Diplomarbeit

Microbial community in the high canopy of the Bornean tropical rainforest: molecular diversity

Ausgeführt am Institut für

Verfahrenstechnik, Umwelttechnik, und Technische Biowissenschaften

der Technischen Universität Wien

unter der Leitung von

Prof. Dr.rer.nat. Irina S. Druzhinina

Dr.techn. Dipl.-Ing Komal Chenthamara

und

DI. Mohammad Javad Rahimi

durch

H.Oya Akyıldız, BSc

1429122

Albertplatz 5/2/1

1080, Wien

Datum

Unterschrift Student

Unterschrift Betreuer

Contents

List of Tables

Table of Figures

Abbreviations

ITS1 and 2	Internal transcribed spacers 1 and 2 of the rRNA gene cluster
tef1α	gene encoding the translation elongation factor-1 alpha
***rpb*2**	gene encoding RNA polymerase subunit B II
PCR	Polymerase Chain Reaction
BLAST	Basic Local Alignment Search Tool
NCBI	National Center for Biotechnology Information
COCY	*Colobopsis cylindrica*
PDA	Potato Dextrose Agar
EDTA	ethylenediaminetetraacetic acid
MAFFT	Multiple Alignment using Fast Fourier Transform
COGs	Clusters of Orthologous Groups

Abstract

Fungi are the most diverse organisms on Earth. However, lots of fungi are still not identified. Failures to correctly identify fungi prevents the progression on the study of species diversity, fungal-fungal interactions, and environmental adaptations. Analysis of data generated with molecular methods can be efficiently applied for identification of fungi. In this study molecular methods were used to identify different fungi from poorly explored habitats such as rain forest of Brunei, Borneo. Borneo has significant amount of biodiversity that is understudied and available for exploration. Therefore, Borneo rainforest is a remarkable area for researcher to explore microorganisms like fungi. Identification and study of unknown fungi species can lead to discover of new sources of enzymes and bioactive metabolites. Borneo is a home of dipterocarp species and ants which spend most of their time on Dipterocarpacea canopies, exploring for food or nesting grounds. For this reason, samples from a different region of ant territories like their nest, leaves phyllosphere (including epiphyte and endophyte), and the ants themselves were collected and isolated. The ITS1 and 2 were combined with *tef1α* (translation elongation factor-1 alpha) and used as markers for identification of fungi. The DNA sequences were compared with other published sequences via NCBI BLAST. The sequences were aligned via MAFFT. For phylogenetic inference, maximum parsimony analysis was used by using MEGA X. A large part of 524 samples is composed of Ascomycota, while 14 samples belong to Basidiomycota and Mucoromycota. The strains were divided into groups according to their isolated area which are phyllosphere, epiphytic & endophytic fungi from *Shorea* sp. and *Ficus* sp. , *C. bruneiensis* and *C. explodens'* nests and phylogenetic trees were constructed. Species from orders Hypocreales (f.e. *Trichoderma* sp.*,* *Fusarium* sp.), Xylariales (f.e. *Pestalotiopsis* sp. and *Arthrinium* sp.) and Eurotiales (f.e. *Penicillium* sp.) were found dominating. Yeasts are mainly represented by *Debaryomyces* and *Candida* genera from Saccharomycetales order. The study showed that, ants' nests possess a less biodiversity than leaves. On the other hand, nests are mostly home of black fungi from several taxonomic groups.

Introduction

Diversity of fungi

Fungi comprise one of the most diverse groups of eukaryotes [2]. Approximately 120,000 fungal species have been formally taxonomically described with the estimated total number of species exceeding several millions [2-4]. The estimations obtained by comparing the number of fungi with plants in the specific geographic region and the number of fungi specific to the plant species and communities. For example in 2001, in the British Isles, there are about six times more fungus species than vascular plant species [4]. The number of culturable fungal species was estimated as 2.2-3.8 million [2]. However it can be larger, 5 million according to Blackwell [5], or according to latest research (2019) 12 million [6]. As it can be seen, in the best case scenario just 8% of world's fungi have been described. These up to over 90% undescribed species may be discovered in specialised habitats like Southeastern Asia which have not yet been explored at all, or have been only poorly investigated. [7]

Classification of fungi

Until the 1990s, fungi were defined and classified according to their morphological and biochemical characteristics [8, 9]. The main groups (phyla) according to this traditional classification are Chytridiomycota, Zygomycota, Ascomycota, and Basidiomycota [10-12]. Because the phenotypic features may vary due to external factors, morphological characters may not reflect phylogenetic relationships [13]. The development of molecular tools has brought a much simpler, faster and practical approach to the study of cryptic (species recognised only by analysis of DNA sequences) organism fungi. Molecular methods not only provide a database based on DNA sequencing but also facilitate the testing of ecological hypotheses and provide a better understanding of the structure and functioning of ecosystems [14]. A classification system based on morphological and molecular data is a more accurate approach. The phylogenetic classification was modified by many researchers [9, 15-19] (Figure 1).

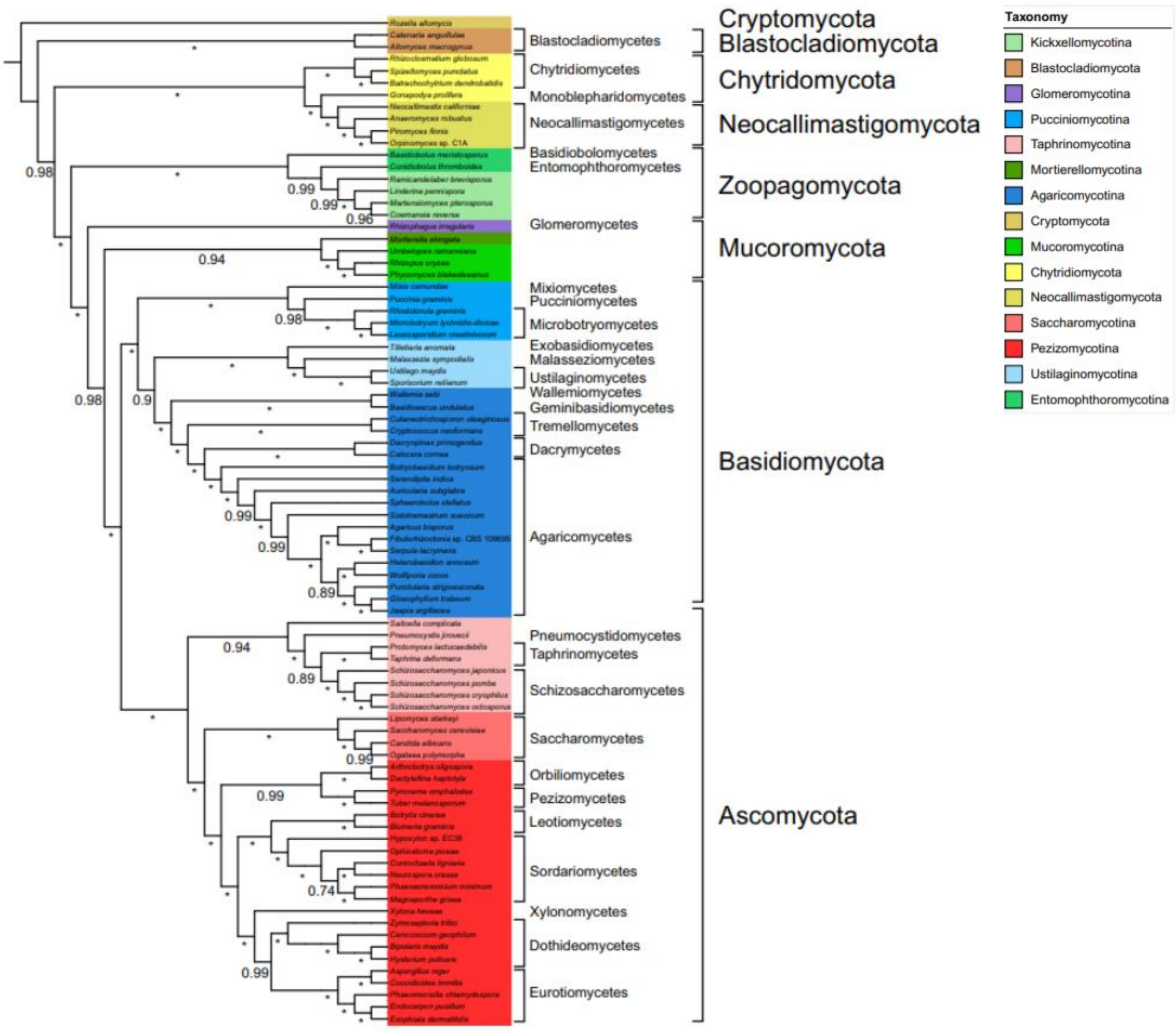


Figure 1 Phylogeny of Fungi. Bayesian phylogeny of 84 fungal species from an 8529-character superalignment derived from 72 ubiquitous fungal COG families sampled in Gblocks using PhyloBayes MPI with a CAT +GTR model. Posterior probabilities shown on branches with a burn-in of 1000 trees. Maximum posterior probability support designated with an asterisk (*) [19].

In this classification (Figure 1), all the traditional phyla are represented; Ascomycota, Basidiomycota, Zygomycetes (Mucoromycota containing Glomeromycotina and Zoopagomycota) and Chytridiomycota. Ascomycota and Basidiomycota form the Dikarya. Glomeromycotina is the closest relatives of Dikarya [18].

Identification of fungi

In 2003, Hebert and his colleagues proposed a standard method for identifying species and placing unknown sequences in higher taxa [20]. They have shown that the COI gene, previously used by Xu [21], can be used as a tool for phylogenetic analysis of published DNA primers. Nowadays DNA barcoding became as the most reliable, simple and precise method suitable for the identification of such highly diverse groups of organisms [22]. In DNA barcoding identification all organisms depend on DNA sequences of a diagnostic DNA fragment (genetic barcode) and comparison with a reference library.

Selection of DNA regions in order to successfully identify species is crucial and the number of DNA fragments suitable for DNA barcoding is limited. DNA loci that are appropriate for DNA barcoding should fulfill several strict criteria. First, such fragments should be universal, i.e., present in genomes of all targeted organisms. For instance, as all living cells contain ribosomes, genes encoding rRNA are suitable DNA-barcoding loci. Second, these fragments most have low intra-specific and high inter-specific variability. As most protein-coding sequences in eukaryotes are highly conserved, they are unlikely to be used for molecular identification. Thus, DNA barcoding frequently relies on such fragments as intergenic spacers of the universal gene clusters, introns of housekeeping genes or genes present in genomes of endosymbiotic organelles (mitochondria or plastids). On the other hand, the barcode marker must have conserved flanking sites for developing universal PCR primers to detect most or all intra-specific group of organisms [23]. Third, the length of the barcode sequence should be short enough to be used for amplification and sequencing methods. Fourth, the DNA barcoding loci should be accepted or standardized in the scientific community, and therefore respective sequences for a broad taxonomic diversity of a given group should be sufficiently represented in public databases of DNA sequences. Thus, although advances in genomics may aid the search for suitable DNA barcoding markers, their introduction may be inefficient if public databases do not contain sufficient reference sequences required for identification.

To identify different organismal groups by means of barcoding different gene regions are examined. For instance, a portion of the cytochrome c oxidase (*co1* or *cox1*) mitochondrial gene is the most known barcode for animals, and some protists. Beside of this, COII, *cytB* and *12S rRNA* are also used [23, 24].

In plants, however, mitochondrial genes exhibit low mutation rates and are not suitable for DNA barcoding. A few candidate genes have been found in the chloroplast genome. It is considered that one of the most variable coding genes of angiosperms is chloroplast gene encoding the maturase K (*matK*) [25].

Internal transcribed spacers (ITS) of rRNA gene cluster and *tef1* (translation elongation factor-1 alpha) as a nuclear marker for DNA barcoding

Sequence of 16S rRNA gene is the part of the 30S small subunit of a prokaryotic ribosome is widely used in identification of bacteria and archaea [26].

Similar to prokaryotes, fungi were also identified based on the sequences of genes encoding rRNA, such as the 28 S rRNA (LSU- Large subunit ribosomal ribonucleic acid) or 18 S rRNA (SSU- Small subunit ribosomal ribonucleic acid) genes [27]. However, due to an insufficient polymorphism of these loci in most fungal genera, the other region of the rRNA gene cluster was proposed for DNA barcoding. The fragment spanning from the 3' end of the 18 S rRNA gene over the internal transcribed spacer 1 (ITS1), the 5.8 S rRNA gene, the internal transcribed spacer 2 (ITS2) and ending in the 5' area of the gene encoding 28 S rRNA (Figure 2) is now standardized as the universal fungal DNA barcode marker named ITS1 and 2 of the rRNA gene cluster [22, 28, 29] (Figure 2).

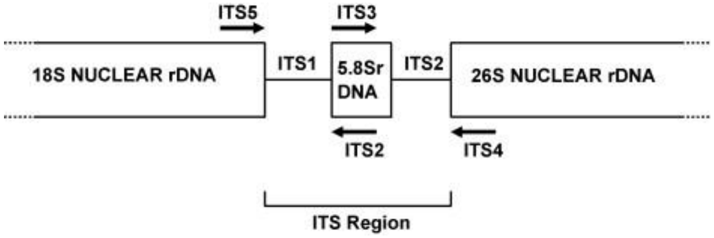


Figure 2 Organization of the internal transcribed spacer (ITS) region[1]

ITS1 and 2 rRNA is a quantitatively dominant marker in public databases. ITS1 and 2 has all the features to be an appropriate DNA barcode. The highly reliable PCR primers developed almost three decades ago by White and his colleagues allow reliable and easy PCR amplification of the fragment [30, 31]. Amplification is also facilitated by the fact that the rRNA operon has multiple copies in most fungal genomes and small size, making PCR typically successful. The presence of a highly conserved but short sequence of the 5.8 S rRNA gene inside the ITS1 and 2 fragment also aids multiple sequence alignment and makes the sequence similarity search reliable, which together helps identification. Consequently, public databases of nucleotide sequences have included comprehensive sets of fungal ITS1 and 2 sequences that are suitable for comparison and molecular identification. Moreover, several research communities have developed curated databases of reference ITS1 and 2 sequences for individual fungal groups [29, 32]. However, ITS region is not suitable region at species level identification in certain fungal clades like some genera in Hypocreales and Eurotiales, since these taxa insufficient variability in their ITS regions. Therefore, using the ITS alone for identification might not be sufficient and it may be necessary to sequence one or more single-copy protein-coding genes [28].

Translation elongation factor 1-a (*tef1α* or *tef1*) and the second largest subunit of RNA polymerase II (*rpb2*) are the most commonly used marker included in the Assembling the Fungal Tree of Life (AFTOL) project [33, 34]. *tef1* together with ITS1 and 2 are widely using for fungi DNA barcoding [30]. Regions of eukaryotic *tef1α* gene are highly conserved and therefore are preferred in phylogenetic inferences. Another reason for its preference is that it is present as a single copy in the genome [35, 36].

The sequence of the whole gene *tef1* gene is more than 2,000 base-pairs long (Figure 3). It consists of six exons separated by five introns. For the purpose of DNA barcoding, usually a fragment of 500 – 600 base-pairs is sufficient. However, it became apparent that the best result can be obtained if the large (4th) intron of the *tef1* gene is used [37] The fragment spanning the large (4th) intron is widely accepted as the most polymorphic locus that may also be used for DNA barcoding of Hypocreales [30, 37].

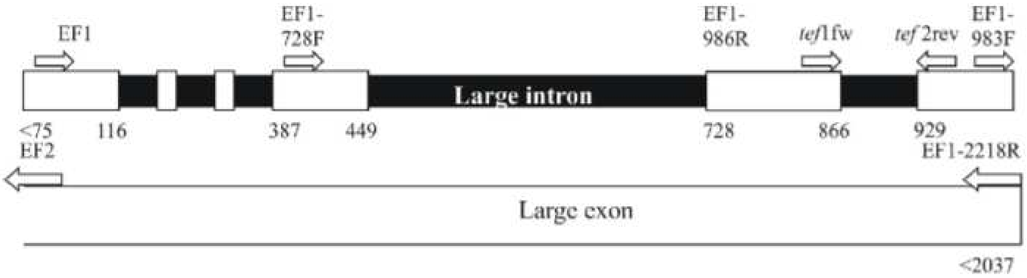


Figure 3 Schematic structure of *tef1* gene in *Trichoderma* spp. and location of primers for phylogenetic analyses [38]

tef1 is not universally present in order Hypocreales like *Trichoderma* and *Fusarium* spp., it still needs to be developed. From genomic studies, *tef1* was characterized as a single universal barcode candidate [30, 33, 38]. Thus, the *rpb*2 gene is a suitable alternative marker as an alternative marker for fungal community analyses [39].

Application of public databases for the taxonomic assignment of the species

The taxonomic assignment of the species achieves by matching of sequences to reference sequences deposited in public databases such as NCBI GenBank. BLAST (The Basic Local Alignment Search Tool is an online program used to identify by comparing sequences of samples with reference samples in the database). If the reference database contains sequences of species, the identification can be defined by species level. These databases contain the DNA barcodes assigned to previously identified taxa. Several reference databases exist depending on the organism group and the genetic marker used. One of the most common database using as an important resource for bioinformatics tools in biotechnology and biomedicine is National Center for Biotechnology Information (NCBI). NCBI houses a series of databases but the major databases include GenBank for DNA sequences [40-42].

The species identity is then assigned based on the scores of the sequence similarity search, which is strongly influenced by the completeness and correctness of the reference database and by the length and composition of the query sequence [43].

Fungi as a source of natural products

Natural products are naturally derived metabolites or by-products from microorganisms and plants. These products are important source for human for thousands of years in the most critical aspects of health care, agriculture and industry [44-46]. Nowadays natural products remain a major source of approved drugs and still play an important role in supplying chemical diversity [47]. Since ancient times, health practices have incorporated the medicinal properties of fungi [44]. For obtaining of some important medication such as antibiotics, immunosuppressant cyclosporine, and antihypercholesterolemic agents lovastatin fungal secondary metabolites have been used [48]. More than half of the compounds that have been isolated from fungi between 1993 and 2001, were shown antibacterial, antifungal or antitumour activity [49]. Antibiotic resistance is continually increasing and it is already a worldwide problem, the antimicrobial compounds from fungi can be potential sources of the new antibiotics [50, 51].

The other usage of natural products from fungi is industrial processes e.g. the production of enzymes, vitamins, polysaccharides etc. [52]. Some of these products are widely producing recently while others are potentially valuable in biotechnology. Fungi produced lipases and esterase have a huge potential in areas such as food technology, biomedical sciences, and chemical industries. Nowadays the plastic and petroleum product pollution become one of the most important global problem and there is a lack of applicable approach for that. Some enzymes such as lipase, esterase, and cutinase produce by filamentous fungi have a good potential to break down plastics [53, 54]. Esterase enzyme produced by some *Fusarium* spp. strains can degrade polyethylene terephthalate (PET) and lead to fungi to grow in medium with PET as solo carbon source [53]

A review published by Schueffler and Anke shown fungal natural products that were discovered between 2009 and 2013 shown the enormous potential of the fungal secondary metabolites that can use in different proposes [55]. Endophytic fungi which maintain at least a part of their life in the plant without damaging it, and in some cases give the plant additional advantages such as drought, disease and insect protection, are known group of fungi as abundant and various bioactive secondary metabolite producers [56]. Isolated metabolites, i.e. alkaloids, terpenoids, quinines, isocoumarin derivatives, flavonoids, phenols, peptides, and phenolic acids are good sources for antibiotics, immunosuppressive and anticancer compounds [57].

Biodiversity of Borneo rain forests

There is significant amount of biodiversity that is understudied and available for exploration at some tropical environments. Particular niches and/or poorly explored habitats such as deep side of the virgin rain forest could be interesting area to exploring new taxa. These areas are likely to be under disproportionate pressure as medical research turns to biodiverse areas for new drugs [7].

Tropical rainforests in Southeast Asia are characterized by a high species diversity and the dipterocarp species dominate the forest canopy [58]. In particular, Borneo is home of at least 222 species of mammals (44 of which are endemic), 420 resident birds (37 endemic), 100 amphibians, 394 fish (19 endemic), and 15,000 plants (6,000 endemic) [59] and highest species diversity of trees among the world's tropical rainforests [60]. Borneo is the hotspot of *Shorea* diversity with 138 species, of which 91 are endemic to the island and almost 20% of the trees in Borneo belongs to Dipterocarpaceae [61, 62].

Ants are the dominant arthropod family in the canopies of lowland tropical rain forests [63, 64]. Ant-plant mutualisms are pervasive and important components of tropical ecosystems. These ants spend most of their time on Dipterocarpacea canopies, exploring for food or nesting grounds. Here, ants deposit fecal droplets as a general excretion of waste on leaves which will be observed by the plant or epiphytic microorganisms as a nutrient [65]. On the other hand, the plant provides the food (nectars) and nest to the ants. Ants using certain fungi and bacteria for a different reason and the role of these symbionts are critical for the ants. They can provide nutrients [66] or hygiene [67, 68]

In Borneo forest canopy, 70% of ants were found to belong to the *Colobopsis cylindricus* (COCY) complex and are also nicknamed Borneo’s exploding ants [69]. Borneo’s exploding ants occupy mostly Dipterocarp trees in the lowland rainforest. Minor workers of this ants are known for hypertrophy of mandibular glands (MG) through the thorax to the end of the gaster [70] and for its release of glandular products in territorial combat [71].

From the surroundings of the Kuala Belalong Field Studies Centre (KBFSC) in Brunei, at least 15 species of exploding ants are known[72], most of them are probably new to science. Recently the first species of Borneo's exploding ants, *Colobopsis explodens* [73]

To understand more about the ant's activities and their physiology, other colleges investigate the microbial diversity on their habitat and determine the possible role of them the ecological effect of these ants. For this reason, they have collected the samples from a different region of ant territories like their nest, leaves phyllosphere (including epiphyte and endophyte), and the ants their self and isolated them.

The aim of the Thesis

Since the microbial diversity of Borneo rain forest remains largely unknown, this is a remarkable area for the researcher to explore microorganisms like fungal species as new sources of enzymes and bioactive metabolites.

The major aim of the thesis was exploring the biodiversity of the fungi isolated from the phyllosphere of *Shorea* spp. and other trees in lowland dipterocarp rain forest. To achieve these aims the following tasks should be completed:

1) Molecular identification of the isolated fungi based on DNA barcoding using ITS1 and 2 and *tef1*.
    a. A sequence similarity search against public databases
    b. Construction of identification phylogram
2) Save the fungi strains in a collection and collect all information about them in a database to conserve the fungi and use them to further experiments.

Materials & methods

Materials from the habitat of Bornean "exploding ants"

This research was based on the materials sampled during the WWTF LS13-048 Project "Voluntary Self-Sacrifice in Exploding Ants: a mechanism to defend co-evolved microbiomes" that started in 2014 and was completed in 2019 in the Group of Microbiology and Applied Genomics, ICEBE.

South-East Asian "exploding ants" (the *Colobopsis cylindrica* or COCY group) live in the canopy of the tropical rain forest and are considered ecosystem-forming organisms. They have distinctive hypertrophied mandibular gland reservoirs (MGR) that proliferate through the entire body and fill the abdomen. In territorial combat, worker ants use the sticky and irritant contents of their enlarged MGR to kill rival arthropods. In species where this defensive behavior is advanced, this happens via the characteristic suicidal "exploding" by voluntary rupture of the abdominal integument (autothysis). In animals, mutualistic microbes help in food digestion, detoxification of harmful substances, and contribute to hygiene. Microbiomes of *C. explodens* and *C. bruneiensis* consisted of bacteria present in the environment but lacked the most common environmental bacteria like *Bacillus* spp., *Clostridium* spp. and *Staphylococcus* spp. The diversity of fungi in *C. explodens* nests mainly consisted of opportunistic and cosmopolitan molds, while stress-tolerant fungi from the ecological group of black yeasts colonized the nests of *C. bruneiensis*. It was proposed that due to the remarkable resistance of these fungi to extreme environments, they can grow in COCY nests and provide protection against microorganisms causing insect diseases.

Nests of *Colobopsis explodens* and *C. bruneiensis* nom. prov.

Nests from *C. explodens* and *C. bruneiensis* nom. prov. (the formal species description is in preparation by Drs. H. Zettel and I. S. Druzhinina, personal communication) were sampled in the lowland dipterocarp rainforest at the Kuala Belalong Field Studies Centre (KBFSC), Temburong

District, Brunei Darussalam (4° 32' 35.5" N, 115° 09' 09.3" E) by the field researcher A. Kopchinskiy (TU Wien) during two sampling expeditions in 2015 and 2017 (Figure 4).

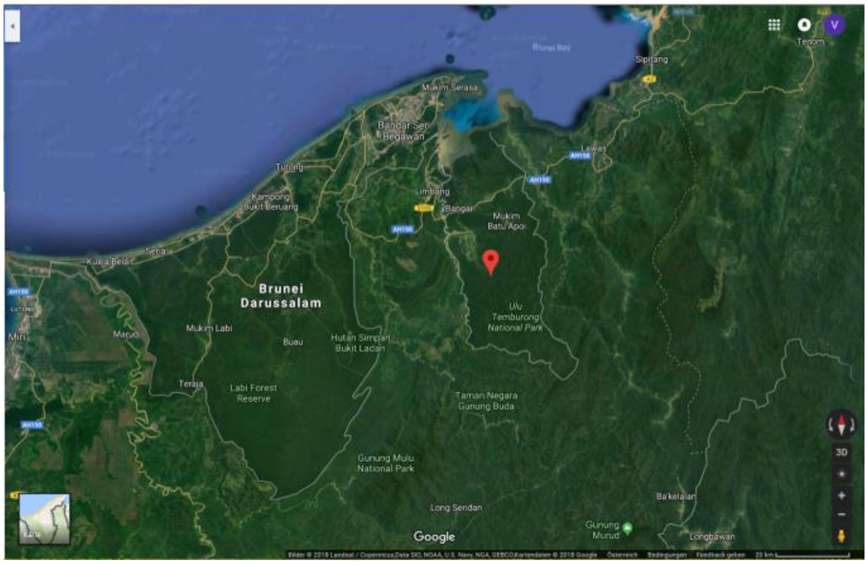


Figure 4 Location of the KBFSC in Brunei Darussalam, Borneo, shown on Google Satellite.

Pieces of the nests contained the ants were transferred to the laboratory. The nests were cut to 1 cm thickness sections at the sterile condition. At sterile condition, different areas of nest slices (carton structures, material from inside the nest and stem surface of outside host tree) were scraped off separately with a sterile scalpel. Natural and artificial nest in forest were shown in Figure 5.

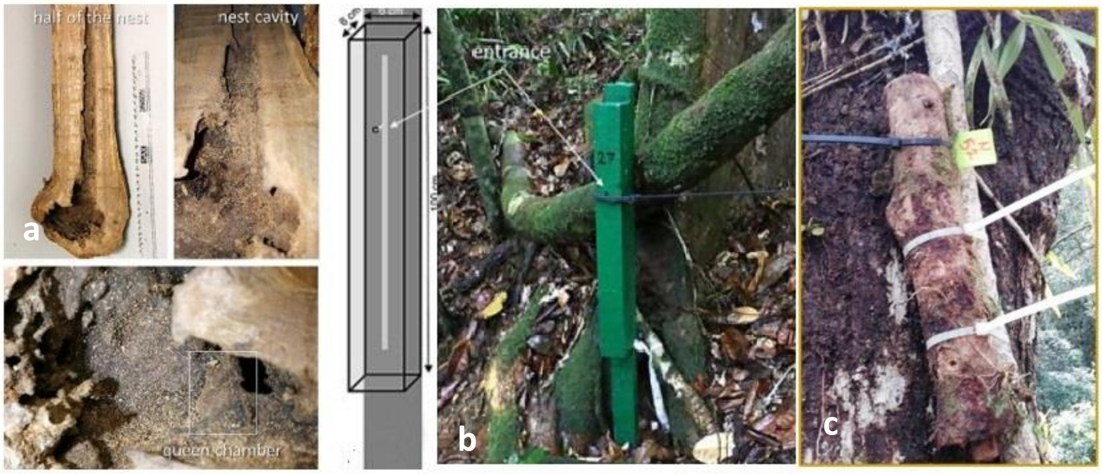


Figure 5 Natural C. explodens *nest (YG-FF) was found in a dead branch of* S. johorensis (a), C. explodens *artificial nest (b),* C. bruneiensis *natural nest (c).*

Bodies of *C. explodens* and *C. bruneiensis* nom. prov.

