1	2
otu_350	<i>Corticium species 1</i>	Saprotroph	1	29
otu_1245	<i>Crepidotaceae species 1.1</i>	Wood decay	1	2
otu_251	<i>Cryptococcus species 1</i>	Saprotroph	1	65
otu_367	<i>Cunninghamellaceae species 1.1</i>	Undetermined	3	100
otu_975	<i>Cunninghamellaceae species 2.1</i>	Undetermined	1	2
otu_871	<i>Cutaneotrichosporon species 1</i>	Saprotroph	1	5
otu_404	<i>Cylindrobasidium species 1</i>	Undetermined	1	17
otu_375	<i>Cyphellaceae species 1.1</i>	Undetermined	1	19
otu_61	<i>Cystobasidiomycetes species 1.2</i>	Undetermined	1	1136
otu_811	<i>Dacryobolus species 1</i>	Plant pathogen	1	5
otu_905	<i>Debaryomyces species 10</i>	Saprotroph	3	10
otu_1198	<i>Debaryomyces species 19</i>	Saprotroph	1	18
otu_2	<i>Debaryomyces species 2</i>	Saprotroph	72	255672
otu_120	<i>Debaryomyces species 20</i>	Saprotroph	10	1662
otu_18	<i>Debaryomyces species 21</i>	Saprotroph	28	36255
otu_208	<i>Debaryomyces species 4</i>	Saprotroph	4	235
otu_405	<i>Debaryomyces species 5</i>	Saprotroph	5	111
otu_530	<i>Debaryomyces species 6</i>	Saprotroph	3	60
otu_659	<i>Debaryomyces species 7</i>	Saprotroph	2	11
otu_668	<i>Debaryomyces species 7</i>	Saprotroph	6	113
otu_751	<i>Debaryomyces species 8</i>	Saprotroph	1	11
otu_862	<i>Debaryomyces species 9</i>	Saprotroph	30	2147
otu_1118	<i>Debaryomycetaceae species 1.1</i>	Undetermined	1	4
otu_669	<i>Debaryomycetaceae species 1.2</i>	Undetermined	3	16
otu_715	<i>Deconica species 1</i>	Saprotroph	1	6
otu_575	<i>Dothideomycetes species 1.1</i>	Undetermined	1	11
otu_1083	<i>Dothideomycetes species 2.1</i>	Undetermined	1	2

otu_971	<i>Engyodontium species 1</i>	Entomopathogenic	1	2
otu_954	<i>Eurotiomycetes species 3.3</i>	Undetermined	1	2
otu_1011	<i>Exidiaceae species 1.1</i>	Undetermined	1	2
otu_127	<i>Exobasidiomycetes species 2.1</i>	Undetermined	1	325
otu_175	<i>Exophiala species 2</i>	Saprotroph	3	215
otu_161	<i>Filobasidium species 1</i>	Saprotroph	1	296
otu_910	<i>Fomitiporia species 1</i>	Plant pathogen	1	3
otu_1128	<i>Fusarium species 1</i>	Plant pathogen	1	2
otu_1194	<i>Fusarium species 10</i>	Plant pathogen	1	4
otu_1057	<i>Fusarium species 12</i>	Plant pathogen	1	2
otu_748	<i>Fusarium species 16</i>	Plant pathogen	1	9
otu_886	<i>Fusarium species 17</i>	Plant pathogen	1	3
otu_258	<i>Fusarium species 18</i>	Plant pathogen	4	205
otu_1094	<i>Fusarium species 19</i>	Plant pathogen	1	2
otu_1148	<i>Fusarium species 20</i>	Plant pathogen	1	2
otu_1156	<i>Fusarium species 21</i>	Plant pathogen	1	2
otu_1181	<i>Fusarium species 22</i>	Plant pathogen	1	4
otu_213	<i>Fusarium species 23</i>	Plant pathogen	3	79
otu_368	<i>Fusarium species 24</i>	Plant pathogen	5	78
otu_411	<i>Fusarium species 25</i>	Plant pathogen	4	112
otu_494	<i>Fusarium species 26</i>	Plant pathogen	1	11
otu_611	<i>Fusarium species 27</i>	Plant pathogen	1	13
otu_67	<i>Fusarium species 28</i>	Plant pathogen	11	1325
otu_737	<i>Fusarium species 29</i>	Plant pathogen	1	6
otu_523	<i>Fusarium species 3</i>	Plant pathogen	1	10
otu_854	<i>Fusarium species 30</i>	Plant pathogen	2	9
otu_939	<i>Fusarium species 31</i>	Plant pathogen	1	2
otu_1121	<i>Fusarium species 32</i>	Plant pathogen	1	2
otu_359	<i>Fusarium species 33</i>	Plant pathogen	1	23
otu_417	<i>Fusarium species 35</i>	Plant pathogen	1	28
otu_1102	<i>Fusarium species 36</i>	Plant pathogen	1	2
otu_564	<i>Fusarium species 4</i>	Plant pathogen	1	9
otu_1097	<i>Fusarium species 6</i>	Plant pathogen	1	2
otu_1178	<i>Fusarium species 7</i>	Plant pathogen	1	8
otu_188	<i>Fusarium species 8</i>	Plant pathogen	3	151
otu_26	<i>Fusarium species 9</i>	Plant pathogen	12	9913
otu_294	<i>Fuscoporia species 1</i>	Saprotroph	1	49
otu_908	<i>Fuscoporia species 2</i>	Saprotroph	1	5
otu_212	<i>Gliomastix species 1</i>	Saprotroph	4	134

otu_850	<i>Gliomastix species 10</i>	Saprotroph	1	7
otu_872	<i>Gliomastix species 11</i>	Saprotroph	1	3
otu_907	<i>Gliomastix species 12</i>	Saprotroph	1	3
otu_153	<i>Gliomastix species 13</i>	Saprotroph	6	3216
otu_204	<i>Gliomastix species 2</i>	Saprotroph	2	4
otu_214	<i>Gliomastix species 3</i>	Saprotroph	1	193
otu_226	<i>Gliomastix species 4</i>	Saprotroph	1	96
otu_28	<i>Gliomastix species 5</i>	Saprotroph	20	26018
otu_713	<i>Gliomastix species 7</i>	Saprotroph	2	12
otu_848	<i>Gliomastix species 8</i>	Saprotroph	1	5
otu_1027	<i>Gliomastix species 9</i>	Saprotroph	2	22
otu_269	<i>Gloeoporus species 2</i>	Wood decay	1	62
otu_596	<i>Gloeoporus species 3</i>	Wood decay	1	10
otu_1163	<i>Glomerellales species 1.1</i>	Undetermined	1	2
otu_744	<i>Glomerellales species 1.2</i>	Undetermined	1	17
otu_1080	<i>Graphium species 1</i>	Saprotroph	1	4
otu_1082	<i>Graphium species 2</i>	Saprotroph	1	2
otu_192	<i>Graphium species 3</i>	Saprotroph	2	133
otu_326	<i>Graphium species 4</i>	Saprotroph	2	49
otu_614	<i>Graphium species 5</i>	Saprotroph	1	6
otu_552	<i>Gymnopilus species 4</i>	Wood decay	2	15
otu_943	<i>Gymnopus species 2</i>	Saprotroph	1	2
otu_927	<i>Gymnopus species 3</i>	Saprotroph	1	2
otu_966	<i>Helotiales species 1.1</i>	Undetermined	1	2
otu_467	<i>Herpotrichiellaceae species 3.1</i>	Undetermined	1	20
otu_242	<i>Hydnodontaceae species 1.1</i>	Undetermined	1	63
otu_1031	<i>Hymenochaetaceae species 1.1</i>	Undetermined	1	2
otu_448	<i>Hymenochaetaceae species 2.1</i>	Undetermined	1	66
otu_268	<i>Hyphodermella species 1</i>	Saprotroph	3	82
otu_705	<i>Hyphodontia species 1</i>	Saprotroph	2	9
otu_666	<i>Hyphodontia species 3</i>	Saprotroph	1	12
otu_442	<i>Hyphodontia species 4</i>	Saprotroph	1	16
otu_1010	<i>Hypholoma species 1</i>	Wood decay	1	4
otu_1173	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	2
otu_653	<i>Hypocreales Incertae sedis species</i>	Undetermined	3	7
otu_774	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	5
otu_775	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	3
otu_1179	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	2
otu_758	<i>Hypocreales Incertae sedis species</i>	Undetermined	4	18