During cutting the nests, we collected the ants in sterile 2 mL wells and preserved by freezing in -80°C until the use. Then washed their cuticle surface of the ants via submerging and shaking in 2 mL reaction tubes containing sterile ultrapure water at 700rpm for 20-40 min. The ants' body than was transferred to another tube. The falcon tube was centrifuged, and the pellet was collected. The washed ants were surface sterilized with 70% ethanol, the different part of the ants' body (head and abdomen) were separated using the stereomicroscope and sterile forceps, crushed and mixed with sterile water.

Leaves of *Shorea johorensis* and *Ficus* sp.

To isolation of the fungi from the *Shorea johorensis* and *Ficus* sp. leaves (the two main COCY ant's inhabiting plants), the fresh leaves were transferred to the laboratory. The phyllosphere microorganisms were removed by submerging a leaf in 20 mL sterile water containing 0.1% WT80 in a sterile Petri plate and collecting epiphytes by applying an electric toothbrush over the adaxial and abaxial leaf surfaces for 2 min in total. The resulting suspension of was centrifuged in 50 mL falcon tubes and centrifuged and pellets were collected. Here we collected mostly epiphytic and some facultatively endophytic organisms.

The cleaned leaves were used to the isolation of the endophytic fungi. Therefore, leave surface were disinfected by submerging in 70% ethanol (v/v) for 1 min, then 15 s in a solution of 15% hydrogen peroxide (v/v) and then submerging again for 1 min in 70% ethanol. The leave was rinsed five times with sterile distilled water.

Isolation of pure fungal cultures and cultivation condition

To isolate the pure fungal cultures from the samples (ant and nest materials and phyllosophere) they were transferred into 2 mL tubes contain 1 mL WT80, shacked them for 2 min vigorously, subjected to the standard serial diluted procedure and were spread on the Potato Dextrose Agar (PDA)+ supplemented with 0.01% Triton 100X and 0.5 g/L chloramphenicol. The plates were incubated at 28^{o}C and checked daily for two weeks. Every new colony with unique morphophysiological properties was picked and transferred to the fresh PDA plates.

To isolate endophytic fungi, after surface disinfection of the leaves, at the sterile condition, we cut them to 1 cm^2 pieces and placed on 9 cm Petri dishes containing tap water-yeast extract agar (TWYE; containing 0.25 g of yeast extract, 0.5 g of K_2HPO_4, and 18 g of agar per liter of tap water+ chloramphenicol (0.5 g/l) and Pen-Strep (100 un/mL) to prevent growth of bacteria. The Petri dishes were incubated at 25°C for 30 days and checked daily, and all fungal colonies found were isolated, purified and maintained in PDA for later testing. The cultures were transferred to fresh plates until the pure cultures were obtained.

All the pure strains were got the collection numbers (TUCIM) and preserved in duplicate cryotubes in 25% glycerol at -80^{o}C. The strains and their origins of isolation were listed in Table 1.

Table 1 Source of isolated strains

Source of isolation			Total number	Strains (TUCIM)
***Shorea* sp. leaves**	**Endophythes**		39	6022, 6023, 6026, 6030, 6034, 6007, 6014, 6018, 6020, 6024, 6025, 6027, 6056, 6029, 6015, 6028, 6021, 6032, 6010, 6012, 6019, 6031, 6017, 6009, 6006, 6011, 6033, 6013, 6005, 6035, 6037, 6046, 6040, 6054, 6043, 6065, 6082, 6053, 6051
	Epiphytes		280	6231, 5961, 5986, 5962, 5997, 6239, 5949, 5954, 5957, 5960, 5978, 5983, 6002, 6066, 6073, 5995, 5965, 5968, 5970, 5982, 6000, 5967, 5988, 5992, 5951, 5994, 6235, 5959, 5972, 5991, 6237, 5956, 6241, 6236, 6004, 5969, 5979, 5996, 5966, 6001, 5973, 5955, 5950, 6003, 5971, 5952, 5985, 5977, 5993, 5987, 5980, 5974, 5958, 6240, 6238, 6083, 6076, 6245, 6074, 6080, 6063, 6484, 6485, 6486, 6487, 6488, 5492, 5630, 5833, 5503, 5508, 5567, 5566, 5568, 5569, 5570, 5571, 5572, 5594, 5595, 5596, 5597, 5598, 5599, 5606, 5607, 5612, 5613, 5614, 5615 5608, 5609, 5610, 5611, 5622, 5623, 5724, 5725, 5726, 5727, 5740, 5741, 5748, 5749, 5616, 5617, 5619, 5618, 5620, 5621, 5624, 5625, 5626, 5627, 5713, 5768, 5628, 5629, 5631, 5632, 5645, 5633, 5634, 5635, 5636, 5637, 5638, 5639, 5641, 5642, 5643, 5644, 5777, 5784, 5646, 5647, 5766, 5648, 5649, 5650, 5651, 5652, 5653, 5710, 5711, 5712, 5714, 5715, 5716, 5717, 5718, 5719, 5722, 5723, 5729, 5738, 5742, 5743, 5728, 5739, 5730, 5731, 5732, 5733, 5734, 5735, 5736, 5737, 5744, 5745, 5746, 5747, 5750, 5751, 5752, 5753, 5754, 5755, 5756, 5757, 5758, 5759, 5760, 5761, 5763, 5796, 5762, 5764, 5765, 5767, 5770, 5769, 5772, 5787, 5792, 5793, 5794, 5795, 5771, 5773, 5774, 5775, 5776, 5778, 5779, 5780, 5816, 5781, 5813, 5782, 5783, 5785, 5786, 5788, 5789, 5790, 5791, 5797, 5798, 5799, 5800, 5805, 5801, 5802, 5804, 5803, 5806, 5807, 5809, 5808, 5810, 5830, 5811, 5812, 5814, 5815, 5819, 5817, 5818, 5820, 5821, 5822, 5823, 5824, 5825, 5826, 5827, 5828, 5829, 5831, 5836, 5837, 5838, 5839, 5840, 5841, 5843, 5844, 5845, 5846, 5984, 5640
	Phyllosphere		18	5488, 5497, 5502, 5501, 5491, 5490, 5493, 5499, 5495, 5498, 5496, 5507, 5494, 5506, 5508, 5567, 5566, 5568
***Ficus* sp. leaves**	**Endophytes**		28	6032, 6011, 6035, 6038, 6057, 6055, 6045, 6052, 6037, 6047, 6046, 6040, 6054, 6043, 6065, 6082, 6053, 6051, 6058, 6039, 6042, 6044, 6050, 6036, 6049, 6041 6059, 6048
	Epiphytes		51	5961, 6239, 5949, 5954, 5957, 5960, 5978, 5983, 6002, 6066, 6073, 5992, 6241, 6078, 6079, 6081, 5952, 6083, 6085, 6245, 6244, 6084, 6075, 6077, 6070, 6074, 6080, 6068, 6071, 6067, 6064, 6072, 6063, 6484, 6485, 6486, 6487, 6488, 5508, 5567, 5566, 5568, 5596, 5643, 5775, 5791, 5818, 5984, 6065, 6082, 6303,
Nest	**YGFF [1]**	**inside**	8	6086, 6087, 6199, 6197, 6198, 6260, 6262, 6200
		carton	13	6201, 6206, 6203, 6204, 6218, 6261, 6209, 6205, 6216, 6217, 6219, 6208, 6200
		outside	25	5488, 5489, 5490, 5491, 5492, 5493, 5494, 5506, 5507, 5495, 5499, 5497, 5496, 5498, 5500, 5505, 5503, 6302, 6089, 6088, 6092, 6097, 6300, 6090, 6194,
	MIT1 [2]	**inside**	20	6164, 6167, 6170, 6165, 6169, 6168, 6243, 6091, 6193, 6247, 6257, 6270, 6271, 6275, 6282, 6272, 6274, 6273, 6248, 6100
		carton	19	6172, 6171, 6195, 6193, 6194, 6247, 6257, 6276, 6280, 6281, 6283, 6269, 6277, 6278, 6279, 6248, 6100, 6301, 6099
		outside	54	6175, 6176, 6246, 6173, 6188, 6095, 6179, 6186, 6184, 6182, 6180, 6178, 6094, 6183, 6177, 6012, 6242, 6181, 6185, 6191, 6174, 6189, 6291, 6292, 6304, 6249, 6250, 6288, 6293, 6285, 6294, 6295, 6298, 6299, 6286, 6297, 6289, 6290, 6310, 6311, 6312, 6306, 6251, 6187, 6303, 6305, 6308, 6093, 6096, 6098, 6313, 6309, 6102, 6192
	Artificial nest [3]		8	6224, 6225, 6253, 6254, 6255, 6227, 6226, 6252
	***C. bruneiensis* 2017**	**inside**	56	6975, 6979, 6980, 6981, 6983, 6984, 6985, 6986, 6989, 6990, 6991, 6995, 6996, 6997, 6998, 6999, 7001, 7002, 6195, 6270, 6271, 6275, 6276, 6280, 6281, 6282, 6283, 6089, 6164, 6167, 6170, 6172, 6192, 6193, 6194, 6269, 6277, 6278, 6301, 6088, 6243, 6247, 6257, 6248, 6091, 6092, 6274, 6279, 6165, 6169, 6097, 6099, 6168, 6100, 6171, 6297
		outside	55	7004, 7006, 7007, 7008, 7009, 7010, 6302, 6291, 6292, 6304, 6310, 6311, 6312, 6306, 6175, 6176, 6246, 6249, 6251, 6250, 6173, 6288, 6188, 6095, 6179, 6186, 6187, 6184, 6303, 6293, 6182, 6180, 6178, 6285, 6294, 6295, 6298, 6305, 6090, 6308, 6093, 6094, 6096, 6183, 6177, 6299, 6102, 6098, 6185, 6191, 6174, 6286, 6289
Ants[4]			38	6234, 6322, 6323, 6324, 6326, 6328, 6331, 6334, 6335, 6336, 6337, 6233, 6321, 6258, 6264, 6268, 6229, 6316, 6318, 6319, 6320, 6327, 6329, 6330, 6315, 6317, 6230, 6325, 6259, 6228, 6332, 6207, 6265, 6267, 6256, 6263, 6008, 6232

YGFF[1] is C. explodens nest

MIT1[2] is C. bruneiensis nest 2015

Artificial nest[3] of C. explodens

Ants[4] couldn't defined

Molecular techniques

DNA Extraction

Materials

- Young (36-72 hours) cultures of the fungi strain
- Lysing buffer (400 mM Tris-HCl [pH 8.0], 60 mM EDTA [pH 8.0], 150 mM NaCl, 1% sodium dodecyl sulfate)
- Potassium acetate buffer (60 mL of 5 M potassium acetate, 11.5 mL of glacial acetic acid, 28.5 mL of distilled water [pH 4.8])
- Nanodrop spectrophotometer (Thermo Scientific, NanoDrop ONE^c)
- Standard equipment for agarose gel electrophoresis

Method

- 50- 100 mg of fresh fungal mycelia were transferred to sterile 2 mL tube contain 4 small glass beads (2 mm) and add 500 µL of lysis buffer. Vortexed vigorously for at least 1 minute.
- The tube incubated for 10 min at 65 ̊C.
- The mixture cooled down and 150 µL of potassium acetate were added.
- Vortexed briefly and spun at 10000 rpm for 1 min.
- The supernatant carefully was transferred to a new 1.5-mL tube and centrifuged at 10000 rpm for 1 min.
- An equal volume of 100% isopropyl alcohol were added and is mixed by inversion briefly.
- The tube is spun for 5 min at high speed, and the supernatant were discarded. The DNA pellet were visible after this step.
- The DNA pellet were washed by adding 300 µL of 70% ethanol. Spun at 10000 rpm for 1 min and the supernatant were discarded.
- The DNA pellet were air dried from residue ethanol and were dissolved in 50 µL of deionized H_2O.
- To quantify the DNA concentration Nanodrop spectrophotometer (Thermo Scientific, NanoDrop ONE^c) were used.

- To check the presence the detectable genomic DNA, agarose gel electrophoresis was carried on.

Polymerase Chain Reaction (PCR)

Materials

- Standard disposables and reagents for PCR
    - GoTaqG2 Flexi polymerase (Promega, Madison, Wisconsin, USA)
    - 10× GoTaq Flexi Buffer (Promega)
    - dNTP (Promega)
    - $MgCl_2$ (Promega)
- Oligonucleotide primers for PCR (Microsynth, Balgach, Switzerland) (Table 2)
- PCR thermocycler (Peqlab, Peqstar thermal cycler)
- Standard equipment for agarose gel electrophoresis
- Standard equipment for DNA quantification
- Arranged Sanger sequencing service for PCR products

Table 2 PCR primers' parameters

Gene	Name	Sequence 5'–3'	Reference
ITS 1&2	SR6R	AAGWAAAAGTCGTAACAAGG	[74]
	LR1	GGTTGGTTTCTTTTCCT	
tef1	EF1 728 f	CATCGAGAAGTTCGAGAAGG	[75]
	TEF1-LLE rev	AACTTGCAGGCAATGTGG	
rpb2	fRPB2-5F	GAYGAYMGWGATCAYTTYGG	[76]
	fRPB2-7cR	CCCATRGCTTGTYYRCCCAT	

Method

- Prepare the PCR reaction according to the standard protocol using following reagents (Table 3):

Table 3 PCR mixture components and concentrations

CR Mastermix	**ITS1 and 2**	***tef1***	***rpb2***
Promega buffer 10x	10	10	5
Promega Nucleotides 2 mM^1	4	4	1
$MgCl_2$ 25mM	6	6	5
forward Primer 6.25 µM^2	2	2	2.5
reverse Primer 6.25 µM^2	2	2	2.5
Promega GoTaq 1	0.1	1	0.1
PCR water	20.9	20	25.90
DNA sample	5	5	5
	50	50	50

- Depend on the loci, we set up the PCR thermocycler and run the machine. The programs summarized at below table (Table 4).

Table 4 PCR Program

PCR program		**ITS 1 & 2**		***tef1***		***rpb2***	
PCR Step		**Temp. [°C]**	**Time [sec]**	**Temp. [°C]**	**Temp. [°C]**	**Temp. [°C]**	**Time [sec]**
initial denaturation		94	60	94	60	95	300
30 cycles	94	60	94	60	60	60	60
	50	60	56	60	60	90	90
	72	90	72	50	50	90	90
final extension		72	420	74	420	72	420
pause		4	∞	4	∞	4	∞

Agarose gel electrophoresis

After the PCR, products were analyzed by gel electrophoresis. the PCR products and marker gene Ruler 1kb DNA ladder (Thermo Fisher Scientific) were loaded to and 1% agarose (Rotiphorese, Agarose Standard) and run the electrophoresis at 100V/ 400mA for 20 min. The appearance of the DNA bands in the gel were examined by Gel-Doc system.

PCR Purification

After the presentation of the amplicon confirmed by nucleic acid gel electrophoresis to send the samples for Sanger sequencing DNA quantification PCR purification or gel extraction protocol should be followed. The DNA purification procedure purify the amplicon from the PCR reagents and primer dimers and provide higher yield of the amplicon.

To purify amplicons fragments from PCR, mi-PCR Purification Kit (Metabion) was used and the protocol summarized below:

The PCR product and PX buffer were mixed and transferred to the GP Column tubes. After centrifugation for 1 min at high speed, the flow through was discarded. In this step the DNA bind to the silicon filter in the column. At the next steps, the bind DNA were washed with two whishing buffers (WN and WS Buffer) and finally 20-25 µL water or Elution Buffer were added directly on center of the column. The column was stand for 10 min and then centrifuged for 5 min at high speed to elute DNA.

Sanger Sequencing

DNA samples were measured for concentration using Nanodrop and diluted to 10-12 ng/µL and sent to Microsynth (Switzerland) for sequencing.

DNA Barcoding and construction of identification of phylograms

A sequence similarity search against public databases

For the molecular identification DNA barcode sequences were obtained with PCR. Based on a BLAST (Basic Local Alignment Search Tool) sequence similarity search done using the National Center for Biotechnology Information (NCBI) online BLAST tool the 100 species with the highest identity score were determined. All sequences with a high identity were saved as FASTA format (attached to the work with a CD) and aligned with our reference sequence (Attachment 1).

Sequence Alignment

For the first investigation, the sequences were aligned using MAFFT with accurate settings. Some of the sequences were excluded due to their poor quality, meaning the sequences amplified were too short to be aligned.

The sequences were explored using Aliview program. Later, non-conserved region was removed using GBlocks with parameters selected for less stringent conditions.

Construction of identification phylogram

Evolutionary analyses were conducted in MEGA X. The maximum parsimony tree was obtained using the Subtree-Pruning-Regrafting (SPR) algorithm with search level 1 in which the initial trees were obtained by the random addition of sequences (10 replicates). The analysis involved 524 nucleotide sequences. The bootstrap consensus tree was inferred from 1000 replicates taken to represent the evolutionary history of the taxa analyses. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed.

Results and Discussion

DNA Amplification Results

In this study, totally 524 strains were isolated from the different samples (leaves, ant nests and ants) and their collection numbers listed in Table 1. ITS 1,2 regions were successfully sequenced for 456 strains. ITS1 and 2 sequences are not a suitable DNA barcode for identification of the fungi belong to Hypocreales family at level of species and phylogenic studies; therefore, after identification of them at the genus level by using ITS1 and 2 sequences, we performed *tef1* amplification. *Trichoderma* is belonging to the order Hypocreales. Therefore, ITS PCR were not necessary, and we did not sequence it for *Trichoderma* strains., therefore we performed only *tef1* for all isolated *Trichoderma* strains (89).

Phylogenetic Analysis Results

In our study, homologous sequences were first subjected to the sequence similarity search against the GenBank (NCBI) database using the following parameters: threshold (10), match/mismatch scores (1,-2) and gap costs (linear). The first 100 best hits were examined for reliability considering their respective publications. All strains were divided according to their isolation sources. As a result, six separate taxonomic groups were generated for phylogenetic analysis. After the DNA sequences were aligned, they were analysed by MP method in MEGA X program using SPR algorithm.

The sunburst chart here shows the precise summary of the composition of isolated 524 fungal strains to their taxonomical family (Figure 6). As can be seen, the majority of species belongs to the Ascomycota group, and only 2.6% of this collection belongs to the group Basidiomycota and one strain belongs to Mucoromycota.

Within Ascomycota, species from orders Hypocreales, Xylariales and Eurotiales dominate. More precisely, plant pathogens such as *Fusarium* spp., species of high biotechnological applications such as *Penicillium* sp. and *Trichoderma sp.* are abundant. These three genera together constitute almost 223 isolates. Yeasts are mainly represented by *Debaryomyces* and *Candida* genera from Saccharomycetales order.

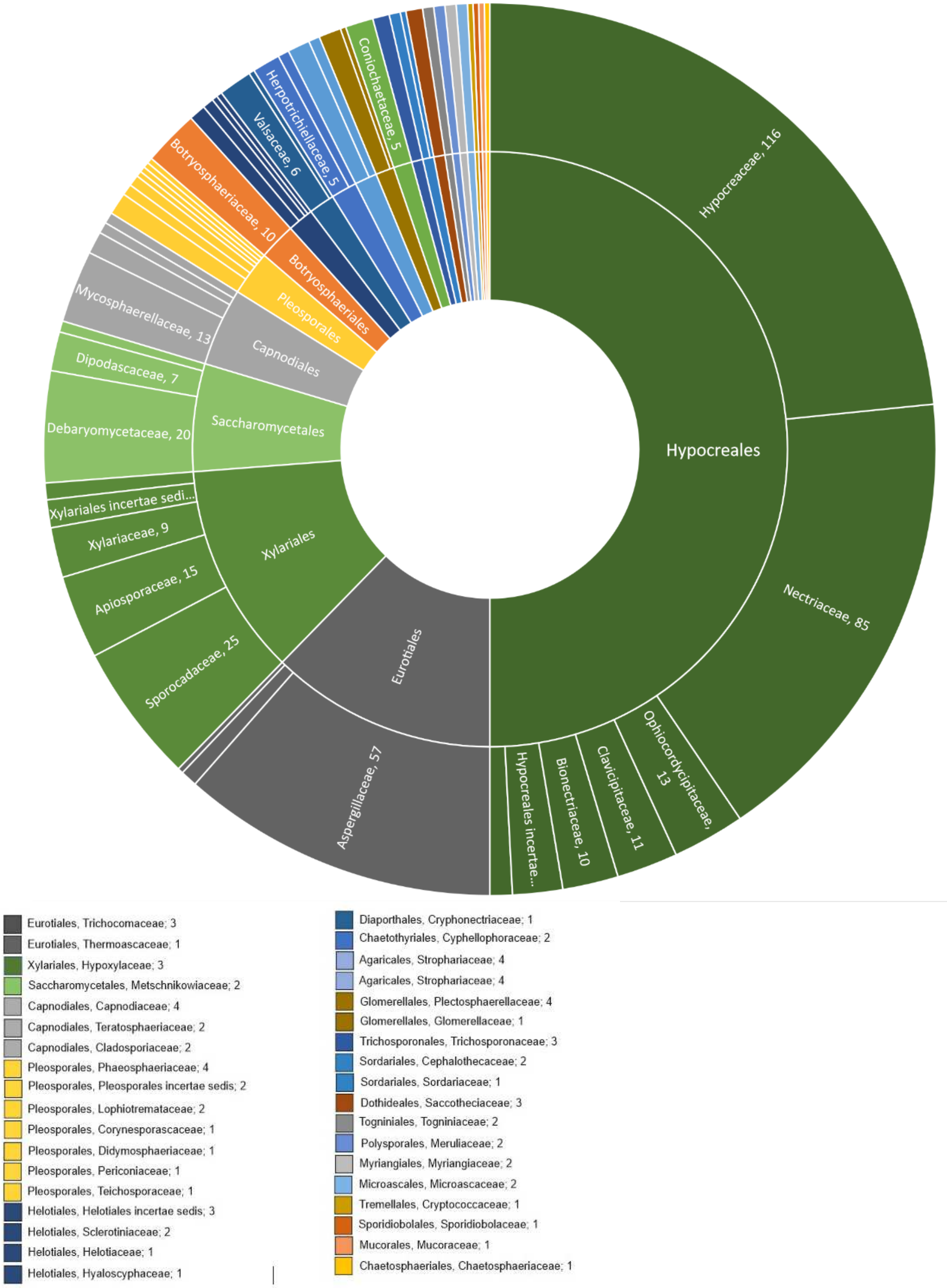


Figure 6 Isolated 524 fungal strains to their taxonomical order & family. Totally 26 order assigned, and 1 unknown remained. The number next to the name of the family represents the number of species in that particular family.

The largest part of the isolated fungi belongs to Hypocreales within the class Sordariomycetes. Hypocreales species are notable for their ability to derive nutrition from diverse nutrient sources such as plant materials, insects, or other fungi to causing infection in human and other mammals. In our study, we isolated different fungi genera of different origins from all characterized family of Hypocreales and most important families and genera within order Hypocreales.

Because of their different phyla, 14 strains were analyzed separately. As a result, 13 strains belong to Basidiomycota and 1 belongs to Mucoromycota. There was a total of 536 positions in the final dataset. *Cryptococcus* sp. and *Trichosporon dermatis* are sharing same clade because they belong to same Tremellomycetes class. (*Figure 7*)

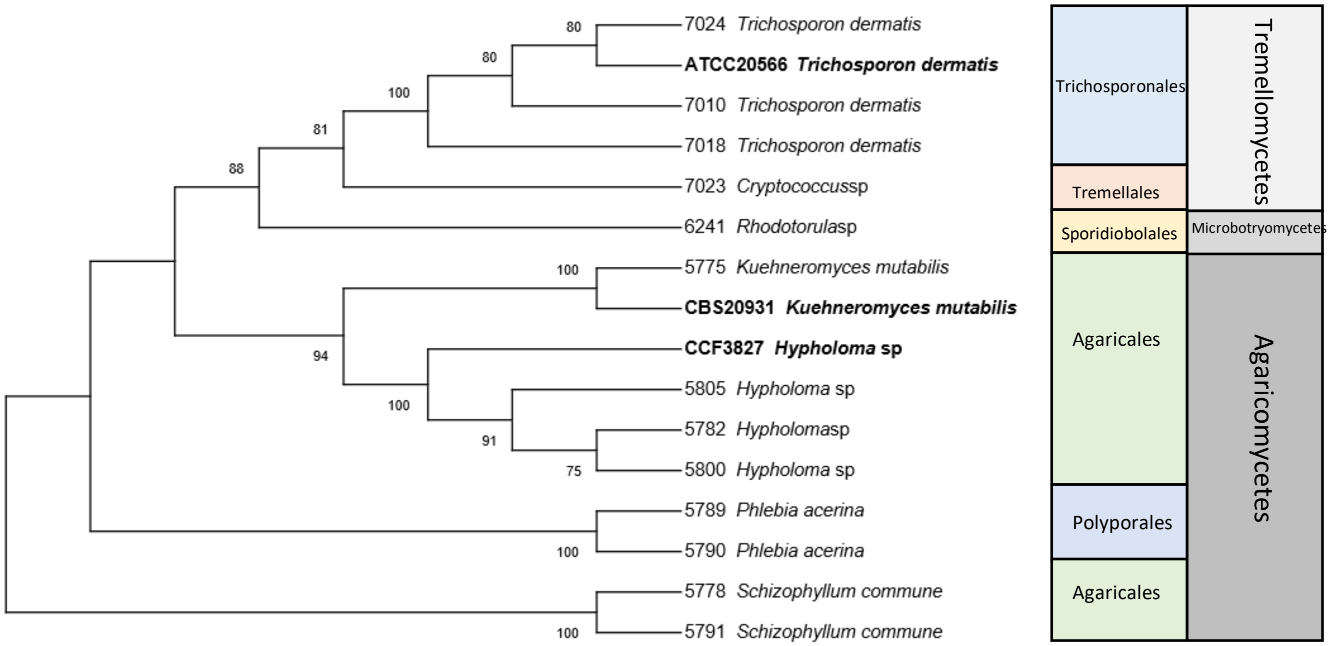
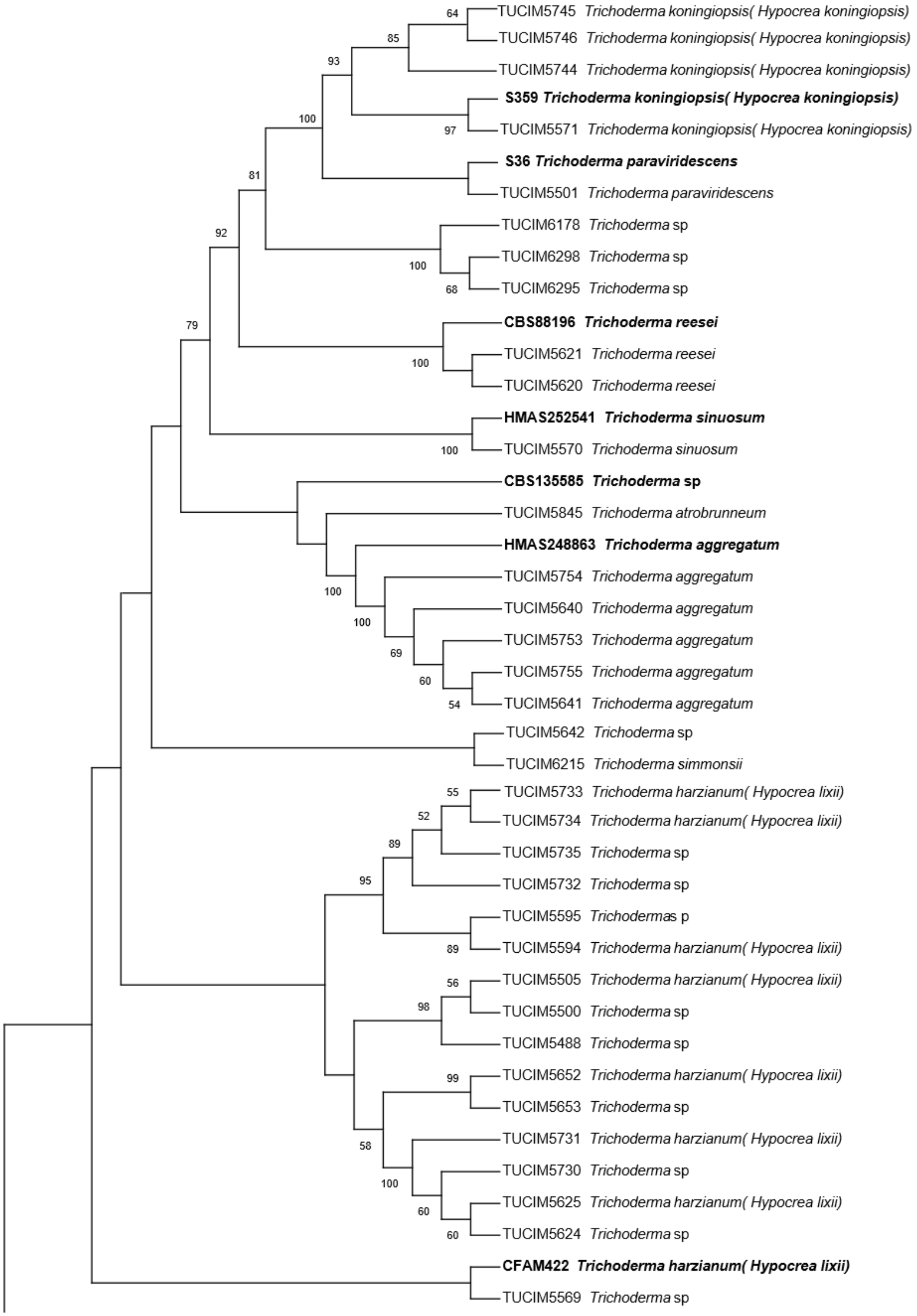


Figure 7 Tree of fungi which belong to Basidiomycota phylum. References were shown as bold type.

Since the ITS region is not suitable region at species level identification in Hypocreales*,* we expected to get unsufficient results with *Trichoderma* strains based on ITS1,2 analysis. Therefore phylogenic analysis based on *tef1* sequences carried on for the *Trichoderma* strains and the phylogenic tree is placed in Figure 8.


64
TUCIM5745 Trichoderma koningiopsis(Hypocrea koningiopsis)
85
TUCIM5746 Trichoderma koningiopsis(Hypocrea koningiopsis)
93
TUCIM5744 Trichoderma koningiopsis(Hypocrea koningiopsis)
S359 Trichoderma koningiopsis(Hypocrea koningiopsis)
100
97
TUCIM5571 Trichoderma koningiopsis(Hypocrea koningiopsis)
S36 Trichoderma paraviridescens
81
TUCIM5501 Trichoderma paraviridescens
92
TUCIM6178 Trichoderma sp
TUCIM6298 Trichoderma sp
100
68
TUCIM6295 Trichoderma sp
79
CBS88196 Trichoderma reesei
TUCIM5621 Trichoderma reesei
100
TUCIM5620 Trichoderma reesei
HMAS252541 Trichoderma sinuosum
100
TUCIM5570 Trichoderma sinuosum
CBS135585 Trichoderma sp
TUCIM5845 Trichoderma atrobrunneum
HMAS248863 Trichoderma aggregatum
TUCIM5754 Trichoderma aggregatum
100
100
TUCIM5640 Trichoderma aggregatum
69
TUCIM5753 Trichoderma aggregatum
60
TUCIM5755 Trichoderma aggregatum
54
TUCIM5641 Trichoderma aggregatum
TUCIM5642 Trichoderma sp
TUCIM6215 Trichoderma simmonsii
55
TUCIM5733 Trichoderma harzianum(Hypocrea lixii)
52
TUCIM5734 Trichoderma harzianum(Hypocrea lixii)
89
TUCIM5735 Trichoderma sp
95
TUCIM5732 Trichoderma sp
TUCIM5595 Trichodermas p
89
TUCIM5594 Trichoderma harzianum(Hypocrea lixii)
56
TUCIM5505 Trichoderma harzianum(Hypocrea lixii)
98
TUCIM5500 Trichoderma sp
TUCIM5488 Trichoderma sp
99
TUCIM5652 Trichoderma harzianum(Hypocrea lixii)
TUCIM5653 Trichoderma sp
58
TUCIM5731 Trichoderma harzianum(Hypocrea lixii)
100
TUCIM5730 Trichoderma sp
60
TUCIM5625 Trichoderma harzianum(Hypocrea lixii)
60
TUCIM5624 Trichoderma sp
CFAM422 Trichoderma harzianum(Hypocrea lixii)
TUCIM5569 Trichoderma sp

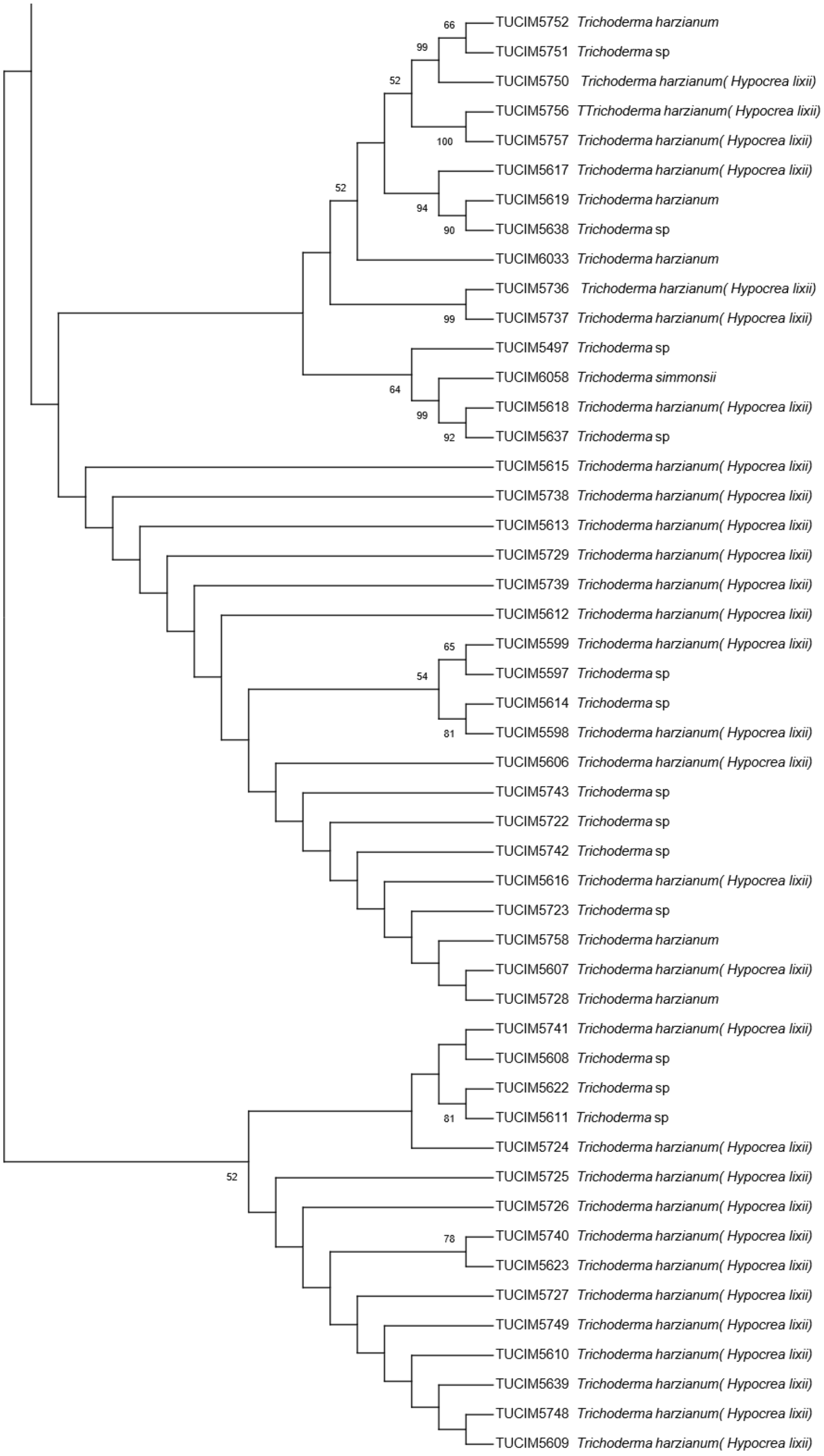


Figure 8 Trichoderma *species based on* tef1*. References were shown as bold type.*

As it was described at Schoch and his colleagues' research [28], some groups of fungi have the low intraspecies polymorphisms in their ITS1 and 2 sequences. Therefore, to their identification and the biodiversity study the scientist using other markers. For example, the genus belongs to order Hypocreales, *tef*1 gene is most suitable marker. Above we genetically analyzed 89 *Trichoderma* strains based on their *tef*1 sequences. From them 43 were belong to *T. harzianum* genus.

The Diversity of Fungi in the Phyllosphere

The phyllosphere generally forms a large, multifaceted habitat for a vast diversity of living organisms. The phyllosphere fungi living on the surface (epiphyte) and the interior tissue (endophyte) of leaves and exhibit high species diversity [77]. Both endophytic bacteria and endophytic fungi can co-exist in a single host plant. These fungi play important roles in host plant. For example, phyllosphere fungi can limit phytopathogenic fungi, mediate defense against herbivores, influence resistance to abiotic stressors such as drought, high temperature water stress [78]. Endophytes enter inside the living plant tissues such as leaves, flowers, stems and cotyledons and at least part of their life without causing any apparent disease symptoms in the host. The both epi and endophytic fungi have ability to produce secondary metabolites but the endophytes are much more known to produce a diverse range of natural products [79]. Metabolites produced by endophitic fungi like alkaloids, flavonoids, peptides, phenols and phenolic acids are good sources of new drugs such as antibiotics, immunosuppressant and anticancer compounds. Invitro studies showing antibacterial, antifungal, anticancer, antiviral, antioxidant, insecticide, antidiabetic and immunosuppressive activities [80].

Several roles determining the composition of endophytic fungi assemblages. For example, geographic location greatly influence endophyte community composition. A plant can be colonized by endophytic fungi that originate from a neighbor plant [81]. Another important factor is the plant host. The host species have a significant effect on endophytic fungal assemblages. Results of some studies were found that closely related host species to have distinct foliar endophytic fungi (FEF) patterns [82]. A recent study on 46 species of *Ficus* spp. sampled from same geographic environment shown both evolutionary and ecological factors are involved in shaping fungal endophyte population [83].

Here we investigated and analyzed the fungal communities of two the exploding ants habitant trees *Shorea johorensis* and *Ficus* sp. leaves. The samplings were carried on at two time periods on 2014 and 2015. Borneo is the hotspot of *Shorea* diversity. Almost 20% of the trees in Borneo belongs to Dipterocarpaceae and 91 species of 138 Dipterocarpaceae in Borneo are endemic [61, 62]. *S. johorensis* is only found in Sumatra, Peninsular Malaysia and Borneo and is in the Nature's Red List of Threatened Species (Figure 9). The size of the trees are typically to 65 m tall. The tested tree was the host of *C. explodens* nest and its leaves was visited daily by the ants.

Figure 9 Leaves of S. johorensis*. the size of the leaves can reach to more than 20 cm.*

The first samples were *Shorea* leaves cultivated by puting the leaves on PDA medium supplemented with choloramphenicol to prevent the growth of bacteria and the plates incubated for one year at +4°C and the single colonies from epiphyte and endophyte were transfered to new plates. Because of long incubation in low temperature, the slow growing fungi had more opportunity to grow. The second sampling carried on at 2015 and this time the epiphytic and endophytic fungi were isolated based on standard protocols. Two type of leaves were tested (*S. johorensis* and *Ficus* sp.). *Ficus* spp. are one of the most important trees in most tropical rainforest and frequently present in southeast asia tropical rainforest. *Ficus* species produce carbohydrate reach extrafloral nectar and also one of the main COCY ants visitors in Brunei rainforest.

Shorea phyllosphere 2014

195 fungi strain of 65 species isolated from the phyllosphere of *S. johorensis* leaves samples colected at 2014. In Table 5 Table 6 the isolated strain listed. The identification of the strains were based on their ITS1, 2 (for all isolates) or *tef1* (for *Trichoderma* and *Fusarium* strains) sequence in NCBI database (Table 6).

Table 5 Species from Shorea *phyllosphere 2014. The identity values below 95% are marked in red. Basidiomycota cells are marked in green.*

		Genus, species	Ident/Cov	Family	Order	Class
5753-5754-5755	3	*Trichoderma aggregatum* HMAS:248863	95%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5640-5641	2	*Trichoderma aggregatum*	95%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5488	1	*Trichoderma* sp. CBS:135585	96%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5497	1	*Trichoderma* sp.	96%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5569	1	*Trichoderma* sp.	97%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5594	1	*Trichoderma harzianum*	98%, 93%	Hypocreaceae	Hypocreales	Sordariomycetes
5597	1	*Trichoderma* sp.	96%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5599	1	*Trichoderma harzianum*	98%, 94%	Hypocreaceae	Hypocreales	Sordariomycetes
5598	1	*Trichoderma harzianum*	98%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5595	1	*Trichoderma* sp.	96%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5612	1	*Trichoderma harzianum*	98%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5606-5607--5613-5615	4	*Trichoderma harzianum*	98%, 93%	Hypocreaceae	Hypocreales	Sordariomycetes
5614-5608-5611-5622-5724-	5	*Trichoderma* sp.	96%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5725-5726-5748-5749-5617-5619-5625	7	*Trichoderma harzianum*	97%, 92%	Hypocreaceae	Hypocreales	Sordariomycetes
5609-5610-5623-5727-5740-5741	6	*Trichoderma harzianum*	97%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5616	1	*Trichoderma harzianum*	98%, 96%	Hypocreaceae	Hypocreales	Sordariomycetes
5618	1	*Trichoderma harzianum*	97%, 93%	Hypocreaceae	Hypocreales	Sordariomycetes
5624-5637-5638	3	*Trichoderma* sp.	95%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5639	1	*Trichoderma harzianum*	99%, 96%	Hypocreaceae	Hypocreales	Sordariomycetes
5642-5653	1	*Trichoderma* sp	96%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5652-5731-5733-5734	4	*Trichoderma harzianum*	98%, 94%	Hypocreaceae	Hypocreales	Sordariomycetes
5722-5723-5742-5743	4	*Trichoderma* sp	97%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes

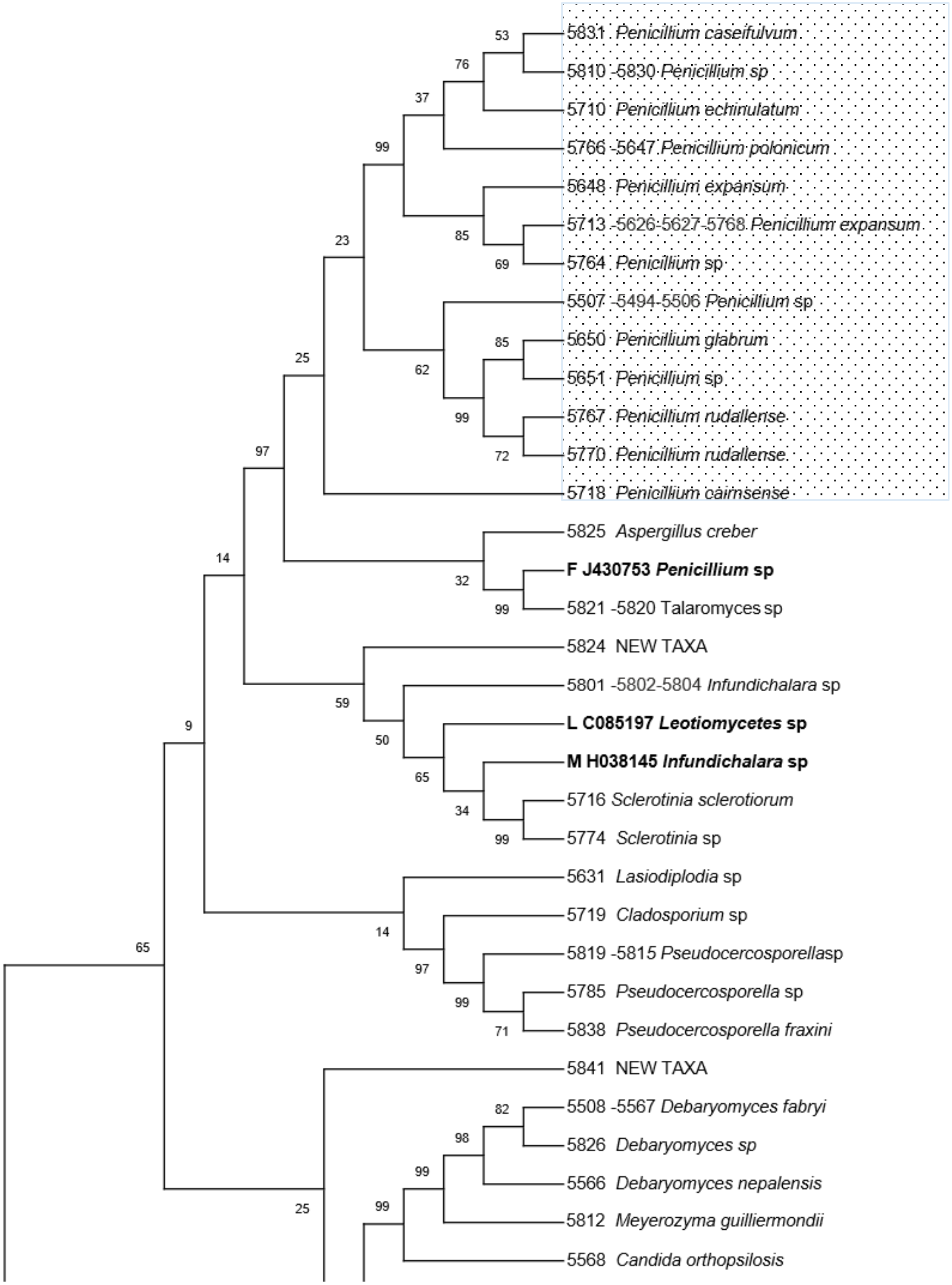
5729-5738-5739-5736	4	*Trichoderma harzianum*	98%, 91%	Hypocreaceae	Hypocreales	Sordariomycetes
5730-5732-5735	3	*Trichoderma* sp	96%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5736	1	*Trichoderma harzianum*	97%, 91%	Hypocreaceae	Hypocreales	Sordariomycetes
5751-5752-5756-5757	4	*Trichoderma harzianum*	96%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5758	1	*Trichoderma harzianum*	97%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5500-5505	2	*Trichoderma* sp	96%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5571	1	*Trichoderma koningiopsis*	97%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5620-5621	2	*Trichoderma ressei* CBS 881.96	98%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5570	1	*Trichoderma sinuosum*	98%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5502	1	*Trichoderma sparsum*	97%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
5501	1	*Trichoderma paraviridescens*	86%, 98%	Hypocreaceae	Hypocreales	Sordariomycetes
5845	1	*Trichoderma atrobrunneum*	100%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5643	1	*Trichoderma harzianum*	93%, 96%	Hypocreaceae	Hypocreales	Sordariomycetes
5744-5745-5746-5747	4	*Trichoderma koningiopsis*	95%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5649	1	*Trichoderma ovalisporum*	93%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
5761-5759-5760-5763-5796	5	*Fusarium oxysporum*	99%, 97%	Nectriaceae	Hypocreales	Sordariomycetes
5762	1	*Fusarium oxysporum*	99%,99%	Nectriaceae	Hypocreales	Sordariomycetes
5795-5769-5772-5787-5792-5793-5794	7	*Fusarium oxysporum*	99%, 97%	Nectriaceae	Hypocreales	Sordariomycetes
5843	1	*Fusarium oxysporum*	99%, 74%	Nectriaceae	Hypocreales	Sordariomycetes
5634	1	*Paracremonium inflatum* CBS 315.73	98%, 99%	Nectriaceae	Hypocreales	Sordariomycetes
5491	1	*Paracremonium* sp. CBS 482.78	87%, 99%	Nectriaceae	Hypocreales	Sordariomycetes
5503-5833	2	*Fusicolla* sp. CBS 634.76	96%, 80%	Nectriaceae	Hypocreales	Sordariomycetes
5628	1	Ovicillium sp. CBS_403.89	99%, 87%	Bionectriaceae	Hypocreales	Sordariomycetes
5633	1	*Leucosphaerina arxii* CBS 737.84	88%, 99%	Hypocreales incertae sedis	Hypocreales	Sordariomycetes
5844	1	*Simplicillium* sp. CBS 454.70	100%, 97%	Cordycipitaceae	Hypocreales	Sordariomycetes
5492, 5630	2	*Stromatonectria caraganae* CBS 125579	99%, 86%	Bionectriaceae	Hypocreales	Sordariomycetes
5490, 5493	2	*Trichothecium* sp.	95%, 96%	Hypocrealesincertaesedis	Hypocreales	Sordariomycetes
5765	1	*Trichothecium* sp.	95%, 96%	Hypocrealesincertaesedis	Hypocreales	Sordariomycetes
5846	1	*Trichothecium* sp.	95%, 96%	Hypocrealesincertaesedis	Hypocreales	Sordariomycetes
5629	1	*Verticillium* sp. CBS 748.73	100%, 97%	Hypocrealesincertaesedis	Hypocreales	Sordariomycetes
5828	1	*Ilyonectria* sp.	100%, 97%	Nectriaceae	Hypocreales	Sordariomycetes
5499-5495	2	*Pestalotiopsis* sp.	100%, 95%	Sporocadaceae	Xylariales	Sordariomycetes
5498	1	*Pestalotiopsis* sp.	100%, 97%	Sporocadaceae	Xylariales	Sordariomycetes

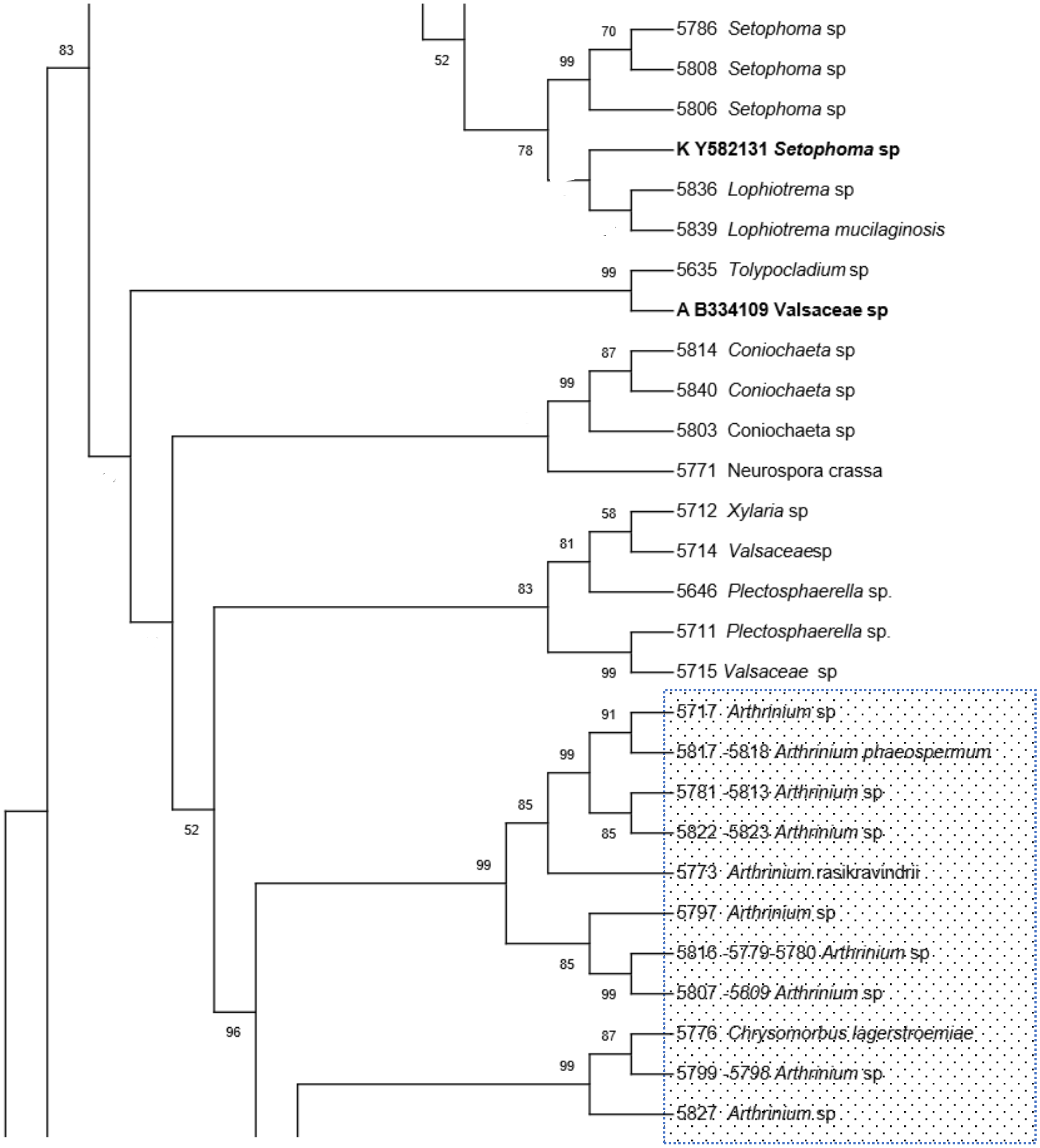
5496	1	*Neopestalotiopsis clavispora*	100%, 97%	Sporocadaceae	Xylariales	Sordariomycetes
5572	1	*Pestalotiopsis* sp.	100%, 97%	Sporocadaceae	Xylariales	Sordariomycetes
5632-5645	2	*Pestalotiopsis* sp.	100%, 97%	Sporocadaceae	Xylariales	Sordariomycetes
5636	1	*Pestalotiopsis* sp.	100%, 97%	Sporocadaceae	Xylariales	Sordariomycetes
5644-5777-5784	3	*Pestalotiopsis* sp.	100%, 95%	Sporocadaceae	Xylariales	Sordariomycetes
5783	1	*Pestalotiopsis* sp.	100%, 96%	Sporocadaceae	Xylariales	Sordariomycetes
5788	1	*Pestalotiopsis* sp.	100%, 97%	Sporocadaceae	Xylariales	Sordariomycetes
5829	1	*Pestalotiopsis* sp.	100%, 99%	Sporocadaceae	Xylariales	Sordariomycetes
5712	1	*Xylaria* sp.	99%, 97%	Xylariaceae	Xylariales	Sordariomycetes
5714	1	*Valsaceae sp*	96%, 96%	Valsaceae	Diaporthales	Sordariomycetes
5646	1	*Plectosphaerella cucumerina*	100%, 97%	Plectosphaerellaceae	Glomerellales	Sordariomycetes
5711	1	*Plectosphaerella sp.*	100%, 100%	Plectosphaerellaceae	Glomerellales	Sordariomycetes
5715	1	*Valsaceae sp*	100%, 95%	Valsaceae	Diaporthales	Sordariomycetes
5717	1	*Arthrinium* sp.	83%, 93%	Apiosporaceae	Xylariales	Sordariomycetes
5773	1	*Arthrinium rasikravindrae*	100%, 95%	Apiosporaceae	Xylariales	Sordariomycetes
5816- 5779-5780	3	*Arthrinium* sp.	100%, 94%	Apiosporaceae	Xylariales	Sordariomycetes
5781	1	*Arthrinium* sp.	100%, 95%	Apiosporaceae	Xylariales	Sordariomycetes
5813	1	*Arthrinium phragmites*	91%, 98%	Apiosporaceae	Xylariales	Sordariomycetes
5797	1	*Arthrinium* sp. CBS 872.73	100%, 94%	Apiosporaceae	Xylariales	Sordariomycetes
5799-5798	2	*Arthrinium* sp. CBS:200.57	97%, 95%	Apiosporaceae	Xylariales	Sordariomycetes
5807-5809	2	*Arthrinium marii* CBS:200.57	98%, 95%	Apiosporaceae	Xylariales	Sordariomycetes
5817	1	*Arthrinium* sp.	100%, 94%	Apiosporaceae	Xylariales	Sordariomycetes
5822- 5823	2	*Arthrinium marii* CBS:200.57	97%, 96%	Apiosporaceae	Xylariales	Sordariomycetes
5827	1	*Arthrinium* sp.	98%, 95%	Apiosporaceae	Xylariales	Sordariomycetes
5837	1	*Pestalotiopsis* sp.	100%, 97%	Sporocadaceae	Xylariales	Sordariomycetes
5776	1	*Chrysomorbus lagerstroemiae*	86%, 96%	Cryphonectriaceae	Diaporthales	Sordariomycetes
5803	1	*Coniochaeta* sp.	99%, 98%	Coniochaetaceae	Coniochaetales	Sordariomycetes
5814	1	*Coniochaeta* sp.	90%, 100%	Coniochaetaceae	Coniochaetales	Sordariomycetes
5840	1	*Coniochaeta velutina* CBS 579.71	90%, 100%	Coniochaetaceae	Coniochaetales	Sordariomycetes
5771	1	*Neurospora crassa*	100%, 91%	Sordariaceae	Sordariales	Sordariomycetes
5635	1	*Tolypocladium sp*	97%, 95%	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
5811	1	*Plectosphaerella cucumerina*	100%, 97%	Plectosphaerellaceae	Glomerellales	Sordariomycetes
5786- 5806-5808	1	*Setophoma* sp.	100%, 90%	Phaeosphaeriaceae	Pleosporales	Dothideomycetes
5836	1	*Lophiotrema mucilaginosis*	90%, 40%	Lophiotremataceae	Pleosporales	Dothideomycetes
5839	1	*Lophiotrema mucilaginosis*	100%, 95%	Lophiotremataceae	Pleosporales	Dothideomycetes
5719	1	*Cladosporium* sp.	100%, 98%	Cladosporiaceae	Capnodiales	Dothideomycetes
5631	1	*Lasiodiplodia* sp. CBS111530	98%, 99%	Botryosphaeriaceae	Botryosphaeriales	Dothideomycetes
5507-5494-5506	3	*Penicillium* sp	96%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes

5713-5626-5627-5768	4	*Penicillium expansum* ATCC 7861	100%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5766-5647	2	*Penicillium polonicum*	100%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5650	1	*Penicillium glabrum* CBS 125543	100%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5651	1	*Penicillium* sp	99%, 100%	Aspergillaceae	Eurotiales	Eurotiomycetes
5718	1	*Penicillium cairnsense*	100%, 98%	Aspergillaceae	Eurotiales	Eurotiomycetes
5810- 5830	2	*Penicillium* sp	99%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5710	1	*Penicillium echinulatum*	100%, 100%	Aspergillaceae	Eurotiales	Eurotiomycetes
5648	1	*Penicillium expansum* ATCC 7861	100%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5770	1	*Penicillium rudallense*	100%, 100%	Aspergillaceae	Eurotiales	Eurotiomycetes
5767	1	*Penicillium rudallense*	100%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5764	1	*Penicillium* sp	92%, 95%	Aspergillaceae	Eurotiales	Eurotiomycetes
5831	1	*Penicillium robsamsonii* CBS 140573	99%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5821-5820	2	*Talaromyces* sp. CBS 408.93	100%, 99%	Trichocomaceae	Eurotiales	Eurotiomycetes
5825	1	*Aspergillus creber*	100%, 99%	Aspergillaceae	Eurotiales	Eurotiomycetes
5716- 5774	2	*Sclerotinia sclerotiorum* ATCC 46762	97%, 99%	Sclerotiniaceae	Helotiales	Leotiomycetes
5801-5802-5804	3	*Infundichalara* sp. CBS:175.74	89%, 95%	Helotialesincertaesedis	Helotiales	Leotiomycetes
5508-5567	2	*Debaryomyces fabryi*	100%, 99%	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
5566	1	*Debaryomyces nepalensis* CBS 2334	100%, 99%	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
5826	1	*Debaryomyces subglobosus*	100%, 98%	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
5568	1	*Candida orthopsilosis*	100%, 99%	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
5812	1	*Meyerozyma guilliermondii* CBS:12037	100%, 100%	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
5785	1	*Pseudocercosporella* sp	99%, 97%	Mycosphaerellaceae	Capnodiales	Dothideomycetes
5838	1	*Pseudocercosporella fraxini*	99%, 96%	Mycosphaerellaceae	Capnodiales	Dothideomycetes
5819-5815	2	*Pseudocercosporella fraxini*	99%, 98%	Mycosphaerellaceae	Capnodiales	Dothideomycetes
5824	1	NEW TAXA TUCIM 5824				
5841	1	NEW TAXA TUCIM 5841				
5778	1	*Schizophyllum* sp.	100%, 99%	Schizophyllaceae	Agaricales	Agaricomycetes [1]
5791	1	*Schizophyllum* sp.	100%, 99%	Schizophyllaceae	Agaricales	Agaricomycetes [1]
5782	1	*Hypholoma* sp.	99%, 100%	Strophariaceae	Agaricales	Agaricomycetes [1]
5800-5805	2	*Hypholoma* sp.	99%, 99%	Strophariaceae	Agaricales	Agaricomycetes [1]
5790-5789	2	*Phlebia acerina*	99%, 99%	Meruliaceae	Polyporales	Agaricomycetes [1]

1- Basidiomycota phylum

Genus belong to Sordariomycetes class mostly from Hypocreales (*Trichoderma* spp. and *Fusarium* spp.) and Xylariales (*Pestalotiopsis* spp.) were the most prevalence fungi isolated from the phyllosphere (150 strains from 195 total isolated strains). Seven basidiomycetes strains were also isolated. During the investigation we also found some fungi which were potentially new as phylum or family or genus.


53
5831 Penicillium caseifulvum
76
5810 -5830 Penicillium sp
37
5710 Penicillium echinulatum
99
5766 -5647 Penicillium polonicum
5648 Penicillium expansum
85
5713 -5626-5627-5768 Penicillium expansum
23
69
5764 Penicillium sp
5507 -5494-5506 Penicillium sp
85
5650 Penicillium glabrum
25
62
5651 Penicillium sp
99
5767 Penicillium rudallense
97
72
5770 Penicillium rudallense
5718 Penicillium cairnsense
5825 Aspergillus creber
14
F J430753 Penicillium sp
32
99
5821 -5820 Talaromyces sp
5824 NEW TAXA
5801 -5802-5804 Infundichalara sp
59
L C085197 Leotiomycetes sp
9
50
M H038145 Infundichalara sp
65
5716 Sclerotinia sclerotiorum
34
99
5774 Sclerotinia sp
5631 Lasiodiplodia sp
5719 Cladosporium sp
14
5819 -5815 Pseudocercosporellasp
65
97
5785 Pseudocercosporella sp
99
71
5838 Pseudocercosporella fraxini
5841 NEW TAXA
82
5508 -5567 Debaryomyces fabryi
98
5826 Debaryomyces sp
99
5566 Debaryomyces nepalensis
25
99
5812 Meyerozyma guilliermondii
5568 Candida orthopsilosis


83
52
70
5786 *Setophoma* sp
99
5808 *Setophoma* sp
5806 *Setophoma* sp
78
K Y582131 *Setophoma* sp
5836 *Lophiotrema* sp
5839 *Lophiotrema mucilaginosis*
99
5635 *Tolypocladium* sp
A B334109 Valsaceae sp
87
5814 *Coniochaeta* sp
99
5840 *Coniochaeta* sp
5803 Coniochaeta sp
5771 Neurospora crassa
58
5712 *Xylaria* sp
81
5714 *Valsaceae*sp
83
5646 *Plectosphaerella* sp.
5711 *Plectosphaerella* sp.
99
5715 *Valsaceae* sp
91
5717 *Arthrinium* sp
99
5817 -5818 *Arthrinium phaeospermum*
85
5781 -5813 *Arthrinium* sp
52
85
5822 -5823 *Arthrinium* sp
99
5773 *Arthrinium* rasikravindrii
5797 *Arthrinium* sp
85
5816 -5779-5780 *Arthrinium* sp
99
5807 -5809 *Arthrinium* sp
96
87
5776 *Chrysomorbus lagerstroemiae*
99
5799 -5798 *Arthrinium* sp
5827 *Arthrinium* sp

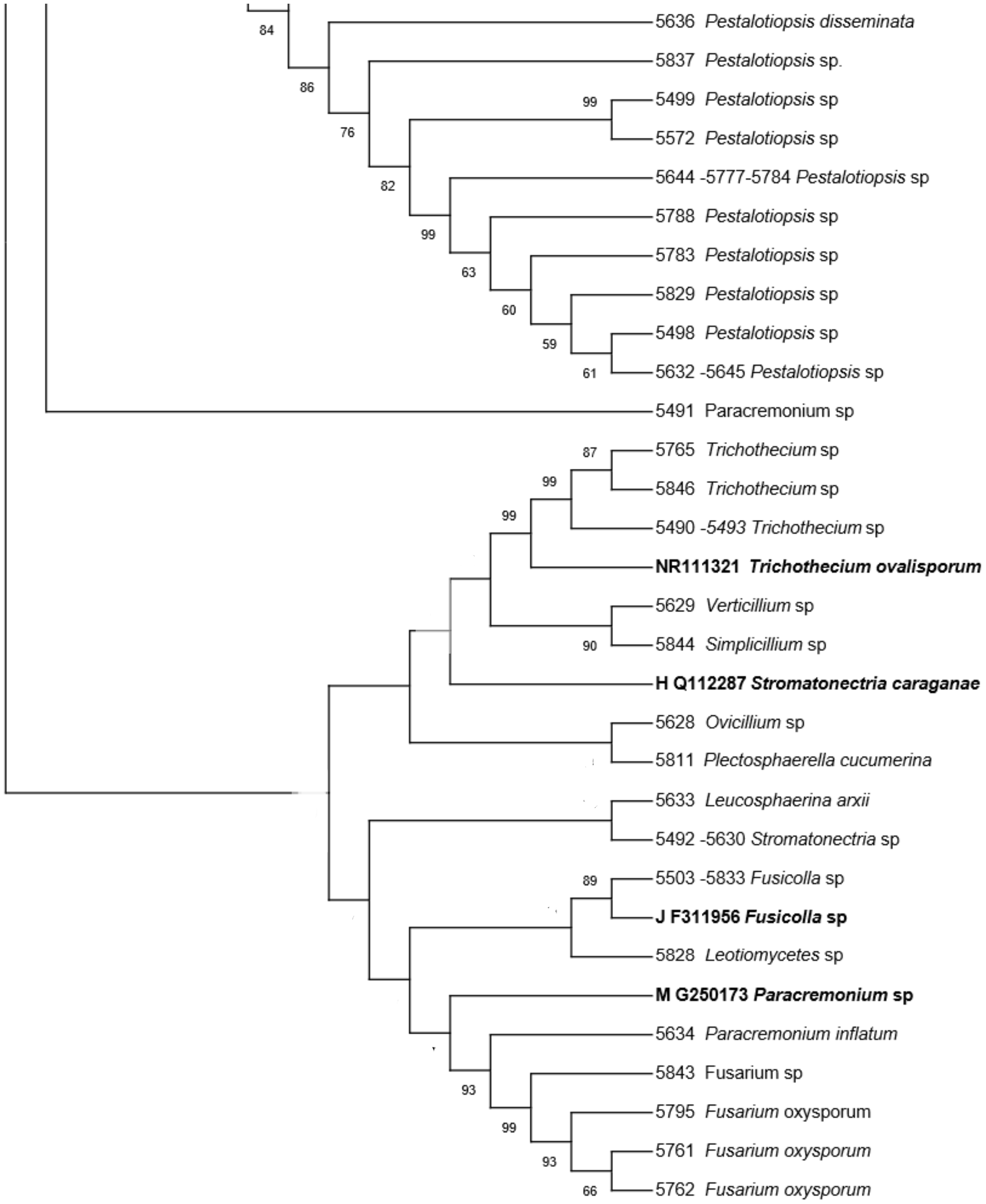


Figure 10 Shorea phyllosphere 2014 excluded Trichoderma. *The highest parts belong to* Arthrinium *and* Penicillium *sp. which were shown. References were shown as bold type.*

188 fungal strains isolated from *S. johorensis* phyllosphere without Basidiomycota species (7) and *Trichoderma* sp. (89) were analyzed. As can be seen from the tree, *Penicillium* and *Arthrinium*

species are most abundant (Figure 10). TU CIM 5824 and TU CIM 5841 were found on BLAST as *Incrucipulum pseudosulphurellum* (TNS:F-81441) with 86% similarity, *Paraphaeosphaeria neglecta* (CBS:627.94) with 80% similarity, respectively. Unfortunately, in the tree there are many mistakes. For this to make new tree according to their order or to construct another phylogenetic tree f.e. Maximum Likelihood.

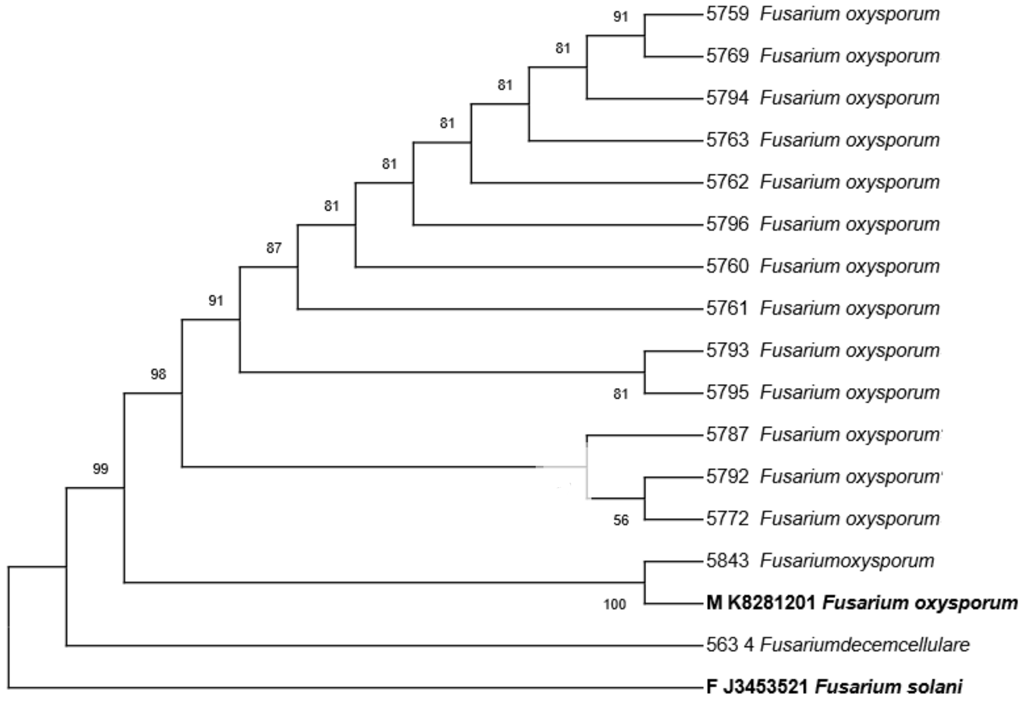


Figure 11 Tree of Fusarium species *from* Shorea *phyllosphere. References were shown as bold type.*

The *Fusarium* genus is the most numerous but not the most diverse genus, 15 sequences in the alignment are almost identical and identified (BLAST). The strains which isolated from epiphytes belong to mostly *Fusarium oxysporum* genus (Figure 11).

S. johorensis and *Ficus* sp. epiphytic fungi

Below you can see the list of the strains and phylogenic analysis of epiphytic fungi isolated from *S. johorensis* and *Ficus* sp. We used some type strains in phylogenic analysis to identification of the strains with similarity less than 95% (Table 6).

The epiphytic fungi pattern of the both tested trees shown similar but mostly from different colonies. Genus belong to Hypocreales (like *Fusarium* sp., and *Trichoderma* sp.), Saccharomycetales and Eurotiales (*Penicillium* sp.) were the most prevalence strains isolated from the both plant leaves. However, each plant strain also had its specific fungi.

In *S. johorensis* a genus belong to Hypocreales TUCIM 5984 were the more frequent isolated fungi from the surface of the leaves. We were able to identify this strain to the level of order because of very low ITS similarity (87% similarity to strain *Pochonia* sp. CBS 892.72 with accession number KM231844 in 2015). Real yeasts belong to order Saccharomycetales (*Geotrichum* sp., *Candida* spp and *Debaryomyces* sp.), Eurotiales (*Penicillium* sp. and *Talaromyces* sp.) and *Readeriella* spp. were the next frequent isolated fungi from *S. johorensis* epiphytic fungi. Capnodiales (*Readeriella* spp.) and *Geotrichum* sp. frequently isolated from the *Shorea* leaves but not from *Ficus*.

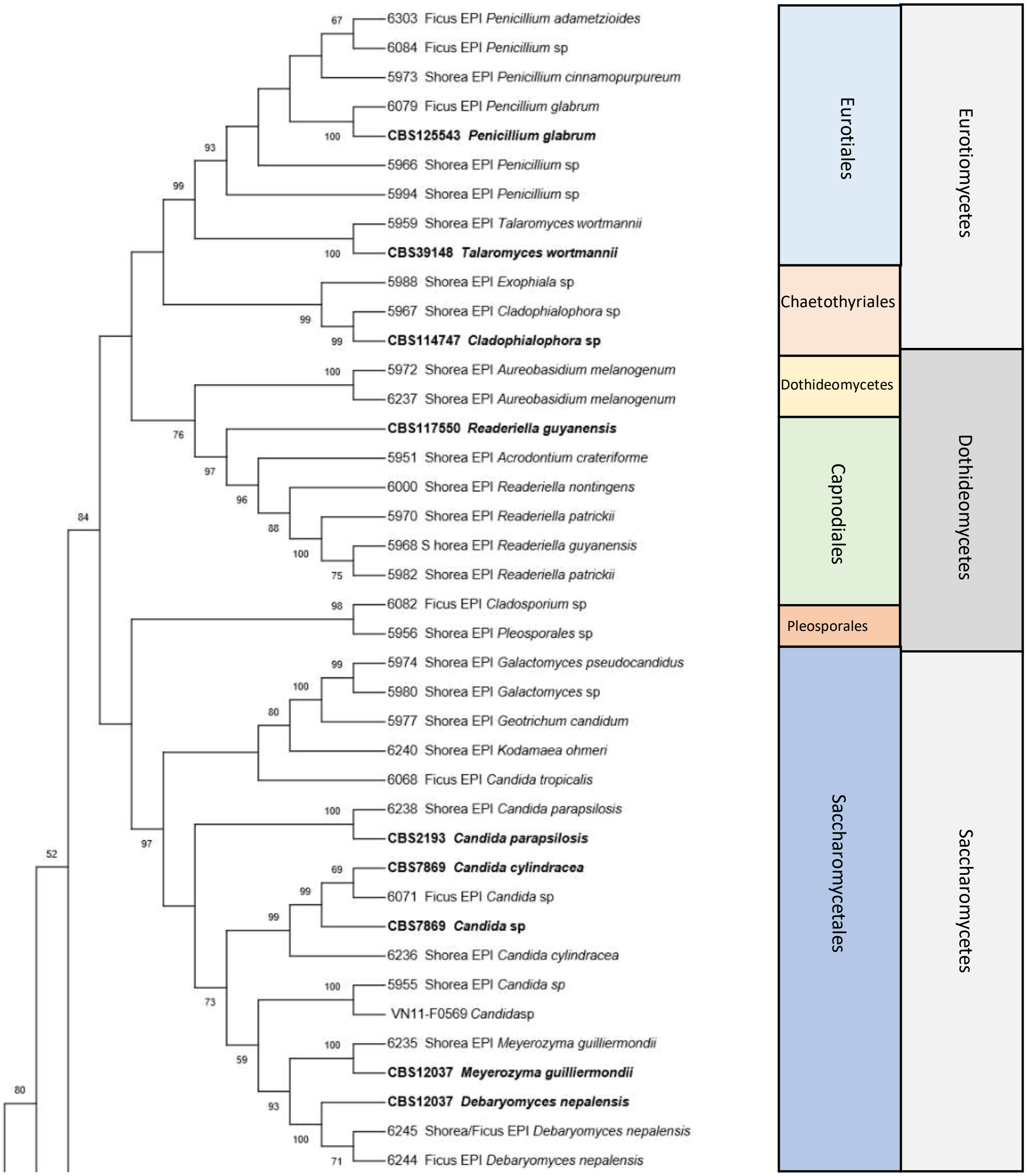
Some strains isolated from *Shorea* epiphyte were probably new as family or genus.

- *Hypocreales* sp. TUCIM 5984 (87% similarity to strain *Pochonia* sp. CBS 892.72)
- *Hypocreales* sp. TUCIM 5950 (87% similarity to strain *Paracremonium inflatum* CBS 482.78)
- *Readeriella* sp. TUCIM 5968 (98% similarity to strain *Readeriella guyanensis* CBS 117550)
- *Readeriella* sp. TUCIM 6000 (90% similarity to strain *Readeriella nontingens* CPC:14444)
- *Chaetothyriales* sp. TUCIM 5967 (93% similarity to strain *Cladophialophora chaetospira* CBS 114747)

Some special *Ficus* epiphytic fungi isolates were also unique and listed below:

- *Hypocreales* sp TUCIM 6064 (88% similarity to strain *Coccinonectria pachysandricola* CBS 476.92)
- *Pleosporales* sp TUCIM 6082 (81% similarity to strain *Corynespora smithii* L133)

Phylogenetic tree of *S. johorensis* and *Ficus* sp. epiphytic fungi was shown below Figure 12.


6303 Ficus EPI Penicillium adametzioides
6084 Ficus EPI Penicillium sp
5973 Shorea EPI Penicillium cinnamopurpureum
6079 Ficus EPI Pencillium glabrum
CBS125543 Penicillium glabrum
5966 Shorea EPI Penicillium sp
5994 Shorea EPI Penicillium sp
5959 Shorea EPI Talaromyces wortmannii
CBS39148 Talaromyces wortmannii
5988 Shorea EPI Exophiala sp
5967 Shorea EPI Cladophialophora sp
CBS114747 Cladophialophora sp
5972 Shorea EPI Aureobasidium melanogenum
6237 Shorea EPI Aureobasidium melanogenum
CBS117550 Readeriella guyanensis
5951 Shorea EPI Acrodontium crateriforme
6000 Shorea EPI Readeriella nontingens
5970 Shorea EPI Readeriella patrickii
5968 S horea EPI Readeriella guyanensis
5982 Shorea EPI Readeriella patrickii
6082 Ficus EPI Cladosporium sp
5956 Shorea EPI Pleosporales sp
5974 Shorea EPI Galactomyces pseudocandidus
5980 Shorea EPI Galactomyces sp
5977 Shorea EPI Geotrichum candidum
6240 Shorea EPI Kodamaea ohmeri
6068 Ficus EPI Candida tropicalis
6238 Shorea EPI Candida parapsilosis
CBS2193 Candida parapsilosis
CBS7869 Candida cylindracea
6071 Ficus EPI Candida sp
CBS7869 Candida sp
6236 Shorea EPI Candida cylindracea
5955 Shorea EPI Candida sp
VN11-F0569 Candidasp
6235 Shorea EPI Meyerozyma guilliermondii
CBS12037 Meyerozyma guilliermondii
CBS12037 Debaryomyces nepalensis
6245 Shorea/Ficus EPI Debaryomyces nepalensis
6244 Ficus EPI Debaryomyces nepalensis
67
100
93
99
100
99
99
100
76
97
96
84
88
100
75
98
99
100
80
100
97
52
69
99
99
100
73
100
59
80
93
100
71
Eurotiales
Chaetothyriales
Dothideomycetes
Capnodiales
Pleosporales
Saccharomycetales
Eurotiomycetes
Dothideomycetes
Saccharomycetes

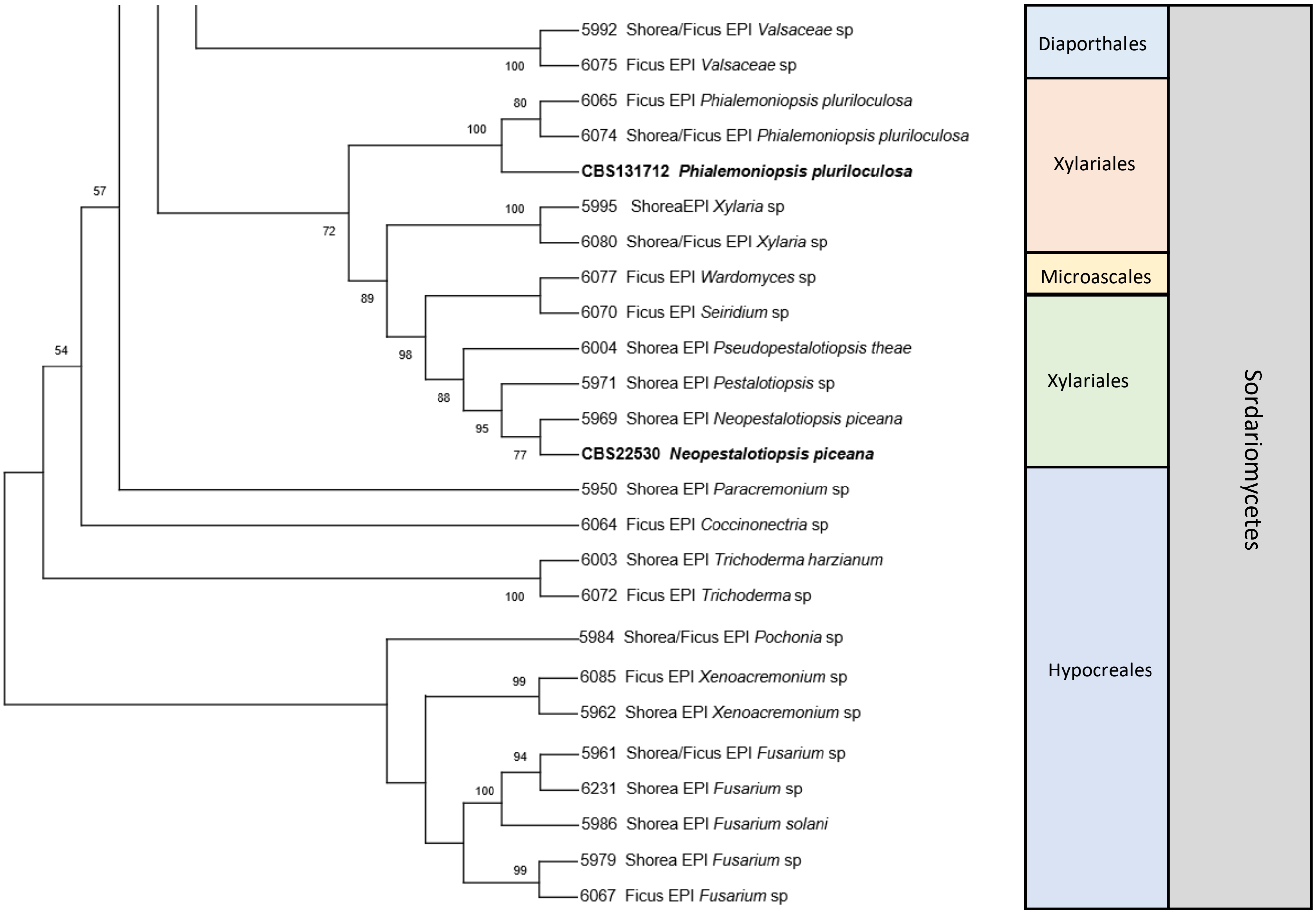


Figure 12 Tree of S. johorensis *and* Ficus *sp. epiphytic fungi. References were shown as bold type.*