otu_778	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	5
otu_1189	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	2
otu_10	<i>Hypocreales Incertae sedis species</i>	Undetermined	73	128406
otu_670	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	7
otu_965	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	2
otu_300	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	50
otu_562	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	12
otu_734	<i>Hypocreales Incertae sedis species</i>	Undetermined	1	7
otu_641	<i>Hypocreales incertae sedis species</i>	Undetermined	2	14
otu_238	<i>Hypocreales incertae sedis species</i>	Undetermined	1	107
otu_940	<i>Hypocreales incertae sedis species</i>	Undetermined	1	2
otu_735	<i>Hypocreales incertae sedis species</i>	Undetermined	1	9
otu_957	<i>Hypocreales incertae sedis species</i>	Undetermined	1	2
otu_319	<i>Hypocreales incertae sedis species</i>	Undetermined	3	93
otu_736	<i>Hypocreales incertae sedis species</i>	Undetermined	1	11
otu_20	<i>Hypocreales incertae sedis species</i>	Undetermined	4	10
otu_34	<i>Hypocreales incertae sedis species</i>	Undetermined	3	8534
otu_1136	<i>Hypocreales incertae sedis species</i>	Undetermined	1	8
otu_769	<i>Hypocreales incertae sedis species</i>	Undetermined	1	3
otu_232	<i>Hypocreales incertae sedis species</i>	Undetermined	1	210
otu_521	<i>Hypocreales incertae sedis species</i>	Undetermined	1	13
otu_1151	<i>Hypocreales incertae sedis species</i>	Undetermined	1	2
otu_128	<i>Hypocreales incertae sedis species</i>	Undetermined	3	542
otu_304	<i>Hypocreales incertae sedis species</i>	Undetermined	1	74
otu_558	<i>Hypocreales incertae sedis species</i>	Undetermined	1	9
otu_1120	<i>Hypocreales incertae sedis species</i>	Undetermined	1	2
otu_733	<i>Hypocreales incertae sedis species</i>	Undetermined	2	25
otu_890	<i>Hypocreales incertae sedis species</i>	Undetermined	1	3
otu_1169	<i>Hypocreales incertae sedis species</i>	Undetermined	1	2
otu_604	<i>Hypocreales incertae sedis species</i>	Undetermined	1	9
otu_578	<i>Hypocreales incertae sedis species</i>	Undetermined	3	19
otu_468	<i>Hypocreales incertae sedis species</i>	Undetermined	1	15
otu_675	<i>Hypocreales incertae sedis species</i>	Undetermined	1	17
otu_1176	<i>Hypocreales incertae sedis species</i>	Undetermined	1	2
otu_752	<i>Hypocreales incertae sedis species</i>	Undetermined	1	8
otu_186	<i>Hypocreales incertae sedis species</i>	Undetermined	1	127
otu_837	<i>Hypocreales incertae sedis species</i>	Undetermined	1	3
otu_384	<i>Hypocreales incertae sedis species</i>	Undetermined	1	18
otu_1071	<i>Hypocreales incertae sedis species</i>	Undetermined	1	2

otu_312	<i>Hypocreales species 1.1</i>	Undetermined	1	48
otu_477	<i>Hypocreales species 10.2</i>	Undetermined	1	12
otu_665	<i>Hypocreales species 12.1</i>	Undetermined	1	10
otu_1096	<i>Hypocreales species 14.2</i>	Undetermined	1	2
otu_532	<i>Hypocreales species 15.2</i>	Undetermined	1	13
otu_716	<i>Hypocreales species 15.3</i>	Undetermined	1	4
otu_888	<i>Hypocreales species 16.1</i>	Undetermined	1	3
otu_663	<i>Hypocreales species 16.2</i>	Undetermined	1	5
otu_856	<i>Hypocreales species 16.3</i>	Undetermined	1	3
otu_976	<i>Hypocreales species 16.4</i>	Undetermined	1	2
otu_150	<i>Hypocreales species 16.5</i>	Undetermined	4	296
otu_786	<i>Hypocreales species 16.6</i>	Undetermined	1	3
otu_1036	<i>Hypocreales species 17.1</i>	Undetermined	1	2
otu_459	<i>Hypocreales species 3.1</i>	Undetermined	1	22
otu_11	<i>Hypocreales species 5.1</i>	Undetermined	30	47429
otu_281	<i>Hypocreales species 6.1</i>	Undetermined	5	104
otu_1113	<i>Hypocreales species 6.10</i>	Undetermined	1	4
otu_30	<i>Hypocreales species 6.11</i>	Undetermined	8	17
otu_427	<i>Hypocreales species 6.12</i>	Undetermined	1	14
otu_536	<i>Hypocreales species 6.13</i>	Undetermined	3	43
otu_679	<i>Hypocreales species 6.2</i>	Undetermined	6	20
otu_1114	<i>Hypocreales species 6.3</i>	Undetermined	1	2
otu_1223	<i>Hypocreales species 6.4</i>	Undetermined	1	4
otu_609	<i>Hypocreales species 6.6</i>	Undetermined	1	14
otu_366	<i>Hypocreales species 6.7</i>	Undetermined	1	25
otu_568	<i>Hypocreales species 6.8</i>	Undetermined	2	17
otu_425	<i>Hypocreales species 6.9</i>	Undetermined	3	33
otu_74	<i>Hypocreales species 7.1</i>	Undetermined	1	1036
otu_1228	<i>Hypocreales species 8.1</i>	Undetermined	1	4
otu_760	<i>Hypocreales species 8.2</i>	Undetermined	1	6
otu_906	<i>Hypocreales species 8.3</i>	Undetermined	1	5
otu_874	<i>Hypocreales species 9.1</i>	Undetermined	1	3
otu_183	<i>Irpex species 2</i>	Wood decay	2	166
otu_972	<i>Junghuhnia species 1</i>	Wood decay	1	2
otu_278	<i>Kneiffiella species 3</i>	Wood decay	5	87
otu_1218	<i>Lasiodiplodia species 1</i>	Plant pathogen	1	2
otu_222	<i>Lasiodiplodia species 2</i>	Plant pathogen	1	123
otu_554	<i>Lecanicillium species 1</i>	Entomopathogenic	1	9
otu_97	<i>Lecanicillium species 2</i>	Entomopathogenic	2	631