Table 6 Shorea johorensis *and* Ficus *sp. epiphytic fungi. The similarity values below 95% are marked in red*

TUCIM No.	total	origin	Genus/Species	ITS-Cov/*Ident*	Family	Order	Class
5984, 5954, 5957, 5960, 5978, 5983, 6002, 6066, 6073	9	*Shorea/ Ficus* EPI	*Pochonia* sp. CBS 892.72	99%, 88%,		Hypocreales	Sordariomycetes
5961, 6083	2	*Shorea/ Ficus* EPI	*Fusarium* sp.	97%, 98%	Nectriaceae	Hypocreales	Sordariomycetes
5986	1	*Shorea* EPI	*Fusarium solani*	98%, 100%	Nectriaceae	Hypocreales	Sordariomycetes
6231, 6076	2	*Shorea* EPI	*Fusarium* sp.	100%, 98%	Nectriaceae	Hypocreales	Sordariomycetes
5979	1	*Shorea* EPI	*Fusarium* sp.	100%, 100%	Nectriaceae	Hypocreales	Sordariomycetes
6067	1	*Ficus* Epi	*Fusarium* sp.	99%, 100%	Nectriaceae	Hypocreales	Sordariomycetes
5950	1	*Shorea* EPI	*Paracremonium* sp. CBS 482.78	100%, 87%		Hypocreales	Sordariomycetes
6085	1	*Ficus* Epi	*Xenoacremonium* sp.	98%, 99%	Nectriaceae	Hypocreales	Sordariomycetes
5962, 5997	2	*Shorea* EPI	*Xenoacremonium* sp	99%, 99%	Nectriaceae	Hypocreales	Sordariomycetes
6003	1	*Shorea* EPI	*Trichoderma harzianum*	99%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6072	1	*Ficus* Epi	*Trichoderma* sp.	98%, 98%	Hypocreaceae	Hypocreales	Sordariomycetes
6064	1	*Ficus* Epi	*Coccinonectria sp.* CBS 476.92	89%, 92%		Hypocreales	Sordariomycetes
6065	1	*Ficus* Epi	*Phialemoniopsis pluriloculosa*	96%, 99%	Togniniaceae	Diaporthales	Sordariomycetes
5995	1	*Shorea* EPI	*Xylaria* sp.	95%, 99%	Hypoxylaceae	Xylariales	Sordariomycetes
6074	1	*Shorea/ Ficus* EPI	*Phialemoniopsis pluriloculosa* CBS 131712	98%, 99%	Xylariales incertae sedis	Xylariales	Sordariomycetes
6080	1	*Shorea/ Ficus* EPI	*Xylaria* sp.	93%, 99%	Xylariaceae	Xylariales	Sordariomycetes
5992	1	*Shorea/ Ficus* EPI	*Valsaceae* sp.	96%, 97%	Valsaceae	Diaporthales	Sordariomycetes
6075	1	*Ficus* Epi	*Valsaceae* sp.	94%, 91%	Valsaceae	Diaporthales	Sordariomycetes
6077	1	*Ficus* Epi	*Wardomyces* sp.	97%, 98%	Microascaceae	Microascales	Sordariomycetes
6070	1	*Ficus* Epi	*Seiridium* sp.	98%, 98%	Sporocadaceae	Xylariales	Sordariomycetes
5969	1	*Shorea* EPI	*Neopestalotiopsis piceana* CBS 225.30	98%, 100%	Sporocadaceae	Xylariales	Sordariomycetes
6004	1	*Shorea* EPI	*Pseudopestalotiopsis theae*	99%, 100%	Sporocadaceae	Xylariales	Sordariomycetes
5971	1	*Shorea* EPI	*Pestalotiopsis* sp.	97%, 100%	Sporocadaceae	Xylariales	Sordariomycetes
5951	1	*Shorea* EPI	*Acrodontium crateriforme*	98%, 99%	Teratosphaeriaceae	Capnodiales	Dothideomycetes
5965, **5968**	2	*Shorea* EPI	*Readeriella guyanensis* CBS 117550	99%, 99%	Teratosphaeriaceae	Capnodiales	Dothideomycetes
5970	1	*Shorea* EPI	*Readeriella patrickii CBS 124987*	94%, 91%	Teratosphaeriaceae	Capnodiales	Dothideomycetes
5972, 5991	2	*Shorea* EPI	*Aureobasidium melanogenum*	98%, 100%	Saccotheciaceae	Dothideales	Dothideomycetes
5982	1	*Shorea* EPI	*Readeriella patrickii* CBS 124987	97%, 91%	Teratosphaeriaceae	Capnodiales	Dothideomycetes
6000	1	*Shorea* EPI	*Readeriella nontingens*	96%, 91%	Teratosphaeriaceae	Capnodiales	Dothideomycetes
6082	1	*Ficus* Epi	*Cladosporium* sp.	100%, 99%	Cladosporiaceae	Capnodiales	Dothideomycetes
5956	1	*Shorea* EPI	*Pleosporales* sp	51%, 91%		Pleosporales	Dothideomycetes
6237	1	*Shorea* EPI	*Aureobasidium melanogenum*	98%, 100%	Saccotheciaceae	Dothideales	Dothideomycetes
5959	1	*Shorea* EPI	*Talaromyces wortmannii* CBS 391.48	98%, 100%	Trichocomaceae	Eurotiales	Eurotiomycetes
5966, 5996, 6001	3	*Shorea* EPI	*Penicillium* sp	99%, 99%	Trichocomaceae	Eurotiales	Eurotiomycetes
5994	1	*Shorea* EPI	*Penicillium* sp	97%, 100%	Trichocomaceae	Eurotiales	Eurotiomycetes
5973	1	*Shorea* EPI	Penicillium cinnamopurpureum	98%, 100%	Trichocomaceae	Eurotiales	Eurotiomycetes

6078, **6079,** 6081	3	*Ficus* Epi	*Penicillium glabrum* CBS 125543	99%, 100%	Trichocomaceae	Eurotiales	Eurotiomycetes
6084	1	*Ficus* Epi	*Penicillium* sp	98%, 100%	Trichocomaceae	Eurotiales	Eurotiomycetes
6303	1	*Ficus* Epi	*Penicillium adametzioides*	99%, 100%	Trichocomaceae	Eurotiales	Eurotiomycetes
5967	1	*Shorea* EPI	*Cladophialophora* sp. CBS 114747	99%, 93%	Herpotrichiellaceae	Chaetothyriales	Eurotiomycetes
5988	1	*Shorea* EPI	*Exophiala* sp.	98%, 87%		Chaetothyriales	Eurotiomycetes
6245, 6239	2	*Shorea/ Ficus* EPI	*Debaryomyces nepalensis*	99%, 99%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
6244	1	*Ficus* Epi	*Debaryomyces nepalensis* *CBS:12037*	98%, 99%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
6235	1	*Shorea* EPI	*Meyerozyma guilliermondii* CBS:12037	98%, 100%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
6236	1	*Shorea* EPI	*Candida cylindracea* CBS:7869	96%, 94%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
6238	1	*Shorea* EPI	*Candida parapsilosis* CBS:2193	98%, 100%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
6240	1	*Shorea* EPI	*Kodamaea ohmeri*	99%, 100%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
6068	1	*Ficus* Epi	*Candida tropicalis*	98%, 100%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
6071	1	*Ficus* Epi	*Candida* sp. CBS:7869	98%, 99%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
5955	1	*Shorea* EPI	Candida *sp*	99%, 90%	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
5958, 5993, **5977,** 5985,	4	*Shorea* EPI	*Geotrichum candidum*	100%, 99%	Dipodascaceae	Saccharomycetales	Saccharomycetes
5974,	2	*Shorea* EPI	*Galactomyces pseudocandidus*	96%, 93%	Dipodascaceae	Saccharomycetales	Saccharomycetes
5980, 5987	1	*Shorea* EPI	*Galactomyces* sp	99%, 93%	Dipodascaceae	Saccharomycetales	Saccharomycetes

S. johorensis and *Ficus* sp. endophytic fungi

Compare to epiphytic fungi, there were few overlap between endophytic fungi of *S. johorensis* and *Ficus* sp. (Except *Trichoderma* spp. and *Pestalotiopsis* spp. which present at high quantity in both plants leaves) and they mostly shown own specific fungi pattern. All the isolated strains belong to Sordariomycetes and Dothideomycetes classes (Table 7).

The most dominant fungi isolated from *Shorea* leaves belong to several species in order Diaporthales (we couldn't identify them because of their low ITS identity after blasting in NCBI), *Gliocephalotrichum* sp. and *Trichoderma* spp. below is the list of the potential new family or genus fungi isolated from the *S. johorensis* endophyte:

- Diaporthales TUCIM 6025 (100% similarity to strain *Purpureocillium lilacinum* Kw-3411)
- Diaporthales TUCIM 6022 (98% similarity to strain *Coniochaeta* sp. BRO-2013)
- Diaporthales TUCIM 6026 (99% similarity to strain *Daldinia eschscholtzii* JMRC:SF:11930)
- Diaporthales TUCIM 6029 (96% similarity to strain *Valsaceae* sp. GS52)

- Diaporthales TUCIM 6030 (100% similarity to strain *Phomopsis* sp. TW24)
- Myriangiales TUCIM 6017 (82% similarity to strain *Anhellia nectandrae* VIC 31767)
- Capnodiales TUCIM 6021 (91% similarity to strain *Readeriella nontingens* CPC:14444)

Diaporthales strains TUCIM 6022, 6023 *Coniochaeta* sp (BRO-2013) and 6034 *Sordariomycetes* sp. (JMUR-2016) are redundant based on their ITS sequences but their same age colonies showing different pigmentation but same morphology (Figure 13).

Figure 13 the one-week old colony of TUCIM 6022. 6023 and 6024 (from left to right)

Trichoderma spp, *Lasiodiplodia* sp. and *Clonostachys rosea* were the most isolated fungi from endophyte of *Ficus* leaves (Figure 14).

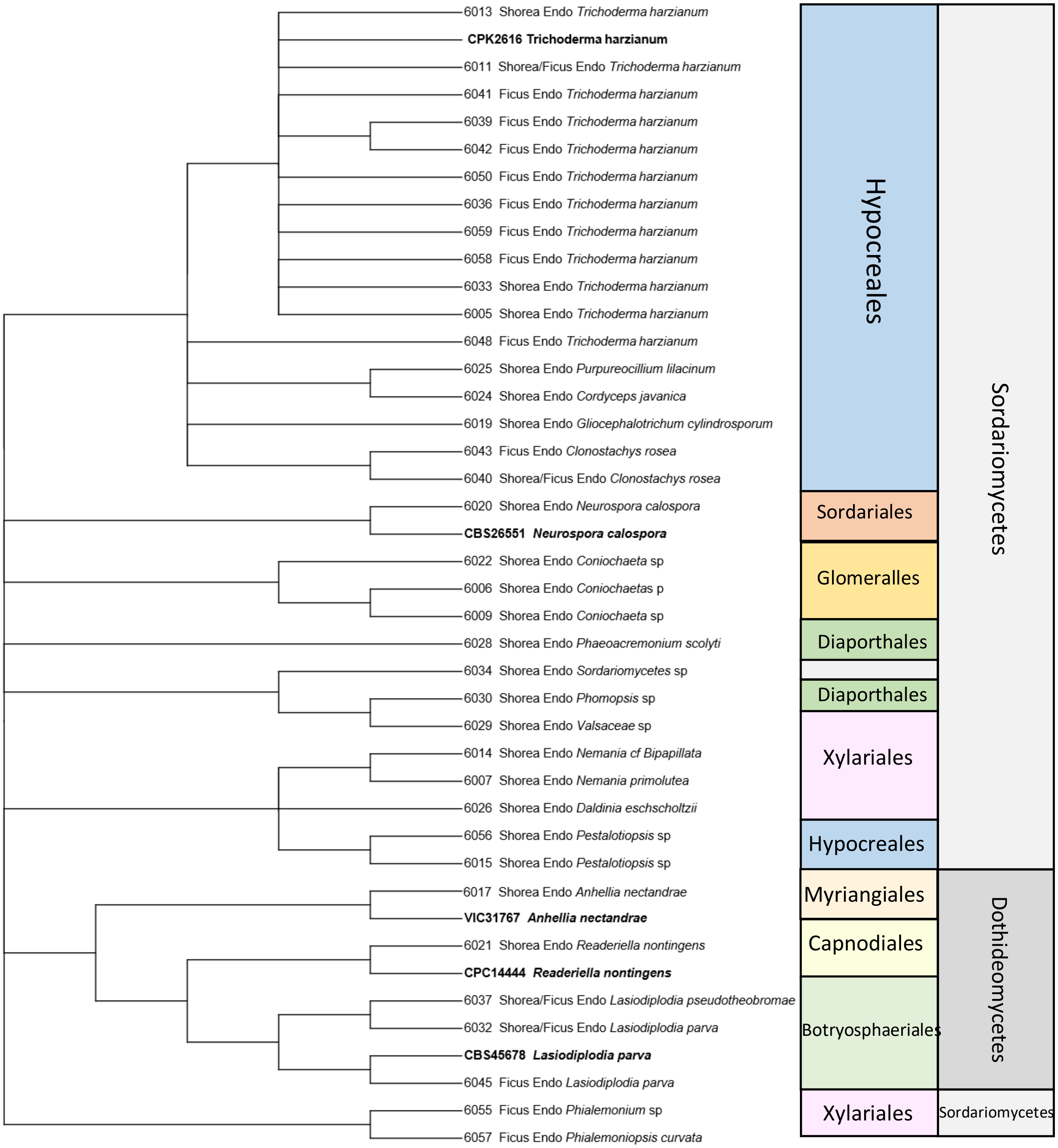


Figure 14Tree of S. johorensis and Ficus sp. endophytic fungi. References were shown as bold type

.

Table 7 *S. johorensis* and *Ficus* sp. endophytic fungi. The identity values below 95% are marked in red.

TUCIM No.	**total**	**origin**	**Genus/Species**	**ITS-Cov/*Ident***	**Family**	**Order**	**Class**
6011, 6051	2	*Shorea/ Ficus* Endo	*Trichoderma harzianum*	99%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6033	1	*Shorea* Endo	*Trichoderma harzianum*	99%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6013	1	*Shorea* Endo	*Trichoderma harzianum*	99%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6005	1	*Shorea* Endo	*Trichoderma harzianum*	99%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6036, 6049	2	*Ficus* Endo	*Trichoderma harzianum*	98%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6039, 6044	2	*Ficus* Endo	*Trichoderma harzianum*	99%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6042	1	*Ficus* Endo	*Trichoderma harzianum*	97%, 97%	Hypocreaceae	Hypocreales	Sordariomycetes
6050	1	*Ficus* Endo	*Trichoderma harzianum*	98%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6041	1	*Ficus* Endo	*Trichoderma harzianum*	98%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6059	1	*Ficus* Endo	*Trichoderma harzianum*	100%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6058	1	*Ficus* Endo	*Trichoderma harzianum*	99%, 99%	Hypocreaceae	Hypocreales	Sordariomycetes
6048	1	*Ficus* Endo	*Trichoderma atroviride*	99%, 100%	Hypocreaceae	Hypocreales	Sordariomycetes
6043, 6046, 6054	3	*Ficus* Endo	*Clonostachys rosea*	97%, 99%	Bionectriaceae	Hypocreales	Sordariomycetes
6040, **6032**	2	*Shorea/ Ficus* Endo	*Clonostachys rosea*	99%, 99%	Bionectriaceae	Hypocreales	Sordariomycetes
6010, 6012, **6019,** 6031	4	*Shorea* Endo	*Gliocephalotrichum cylindrosporum*	98%, 99%	Nectriaceae	Hypocreales	Sordariomycetes
6056	1	*Shorea* Endo	*Pestalotiopsis* sp.	97%, 99%	Sporocadaceae	Xylariales	Sordariomycetes
6025	1	*Shorea* Endo	*Purpureocillium lilacinum*	98%, 100%	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6024,6027	2	*Shorea* Endo	*Cordyceps javanica*	92%, 100%	Cordycipitaceae	Hypocreales	Sordariomycetes
6020,	1	*Shorea* Endo	*Neurospora calospora* CBS 265.51	100%, 99%	Sordariaceae	Sordariales	Sordariomycetes
6014, 6018,	2	*Shorea* Endo	*Nemania cf. Bipapillata*	94%, 100%	Xylariaceae	Xylariales	Sordariomycetes
6007	1	*Shorea* Endo	*Nemania primolutea*	99%, 95%	Xylariaceae	Xylariales	Sordariomycetes
6022, 6023,	2	*Shorea* Endo	*Coniochaeta* sp.	100%, 98%	Coniochaetaceae	Coniochaetales	Sordariomycetes
6034	1	*Shorea* Endo	*Sordariomycetes* sp.	99%, 86%			Sordariomycetes
6026	1	*Shorea* Endo	*Daldinia eschscholtzii*	100%, 99%	Hypoxylaceae	Xylariales	Sordariomycetes
6030	1	*Shorea* Endo	*Phomopsis* sp.	100%, 100%	Valsaceae	Diaporthales	Sordariomycetes
6029	1	*Shorea* Endo	*Valsaceae* sp	95%, 96%	Castanediellaceae	Xylariales	Sordariomycetes
6038, **6055**	2	*Ficus* Endo	*Phialemonium* sp.	98%, 99%	Xylariales incertae sedis	Xylariales	Sordariomycetes
6057	1	*Ficus* Endo	*Phialemoniopsis curvata*	98%, 97%	Xylariales incertae sedis	Xylariales	Sordariomycetes
6015	1	*Shorea* Endo	*Pestalotiopsis* sp.	98%, 99%	Sporocadaceae	Xylariales	Sordariomycetes
6028	1	*Shorea* Endo	*Phaeoacremonium scolyti*	93%, 98%	Togniniaceae	Togniniales	Sordariomycetes
6006	1	*Shorea* Endo	*Coniochaeta* sp.	100%, 99%	Glomerellaceae	Glomerellales	Sordariomycetes
6009	1	*Shorea* Endo	*Coniochaeta* sp	97%, 98%	Coniochaetaceae	Coniochaetales	Sordariomycetes
6017	1	*Shorea* Endo	Anhellia sp. VIC 31767	93%, 82%	Myriangiaceae	Myriangiales	Dothideomycetes
6037	1	*Shorea/ Ficus* Endo	*Lasiodiplodia pseudotheobromae*	99%, 99%	Botryosphaeriaceae	Botryosphaeriales	Dothideomycetes
6032	1	*Shorea/ Ficus* Endo	*Lasiodiplodia parva* CBS 456.78	99%, 99%	Botryosphaeriaceae	Botryosphaeriales	Dothideomycetes
6045, 6052, 6047	3	*Ficus* Endo	*Lasiodiplodia parva* CBS 456.78	92%, 99%	Botryosphaeriaceae	Botryosphaeriales	Dothideomycetes
6021	1	*Shorea* Endo	*Readeriella nontingens* CPC:14444	96%, 90%	Teratosphaeriaceae	Capnodiales	Dothideomycetes

The diversity of ant assosiated fungi:

C. explodens natural nest (YGFF)

The quantity of the fungi from inside of *C. explodens* natural nest (YGFF) were not diverse compared to the outer surface. However, the populations of the fungi were different. In carton part, *Xenoacremonium recifei* (CBS 541.89 with 99% similarity) was the dominant taxon and other black fungi included Chaetothyriales (CBS 128948 with 88% similarity) and *Fonsecaea minima* (CBS 126022 with 92% similarity) were in minority (Figure 15). *Trichoderma* genus and Saccharomyces were mostly present at inner part of the nest. Based on *tef*1 sequence identification, the *Trichoderma* strains isolated from the interior of the nest (TUCIM 6215) are new as species and not described yet (93% similar to *T. harzianum* culture-collection DAOM:233448). The YGFF nest strains and their phylogenic analysis listed below (Table 8, Table 9):

Table 8 YGFF nest strains and their phylogenic analysis. The identity values below 95% are marked in red

TUCIM No.	**total**	**Genus/Species**	**ITS-Cov/*Ident***	**origin**	**Family**	**Order**	**Class**
6203, 6204, 6086, 6087	4	*Xenoacremonium recifei* CBS 541.89	99%, 99%	Inside/Out	Nectriaceae	Hypocreales	Sordariomycetes
6218	1	*Xenoacremonium recifei* CBS 541.89	98%, 99%	Inside	Nectriaceae	Hypocreales	Sordariomycetes
6201	1	*Campylocarpon fasciculare*	90%,96%	Inside	Nectriaceae	Hypocreales	Sordariomycetes
6207	1	*Phialemoniopsis pluriloculosa* CBS 131712	95%, 99%	Inside	Xylariales incertae sedis	Xylariales	Sordariomycetes
6209	1	*Penicillium citrinum*	97%, 100%	Inside/Out	Trichocomaceae	Eurotiales	Eurotiomycetes
6205	1	*Chaetothyriales* sp. CBS 128948	99%, 86%	Inside		Chaetothyriales	Eurotiomycetes
6200	1	*Fonsecaea minima* CBS 126022	98%, 92%	Inside	Herpotrichiellaceae	Chaetothyriales	Eurotiomycetes
6217	1	*Penicillium expansum* ATCC 7861	99%, 100%	Outer layer	Trichocomaceae	Eurotiales	Eurotiomycetes
6216, 6219	2	*Penicillium chrysogenum*	99%, 99%	Outer layer	Trichocomaceae	Eurotiales	Eurotiomycetes
6209	1	*Penicillium citrinum*	97%, 100%	Outer layer	Trichocomaceae	Eurotiales	Eurotiomycetes
6260, 6261, 6262, 6263	4	*Schwanniomyces vanrijiae var. vanrijiae* CBS:3024	96%, 100%	Inside/Out	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
6208	1	*Mucor* sp.	96%, 98%	Inside	Mucoraceae	Mucorales	Mucoromycotina

Table 9 YGFF nest strains and their phylogenic analysis with marker tef1-*α*

TUCIM No.	total	Genus/Species	ITS-Cov/*Ident*	origin	Family	Order	Class
6212	1	*Trichoderma* sp.	99%, 99%	Inside	Hypocreaceae	Hypocreales	Sordariomycetes
6214, 6220	2	*Trichoderma* sp.	100%, 99%	out	Hypocreaceae	Hypocreales	Sordariomycetes
6210, 6211, 6213, 6215	4	*Trichoderma* sp.	99%, 99%	Inside/Out	Hypocreaceae	Hypocreales	Sordariomycetes
6221, 6222, 6223	3	*Trichoderma* sp.	100%, 99%	Inside	Hypocreaceae	Hypocreales	Sordariomycetes

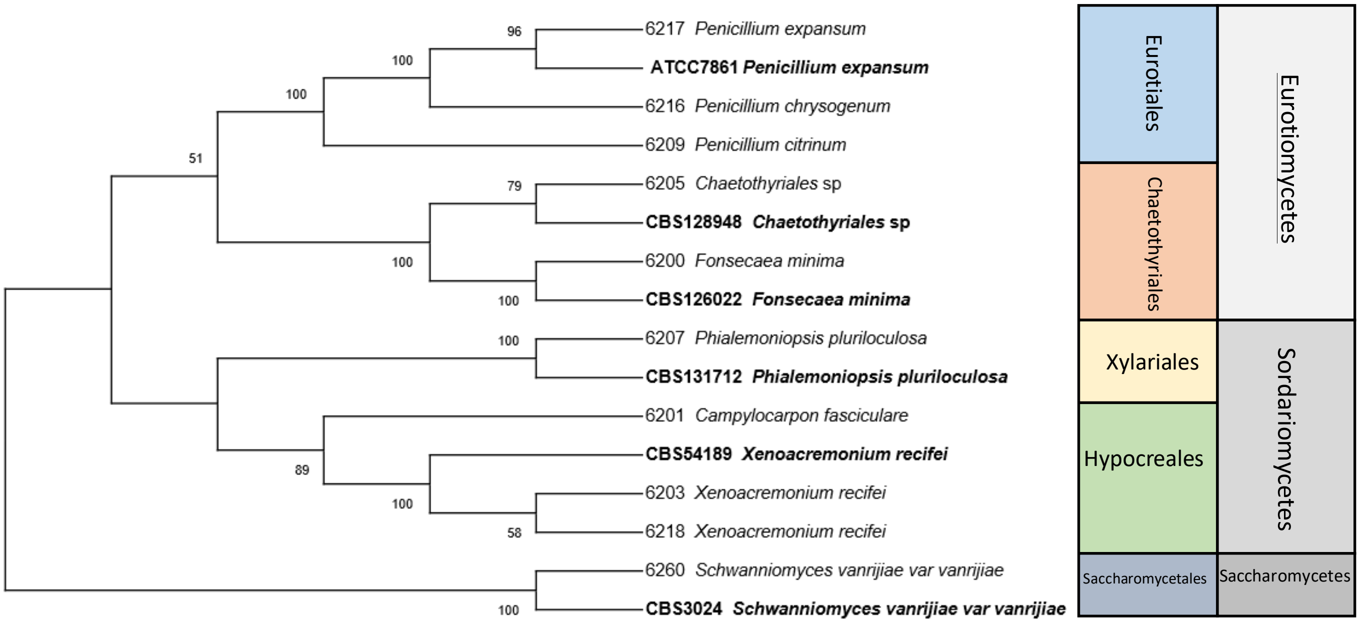


Figure 15 Tree of fungi from C. explodens *natural nest (YGFF). References were shown as bold type.*

C. bruneiensis nest 2015 (MIT1)

In *C. bruneiensis* 2015 nest cavity wall and carton structures inside, a patch of black dimorphic yeast-like fungi from the order Pleosporales (*Pleosporales* sp. TUCIM 6192) covered especially the inner area (Figure 16). Based on ITS 1-2 and *rpb*2 DNA barcoding analysis, we could not identify this fungus on level of family and genus (ITS1-2 coverage 50%, Similarity 91%).

*Figure 16 microscopic analysis of the BBQ nest 2015: A patch of fungi belong to family Pleosporales (*Pleosporales *sp. TUCIM 6192) covered the inner surface of the nest*

In microscopy analysis, we observed the patch of sporulating fungus covered all interior part of the nest. The yeast-like stages were never observed in the nest.

This fungus dominated the cultivable diversity (more than 99%). TUCIM 6192 has slow growth rate on PDA plates at 28°C at initial culture of the nest material, after four days of cultivation on PDA medium, the fungi colony switch from the mycelial to yeasty but after one week, the colony switch back to mycelial form (Figure 17). Interestingly, no evidence for conidiation was found in the medium while we observed the conidiation in the nest.

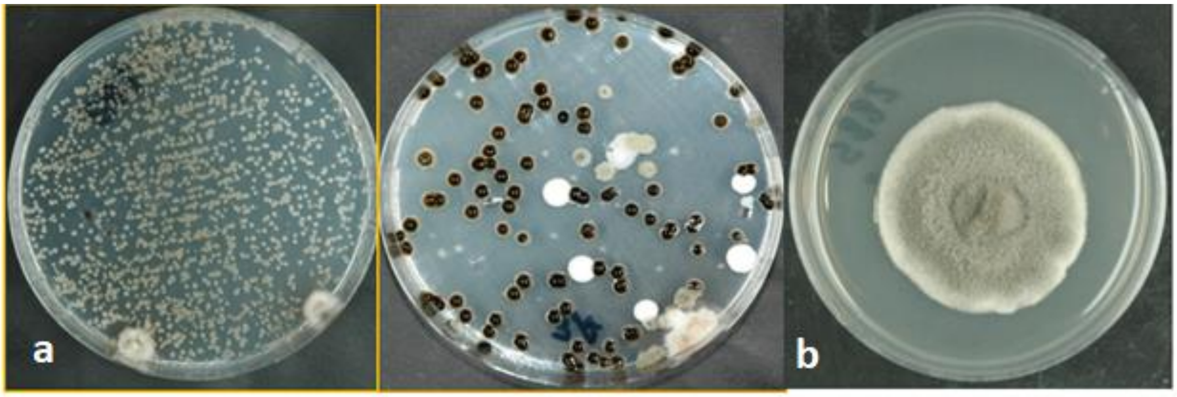


Figure 17 a) Fungi plate culture of C. bruneiensis *2015 nest. The left plate was belonging to 4 days culture of the inner part of the nest. More than 99% of the grown fungi were belong to the same strain (TUCIM 6192). b) One-week old culture of the interior of* C. bruneiensis *nest.*

The fungal diversity isolated from inside and outer layer of the MIT1 nest (*C. bruneiensis* 2015) were listed in Table 10. The identification of these strains was based on ITS1-2 gene barcoding (Figure 18).