otu_255	<i>Lecanoromycetes species 2.1</i>	Undetermined	1	64
otu_274	<i>Lecanoromycetes species 2.3</i>	Undetermined	1	68
otu_876	<i>Lecanoromycetes species 2.4</i>	Undetermined	1	3
otu_819	<i>Lecanoromycetes species 4.1</i>	Undetermined	1	6
otu_298	<i>Lecanoromycetes species 5.2</i>	Undetermined	2	67
otu_591	<i>Lecanoromycetes species 5.3</i>	Undetermined	2	12
otu_781	<i>Lecanoromycetes species 5.4</i>	Undetermined	1	5
otu_206	<i>Lentinellus species 1</i>	Saprotroph	1	92
otu_41	<i>Lentinus species 2</i>	Wood decay	2	3309
otu_31	<i>Leptobacillium species 1</i>	Undetermined	11	25806
otu_673	<i>Leptobacillium species 10</i>	Undetermined	1	8
otu_745	<i>Leptobacillium species 11</i>	Undetermined	2	868
otu_880	<i>Leptobacillium species 12</i>	Undetermined	1	11
otu_1230	<i>Leptobacillium species 2</i>	Undetermined	1	2
otu_740	<i>Leptobacillium species 3</i>	Undetermined	1	6
otu_742	<i>Leptobacillium species 4</i>	Undetermined	1	14
otu_1139	<i>Leptobacillium species 5</i>	Undetermined	1	2
otu_221	<i>Leptobacillium species 6</i>	Undetermined	1	175
otu_280	<i>Leptobacillium species 7</i>	Undetermined	1	267
otu_430	<i>Leptobacillium species 8</i>	Undetermined	2	39
otu_498	<i>Leptobacillium species 9</i>	Undetermined	1	37
otu_569	<i>Leptosporomyces species 1</i>	Saprotroph	1	17
otu_1029	<i>Malassezia species 1</i>	Saprotroph	1	2
otu_135	<i>Malassezia species 14</i>	Saprotroph	3	16
otu_504	<i>Malassezia species 15</i>	Saprotroph	3	28
otu_53	<i>Malassezia species 16</i>	Saprotroph	18	5987
otu_785	<i>Malassezia species 2</i>	Saprotroph	1	3
otu_808	<i>Malassezia species 3</i>	Saprotroph	4	43
otu_25	<i>Malassezia species 4</i>	Saprotroph	12	28413
otu_92	<i>Malassezia species 6</i>	Saprotroph	10	878
otu_193	<i>Malasseziomycetes species 1.1</i>	Undetermined	2	141
otu_43	<i>Malasseziomycetes species 1.3</i>	Undetermined	3	3277
otu_94	<i>Marasmiaceae species 1.2</i>	Plant pathogen	1	1046
otu_24	<i>Marasmiellus species 1</i>	Plant pathogen	3	3507
otu_1127	<i>Metacordyceps species 1</i>	Entomopathogenic	1	2
otu_565	<i>Metacordyceps species 2</i>	Entomopathogenic	4	45
otu_58	<i>Metapochonia species 10</i>	Entomopathogenic	1	1630
otu_580	<i>Metapochonia species 11</i>	Entomopathogenic	1	19
otu_1131	<i>Metapochonia species 13</i>	Entomopathogenic	2	4

otu_207	<i>Metapochonia species 14</i>	Entomopathogenic	2	272
otu_273	<i>Metapochonia species 15</i>	Entomopathogenic	1	118
otu_299	<i>Metapochonia species 16</i>	Entomopathogenic	2	34
otu_334	<i>Metapochonia species 17</i>	Entomopathogenic	6	385
otu_1152	<i>Metapochonia species 18</i>	Entomopathogenic	1	2
otu_414	<i>Metapochonia species 19</i>	Entomopathogenic	2	29
otu_122	<i>Metapochonia species 2</i>	Entomopathogenic	21	1783
otu_495	<i>Metapochonia species 21</i>	Entomopathogenic	1	23
otu_533	<i>Metapochonia species 22</i>	Entomopathogenic	1	16
otu_610	<i>Metapochonia species 23</i>	Entomopathogenic	2	23
otu_868	<i>Metapochonia species 3</i>	Entomopathogenic	1	5
otu_869	<i>Metapochonia species 4</i>	Entomopathogenic	1	11
otu_902	<i>Metapochonia species 5</i>	Entomopathogenic	1	9
otu_195	<i>Metapochonia species 6</i>	Entomopathogenic	1	112
otu_534	<i>Metapochonia species 7</i>	Entomopathogenic	1	27
otu_1224	<i>Metapochonia species 8</i>	Entomopathogenic	1	2
otu_14	<i>Metapochonia species 9</i>	Entomopathogenic	35	65889
otu_6	<i>Metarhizium species 1</i>	Entomopathogenic	32	62691
otu_1236	<i>Metarhizium species 3</i>	Entomopathogenic	1	2
otu_493	<i>Mucor species 1</i>	Saprotroph	1	12
otu_1232	<i>Mucoromycotina species 1.1</i>	Undetermined	1	2
otu_277	<i>Mycena species 1</i>	Saprotroph	1	51
otu_632	<i>Mycena species 2</i>	Saprotroph	1	7
otu_47	<i>Mycenaceae species 1.1</i>	Undetermined	2	2859
otu_1202	<i>Mycenaceae species 1.2</i>	Undetermined	1	4
otu_574	<i>Myxarium species 1</i>	Wood decay	1	18
otu_746	<i>Myxospora species 2</i>	Undetermined	1	8
otu_882	<i>Myxospora species 3</i>	Undetermined	1	3
otu_1167	<i>Myxospora species 4</i>	Undetermined	1	4
otu_1170	<i>Myxospora species 5</i>	Undetermined	1	2
otu_1177	<i>Myxospora species 6</i>	Undetermined	2	4
otu_239	<i>Myxospora species 7</i>	Undetermined	1	125
otu_286	<i>Myxospora species 8</i>	Undetermined	1	63
otu_35	<i>Myxospora species 9</i>	Undetermined	7	7925
otu_32	<i>Naganishia species 2</i>	Undetermined	2	8
otu_766	<i>Nectria species 10</i>	Plant pathogen	1	5
otu_829	<i>Nectria species 11</i>	Plant pathogen	1	2
otu_884	<i>Nectria species 12</i>	Plant pathogen	1	3
otu_901	<i>Nectria species 13</i>	Plant pathogen	1	6

otu_933	<i>Nectria species 14</i>	Plant pathogen	1	2
otu_37	<i>Nectria species 15</i>	Plant pathogen	1	3703
otu_864	<i>Nectria species 16</i>	Plant pathogen	1	7
otu_1196	<i>Nectria species 17</i>	Plant pathogen	1	2
otu_1219	<i>Nectria species 18</i>	Plant pathogen	1	2
otu_13	<i>Nectria species 19</i>	Plant pathogen	25	25796
otu_1188	<i>Nectria species 3</i>	Plant pathogen	1	2
otu_197	<i>Nectria species 4</i>	Plant pathogen	1	107
otu_289	<i>Nectria species 5</i>	Plant pathogen	2	69
otu_324	<i>Nectria species 6</i>	Plant pathogen	1	51
otu_571	<i>Nectria species 7</i>	Plant pathogen	1	12
otu_1192	<i>Nectria species 8</i>	Plant pathogen	1	2
otu_749	<i>Nectria species 9</i>	Plant pathogen	1	13
otu_671	<i>Nectriaceae species 1.1</i>	Undetermined	1	8
otu_1140	<i>Nectriaceae species 1.2</i>	Undetermined	1	8
otu_224	<i>Nectriaceae species 1.3</i>	Undetermined	3	148
otu_429	<i>Nectriaceae species 1.4</i>	Undetermined	1	12
otu_1143	<i>Nectriaceae species 2.1</i>	Undetermined	1	2
otu_1081	<i>Nectriaceae species 3.1</i>	Undetermined	1	2
otu_522	<i>Nectriaceae species 3.2</i>	Undetermined	5	38
otu_855	<i>Nectriaceae species 3.3</i>	Undetermined	1	6
otu_823	<i>Nectriaceae species 4.1</i>	Undetermined	1	3
otu_1165	<i>Nectriaceae species 5.2</i>	Undetermined	1	2
otu_1190	<i>Nectriaceae species 5.3</i>	Undetermined	1	2
otu_1180	<i>Nectriaceae species 5.4</i>	Undetermined	1	2
otu_1195	<i>Nectriaceae species 5.5</i>	Undetermined	1	2
otu_284	<i>Nectriaceae species 6.1</i>	Undetermined	1	61
otu_447	<i>Nectriaceae species 6.2</i>	Undetermined	1	16
otu_570	<i>Nectriaceae species 7.2</i>	Undetermined	2	21
otu_844	<i>Nectriaceae species 7.3</i>	Undetermined	1	7
otu_873	<i>Nectriaceae species 7.4</i>	Undetermined	1	5
otu_881	<i>Nectriaceae species 7.5</i>	Undetermined	1	5
otu_1014	<i>Omphalotaceae species 1.1</i>	Undetermined	1	2
otu_585	<i>Omphalotaceae species 1.2</i>	Undetermined	1	13
otu_385	<i>Omphalotaceae species 1.3</i>	Undetermined	2	66
otu_431	<i>Omphalotaceae species 1.4</i>	Undetermined	1	37
otu_964	<i>Omphalotaceae species 1.6</i>	Undetermined	1	2
otu_7	<i>Omphalotaceae species 1.7</i>	Undetermined	24	63494
otu_1217	<i>Omphalotaceae species 1.8</i>	Undetermined	1	2