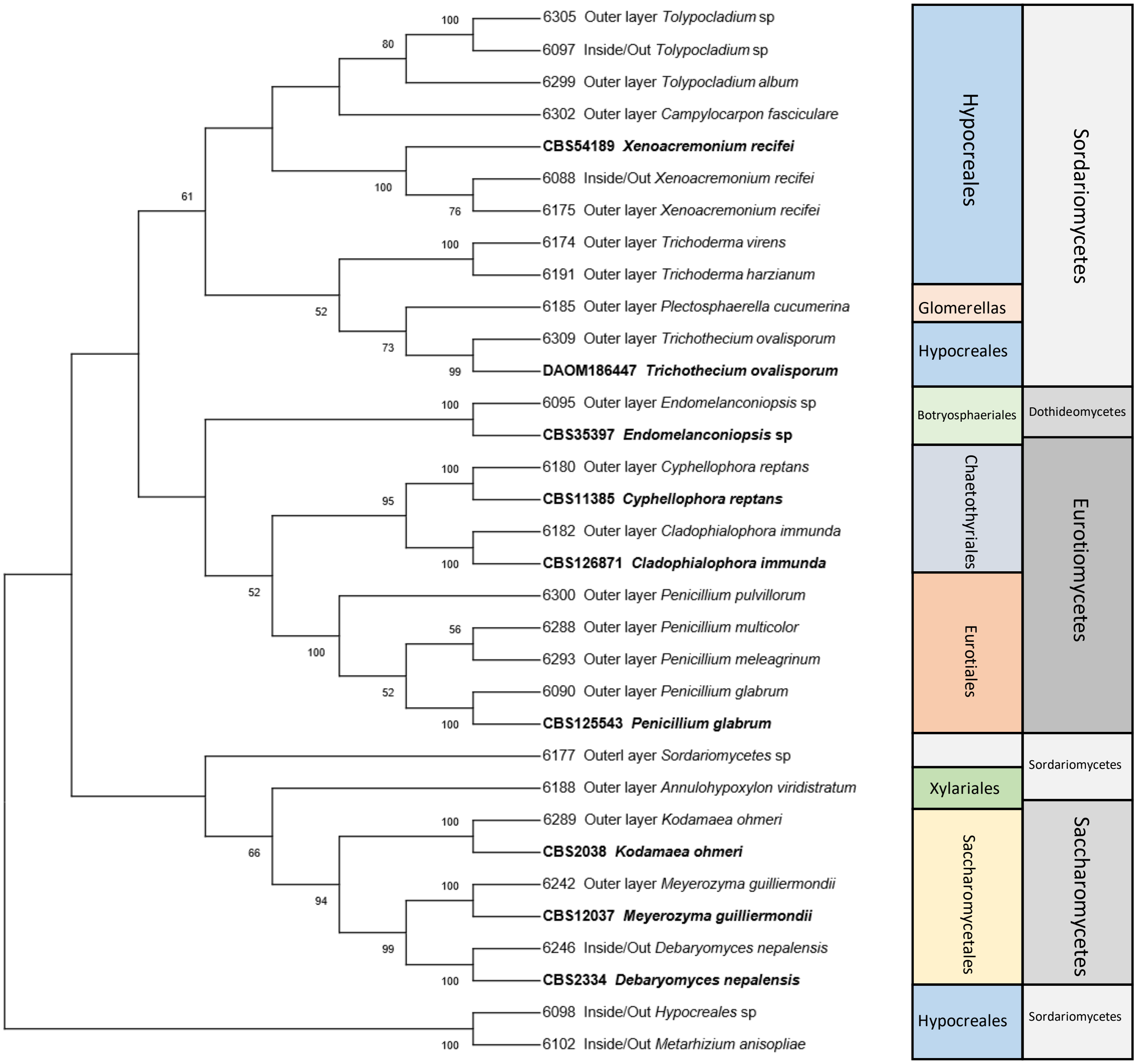


Figure 18 Tree of fungi from C. bruneiensis *nest 2015 (MIT1). References were shown as bold type.*

Table 10 The fungi diversity isolated from inside and outer layer of the MIT1 nest. The identity values below 95% are marked in red

TUCIM No.		Genus/Species	ITS-Cov/*Ident*	origin	Family	Order	Class
6089	1	*Setophoma yingyisheniae*	89%, 100%	Inside	Phaeosphaeriaceae	Pleosporales	Dothideomycetes
6164, 6167, 6170, 6172, **6192**, 6193, 6194, 6269, 6277, 6278, 6301, 6310, 6311, 6312	14	Pleosporales sp.	50%, 91%	Inside		Pleosporales	Dothideomycetes
6181	1	*Hermatomyces krabiensis*	**40%**, 90%	Outer layer	Pleosporales incertae sedis	Pleosporales	Dothideomycetes
6093	1	*Readeriella patrickii* CBS 124987	95%, 91%	Outer layer	Mycosphaerellaceae	Capnodiales	Dothideomycetes
6096, 6094, 6184	3	*Readeriella guyanensis* CBS 117550	99%, 99%	Outer layer	Mycosphaerellaceae	Capnodiales	Dothideomycetes
6183	1	*Capnodium* sp.	99%, 95%	Outer layer	Capnodiaceae	Capnodiales	Dothideomycetes
6286	1	*Cladosporium* sp.	100%, 99%	Outer layer	Cladosporiaceae	Capnodiales	Dothideomycetes
6304, 6276, 6291	3	*Fusarium* sp.	97%, 98%	Inside/Out	Nectriaceae	Hypocreales	Sordariomycetes
6195, 6275, 6282	3	*Fusarium* sp.	98%, 98%	Inside/Out	Nectriaceae	Hypocreales	Sordariomycetes
6270, 6271, 6280, 6281, 6283, 6292	6	*Fusarium* sp.	99%, 98%	Inside/Out	Nectriaceae	Hypocreales	Sordariomycetes
6272, 6274, 6279	3	*Paracremonium inflatum* CBS 482.78	99%, 98%	Inside	Nectriaceae	Hypocreales	Sordariomycetes
6168, **6171**	2	*Ijuhya corynospora* CBS 342.77	79%, 90%	Inside	Bionectriaceae	Hypocreales	Sordariomycetes
6165, 6169	2	*Tolypocladium inflatum*	97%, 99%	Inside	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6100	1	*Stromatonectria caraganae* CBS 125579	95%, 86%	Inside	Bionectriaceae	Hypocreales	Sordariomycetes
6290	1	*Leucosphaerina arxii* CBS 737.84	99%, 88%	Inside/Out	Hypocreales incertae sedis	Hypocreales	Sordariomycetes
6291, 6292	2	*Fusarium* sp	97%, 98%	Inside/Out	Nectriaceae	Hypocreales	Sordariomycetes
6294, 6298, 6285, 6178,	4	*Tolypocladium* sp.	95%, 97%	Outer layer	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6295	1	*Tolypocladium* sp.	97%, 95%	Outer layer	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6308	1	*Leucosphaerina arxii* CBS 737.84	99%, 89%	Outer layer	Hypocreales incertae sedis	Hypocreales	Sordariomycetes
6174, 6297	2	*Trichoderma virens*	99%, 99%	Outer layer	Hypocreaceae	Hypocreales	Sordariomycetes
6309	1	*Trichothecium ovalisporum*	96%, 94%	Outer layer	Hypocreales incertae sedis	Hypocreales	Sordariomycetes
6191	1	*Trichoderma harzianum*	99%, 99%	Outer layer	Hypocreaceae	Hypocreales	Sordariomycetes
6088, 6306	2	*Xenoacremonium recifei* CBS 541.89	100%, 99%	Inside/Out	Nectriaceae	Hypocreales	Sordariomycetes
6175, 6176	2	*Xenoacremonium recifei* CBS 541.89	99%, 98%	Outer layer	Nectriaceae	Hypocreales	Sordariomycetes
6177	1	*Sordariomycetes* sp.	99%, 86%	Outer layer			Sordariomycetes
6299	1	*Tolypocladium album*	94%, 97%	Outer layer	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6302	1	*Campylocarpon fasciculare*	94%, 97%	Outer layer	Nectriaceae	Hypocreales	Sordariomycetes
6305	1	*Tolypocladium* sp.	92%, 99%	Outer layer	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6097	1	*Tolypocladium* sp.	100%, 96%	Inside/Out	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6098	1	*Hypocreales* sp	67%, 81%	Inside/Out		Hypocreales	Sordariomycetes
6102	1	*Metarhizium anisopliae*	47%, 87%	Inside/Out	Clavicipitaceae	Hypocreales	Sordariomycetes
6188	1	*Annulohypoxylon viridistratum*	95%, 99%	Outer layer	Hypoxylaceae	Xylariales	Sordariomycetes
6185	1	*Plectosphaerella cucumerina*	97%, 99%	Outer layer	Plectosphaerellaceae	Glomerellales	Sordariomycetes
6288, 6173	2	*Penicillium multicolor*	98%, 99%	Outer layer	Aspergillaceae	Eurotiales	Eurotiomycetes

6090	1	*Penicillium glabrum* CBS 125543	98%, 99%	Outer layer	Aspergillaceae	Eurotiales	Eurotiomycetes
6293	1	*Penicillium meleagrinum*	100%, 99%	Outer layer	Aspergillaceae	Eurotiales	Eurotiomycetes
6300	1	*Penicillium pulvillorum*	97%, 97%	Outer layer	Aspergillaceae	Eurotiales	Eurotiomycetes
6180	1	*Cyphellophora reptans* CBS 113.85	99%, 89%	Outer layer	Cyphellophoraceae	Chaetothyriales	Eurotiomycetes
6182	1	*Cladophialophora immunda* CBS 126871	98%, 97%	Outer layer	Herpotrichiellaceae	Chaetothyriales	Eurotiomycetes
6095, 6179, 6186, 6187	4	*Endomelanconiopsis* sp. CBS 353.97	97%, 97%	Outer layer	Botryosphaeriaceae	Botryosphaeriales	Dothideomycetes
6242	1	*Meyerozyma guilliermondii* CBS:12037	99%, 99%	Outer layer	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
6289	1	*Kodamaea ohmeri* CBS:2038	99%, 99%	Outer layer	Metschnikowiaceae	Saccharomycetales	Saccharomycetes
6246, 6249, 6251	3	*Debaryomyces nepalensis* CBS 2334	99%, 99%	Inside/Out	Debaryomycetaceae	Saccharomycetales	Saccharomycetes

C. bruneiensis nest 2017

Like *C. bruneiensis* nest 2015, the interior of *C. bruneiensis* 2017 were dominated by the black dimorphic fungi (~10^8/gram nest). Our study shows that a high genetic diversity of fungal symbionts is present in *C. bruneiensis* 2017 compared to nest 2015, mainly belong Chaetothyriales order. Some of these black fungi show the yeast-like form only when in the nest, but they grow in a filamentous form *in vitro* (*Figure 19).* The colony of strain *Chaetothyriales* sp. (TUCIM 6997) can switch to a yeasty form after three weeks of cultivation on PDA medium (Figure 20).

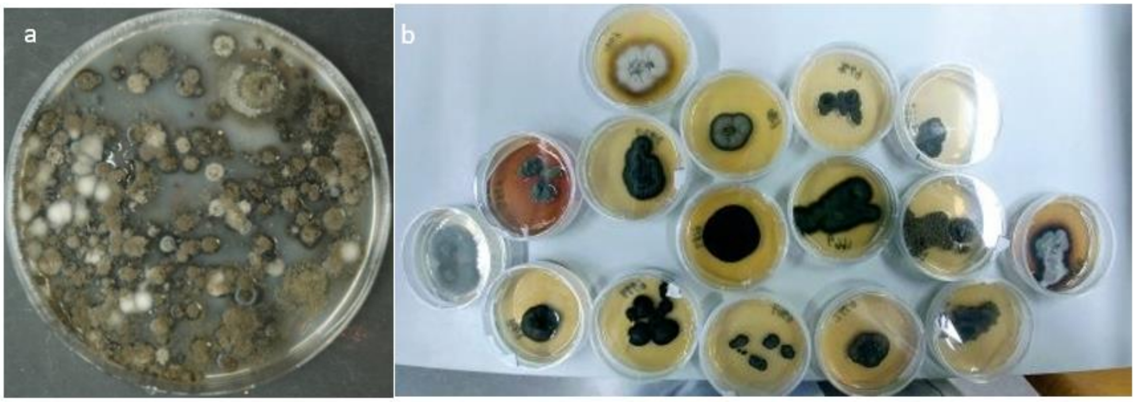


Figure 19 Fungi plate culture of C. bruneiensis *2015. a) is one-week culture plate of* C. bruneiensis *nest sample on PDA medium b) the pure cultures from the strains isolated from plate (a).*

Figure 20 Some of the fungi strains can switch from mycelial form to yeasty after few days of cultivation. Here in this plate the strain at the right side (TUCIM 7996) formed yeasty after one week of cultivation on PDA plate.

Morphology of the fungi from the *C. bruneiensis* nest were shown thick-walled, dark brown hyphae with individual and elongated to globose cells (Figure 21).

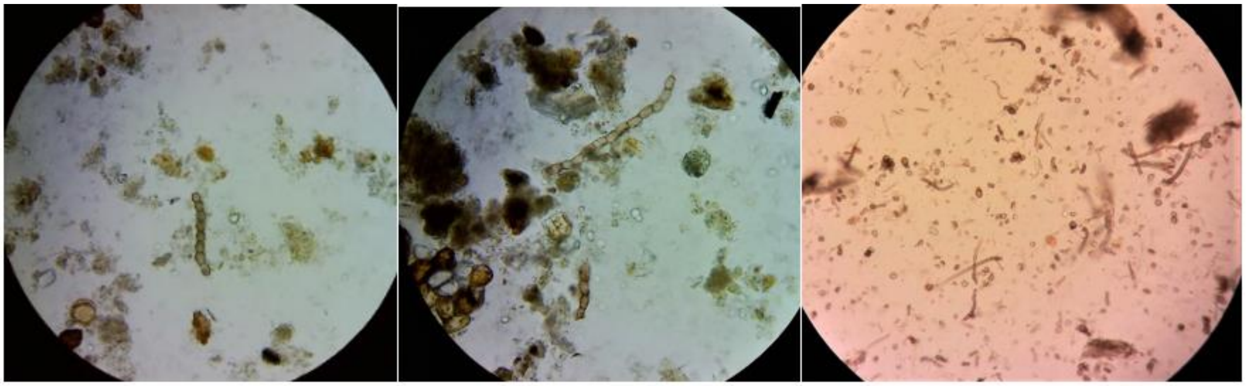


Figure 21 Fungi from C. bruneiensis *nest in microscopy*

Table 11 Fungi from of C. bruneiensis *nest-2017.* [1]*Basidiomycota*

		Identification	Cov/Ident	origin	Family	Order	Class
6332	1	*Tolypocladium album*	96%, 96%	Inside	Ophiocordycipitaceae	Hypocreales	Sordariomycetes
6975	1	*Trichoderma harzianum*	98%, 99%	Inside	Hypocreaceae	Hypocreales	Sordariomycetes
6984, 6985	2	*Schwanniomyces vanrijiae* CBS:3024	98%, 100%	Inside	Debaryomycetaceae	Saccharomycetales	Saccharomycetes
6986	1	*Chloridium virescens* CBS 126074	95%, 99%	Inside	Chaetosphaeriaceae	Chaetosphaeriales	Sordariomycetes
6989	1	*Pseudallescheria apiosperma*	99%, 99%	Inside	Microascaceae	Microascales	Sordariomycetes
6990	1	*Hawksworthiomyces crousii*	89%, 94%	Inside	Ophiostomataceae	Ophiostomatales	Sordariomycetes
7004, 7006	2	*Trichoderma* sp.	99%, 99%	Outer layer	Hypocreaceae	Hypocreales	Sordariomycetes
7008	1	*Xenoacremonium recifei* CBS 541.89	99%, 98%	Outer layer	Nectriaceae	Hypocreales	Sordariomycetes
6991	1	*Cladophialophora immunda*	99%, 91%	Inside	Herpotrichiellaceae	Chaetothyriales	Eurotiomycetes
6995	1	Chaetothyriales sp.	99%, 99%	Inside		Chaetothyriales	Eurotiomycetes
6996, 6997, 7002	3	Chaetothyriales sp.	98%, 98%	Inside		Chaetothyriales	Eurotiomycetes
6998	1	*Neophaeothecoidea proteae* CBS 114129	99%, 87%	Inside	Teratosphaeriaceae	Capnodiales	Dothideomycetes
7007	1	*Penicillium rubens*	98%, 100%	Outer layer	Aspergillaceae	Eurotiales	Eurotiomycetes
6999	1	Fumiglobus pieridicola UBC F23788	96%, 83%	Inside	Capnodiaceae	Capnodiales	Dothideomycetes
7001	1	*Anthopsis catenata* CBS 492.81	90%, 84%	Inside	Cyphellophoraceae	Chaetothyriales	Eurotiomycetes
7009	1	*Debaryomyces nepalensis* CBS 2334	98%, 99%	Outer layer	Saccharomycetaceae	Saccharomycetales	Saccharomycetes
7010	1	*Trichosporon dermatis* ATCC 20566	98%, 98%	Inside	Trichosporonaceae	Tremellales	Tremellomycetes [1]

The fungal diversity isolated from inside and outer layer of the MIT1 nest (*C. bruneiensis* 2017) were listed in (Table 11). The identification of these strains was based on ITS1-2 gene barcoding (Figure 22).

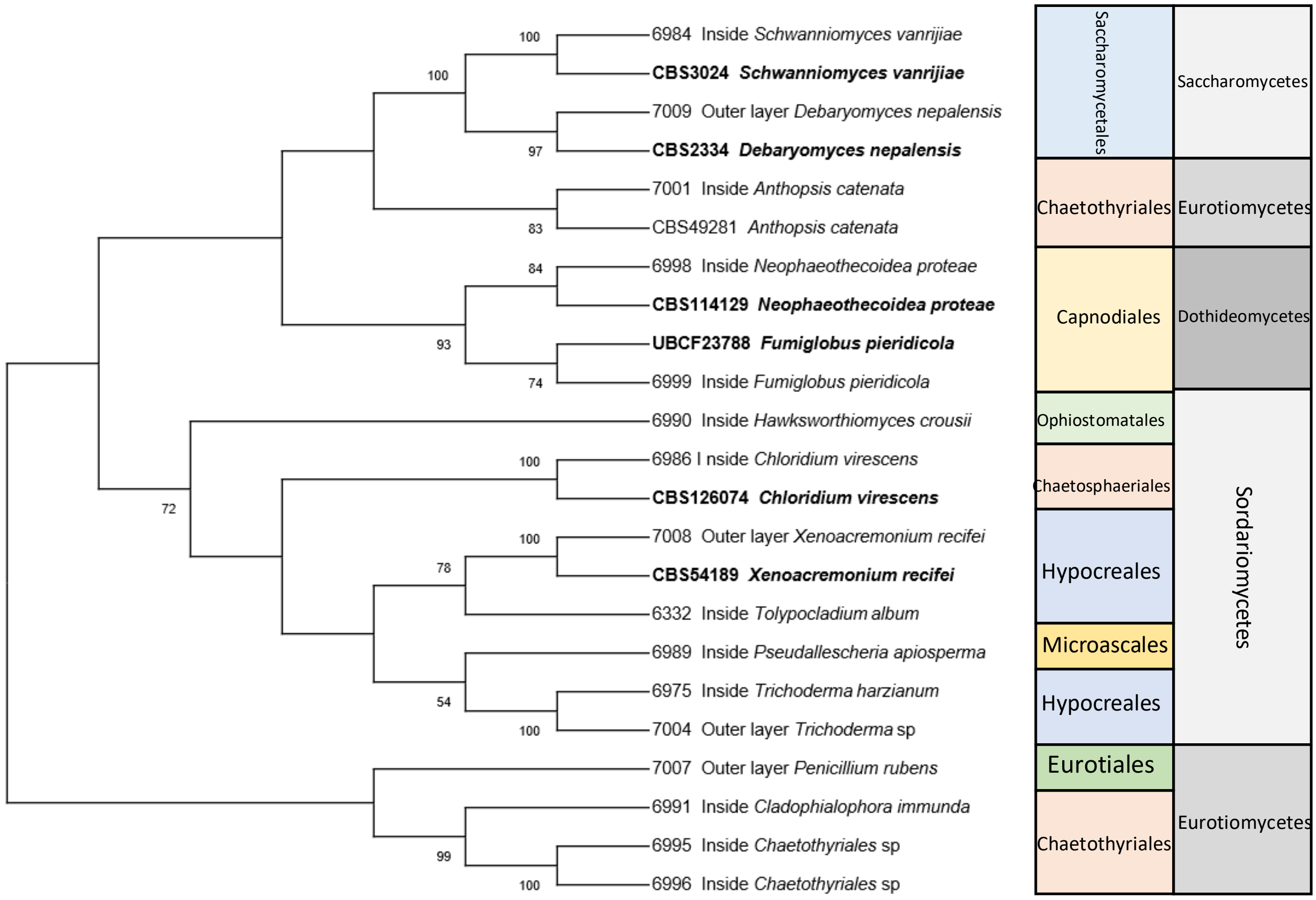


Figure 22 Tree of fungi from C. bruneiensis *nest-2017. References were shown as bold type.*

The outer surface of the both *C. bruneiensis* nest were dominated by opportunistic saprotrophic, potentially plant-pathogenic, and possibly entomopathogenic fungi from the yeasts belong to Saccharomycetaceae family, genera *Penicillium*, *Trichoderma*, *Fusarium*, and *Tolypocladium*, respectively.

In Figure 23 we compare the fungi species isolated from both *C. bruneiensis* nest 2017 and 2015. The black fungi from different classes were the most frequent in quantity and the most fungi groups inside both nests.

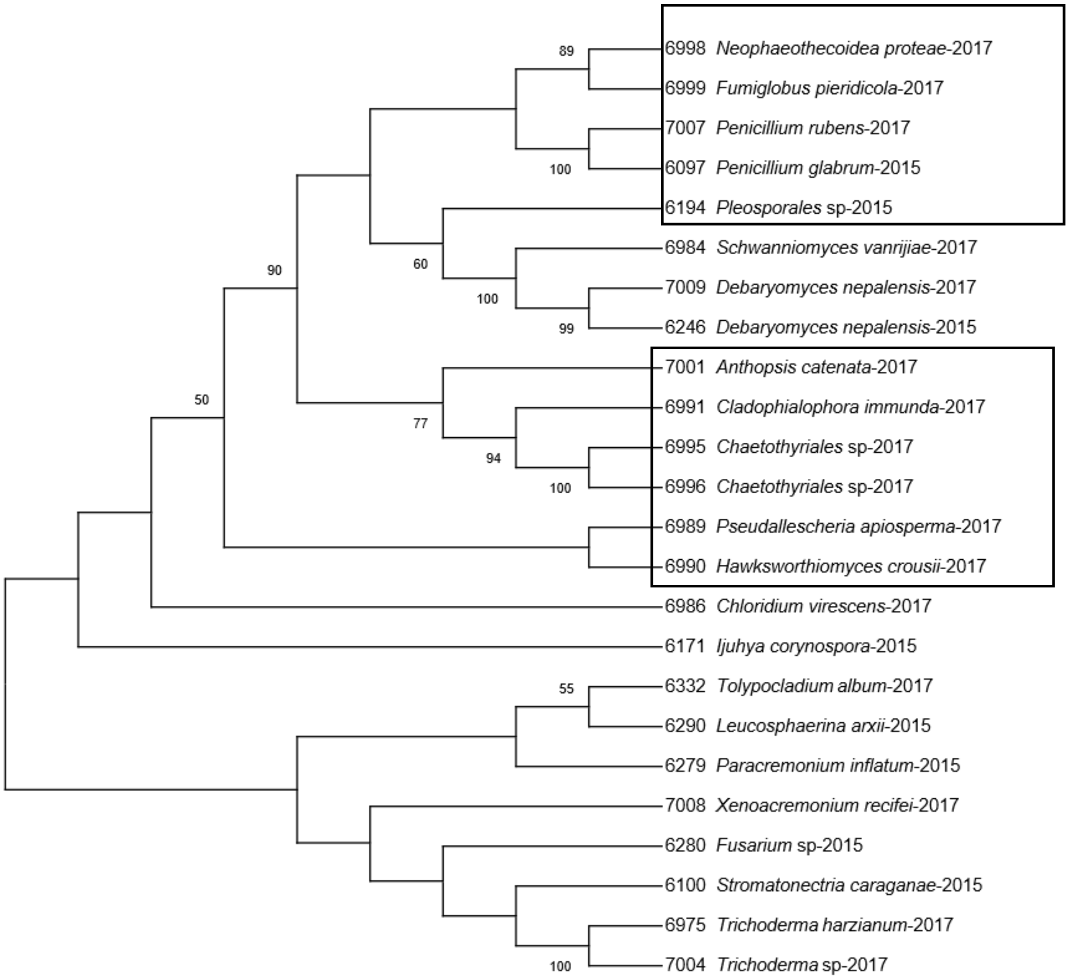


Figure 23 The fungi of the both C. bruneiensis *(2015& 2017) nest. The black fungi are framed.*

Presence of the black dimorphic fungi in the ant's nest is not a new finding. Several studies have shown the colonization of these carton fungi in different ant nests [68]. Black dimorphic fungi, newly described symbionts of the ant-microbe system. These groups of fungi are mostly known from a range of oligotrophic or other extreme environments. The members of this group exhibit a complex ecological versatility, and species are found in habitats characterized by extreme and adverse conditions, e.g. on rock surfaces in hot, arid climates, in toxic niches with hydrocarbons and heavy metals. Some genera produce budding cells or are entirely yeast-like, and therefore are often referred to as black yeasts (BY). Recent studies undescribed the black fungi from ant colonies that clustered in various orders, but mostly belong to of Chaetothyriales and recently been found in the symbiotic association with ants [67, 68]. However, the nature and the details of the association, as well as the taxonomic affiliation of Chaetothyriales, remained unknown. Most of strains of Chaetothyriales appear to be species new to science. Ants, the symbiotic nest bacteria and the host tree produce a large diversity of antimicrobial secondary metabolites such as phenolic and aromatic hydrocarbons [84], it has been suggested that BY might be naturally selected in ant nests because of their high resistance to xenobiotics or their ability to metabolize these chemical substances [67, 85, 86]. The nest chamber has few tiny entrances then there is almost no air circulation in the nest. Accumulation inside of the nest can be harmful to most of the fungi. [67, 85-87]

Conclusion

In this study, 524 fungal strains were examined. As the morphology of fungi alone cannot be used for a correct identification. Therefore, a molecular analysis method was preferred. ITS was used as a universal barcode and *tef1*-α was used for some *Trichoderma* species. Examining and aligning gene sequences with morphological and anatomical results gave a classification. DNA sequences of the ITS regions of each sample were obtained. The ITS region was compared with other published sequences via NCBI BLAST. The reliable results were found in GenBank Database and were chosen. The sequences were aligned via MAFFT. For phylogenetic inference, maximum parsimony analysis was used. A large part of 524 samples is composed of Ascomycota, while 14 samples belong to Basidiomycota and Mucoromycota. The strains were divided into groups according to their isolated area and phylogenetic trees were arranged.

The results showed that, leaves have huge biodiversity. In contrast, *C.explodens* ants' nest is less diverse. Generally, species from orders Hypocreales, Xylariales and Eurotiales dominate. More precisely, plant pathogens such as *Fusarium* spp., species of high biotechnological applications such as *Penicillium* sp. and *Trichoderma* sp. are abundant. The largest part of the isolated fungi belong to Hypocreales within the class Sordariomycetes. Hypocreales species are notable for their ability to derive nutrition from diverse nutrient sources such as plant materials, insects, or other fungi to causing infection in human and other mammals.