otu_841	<i>Ophiocordycipitaceae species 1.1</i>	Entomopathogenic	1	8
otu_1108	<i>Ophiocordycipitaceae species 2.1</i>	Entomopathogenic	1	4
otu_729	<i>Ophiocordycipitaceae species 2.10</i>	Entomopathogenic	1	10
otu_1134	<i>Ophiocordycipitaceae species 2.12</i>	Entomopathogenic	1	2
otu_1111	<i>Ophiocordycipitaceae species 2.13</i>	Entomopathogenic	1	2
otu_1226	<i>Ophiocordycipitaceae species 2.14</i>	Entomopathogenic	1	4
otu_563	<i>Ophiocordycipitaceae species 2.15</i>	Entomopathogenic	1	13
otu_852	<i>Ophiocordycipitaceae species 2.16</i>	Entomopathogenic	1	3
otu_79	<i>Ophiocordycipitaceae species 2.17</i>	Entomopathogenic	2	643
otu_1157	<i>Ophiocordycipitaceae species 2.18</i>	Entomopathogenic	1	2
otu_189	<i>Ophiocordycipitaceae species 2.2</i>	Entomopathogenic	3	288
otu_155	<i>Ophiocordycipitaceae species 2.20</i>	Entomopathogenic	1	198
otu_616	<i>Ophiocordycipitaceae species 2.3</i>	Entomopathogenic	2	25
otu_738	<i>Ophiocordycipitaceae species 2.5</i>	Entomopathogenic	1	8
otu_1110	<i>Ophiocordycipitaceae species 2.6</i>	Entomopathogenic	1	4
otu_1135	<i>Ophiocordycipitaceae species 2.7</i>	Entomopathogenic	1	2
otu_413	<i>Ophiocordycipitaceae species 2.8</i>	Entomopathogenic	1	46
otu_528	<i>Ophiocordycipitaceae species 2.9</i>	Entomopathogenic	1	17
otu_133	<i>Ophiostoma species 1</i>	Plant pathogen	2	323
otu_296	<i>Ophiostoma species 2</i>	Plant pathogen	1	30
otu_292	<i>Orbiliomycetes species 1.27</i>	Undetermined	1	45
otu_822	<i>Panus species 1</i>	Undetermined	1	5
otu_754	<i>Penicillifer species 10</i>	Saprotroph	1	6
otu_974	<i>Penicillifer species 11</i>	Saprotroph	1	4
otu_146	<i>Penicillifer species 12</i>	Saprotroph	1	292
otu_1210	<i>Penicillifer species 13</i>	Saprotroph	1	2
otu_1117	<i>Penicillifer species 16</i>	Saprotroph	2	8
otu_15	<i>Penicillifer species 17</i>	Saprotroph	19	53002
otu_576	<i>Penicillifer species 2</i>	Saprotroph	2	17
otu_200	<i>Penicillifer species 3</i>	Saprotroph	4	365
otu_393	<i>Penicillifer species 4</i>	Saprotroph	3	26
otu_1172	<i>Penicillifer species 5</i>	Saprotroph	1	2
otu_433	<i>Penicillifer species 6</i>	Saprotroph	12	1038
otu_1105	<i>Penicillifer species 7</i>	Saprotroph	1	2
otu_977	<i>Penicillifer species 8</i>	Saprotroph	1	2
otu_329	<i>Peniophora species 1</i>	Wood decay	9	243
otu_308	<i>Peniophora species 10</i>	Wood decay	1	46
otu_1028	<i>Peniophora species 2</i>	Wood decay	3	14
otu_627	<i>Peniophora species 3</i>	Wood decay	2	11

otu_265	<i>Peniophora species 5</i>	Wood decay	5	144
otu_550	<i>Peniophora species 7</i>	Wood decay	1	13
otu_154	<i>Peniophoraceae species 1.1</i>	Undetermined	2	196
otu_225	<i>Peniophorella species 2</i>	Saprotroph	3	127
otu_339	<i>Perenniporia species 1</i>	Wood decay	1	40
otu_1004	<i>Phaeomoniellales species 1.1</i>	Undetermined	1	2
otu_1162	<i>Phaeophlebiopsis species 1</i>	Saprotroph	1	2
otu_710	<i>Phallales species 1.1</i>	Undetermined	3	15
otu_219	<i>Phanerochaete species 1</i>	Wood decay	1	23
otu_320	<i>Phellinus species 1</i>	Plant pathogen	1	44
otu_1182	<i>Phialemoniopsis species 1</i>	Saprotroph	1	2
otu_529	<i>Phialemoniopsis species 2</i>	Saprotroph	1	8
otu_171	<i>Phialemoniopsis species 3</i>	Saprotroph	4	327
otu_496	<i>Phialemoniopsis species 4</i>	Saprotroph	1	14
otu_441	<i>Phlebia species 1</i>	Wood decay	1	16
otu_812	<i>Phlebia species 3</i>	Wood decay	1	3
otu_514	<i>Phlebia species 4</i>	Wood decay	1	12
otu_806	<i>Phlebia species 5</i>	Wood decay	1	3
otu_440	<i>Phlebia species 9</i>	Wood decay	2	26
otu_978	<i>Pholiota species 1</i>	Saprotroph	1	2
otu_1125	<i>Plectosphaerella species 1</i>	Plant pathogen	1	2
otu_33	<i>Plectosphaerella species 3</i>	Plant pathogen	8	1114
otu_124	<i>Plectosphaerella species 4</i>	Plant pathogen	1	270
otu_711	<i>Plectosphaerella species 5</i>	Plant pathogen	1	26
otu_783	<i>Plectosphaerella species 6</i>	Plant pathogen	1	5
otu_646	<i>Plectosphaerella species 7</i>	Plant pathogen	2	22
otu_645	<i>Plectosphaerella species 7</i>	Plant pathogen	3	11
otu_50	<i>Plectosphaerellaceae species 1.2</i>	Undetermined	3	1936
otu_1068	<i>Pleosporales species 1.1</i>	Undetermined	1	2
otu_1023	<i>Pleosporales species 1.2</i>	Undetermined	2	4
otu_531	<i>Pleurotus species 1</i>	Entomopathogenic	1	17
otu_262	<i>Pluteus species 2</i>	Wood decay	1	67
otu_597	<i>Polyporaceae species 2.1</i>	Undetermined	1	6
otu_130	<i>Polyporales species 1.1</i>	Undetermined	1	582
otu_1021	<i>Polyporales species 2.1</i>	Undetermined	1	2
otu_1231	<i>Polyporales species 4.1</i>	Undetermined	1	2
otu_392	<i>Polyporales species 5.1</i>	Undetermined	2	39
otu_136	<i>Polyporales species 6.1</i>	Undetermined	1	310
otu_460	<i>Polyporales species 7.1</i>	Undetermined	1	25

otu_271	<i>Postia species 1</i>	Wood decay	1	74
otu_548	<i>Postia species 2</i>	Wood decay	1	13
otu_712	<i>Pseudochaete species 1</i>	Saprotroph	1	7
otu_137	<i>Puccinia species 1</i>	Plant pathogen	1	260
otu_674	<i>Pucciniomycetes species 1.1</i>	Undetermined	1	9
otu_1045	<i>Purpureocillium species 2</i>	Entomopathogenic	1	2
otu_555	<i>Purpureocillium species 3</i>	Entomopathogenic	1	2
otu_519	<i>Purpureocillium species 4</i>	Entomopathogenic	1	19
otu_520	<i>Purpureocillium species 5</i>	Entomopathogenic	1	28
otu_836	<i>Purpureocillium species 6</i>	Entomopathogenic	1	5
otu_1007	<i>Resinicium species 1</i>	Saprotroph	1	4
otu_95	<i>Resupinatus species 1</i>	Wood decay	2	838
otu_383	<i>Resupinatus species 2</i>	Wood decay	1	61
otu_382	<i>Resupinatus species 3</i>	Wood decay	1	26
otu_1244	<i>Rhizophydiales species 1.1</i>	Undetermined	1	2
otu_263	<i>Rigidoporus species 1</i>	Wood decay	1	76
otu_210	<i>Rigidoporus species 2</i>	Wood decay	1	96
otu_979	<i>Rigidoporus species 4</i>	Wood decay	1	4
otu_337	<i>Roussoella species 1</i>	Saprotroph	1	52
otu_723	<i>Roussoellaceae species 1.1</i>	Saprotroph	1	4
otu_1066	<i>Roussoellaceae species 1.10</i>	Saprotroph	1	4
otu_557	<i>Roussoellaceae species 1.11</i>	Saprotroph	1	23
otu_843	<i>Roussoellaceae species 1.12</i>	Saprotroph	1	5
otu_853	<i>Roussoellaceae species 1.13</i>	Saprotroph	1	5
otu_235	<i>Roussoellaceae species 1.14</i>	Saprotroph	1	481
otu_1069	<i>Roussoellaceae species 1.15</i>	Saprotroph	1	2
otu_603	<i>Roussoellaceae species 1.3</i>	Saprotroph	1	13
otu_842	<i>Roussoellaceae species 1.5</i>	Saprotroph	1	23
otu_492	<i>Roussoellaceae species 1.6</i>	Saprotroph	1	82
otu_1024	<i>Roussoellaceae species 1.8</i>	Saprotroph	1	2
otu_143	<i>Roussoellaceae species 1.9</i>	Saprotroph	2	442
otu_1240	<i>Saccharomyces species 1</i>	Wood decay	1	4
otu_1079	<i>Saccharomycetaceae species 1.1</i>	Undetermined	1	2
otu_1212	<i>Saccharomycetales species 2.1</i>	Undetermined	1	2
otu_458	<i>Sakaguchia species 1</i>	Undetermined	1	17
otu_45	<i>Sampaiozyma species 1</i>	Undetermined	1	2020
otu_1098	<i>Sarcopodium species 1</i>	Saprotroph	1	2
otu_295	<i>Sarcopodium species 2</i>	Saprotroph	2	60
otu_510	<i>Sarocladium species 1</i>	Saprotroph	2	25

otu_928	<i>Sarocladium species 10</i>	Saprotroph	3	8
otu_250	<i>Sarocladium species 11</i>	Saprotroph	32	656
otu_388	<i>Sarocladium species 12</i>	Saprotroph	2	84
otu_391	<i>Sarocladium species 13</i>	Saprotroph	6	39
otu_114	<i>Sarocladium species 14</i>	Saprotroph	4	463
otu_418	<i>Sarocladium species 15</i>	Saprotroph	4	74
otu_419	<i>Sarocladium species 16</i>	Saprotroph	2	36
otu_622	<i>Sarocladium species 17</i>	Saprotroph	3	17
otu_56	<i>Sarocladium species 18</i>	Saprotroph	5	1372
otu_776	<i>Sarocladium species 2</i>	Saprotroph	16	121
otu_434	<i>Sarocladium species 20</i>	Saprotroph	31	284
otu_924	<i>Sarocladium species 21</i>	Saprotroph	5	10
otu_921	<i>Sarocladium species 22</i>	Saprotroph	1	2
otu_1124	<i>Sarocladium species 23</i>	Saprotroph	1	2
otu_3	<i>Sarocladium species 24</i>	Saprotroph	129	1823481
otu_767	<i>Sarocladium species 3</i>	Saprotroph	11	42
otu_77	<i>Sarocladium species 4</i>	Saprotroph	42	3103
otu_435	<i>Sarocladium species 6</i>	Saprotroph	8	107
otu_452	<i>Sarocladium species 7</i>	Saprotroph	1	22
otu_958	<i>Sarocladium species 8</i>	Saprotroph	1	2
otu_475	<i>Sarocladium species 9</i>	Saprotroph	6	34
otu_228	<i>Schizophyllum species 1</i>	Wood decay	1	84
otu_160	<i>Schwanniomyces species 1</i>	Undetermined	2	224
otu_1222	<i>Septobasidiales species 1.2</i>	Undetermined	2	4
otu_335	<i>Simplicillium species 1</i>	Entomopathogenic	1	52
otu_753	<i>Simplicillium species 2</i>	Entomopathogenic	1	13
otu_1209	<i>Simplicillium species 3</i>	Entomopathogenic	1	2
otu_1238	<i>Simplicillium species 4</i>	Entomopathogenic	1	2
otu_42	<i>Simplicillium species 5</i>	Entomopathogenic	1	2811
otu_9	<i>Simplicillium species 6</i>	Entomopathogenic	9	42624
otu_649	<i>Sistotremastrum species 1</i>	Saprotroph	1	8
otu_662	<i>Sordariomycetes incertae sedis</i>	Undetermined	1	5
otu_338	<i>Sordariomycetes incertae sedis</i>	Undetermined	1	34
otu_961	<i>Sordariomycetes species 1.1</i>	Undetermined	1	2
otu_714	<i>Sordariomycetes species 12.10</i>	Undetermined	1	8
otu_119	<i>Sordariomycetes species 12.13</i>	Undetermined	1	432
otu_631	<i>Sordariomycetes species 12.14</i>	Undetermined	3	12
otu_245	<i>Sordariomycetes species 12.18</i>	Undetermined	1	72
otu_647	<i>Sordariomycetes species 13.1</i>	Undetermined	1	8

otu_1187	<i>Sordariomycetes species 13.2</i>	Undetermined	1	2
otu_1216	<i>Sordariomycetes species 14.1</i>	Undetermined	1	2
otu_249	<i>Sordariomycetes species 18.2</i>	Undetermined	2	245
otu_486	<i>Sordariomycetes species 19.1</i>	Undetermined	1	13
otu_399	<i>Sordariomycetes species 6.2</i>	Undetermined	2	25
otu_898	<i>Sordariomycetes species 7.1</i>	Undetermined	1	3
otu_1009	<i>Sordariomycetes species 9.1</i>	Undetermined	1	2
otu_390	<i>Sporidiobolus species 2</i>	Undetermined	1	23
otu_327	<i>Stachybotryaceae species 1.1</i>	Undetermined	1	96
otu_395	<i>Stachybotryaceae species 1.2</i>	Undetermined	1	25
otu_1183	<i>Stachybotryaceae species 2.1</i>	Undetermined	1	8
otu_889	<i>Stachybotryaceae species 2.2</i>	Undetermined	1	3
otu_1186	<i>Stachybotrys species 1</i>	Wood decay	1	4
otu_1193	<i>Stachybotrys species 2</i>	Wood decay	1	4
otu_499	<i>Stachybotrys species 3</i>	Wood decay	1	33
otu_885	<i>Stachybotrys species 4</i>	Wood decay	1	3
otu_346	<i>Steccherinum species 1</i>	Saprotroph	1	33
otu_272	<i>Stephanonectria species 2</i>	Saprotroph	4	57
otu_732	<i>Stephanonectria species 3</i>	Saprotroph	2	10
otu_167	<i>Stereum species 1</i>	Saprotroph	8	445
otu_676	<i>Stereum species 2</i>	Saprotroph	1	5
otu_681	<i>Symptoventuriaceae species 1.1</i>	Undetermined	1	8
otu_923	<i>Talaromyces species 1</i>	Saprotroph	1	2
otu_644	<i>Teloschistaceae species 1.1</i>	Undetermined	1	5
otu_343	<i>Tilletiopsis species 1</i>	Undetermined	1	37
otu_1030	<i>Tinctoporellus species 2</i>	Wood decay	1	6
otu_969	<i>Togniniales species _man 1.2</i>	Undetermined	1	2
otu_1191	<i>Togniniales species _man 1.3</i>	Undetermined	1	4
otu_240	<i>Togniniales species _man 1.7</i>	Undetermined	1	82
otu_40	<i>Tolypocladium species 1</i>	Entomopathogenic	31	10597
otu_106	<i>Tolypocladium species 10</i>	Entomopathogenic	13	1403
otu_1086	<i>Tolypocladium species 11</i>	Entomopathogenic	1	4
otu_1137	<i>Tolypocladium species 12</i>	Entomopathogenic	1	6
otu_1150	<i>Tolypocladium species 13</i>	Entomopathogenic	1	2
otu_1153	<i>Tolypocladium species 14</i>	Entomopathogenic	3	12
otu_1154	<i>Tolypocladium species 15</i>	Entomopathogenic	3	8
otu_1166	<i>Tolypocladium species 16</i>	Entomopathogenic	3	18
otu_1185	<i>Tolypocladium species 17</i>	Entomopathogenic	2	4
otu_1213	<i>Tolypocladium species 18</i>	Entomopathogenic	1	2

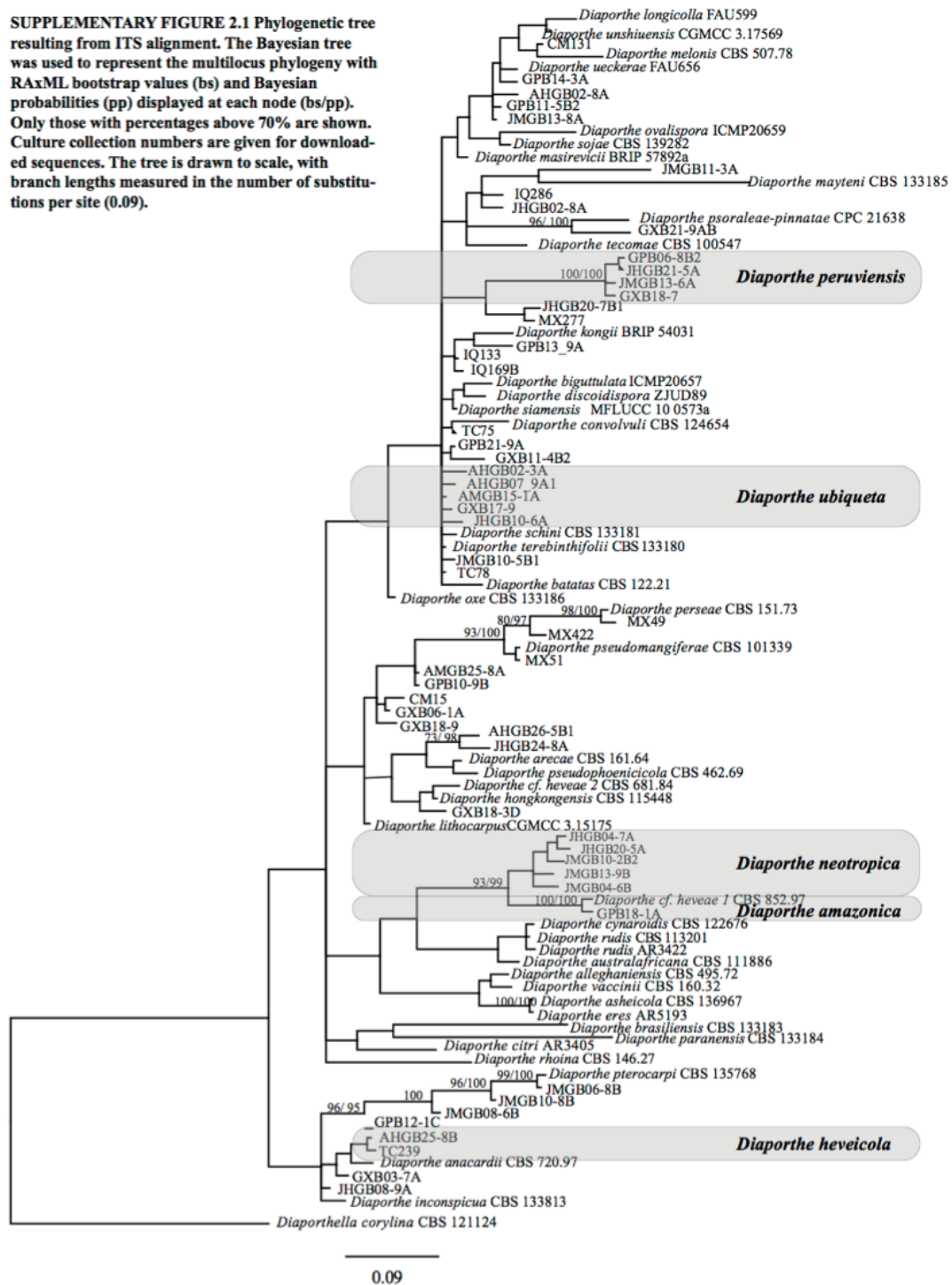
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otu_266	<i>Tolypocladium species 23</i>	Entomopathogenic	2	109
otu_328	<i>Tolypocladium species 24</i>	Entomopathogenic	3	130
otu_353	<i>Tolypocladium species 25</i>	Entomopathogenic	2	53
otu_396	<i>Tolypocladium species 26</i>	Entomopathogenic	2	16
otu_415	<i>Tolypocladium species 27</i>	Entomopathogenic	3	42
otu_449	<i>Tolypocladium species 28</i>	Entomopathogenic	6	89
otu_450	<i>Tolypocladium species 29</i>	Entomopathogenic	6	119
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otu_472	<i>Tolypocladium species 31</i>	Entomopathogenic	1	2
otu_505	<i>Tolypocladium species 32</i>	Entomopathogenic	1	46
otu_526	<i>Tolypocladium species 33</i>	Entomopathogenic	3	36
otu_527	<i>Tolypocladium species 34</i>	Entomopathogenic	1	8
otu_549	<i>Tolypocladium species 35</i>	Entomopathogenic	2	15
otu_620	<i>Tolypocladium species 36</i>	Entomopathogenic	2	13
otu_739	<i>Tolypocladium species 38</i>	Entomopathogenic	1	6
otu_741	<i>Tolypocladium species 39</i>	Entomopathogenic	1	11
otu_22	<i>Tolypocladium species 4</i>	Entomopathogenic	19	24464
otu_857	<i>Tolypocladium species 41</i>	Entomopathogenic	1	7
otu_875	<i>Tolypocladium species 42</i>	Entomopathogenic	1	3
otu_893	<i>Tolypocladium species 43</i>	Entomopathogenic	2	11
otu_963	<i>Tolypocladium species 44</i>	Entomopathogenic	1	2
otu_257	<i>Tolypocladium species 45</i>	Entomopathogenic	6	157
otu_1088	<i>Tolypocladium species 47</i>	Entomopathogenic	1	2
otu_201	<i>Tolypocladium species 49</i>	Entomopathogenic	5	139
otu_428	<i>Tolypocladium species 5</i>	Entomopathogenic	1	41
otu_21	<i>Tolypocladium species 50</i>	Entomopathogenic	23	35337
otu_387	<i>Tolypocladium species 51</i>	Entomopathogenic	2	38
otu_606	<i>Tolypocladium species 53</i>	Entomopathogenic	2	8
otu_688	<i>Tolypocladium species 54</i>	Entomopathogenic	24	994
otu_408	<i>Tolypocladium species 55</i>	Entomopathogenic	7	102
otu_720	<i>Tolypocladium species 57</i>	Entomopathogenic	1	2
otu_730	<i>Tolypocladium species 58</i>	Entomopathogenic	1	10
otu_572	<i>Tolypocladium species 6</i>	Entomopathogenic	1	15

otu_777	<i>Tolypocladium species 60</i>	Entomopathogenic	2	8
otu_858	<i>Tolypocladium species 62</i>	Entomopathogenic	1	3
otu_941	<i>Tolypocladium species 63</i>	Entomopathogenic	3	8
otu_1155	<i>Tolypocladium species 64</i>	Entomopathogenic	1	2
otu_12	<i>Tolypocladium species 65</i>	Entomopathogenic	52	78889
otu_619	<i>Tolypocladium species 7</i>	Entomopathogenic	2	17
otu_1000	<i>Tolypocladium species 8</i>	Entomopathogenic	9	20
otu_1015	<i>Tolypocladium species 9</i>	Entomopathogenic	1	4
otu_288	<i>Torrubiella species 4</i>	Entomopathogenic	1	13
otu_72	<i>Torrubiella species 6</i>	Entomopathogenic	2	208
otu_544	<i>Trametes species 2</i>	Wood decay	1	13
otu_314	<i>Trametes species 3</i>	Wood decay	1	56
otu_182	<i>Trechisporales species 1.1</i>	Undetermined	2	164
otu_246	<i>Trechisporales species 1.2</i>	Undetermined	1	108
otu_407	<i>Trechisporales species 1.3</i>	Undetermined	1	24
otu_967	<i>Tremellales species 1.1</i>	Undetermined	1	2
otu_121	<i>Trichaptum species 1</i>	Wood decay	5	942
otu_462	<i>Trichoderma species 1</i>	Fungicolous	2	25
otu_726	<i>Trichomonascaceae species 1.1</i>	Undetermined	1	13
otu_373	<i>Tubeufiales species 1.1</i>	Undetermined	1	44
otu_756	<i>Tubeufiales species 1.2</i>	Undetermined	1	8
otu_253	<i>Tyromyces species 1</i>	Wood decay	1	60
otu_372	<i>Umbelopsis species 2</i>	Saprotroph	2	34
otu_158	<i>Ustilago species 1</i>	Plant pathogen	3	252
otu_1168	<i>Volutella species 1</i>	Plant pathogen	1	2
otu_1138	<i>Volutella species 10</i>	Plant pathogen	3	22
otu_227	<i>Volutella species 2</i>	Plant pathogen	4	301
otu_287	<i>Volutella species 3</i>	Plant pathogen	2	66
otu_370	<i>Volutella species 4</i>	Plant pathogen	3	98
otu_147	<i>Volutella species 5</i>	Plant pathogen	2	252
otu_660	<i>Volutella species 6</i>	Plant pathogen	1	5
otu_692	<i>Volutella species 7</i>	Plant pathogen	1	4
otu_1100	<i>Volutella species 8</i>	Plant pathogen	1	2
otu_1103	<i>Volutella species 9</i>	Plant pathogen	1	2
otu_291	<i>Volvariella species 1</i>	Saprotroph	1	47
otu_115	<i>Wallemia species 1</i>	Saprotroph	1	416
otu_46	<i>Wallemia species 2</i>	Saprotroph	3	3303
otu_849	<i>Wallrothiella species 1</i>	Undetermined	1	5
otu_547	<i>Wolfiporia species 1</i>	Wood decay	1	10

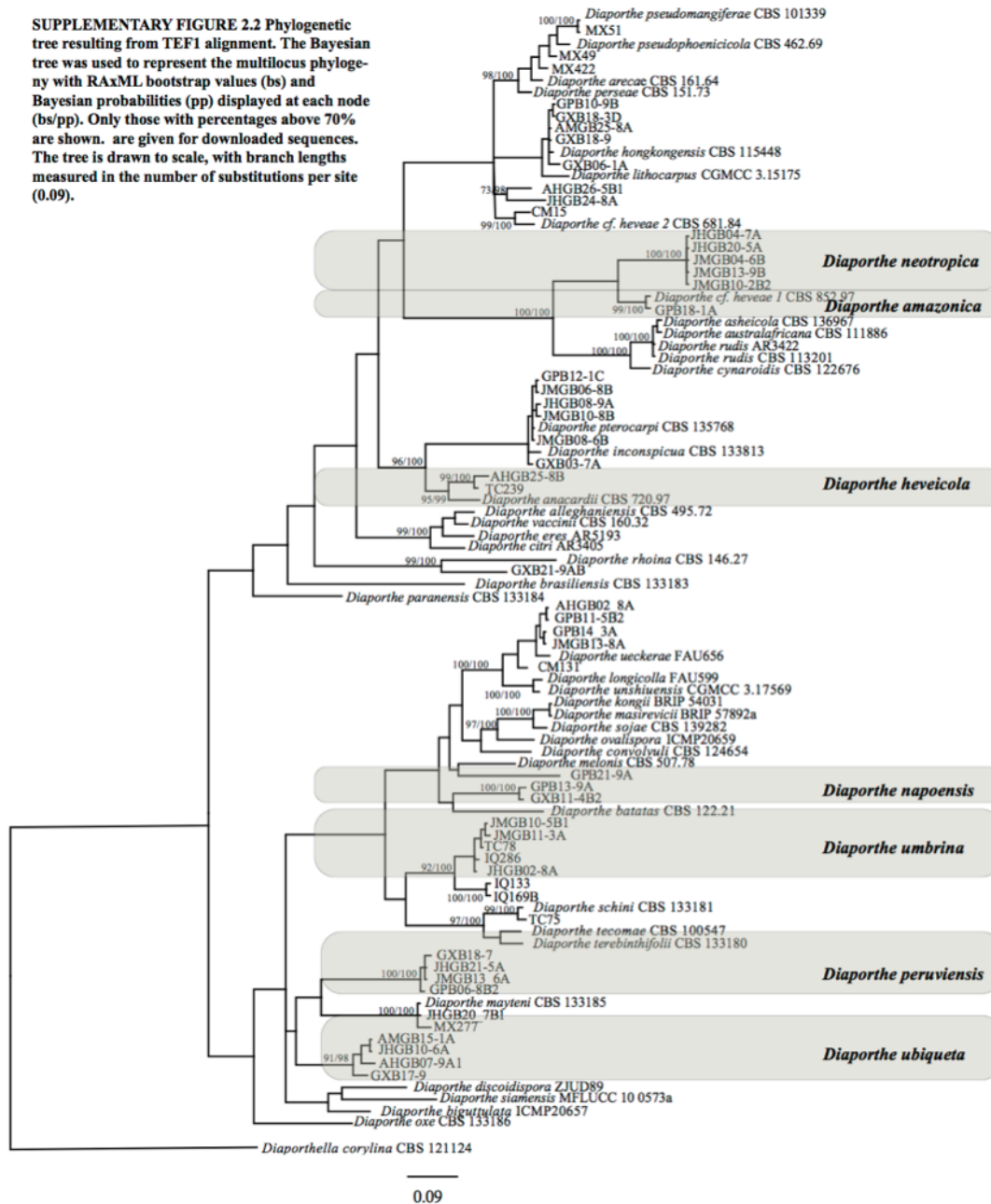
otu_455	<i>Xenasmata species 1</i>	Wood decay	1	20
otu_573	<i>Xenasmata species 2</i>	Wood decay	1	28
otu_365	<i>Xylariales species 4.3</i>	Undetermined	2	30
otu_400	<i>Xylariales species 4.4</i>	Undetermined	1	23
otu_323	<i>Xylobolus species 1</i>	Saprotroph	1	41
otu_163	<i>Xylodon species 1</i>	Saprotroph	5	253
otu_1026	<i>Xylodon species 2</i>	Saprotroph	1	2
otu_590	<i>Xylodon species 3</i>	Saprotroph	1	9
otu_303	<i>Yuchengia species 3</i>	Saprotroph	1	56

SUPPLEMENTARY FIGURE 2.1. Phylogenetic tree resulting from ITS alignment.

SUPPLEMENTARY FIGURE 2.1 Phylogenetic tree resulting from ITS alignment. The Bayesian tree was used to represent the multilocus phylogeny with RAxML bootstrap values (bs) and Bayesian probabilities (pp) displayed at each node (bs/pp). Only those with percentages above 70% are shown. Culture collection numbers are given for downloaded sequences. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (0.09).

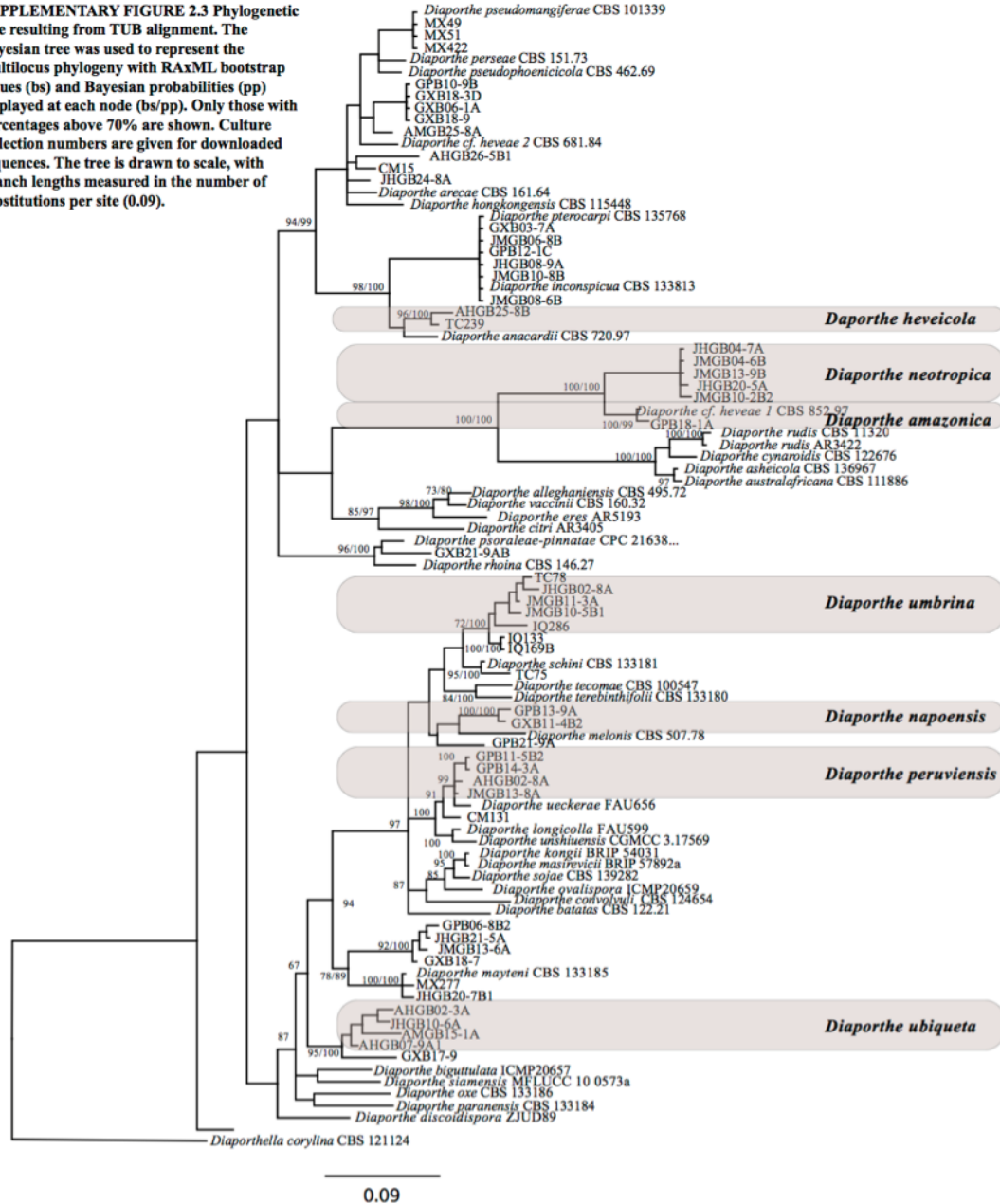


SUPPLEMENTARY FIGURE 2.2. Phylogenetic tree resulting from TEF1 alignment.



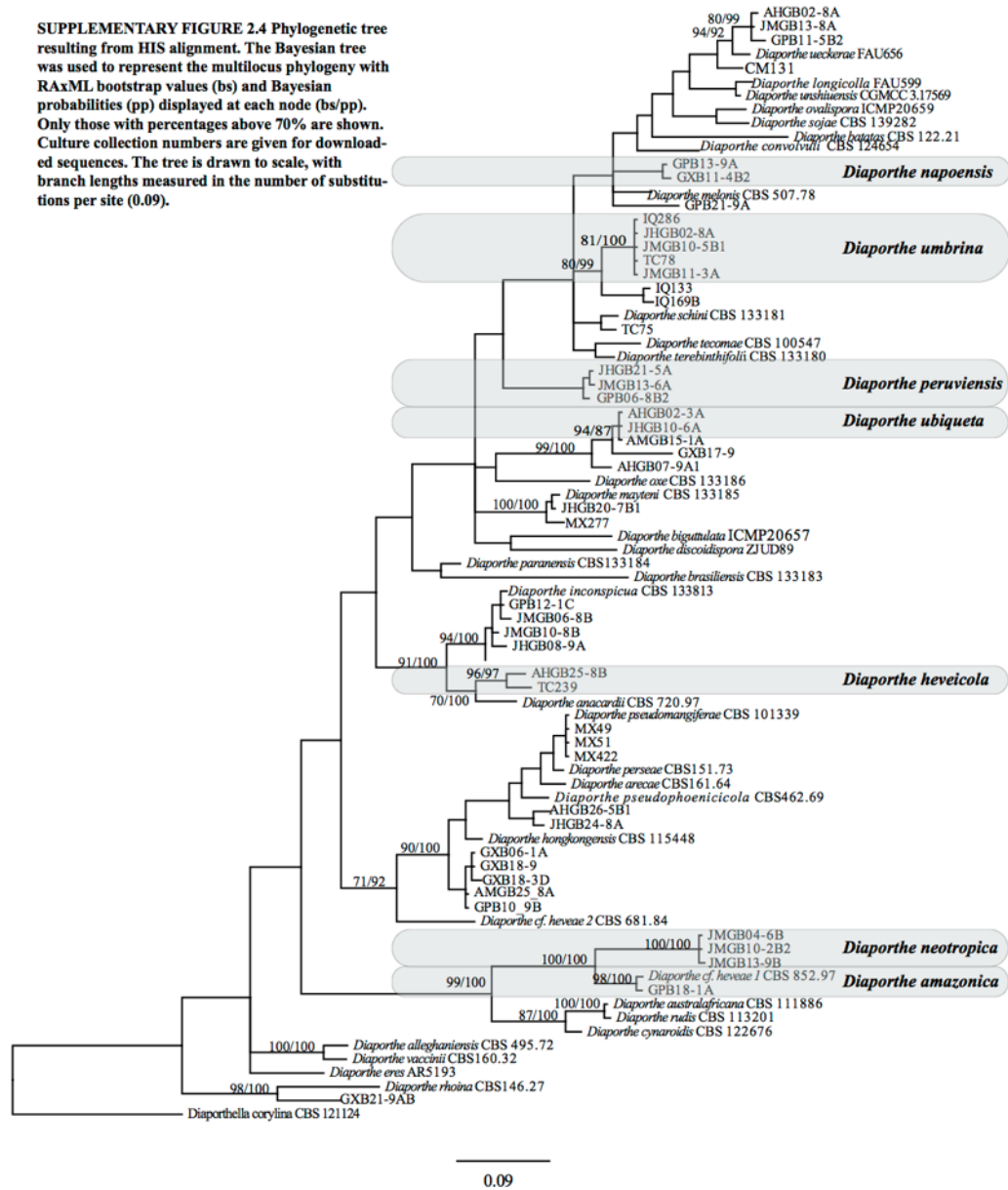
SUPPLEMENTARY FIGURE 2.3. Phylogenetic tree resulting from TUB alignment.

SUPPLEMENTARY FIGURE 2.3 Phylogenetic tree resulting from TUB alignment. The Bayesian tree was used to represent the multilocus phylogeny with RAxML bootstrap values (bs) and Bayesian probabilities (pp) displayed at each node (bs/pp). Only those with percentages above 70% are shown. Culture collection numbers are given for downloaded sequences. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (0.09).



SUPPLEMENTARY FIGURE 2.4. Phylogenetic tree resulting from HIS alignment.

SUPPLEMENTARY FIGURE 2.4 Phylogenetic tree resulting from HIS alignment. The Bayesian tree was used to represent the multilocus phylogeny with RAxML bootstrap values (bs) and Bayesian probabilities (pp) displayed at each node (bs/pp). Only those with percentages above 70% are shown. Culture collection numbers are given for downloaded sequences. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (0.09).



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