In our study, from all three tested nests (*C. explodens, C. bruneiensis* 2015 and *C. bruneiensis* 2017) we isolated 11 species of black dimorphic fungi belong to six orders. In the molecular phylogenetic analyses, the BY (black yeast) fungi from all tested nests were dispersed in different clades. The inside of *C. bruneiensis* nests were dominated BY. In*, C. bruneiensis* 2015 nest, one BY species were the dominant fungi in the nest (more than 99% of the cultivated fungi) but the population of the BY species in *C. bruneiensis* 2017 nest were diverse and contained 12 different species. Result of this work has shown that the diversity of BY species in the ant nests are not ant specific. In *C. explodens* nest, the BY fungi were in minority and seems that the BY don't have critical role for the hosted ants, or probably in that case the other type of symbiotic bacteria serve the role of the BY in the nest.

Outside part of the nest, forest soil and the plants phyllosphere are full of different saprotrophic and entomopathogenic fungi and the ants can transfer these fungi to their nest. But we only observed almost one type of the fungi inside of the nest.

The following studies should also include another regions for more specific results (f.e. *tef1*, *rpb*2 etc), the reliability of the sequences of genes to be used should be assured and different phylogenetic analysis should be performed. On the other hand, researches on the biotechnological potential of these studied species should be developed.

References

1. Baldwin, B.G., et al., *The ITS region of nuclear ribosomal DNA: a valuable source of evidence on angiosperm phylogeny.* Annals of the Missouri botanical garden, 1995: p. 247-277.
2. Hawksworth, D.L. and R. Lucking, *Fungal Diversity Revisited: 2.2 to 3.8 Million Species.* Microbiol Spectr, 2017. **5**(4).
3. Hawksworth, D.L., *The fascination of fungi: exploring fungal diversity.* Mycologist, 1997. **11**(1): p. 18-22.
4. Hawksworth, D.L., *The magnitude of fungal diversity: the 1· 5 million species estimate revisited.* Mycological research, 2001. **105**(12): p. 1422-1432.
5. Blackwell, M., *The Fungi: 1, 2, 3… 5.1 million species?* American journal of botany, 2011. **98**(3): p. 426-438.
6. Wu, B., et al., *Current insights into fungal species diversity and perspective on naming the environmental DNA sequences of fungi.* Mycology, 2019. **10**(3): p. 127-140.
7. Hyde, K.D., et al., *Thailand's amazing diversity: up to 96% of fungi in northern Thailand may be novel.* Fungal diversity, 2018. **93**(1): p. 215-239.
8. Seifert, K.A., *Progress towards DNA barcoding of fungi.* Molecular ecology resources, 2009. **9**: p. 83-89.
9. McLaughlin, D.J., et al., *The search for the fungal tree of life.* Trends in microbiology, 2009. **17**(11): p. 488-497.
10. Barr, D.J., *Evolution and kingdoms of organisms from the perspective of a mycologist.* Mycologia, 1992: p. 1-11.
11. Hawksworth, D., et al., *Dictionary of the fungi*. 1995.
12. Alexopoulos, C. and C. Mims, *Blackwell. M. 1996.* Introductory Mycology. 4th ed. John Wiley & Sons, New York, USA, 869pp.
13. Judd, W.S., et al., *Plant systematics*. 2002: Sinauer Sunderland.
14. Taylor, A., *Recent advances in our understanding of fungal ecology.* Coolia, 2008. **51**(4): p. 197-212.
15. Hibbett, D.S., et al., *A higher-level phylogenetic classification of the Fungi.* Mycological research, 2007. **111**(5): p. 509-547.
16. Jones, M.D., et al., *Validation and justification of the phylum name Cryptomycota phyl. nov.* IMA fungus, 2011. **2**(2): p. 173-175.
17. Powell, M.J. and P.M. Letcher, *6 Chytridiomycota 0 Chytridiomycota, Monoblepharidomycota, 0 Monoblepharidomycota and Neocallimastigomycota 0 Neocallimastigomycota*, in *Systematics and Evolution*. 2014, Springer. p. 141-175.
18. Spatafora, J.W., et al., *A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data.* Mycologia, 2016. **108**(5): p. 1028-1046.
19. McCarthy, C.G. and D.A. Fitzpatrick, *Multiple approaches to phylogenomic reconstruction of the fungal kingdom*, in *Advances in genetics*. 2017, Elsevier. p. 211-266.
20. Hebert, P.D., et al., *Biological identifications through DNA barcodes.* Proceedings of the Royal Society of London. Series B: Biological Sciences, 2003. **270**(1512): p. 313-321.
21. Vrijenhoek, R., *DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates.* Mol Mar Biol Biotechnol, 1994. **3**(5): p. 294-9.
22. Xu, J., *Fungal DNA barcoding.* Genome, 2016. **59**(11): p. 913-932.
23. Fiser Pecnikar, Z. and E.V. Buzan, *20 years since the introduction of DNA barcoding: from theory to application.* J Appl Genet, 2014. **55**(1): p. 43-52.

24. Wilson, J.J., *DNA barcodes for insects.* Methods Mol Biol, 2012. **858**: p. 17-46.
25. Group, C.P.W., et al., *A DNA barcode for land plants.* Proceedings of the National Academy of Sciences, 2009. **106**(31): p. 12794-12797.
26. Rossi-Tamisier, M., et al., *Cautionary tale of using 16S rRNA gene sequence similarity values in identification of human-associated bacterial species.* International journal of systematic and evolutionary microbiology, 2015. **65**(6): p. 1929-1934.
27. Stockinger, H., M. Kruger, and A. Schussler, *DNA barcoding of arbuscular mycorrhizal fungi.* New Phytol, 2010. **187**(2): p. 461-74.
28. Schoch, C.L., et al., *Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi.* Proceedings of the National Academy of Sciences, 2012. **109**(16): p. 6241-6246.
29. Druzhinina, I.S., et al., *An oligonucleotide barcode for species identification in Trichoderma and Hypocrea.* Fungal Genet Biol, 2005. **42**(10): p. 813-28.
30. Stielow, J.B., et al., *One fungus, which genes? Development and assessment of universal primers for potential secondary fungal DNA barcodes.* Persoonia: Molecular Phylogeny and Evolution of Fungi, 2015. **35**: p. 242.
31. White, T.J., et al., *Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics.* PCR protocols: a guide to methods and applications, 1990. **18**(1): p. 315-322.
32. Garnica, S., et al., *Determining threshold values for barcoding fungi: lessons from Cortinarius (Basidiomycota), a highly diverse and widespread ectomycorrhizal genus.* FEMS microbiology ecology, 2016. **92**(4).
33. James, T.Y., et al., *A molecular phylogeny of the flagellated fungi (Chytridiomycota) and description of a new phylum (Blastocladiomycota).* Mycologia, 2006. **98**(6): p. 860-871.
34. Lutzoni, F., et al., *Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits.* American journal of botany, 2004. **91**(10): p. 1446-1480.
35. Roger, A.J., et al., *An evaluation of elongation factor 1 alpha as a phylogenetic marker for eukaryotes.* Molecular biology and evolution, 1999. **16**(2): p. 218-233.
36. Baldauf, S.L. and W.F. Doolittle, *Origin and evolution of the slime molds (Mycetozoa).* Proceedings of the National Academy of Sciences, 1997. **94**(22): p. 12007-12012.
37. Kopchinskiy, A., et al., *TrichoBLAST: a multilocus database for Trichoderma and Hypocrea identifications.* Mycological research, 2005. **109**(6): p. 658-660.
38. Irinyi, L.M., G. Kövics, and E.M. Karaffa, *Classification of Phoma species using new phylogenetic marker.* 2006.
39. Tsang, C.-C., et al., *Taxonomy and evolution of Aspergillus, Penicillium and Talaromyces in the omics era–past, present and future.* Computational and Structural Biotechnology Journal, 2018.
40. Benson, D.A., et al., *GenBank.* Nucleic acids research, 2003. **31**(1): p. 23.
41. Nilsson, R.H., et al., *Taxonomic reliability of DNA sequences in public sequence databases: a fungal perspective.* PloS one, 2006. **1**(1): p. e59.
42. Nilsson, R.H., et al., *A software pipeline for processing and identification of fungal ITS sequences.* Source code for biology and medicine, 2009. **4**(1): p. 1.
43. Wheeler, D.L., et al., *Database resources of the national center for biotechnology information.* Nucleic acids research, 2006. **35**(suppl_1): p. D5-D12.
44. Gould, K., *Antibiotics: from prehistory to the present day.* Journal of Antimicrobial Chemotherapy, 2016. **71**(3): p. 572-575.
45. Atanasov, A.G., et al., *Discovery and resupply of pharmacologically active plant-derived natural products: A review.* Biotechnology advances, 2015. **33**(8): p. 1582-1614.
46. Strobel, G. and B. Daisy, *Bioprospecting for microbial endophytes and their natural products.* Microbiol. Mol. Biol. Rev., 2003. **67**(4): p. 491-502.

47. Aly, A., A. Debbab, and C. Chaidir, *Fifty years of drug discovery from fungi.* Fungal Diversity, 2011. **50**: p. 3-19.
48. Hiestand, P.C., et al., *Prolactin as a modulator of lymphocyte responsiveness provides a possible mechanism of action for cyclosporine.* Proceedings of the National Academy of Sciences, 1986. **83**(8): p. 2599-2603.
49. An, Z., *Handbook of industrial mycology*. 2004: CRC Press.
50. Keller, N.P., *Fungal secondary metabolism: regulation, function and drug discovery.* Nature reviews. Microbiology, 2019. **17**(3): p. 167-180.
51. Organization, W.H., *WHO global strategy for containment of antimicrobial resistance*. 2001, Geneva: World Health Organization.
52. Foster, J.W., *Chemical activities of fungi.* Chemical activities of fungi., 1949.
53. Nimchua, T., D.E. Eveleigh, and H. Punnapayak, *Screening of tropical fungi producing polyethylene terephthalate-hydrolyzing enzyme for fabric modification.* Journal of industrial microbiology & biotechnology, 2008. **35**(8): p. 843.
54. Chen, S., et al., *Cutinase: characteristics, preparation, and application.* Biotechnology advances, 2013. **31**(8): p. 1754-1767.
55. Schueffler, A. and T. Anke, *Fungal natural products in research and development.* Natural product reports, 2014. **31**(10): p. 1425-1448.
56. Higginbotham, S.J., et al., *Bioactivity of fungal endophytes as a function of endophyte taxonomy and the taxonomy and distribution of their host plants.* PloS one, 2013. **8**(9): p. e73192.
57. Clay, K., *Fungal endophytes of grasses: a defensive mutualism between plants and fungi.* Ecology, 1988. **69**(1): p. 10-16.
58. Kamiya, K., et al., *Phylogeny of PgiC gene in Shorea and its closely related genera (Dipterocarpaceae), the dominant trees in Southeast Asian tropical rain forests.* Am J Bot, 2005. **92**(5): p. 775-88.
59. Pio, D. and R. D'Cruz, *WWF: Borneo's Lost World: Newly Discovered Species on Borneo.* WWF Indonesia, Jakarta, 2005.
60. Primack, R.B. and P. Hall, *Biodiversity and Forest Change in Malaysian BorneoLong-term studies of trees provide insight on the conservation and management of Asian rainforests.* BioScience, 1992. **42**(11): p. 829-837.
61. Slik, J., et al., *A floristic analysis of the lowland dipterocarp forests of Borneo.* Journal of Biogeography, 2003. **30**(10): p. 1517-1531.
62. Slik, J.F., et al., *Environmental correlates for tropical tree diversity and distribution patterns in Borneo.* Diversity and Distributions, 2009. **15**(3): p. 523-532.
63. Davidson, D. and L. Patrell-Kim, *Tropical arboreal ants: Why so abundant?* 1996.
64. T. Ryder Wilkie, K., A. Mertl, and J. Traniello, *Species Diversity and Distribution Patterns of the Ants of Amazonian Ecuador*. Vol. 5. 2010.
65. Weiss, M.R., *Defecation behavior and ecology of insects.* Annu Rev Entomol, 2006. **51**: p. 635-61.
66. Defossez, E., et al., *Ant-plants and fungi: a new threeway symbiosis.* New Phytol, 2009. **182**(4): p. 942-9.
67. Teixeira, M.d.M., et al., *Exploring the genomic diversity of black yeasts and relatives (Chaetothyriales, Ascomycota).* Studies in mycology, 2017. **86**: p. 1-28.
68. Voglmayr, H., et al., *The diversity of ant-associated black yeasts: insights into a newly discovered world of symbiotic interactions.* Fungal Biology, 2011. **115**(10): p. 1077-1091.
69. Davidson, D., A.S. Kamariah, and J. Billen, *Histology of structures used in territorial combat by Borneo’s ‘exploding ants’*. Vol. 93. 2011.
70. Maschwitz, U. and E. Maschwitz, *Platzende Arbeiterinnen: Eine neue Art der Feindabwehr bei sozialen Hautflüglern.* Oecologia, 1974. **14**(3): p. 289-294.

71. Jones, T.H., et al., *The Chemistry of Exploding Ants, Camponotus SPP. (Cylindricus COMPLEX).* Journal of Chemical Ecology, 2004. **30**(8): p. 1479-1492.
72. Davidson, D.W., et al., *The Tropical Ant Mosaic in a Primary Bornean Rain Forest.* Biotropica, 2007. **39**(4): p. 468-475.
73. Laciny, A., et al., *Colobopsis explodens sp. n., model species for studies on "exploding ants" (Hymenoptera, Formicidae), with biological notes and first illustrations of males of the Colobopsis cylindrica group.* ZooKeys, 2018. **751**.
74. Smolik, M., et al., *rDNA variability assessed in PCR reactions of selected accessions of Acer.* Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 2011. **39**(1): p. 260-266.
75. Jaklitsch, W.M., et al., *Hypocrea voglmayrii sp. nov. from the Austrian Alps represents a new phylogenetic clade in Hypocrea/Trichoderma.* Mycologia, 2005. **97**(6): p. 1365-1378.
76. Zheng, L., et al., *Identification of a novel Alternaria alternata strain able to hyperparasitize Puccinia striiformis f. sp. tritici, the causal agent of wheat stripe rust.* Frontiers in microbiology, 2017. **8**: p. 71.
77. Vorholt, J.A., *Microbial life in the phyllosphere.* Nature Reviews Microbiology, 2012. **10**(12): p. 828.
78. Remus-Emsermann, M.N. and R.O. Schlechter, *Phyllosphere microbiology: at the interface between microbial individuals and the plant host.* New Phytologist, 2018. **218**(4): p. 1327-1333.
79. Bamisile, B.S., et al., *Fungal endophytes: beyond herbivore management.* Frontiers in microbiology, 2018. **9**: p. 544.
80. Suryanarayanan, T., et al., *Fungal endophytes and bioprospecting.* Fungal biology reviews, 2009. **23**(1-2): p. 9-19.
81. Whitaker, B.K., H.L. Reynolds, and K. Clay, *Foliar fungal endophyte communities are structured by environment but not host ecotype in Panicum virgatum (switchgrass).* Ecology, 2018. **99**(12): p. 2703-2711.
82. Dastogeer, K.M., et al., *Host specificity of endophytic mycobiota of wild Nicotiana plants from arid regions of Northern Australia.* Microbial ecology, 2018. **75**(1): p. 74-87.
83. Liu, J., et al., *Host identity and phylogeny shape the foliar endophytic fungal assemblages of Ficus.* Ecology and Evolution, 2019.
84. Berasategui, A., et al., *Potential applications of insect symbionts in biotechnology.* Applied microbiology and biotechnology, 2016. **100**(4): p. 1567-1577.
85. Jones, T., et al., *The chemistry of exploding ants, Camponotus spp.(cylindricus complex).* Journal of chemical ecology, 2004. **30**(8): p. 1479-1492.
86. Zhao, J., et al., *Isolation and identification of black yeasts by enrichment on atmospheres of monoaromatic hydrocarbons.* Microb Ecol, 2010. **60**(1): p. 149-56.
87. Deng, Y. and S. Lu, *Biosynthesis and Regulation of Phenylpropanoids in Plants*. Vol. 36. 2017. 1-34.

Curriculum Vitae

H. Oya Akyıldız

♀ 20.06.1991

Albertplatz 5/2/1 1080 Vienna
oyaaky@gmail.com

Turkey

Education

Master of Science (2016- 2019)

Vienna Technology University-Technical Chemistry – Biotechnology and Bioanalytic

"Microbial community in the high canopy of the Bornean tropical rainforest: molecular diversity"

Bachelor of Science (2009-2014)

Istanbul Technical University- Chemistry

Thesis: "Alkylation of Active Methylene Compounds in Acidic Medium"

Mustafa Saffet Anatolian High School (2005-2009)

Work experience

Microbiology Intern April 2017-April 2018

Technische Universität Wien/ Research Group for Microbiology and Applied Genomics

Microbiology Intern 2017 Summer

Istanbul University/ Fundamental and Industrial Microbiology Laboratory Intern

Production Intern July 2013

Bayer – Pharmaceuticals

Quality Control Intern June 2013

Era Pharma Solutions

Quality Control Intern June 2012

Biofarma Pharmaceuticals

Qualifications

Language
English (Advanced), Deutsch (B2), Turkish (native), Russian (Beginner)
Interests
Tennis, Piano, Travelling, Puzzles

Attachment 1

				IDENTIFICATION															
					Putative identification														
Sample ID	**Marker**	**Primers**	**Sequence**	**length, bp**	***Species***	***Genus***	Order	Class	Taxon name	Strain ID	GB Accession Number	Similarity, %	E-value	Coverage, %	Number of SNPs	Substrate	Biogeographic region	References	Ref Sequence
TU CIM 5782	ITS1&2	SR6R	ATTATTGAATAAA	669	*Hypholoma* sp.	Hypholoma	Agaricales	Agaricomycet	*Hypholoma fasciculare*	CCF3827	FJ430716	98.95%	0,00E+00	100%	7			Hujslova et al 2010	GAACCTGCGGAAGGATC
TU CIM 5800	ITS1&2	SR6R	CATTATTGAATAA	678	*Hypholoma* sp.	Hypholoma	Agaricales	Agaricomycet	*Hypholoma fasciculare*	CCF3827	FJ430716	98.82%	0	99%	8			Hujslova et al 2010	GAACCTGCGGAAGGATC
TU CIM 5805	ITS1&2	SR6R	ATTATTGAATAAA	677	*Hypholoma* sp.	Hypholoma	Agaricales	Agaricomycet	*Hypholoma fasciculare*	CCF3827	FJ430716	98.96%	0	99%	7			Hujslova et al 2010	GAACCTGCGGAAGGATC
TU CIM 5778	ITS1&2	SR6R	TAACGAATCAAA	617	*Schizophyllum commune*	Schizophyllu	Agaricales	Agaricomycet	*Schizophyllum commune*	15R-5-F01	KX958030	99.51%	0	99%	3	sediment bel	Japan: Shimo	Liu et al 2016	ACGAATCAAACAAGTTC
TU CIM 5791	ITS1&2	SR6R	CAAGTTCATCTTG	605	*Schizophyllum commune*	Schizophyllu	Agaricales	Agaricomycet	*Schizophyllum commune*	15R-5-F01	KX958030	99.83%	0	99%	1	sediment bel	Japan: Shimo	Liu et al 2016	ACGAATCAAACAAGTTC
TU CIM 5775	ITS1&2	SR6R	TTGAATGAACTTG	688	*Kuehneromyces mutabilis*	Kuehneromyc	Agaricales	Agaricomycet	*Kuehneromyces mutabilis*	CBS 209.31	MH855190	95.92%	0	98%	28			Vu et al 2019	AACAAGGTTTCCGTAGG
TU CIM 5789	ITS1&2	SR6R	AACGGGTTGTAG	607	*Phlebia acerina*	Phlebia	Polyporales	Agaricomycet	*Phlebia acerina*	FBCC345	LN611083	99.01%	0	99%	6			Kuuskeri et al 2015	AAGGATCATTATCGAGTT
TU CIM 5790	ITS1&2	SR6R	CATTATCGAGTTT	631	*Phlebia acerina*	Phlebia	Polyporales	Agaricomycet	*Phlebia acerina*	FBCC345	LN611083	99.20%	0	98%	5			Kuuskeri et al 2015	AAGGATCATTATCGAGTT
TU CIM 6241	ITS1&2	SR6R	ATTAGTGATATAG	853	*Rhodotorula* sp.	Rhodotorula	Sporidiobolale	Microbotryom	*Rhodotorula* sp.	Y11	DQ186608	100%	0	99%	0			Yuan et al 2005	ATCATTAGTGATATAGG
TU CIM 6208	ITS1&2	SR6R	NNTAATTTGAGT	619	*Mucor irregularis*	Mucor	Mucorales	Mucoromycet	*Mucor irregularis*	5012	HM639972	98.51%	0	96%	9			Wang et al 2011	GAAAAAAGTTTGAGTTG
TU CIM 7023	ITS1&2	SR6R	TGTTGCTCTGCAA	454	*Cryptococcus* sp.	Cryptococcus	Tremellales	Tremellomyce	*Cryptococcus* sp.	TMS-2011	HQ631024	98.65%	0	97%	1			Shrestha et al 2011	TCTTGGTCATTTAGAGGA
TU CIM 7024	ITS1&2	SR6R	NCATTAGTGATTG	520	*Trichosporon dermatis*	Cutaneotrich	Trichosporon	Tremellomyce	*Trichosporon dermatis*	ATCC 20566	HM802130	99.42%	0	98%	3			Gujjari et al 2011	GTTTCCGTAGGTGAACCT
TU CIM 7018	ITS1&2	SR6R	TTAGTGAATTGCT	507	*Trichosporon dermatis*	Cutaneotrich	Trichosporon	Tremellomyce	*Trichosporon dermatis*	ATCC 20566	HM802130	100%	0	99%	0			Gujjari et al 2011	GTTTCCGTAGGTGAACCT
TU CIM 7010	ITS1&2	SR6R	TTAGTGAATTGCT	518	*Trichosporon dermatis*	Cutaneotrich	Trichosporon	Tremellomyce	*Trichosporon dermatis*	ATCC 20566	HM802130	98.90%	0	98%	1			Gujjari et al 2011	GTTTCCGTAGGTGAACCT
TU CIM 5492	ITS1&2	SR6R	TTACCGAGTTTAC	581	*Stromatonectria caraganae*	Stromatonect	Hypocreales	Sordariomyce	*Stromatonectria caraganae*	CBS 125579	HQ112288	99%	3e-174	86.39%	81	*Colutea arborescens*		Jaklitsch et al 2010	CTACTACCGATTGAATGG
TU CIM 5628	ITS1&2	SR6R	ATTATCGAGTTCT	563	*Ovicillium subglobosum*	Ovicillium	Hypocreales	Sordariomyce	*Ovicillium subglobosum*	CBS_403.89	KU382207	98.58%	0	87%	7	Forest soil		Zare et al 2016	ACGAGGATACTTATCGA
TU CIM 5630	ITS1&2	SR6R	CAACTCCCAAACC	564	*Stromatonectria caraganae*	Stromatonect	Hypocreales	Sordariomyce	*Stromatonectria caraganae*	CBS 125579	HQ112288	86.13%	2e-167	100%	81	*Colutea arborescens*		Jaklitsch et al 2010	CTACTACCGATTGAATGG
TU CIM 6100	ITS1&2	SR6R	TTACCGAGTTTAC	624	*Stromatonectria caraganae*	Stromatonect	Hypocreales	Sordariomyce	*Stromatonectria caraganae*	CBS 125579	HQ112288	85.62%	6e-172	95%	88	*Colutea arborescens*		Jaklitsch et al 2011	CTACTACCGATTGAATGG
TU CIM 6168	ITS1&2	SR6R	TCCCCGCCCCGGC	506	*Ijuhya corynospora*	Ijuhya	Hypocreales	Sordariomyce	*Ijuhya corynospora*	CBS 342.77	KY607539	90.44%	1e-144	79%	39	*Phormium ter*	New Zealand	Ashrafi et al 2017	GTACACACCGCCCGTCG
TU CIM 6171	ITS1&2	SR6R	CATTACCGAGTTC	582	*Ijuhya corynospora*	Ijuhya	Hypocreales	Sordariomyce	*Ijuhya corynospora*	CBS 342.77	KY607539	85.62%	4e-163	99%	85	*Phormium ter*	New Zealand	Ashrafi et al 2017	GTACACACCGCCCGTCG
TU CIM 5949	ITS1&2	SR6R	TTACCGAGTTTAC	561	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.74%	7e-176	99%	69	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5954	ITS1&2	SR6R	TTACCGAGTTTAC	558	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.79%	6e-177	100%	68	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5957	ITS1&2	SR6R	CCGAGTTTACNAC	570	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	3.42%	8e-151	99%	95	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5960	ITS1&2	SR6R	CCAAACCCTTTGT	599	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	84.85%	1e-154	100%	85	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5978	ITS1&2	SR6R	ATTACCGAGTTTA	567	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.79%	6,00E-177	98%	69	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5983	ITS1&2	SR6R	TTACCGAGTTTAC	569	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.65%	3,00E-179	99%	71	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5984	ITS1&2	SR6R	NCATTACCGAGTT	569	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.61%	1,00E-178	99%	71	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6002	ITS1&2	SR6R	CAACTCCCAAACC	554	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.50%	9,00E-170	98%	69	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6066	ITS1&2	SR6R	ATTACCGAGTTTA	573	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.67%	3,00E-179	99%	71	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6073	ITS1&2	SR6R	ATTACCGAGTTTA	568	*Pochonia* sp.	Pochonia sp.	Hypocreales	Sordariomyce	*Pochonia* sp.	CBS 892.72	KM231844	87.79%	6,00E-177	98%	69	*Arcyria sp.*	Netherlands	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5844	ITS1&2	SR6R	ACGAGTTATACAA	587	*Simplicillium lamellicola*	Simplicillium	Hypocreales	Sordariomyce	*Simplicillium lamellicola*	CBS 454.70	MH859793	99.65%	0	97%	2		USA: Georgia	Vu et al 2019	AACAAGGTCTCCGTTGG
TU CIM 5488	ITS1&2	SR6R	CCGAGTTTACAAC	591	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	T9	MG738308	99.66%	0	99%	2	soil	India	Sharma et al 2018	CTTCCGTAGGTGAACCTG
TU CIM 5497	ITS1&2	SR6R	CATTACCGAGTTT	597	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	Cef-B4	KX960805	99.83%	0	99%	1		China	Shan,T 2016	GGAAGTAAAAGTCGTAA
TU CIM 5500	ITS1&2	SR6R	ATTACCGAGTTTA	608	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	TV96	KP263604	99.66%	0	97%	2		Venezuela: B	Pavone et al 2015	TTGGTGACCAGCGGAGG
TU CIM 5505	ITS1&2	SR6R	ATTACCGAGTTTA	603	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	TV96	KP263604	99.66%	0	98%	2		Venezuela: B	Pavone et al 2015	TTGGTGACCAGCGGAGG
TU CIM 5501	ITS1&2	SR6R	CCGAGTTTACAAC	580	*Trichoderma strigosum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma strigosum*	DAOM 234231	EU280114	99.13%	0	99%	5		Guatemala	Hoyos-Carvajal et al 200	TGGAAGTAAAAGTCGTA
TU CIM 5502	ITS1&2	SR6R	ATTACCGAGTTTA	579	*Trichoderma* sp	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp	DAOM 231245	EU280117	99.48%	0	98%	3		Mexico	Hoyos-Carvajal et al 201	TGGAAGTAAAAGTCGTA
TU CIM 5569	ITS1&2	SR6R	TTACCGAGTTTAC	593	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.66%	0	100%	2	coffee plant r	Ethiopia	Mulaw et al 2010	GACATTACCGAGTTTACA
TU CIM 5570	ITS1&2	SR6R	CAACTCCCAAACC	599	*Trichoderma sinuosum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sinuosum*	C.P.K. 2011	FJ860840	99.66%	0	97%	2			Jaklitsch,W.M 2009	CATTACCGAGTTTACAAC
TU CIM 5571	ITS1&2	SR6R	TTACCGAGTTTAC	579	*Trichoderma koningiopsis*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis*	SPXX-FS18	KR296904	99%	0	100%	0	soil	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA
TU CIM 5640	ITS1&2	SR6R	TACCGAGTTTACA	602	*Trichoderma aggregatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma aggregatum*	HMAS 248863	NR_154582	98.29%	0	96%	10			Robbertse et al 2017	CCGAGTTTACAACTCCCA
TU CIM 5642	ITS1&2	SR6R	AACTCCCAAACCC	582	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.31%	0	99%	4	coffee plant r	Ethiopia	Mulaw et al 2010	GACATTACCGAGTTTACA
TU CIM 5643	ITS1&2	SR6R	ACCGAGTTTACAA	582	*Trichoderma* sp.	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp.	17 BRO-2013	KF367564	99.17%	0	100%	5	untreated dri	Portugal	Oliveira et al 2013	ACTCGGTCATTTAGAGG
TU CIM 5649	ITS1&2	SR6R	TTACCGAGTTTAC	580	*Trichoderma koningiopsis*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis*	SPXX-FS18	KR296904	99.83%	0	99%	1	soil	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA
TU CIM 5744	ITS1&2	SR6R	CCGAGTTTACAAC	577	*Trichoderma koningiopsis*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis*	SPXX-FS18	KR296904	99.83%	0	99%	1	soil	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA
TU CIM 5745	ITS1&2	SR6R	ATTACCGAGTTTA	581	*Trichoderma koningiopsis*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis*	SPXX-FS18	KR296904	99.83%	0	99%	1	soil	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA
TU CIM 5746	ITS1&2	SR6R	ATTACCGAGTTTA	581	*Trichoderma koningiopsis*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis*	SPXX-FS18	KR296904	99.83%	0	99%	1	soil	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA

TU CIM 5747	ITS1&2	SR6R	ATTACCGAGTTTA	581	*Trichoderma koningiopsis*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis*	SPXX-FS18	KR296904	99.83%	0	99%	1	soil	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA
TU CIM 6003	ITS1&2	SR6R	CAACTCCCAAACC	593	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	TUB F-834	AY857228	99.49%	0	99%	3			Druzhinina et al 2005	TTTACAACTCCCAAACCC
TU CIM 6005	ITS1&2	SR6R	ATTACCGAGTTTA	148	*Trichoderma* sp.	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp.	CK850	KU702333	97.89%	2e-61□	95%□	3	soil baiting w	USA: North C	Hesse et al 2016	AGGGATCATTACCGAGT
TU CIM 6011	ITS1&2	SR6R	CAACTCCCAAACC	591	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.66%	0	99%	2	coffee plant r	Ethiopia	Mulaw et al 2010	GACATTACCGAGTTTACA
TU CIM 6051	ITS1&2	SR6R	CAACTCCCAAACC	590	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.66%	0	99%	2	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6273	ITS1&2	SR6R	CAACTCCCAAACC	595	*Trichoderma* sp.	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp.	SQR037	GQ497168	100%	0	97%	0			Yang et al 2011	AATTCGTTAGGGTGTACC
TU CIM 6033	ITS1&2	SR6R	TTACCGAGTTTAC	602	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.67%	0	99%	2	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6013	ITS1&2	SR6R	ACTCCCAAACCCA	589	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.66%	0	99%	2	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6036	ITS1&2	SR6R	NCATTACCGAGTT	612	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99%	0	98%	6	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6049	ITS1&2	SR6R	ACCGAGTTTACAA	597	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.16%	0	99%	5	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6039	ITS1&2	SR6R	TTACCGAGTTTAC	606	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.67%	0	99%	2	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6044	ITS1&2	SR6R	GTCATTACCGAGT	610	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.50%	0	98%	3	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6041	ITS1&2	SR6R	ACAACTCCCAAAC	595	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.32%	0	98%	4	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6042	ITS1&2	SR6R	GASSAACCAAAAC	502	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	TUB F-947	EF593404	97.33%	0	97%	13			Nagy et al 2007	AATCCCAATCGTGAGAC
TU CIM 6048	ITS1&2	SR6R	ANGGTGAACCATA	375	*Trichoderma atroviride*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma atroviride*	ZNAF13	KR868399	100%	0	99%	0	Aquaculture f	China	Saravanakumar et al 201	TTGAAGTAAAAAATCGT
TU CIM 6058	ITS1&2	SR6R	CATTACCGAGTTT	600	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	3TSM2	EU871018	99.67%	0	99%	2			Zachow et al 2009	AGGACATTACCGAGTTT
TU CIM 6050	ITS1&2	SR6R	ACTCCCAAACCCA	594	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.49%	0	98%	3	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6059	ITS1&2	SR6R	ACAACTCCCAAAC	588	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	TUB F-1005	AY857234	99.49%	0	100%	3			Druzhinina et al 2005	TTTACAACTCCCAAACCC
TU CIM 6063	ITS1&2	SR6R	CATTACCGAGTTT	159	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CBS 243.71	MH860095	100.00%	2e-72□	96%□	0		Switzerland	Vu et al 2019	ACACCGGAAGTAATAAA
TU CIM 6072	ITS1&2	SR6R	AACTCCCAAACCC	593	*Trichoderma* sp.	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp.	BRO-2013	KF367525	98.46%	0	98%	9	untreated dri	Portugal	Oliveira et al 2013	GGGCAACTACCACTCAG
TU CIM 6174	ITS1&2	SR6R	TACCGAGTTTACA	587	*Trichoderma virens*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma virens*	JIXX-FM26	KR296867	99.83%	0	99%	1	mushroom su	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA
TU CIM 6297	ITS1&2	SR6R	CAACTCCCAAACC	581	*Trichoderma virens*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma virens*	TR039	HQ608079	99.83%	0	98%	1	*Trachymyrme*	USA: Texas	Rodrigues et al 2011	GGAAGTAAAAGTCGTAA
TU CIM 6191	ITS1&2	SR6R	ATTACCGAGTTTA	595	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	CPK 2616	FJ412026	99.49%	0	99%	3	coffee plant r	Ethiopia	Mulaw et al 2011	GACATTACCGAGTTTACA
TU CIM 6230	ITS1&2	SR6R	TTACTGAGTGTTA	551	*Acremonium* sp.	Acremonium	Hypocreales	Sordariomyce	*Acremonium* sp.	G246	KM215633	91.02%	0	100%	50	milk thistle		Raja et al 2015	TTAACTCAGAACAGGTA
TU CIM 6975	ITS1&2	SR6R	TTACCGAGTTTAC	609	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	3TSMC3	EU871021	99.83%	0	98%	1			Zachow et al 2009	GGGACATTACCGAGTTT
TU CIM 6979	ITS1&2	SR6R	ATTACCGAGTTTA	610	*Trichoderma* sp.	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp.	AE-2013	KF746133	99.01%	0	99%	6	*Bradypus vari*	Panama	Higginbotham et al 2014	TTACCGAGTTTACAACTC
TU CIM 6980	ITS1&2	SR6R	TACCGAGTTTACA	593	*Trichoderma* sp.	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp.	AE-2013	KF746133	99.33%	0	100%	4	*Bradypus vari*	Panama	Higginbotham et al 2014	TTACCGAGTTTACAACTC
TU CIM 6981	ITS1&2	SR6R	TCATTACCGAGTT	607	*Trichoderma virens*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma virens*	JIXX-FM26	KR296867	99.33%	0	97%	1	mushroom su	Singapore	Ottenheim et al 2015	CTGCGGAGGGATCATTA
TU CIM 7004	ITS1&2	SR6R	TTACCGAGTTTAC	609	*Trichoderma* sp.	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma* sp.	AE-2013	KF746133	99.50%	0	99%	3	*Bradypus vari*	Panama	Higginbotham et al 2014	TTACCGAGTTTACAACTC
TU CIM 7006	ITS1&2	SR6R	CATTACCGAGTTT	589	*Trichoderma hamatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma hamatum*	TR090	HQ608116	98.09%	0	97%	11	*Trachymyrme*	USA: Texas	Rodrigues et al 2011	GGAAGTAAAAGTCGTAA
TU CIM 6309	ITS1&2	SR6R	TTACCGAGTTTAC	584	*Trichothecium ovalisporum*	Trichothecium	Hypocreales	Sordariomyce	*Trichothecium ovalisporum*	DAOM 186447	NR_111321	94.85%	0	96%	29	*Megachile rotundata*		Schoch et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 5490	ITS1&2	SR6R	NCATTACCGAGTT	577	*Trichothecium ovalisporum*	Trichothecium	Hypocreales	Sordariomyce	*Trichothecium ovalisporum*	DAOM 186447	NR_111321	94.87%	0	96%	29	*Megachile rotundata*		Schoch et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 5493	ITS1&2	SR6R	CACAAACTCCCAA	561	*Trichothecium ovalisporum*	Trichothecium	Hypocreales	Sordariomyce	*Trichothecium ovalisporum*	DAOM 186447	NR_111321	95.25%	0	96%	26	*Megachile rotundata*		Schoch et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 5629	ITS1&2	SR6R	TTATCGAGTTATT	551	*Leptobacillium leptobactrum*	Leptobacillium	Hypocreales	Sordariomyce	*Leptobacillium leptobactrum*	CBS 748.73	EF641867	99.63%	0	97%	2	living lepidop	Ghana	Zare et al 2008	ACGGGATATTATCGAGT
TU CIM 5765	ITS1&2	SR6R	CATTACCGAGTTT	582	*Trichothecium ovalisporum*	Trichothecium	Hypocreales	Sordariomyce	*Trichothecium ovalisporum*	DAOM 186447	NR_111321	94.87%	0	96%	29	*Megachile rotundata*		Schoch et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 5846	ITS1&2	SR6R	CAAACTCCCAACC	558	*Trichothecium ovalisporum*	Trichothecium	Hypocreales	Sordariomyce	*Trichothecium ovalisporum*	DAOM 186447	NR_111321	95.25%	0	96%	29	*Megachile rotundata*		Schoch et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 6091	ITS1&2	SR6R	ACAAACTCCAAAC	513	*Leucosphaerina arxii*	Leucosphaerina	Hypocreales	Sordariomyce	*Leucosphaerina arxii*	CBS 737.84	NR_145040	88.38%	2e-171□	99%	61		USA	Giraldo et al 2012	TTATAGAGTCTTCTGAAC
TU CIM 6092	ITS1&2	SR6R	TTATAGAGTTACA	521	*Leucosphaerina arxii*	Leucosphaerina	Hypocreales	Sordariomyce	*Leucosphaerina arxii*	CBS 737.84	NR_145040	88.13%	1e-173□	100%	64		USA	Giraldo et al 2012	TTATAGAGTCTTCTGAAC
TU CIM 6290	ITS1&2	SR6R	CATTATAGAGTTA	520	*Leucosphaerina arxii*	Leucosphaerina	Hypocreales	Sordariomyce	*Leucosphaerina arxii*	CBS 737.84	NR_145040	88.22%	4e-173□	99%	63		USA	Giraldo et al 2012	TTATAGAGTCTTCTGAAC
TU CIM 6308	ITS1&2	SR6R	CATTATAGAGTCT	527	*Leucosphaerina arxii*	Leucosphaerina	Hypocreales	Sordariomyce	*Leucosphaerina arxii*	CBS 737.84	NR_145040	89.34%	0	99%	58		USA	Giraldo et al 2012	TTATAGAGTCTTCTGAAC
TU CIM 6317	ITS1&2	SR6R	CAAACTCCAAACC	513	*Leucosphaerina arxii*	Leucosphaerina	Hypocreales	Sordariomyce	*Leucosphaerina arxii*	CBS 737.84	NR_145040	88.40%	4e-172□	99%	61		USA	Giraldo et al 2012	TTATAGAGTCTTCTGAAC
TU CIM 5633	ITS1&2	SR6R	CAAACTCCAAACC	513	*Leucosphaerina arxii*	Leucosphaerina	Hypocreales	Sordariomyce	*Leucosphaerina arxii*	CBS 737.84	NR_145040	88.40%	5,00E-172	99%	61		USA	Giraldo et al 2012	TTATAGAGTCTTCTGAAC
TU CIM 6097	ITS1&2	SR6R	TGTGAACATACCT	512	*Tolypocladium* sp.	Tolypocladium	Hypocreales	Sordariomyce	*Tolypocladium* sp.	DS35	KY432335	96.32%	0	100%	19	roots		Wang et al 2017	TGCGGTAGTTACTCCTCC
TU CIM 6098	ITS1&2	SR6R	GNNATTACCGAGT	621	*Hypocreales* sp.		Hypocreales	Sordariomyce	*Hypocreales* sp.	1b0852P152CC6	JQ411375	81.50%	1,00E-88	67%	79	*marine spong*	Panama	Bolanos et al 2015	CTCCCAAACCCCTGTGAA
TU CIM 6099	ITS1&2	SR6R	NCATTACCGAGTT	580	*Unclear*														
TU CIM 6102	ITS1&2	SR6R	CCGAGTTTTCTGA	425	*Metarhizium anisopliae*	Metarhizium	Hypocreales	Sordariomyce	*Metarhizium anisopliae*	MaGD58	MH483706	87.19%□	7,00E-65	47%	26		China	Niu et al 2019	GGGGAATCGGTTCCACT
TU CIM 6165	ITS1&2	SR6R	CATTACCGAGTTT	613	*Unclear*														
TU CIM 6169	ITS1&2	SR6R	CATTACCGAGTTT	569	*Tolypocladium inflatum*	Tolypocladium	Hypocreales	Sordariomyce	*Tolypocladium inflatum*	ANM200T9ZM1I	JF796050	99.10%	0	97%	5	*Haliclona* sp.		Caballero-George et al 20	ATTACCGAGTTTTCACTC
TU CIM 6177	ITS1&2	SR6R	NCATTACCGAGTT	561	*Tolypocladium inflatum*	Tolypocladium	Hypocreales	Sordariomyce	*Tolypocladium inflatum*	ANM200T9ZM1I	JF796050	99.10%	0	98%	5	*Haliclona* sp.		Caballero-George et al 20	ATTACCGAGTTTTCACTC
TU CIM 6178	ITS1&2	SR6R	ATTACCGAGTTAT	560	*Tolypocladium inflatum*	Tolypocladium	Hypocreales	Sordariomyce	*Tolypocladium inflatum*	ANM200T9ZM1I	JF796050	95.88%	0	98%	23	*Haliclona* sp.		Caballero-George et al 20	ATTACCGAGTTTTCACTC

TU CIM 6285	ITS1&2	SR6R	TTACCGAGTTATC	574	*Tolypocladium album*	Tolypocladiun	Hypocreales	Sordariomyce	*Tolypocladium album*	BH-06	LC386577	97.62%	0	95%	13	soil	South Korea	Das et al 2018	TGCGGAGGGATCATTAC
TU CIM 6294	ITS1&2	SR6R	CAACTCCCAAACC	565	*Tolypocladium* sp.	Tolypocladiun	Hypocreales	Sordariomyce	*Tolypocladium* sp.	S3-Z-2-10	KP216881	97.59%	0	95%	13	sediments of	China	Man et al 2015	CCCCTGTGAACATACCTG
TU CIM 6298	ITS1&2	SR6R	TCCCAAACCCCTG	534	*Tolypocladium album*	Tolypocladiun	Hypocreales	Sordariomyce	*Tolypocladium album*	BH-06	LC386577	94.16%	0	99%	31	soil	South Korea	Das et al 2018	TGCGGAGGGATCATTAC
TU CIM 6295	ITS1&2	SR6R	CAACTCCCAAACC	561	*Tolypocladium* sp.	Tolypocladiun	Hypocreales	Sordariomyce	*Tolypocladium* sp.	S3-Z-2-10	KP216881	97.59%	0	95%	13	sediments of	China	Man et al 2015	CCCCTGTGAACATACCTG
TU CIM 6299	ITS1&2	SR6R	TTACCGAGTTATC	575	*Tolypocladium album*	Tolypocladiun	Hypocreales	Sordariomyce	*Tolypocladium album*	BH-06	LC386577	97.62%	0	94%	13	soil	South Korea	Das et al 2018	TGCGGAGGGATCATTAC
TU CIM 6305	ITS1&2	SR6R	TTACCGAGTTTTC	554	*Tolypocladium* sp.	Tolypocladiun	Hypocreales	Sordariomyce	*Tolypocladium* sp.	PNB17_7A1	MH268124	99.61%	0	92%	9	*Hevea guiane*	Peru	Skaltsas et al 2019	TTACCGAGTTTTCAACTC
TU CIM 5491	ITS1&2	SR6R	WCATTACAGAGT	550	*Paracremonium inflatum*	Paracremoniu	Hypocreales	Sordariomyce	*Paracremonium inflatum*	CBS 482.78	KM231830	86.83%	3e-169⍰	99%	74	soil	Colombia	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5503	ITS1&2	SR6R	AACTCCCCAACCC	668	*Fusicolla violacea*	Fusicolla	Hypocreales	Sordariomyce	*Fusicolla violacea*	CBS 634.76	NR_137617	95.74%	0	80%	23	*Diaspidiotus p*	Iran	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5833	ITS1&2	SR6R	AACTCCCCAACCC	535	*Fusicolla violacea*	Fusicolla	Hypocreales	Sordariomyce	*Fusicolla violacea*	CBS 634.76	NR_137617	96.07%	0	99%	21	*Diaspidiotus p*	Iran	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5634	ITS1&2	SR6R	TTTACAACTCCCA	533	*Fusarium decemcellulare*	Fusarium	Hypocreales	Sordariomyce	*Fusarium decemcellulare*	CBS 315.73	KM231809	98.49%	0	99%	8	*Theobroma c*	Malaysia	Lombard et al 2015	AGTAAAAGTCGTAACAA
TU CIM 5759	ITS1&2	SR6R	GGNCATTACCGA	548	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox59	KJ562372	99.81%	0	97%	1	soil	Italy: South T	Caputo et al 2015	AAGTCGTAACAAGGTCT
TU CIM 5760	ITS1&2	SR6R	CCGAGTTTACAAC	531	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox59	KJ562372	99.81%	0	99%	1	soil	Italy: South T	Caputo et al 2015	AAGTCGTAACAAGGTCT
TU CIM 5761	ITS1&2	SR6R	GGNCATTACCGA	549	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox59	KJ562372	99.81%	0	97%	1	soil	Italy: South T	Caputo et al 2015	AAGTCGTAACAAGGTCT
TU CIM 5763	ITS1&2	SR6R	ATTACCGAGTTTA	536	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox59	KJ562372	99.81%	0	99%	1	soil	Italy: South T	Caputo et al 2015	AAGTCGTAACAAGGTCT
TU CIM 5796	ITS1&2	SR6R	CATTACCGAGTTT	536	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox56	KJ562373	99.81%	0	97%	1	soil	Italy: South T	Caputo et al 2015	GCGCCTTACGGCTCTCGT
TU CIM 5762	ITS1&2	SR6R	ATTACCGAGTTTA	535	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox59	KJ562372	99.81%	0	99%	1	soil	Italy: South T	Caputo et al 2015	AAGTCGTAACAAGGTCT
TU CIM 5769	ITS1&2	SR6R	AACCCCTGTGAAC	525	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox59	KJ562372	98.63%	0	97%⍰	7	soil	Italy: South T	Caputo et al 2015	AAGTCGTAACAAGGTCT
TU CIM 5772	ITS1&2	SR6R	CCGAGTTTACAAC	687	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox56	KJ562373	97.73%	0	77%	12	soil	Italy: South T	Caputo et al 2015	GCGCCTTACGGCTCTCGT
TU CIM 5787	ITS1&2	SR6R	TTACCGAGTTTAC	544	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox56	KJ562373	99.44%	0	97%	3	soil	Italy: South T	Caputo et al 2015	GCGCCTTACGGCTCTCGT
TU CIM 5792	ITS1&2	SR6R	TTACCGAGTTTAC	535	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox56	KJ562373	99.25%	0	99%	4	soil	Italy: South T	Caputo et al 2015	GCGCCTTACGGCTCTCGT
TU CIM 5793	ITS1&2	SR6R	ATTACCGAGTTTA	535	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox56	KJ562373	99.81%	0	99%	1	soil	Italy: South T	Caputo et al 2015	GCGCCTTACGGCTCTCGT
TU CIM 5794	ITS1&2	SR6R	CATTACCGAGTTT	547	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox56	KJ562373	99.81%	0	97%	1	soil	Italy: South T	Caputo et al 2015	GCGCCTTACGGCTCTCGT
TU CIM 5795	ITS1&2	SR6R	CCGAGTTTACAAC	541	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	Fox56	KJ562373	99.81%	0	97%	1	soil	Italy: South T	Caputo et al 2015	GCGCCTTACGGCTCTCGT
TU CIM 5828	ITS1&2	SR6R	TTACCGAGTTTAC	522	*Ilyonectria palmarum*	Ilyonectria	Hypocreales	Sordariomyce	*Ilyonectria palmarum*	DiGeSA-BRA1	HF937429	99.80%	0	97%	1	*Brahea armata*	basal stem	Aiello et al 2014	CGTAACAAGGTCTCCGTT
TU CIM 5843	ITS1&2	SR6R	TTACCGAGTTTAC	709	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	CPC 27702	LT746253	99.43%	0	74%	3		Italy:Siracusa	Sandoval-Denis et al 201	CGTAACAAGGTCTCCGTT
TU CIM 5950	ITS1&2	SR6R	CATTACAGAGTGT	538	*Paracremonium inflatum*	Paracremoniu	Hypocreales	Sordariomyce	*Paracremonium inflatum*	CBS 482.78	KM231830	87.11%	1,00E-168	100%	71	soil	Colombia	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5961	ITS1&2	SR6R	ATTCAACTCATCA	548	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.33%	0	97%	9			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6083	ITS1&2	SR6R	TTACCGAGTTATT	555	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.34%	0	97%	11			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 5962	ITS1&2	SR6R	ACCGAGTTATCAA	552	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.27%	0	99%	4	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5997	ITS1&2	SR6R	CCGAGTTATCAAC	539	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.07%⍰	0	100%	5	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 5986	ITS1&2	SR6R	ACCGAGTTATTCA	548	*Fusarium solani*	Fusarium	Hypocreales	Sordariomyce	*Fusarium solani*	LMMM135	KF030977	99.81%	0	98%	1	peritoneal fluid		da Silva-Rocha et al 2015	GGCAACTACCACCCAGG
TU CIM 6010	ITS1&2	SR6R	TTACCGAGTTTAC	527	*Gliocephalotrichum cylindrosp*	Gliocephalotri	Hypocreales	Sordariomyce	*Gliocephalotrichum cylindrosp*	MUCL 18576	NR_145030	100%	0	99%	0			Decock et al 2006	TCCGTTGGTGAACCAGC
TU CIM 6012	ITS1&2	SR6R	TTTACAACTCCCA	529	*Gliocephalotrichum cylindrosp*	Gliocephalotri	Hypocreales	Sordariomyce	*Gliocephalotrichum cylindrosp*	MUCL 18576	NR_145030	99.81%	0	98%	1			Decock et al 2006	TCCGTTGGTGAACCAGC
TU CIM 6019	ITS1&2	SR6R	AACCCATGTGAAT	569	*Gliocephalotrichum cylindrosp*	Gliocephalotri	Hypocreales	Sordariomyce	*Gliocephalotrichum cylindrosp*	MUCL 18576	NR_145030	99.80%⍰	0	97%	1			Decock et al 2006	TCCGTTGGTGAACCAGC
TU CIM 6031	ITS1&2	SR6R	ATTACCGAGTTTA	539	*Gliocephalotrichum cylindrosp*	Gliocephalotri	Hypocreales	Sordariomyce	*Gliocephalotrichum cylindrosp*	MUCL 18576	NR_145030	99.81%	0	97%	1			Decock et al 2006	TCCGTTGGTGAACCAGC
TU CIM 6040	ITS1&2	SR6R	TTACCGAGTTTAC	551	*Clonostachys rosea*	Clonostachys	Hypocreales	Sordariomyce	*Clonostachys rosea*	AH	KR909139	99.45%	0	98%	3	wood		Travadon et al 2016	TCCGTAGGTGAACCTGC
TU CIM 6032	ITS1&2	SR6R	CATTACCGAGTT	530	*Lasiodiplodia parva*	Lasiodiplodia	Botryosphaer	Dothideomyc	*Lasiodiplodia parva*	MH861166	CBS 456.78	99%	0	99.05%	5		Colombia	Vu et al 2019	
TU CIM 6043	ITS1&2	SR6R	NCATTACCGAGTT	557	*Clonostachys rosea*	Clonostachys	Hypocreales	Sordariomyce	*Clonostachys rosea*	AH	KR909139	99.26%	0	97%	4	wood		Travadon et al 2016	TCCGTAGGTGAACCTGC
TU CIM 6046	ITS1&2	SR6R	ACAACTCCCAAAC	543	*Clonostachys rosea*	Clonostachys	Hypocreales	Sordariomyce	*Clonostachys rosea*	AH	KR909139	99.25%	0	97%	4	wood		Travadon et al 2016	TCCGTAGGTGAACCTGC
TU CIM 6054	ITS1&2	SR6R	AACTCCCAAACCC	531	*Clonostachys rosea*	Clonostachys	Hypocreales	Sordariomyce	*Clonostachys rosea*	AH	KR909139	99.24%	0	99%	4	wood		Travadon et al 2016	TCCGTAGGTGAACCTGC
TU CIM 6064	ITS1&2	SR6R	CATTACCGAGTTA	729	*Coccinonectria pachysandricol*	Coccinonectri	Hypocreales	Sordariomyce	*Coccinonectria pachysandricol*	CBS 476.92	KM231775	88.69%	0	92%	63	*Pachysandra*	Netherlands	Lombard et al 2015	AGTAAAAGTCGTAACAA
TU CIM 6067	ITS1&2	SR6R	TTACCGAGTTTAC	519	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	AE-2013	KF746131	99.81%	0	99%	1	*Bradypus vari*	Panama	Higginbotham et al 2014	TTACCGAGTTTACAACTC
TU CIM 6076	ITS1&2	SR6R	CAACTCATCAACC	543	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.31%	0	97%	9			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6231	ITS1&2	SR6R	TTACCGAGTTATT	541	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.34%	0	100%	9			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6085	ITS1&2	SR6R	TTACCGAGTTATC	549	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.26%⍰	0	98%	4	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6086	ITS1&2	SR6R	AACTCCCAAACCC	528	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.43%⍰	0	99%	3	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6087	ITS1&2	SR6R	ATTACCGAGTTAT	543	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.44%	0	99%	3	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6203	ITS1&2	SR6R	ATTACCGAGTTAT	555	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.45%⍰	0	99%	3	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6204	ITS1&2	SR6R	ATCAACTCCCAAA	530	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.43%	0	100%	3	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6088	ITS1&2	SR6R	ATTACCGAGTTAT	541	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.26%	0	100%	4	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT

TU CIM 6306	ITS1&2	SR6R	TTACCGAGTTATC	549	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.27%		0	99%	14	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6175	ITS1&2	SR6R	AACTCCCAAACCC	533	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.24%		0	98%	4	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6176	ITS1&2	SR6R	TGTGAACATACCT	518	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	97.28%		0	99%	14	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6195	ITS1&2	SR6R	AACTCATCAACCC	533	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.30%		0	98%	9			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6270	ITS1&2	SR6R	ATTACCGAGTTAT	549	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.18%		0	99%	10			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6271	ITS1&2	SR6R	ATTACCGAGTTAT	545	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.34%		0	99%	11			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6275	ITS1&2	SR6R	TTCAACTCATCAA	537	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.14%		0	99%	10			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6276	ITS1&2	SR6R	CCGAGTTATTNAA	546	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43511	EF453110	97.81%		0	99%	12			O'Donnell et al 2007	CCGAGTTATTCAACTCAT
TU CIM 6304	ITS1&2	SR6R	CTTCGGCGGGAA	479	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43811	EF453204	98.54%		0	100%	7			O'Donnell et al 2007	CCGAGTTATACAACTCAT
TU CIM 6280	ITS1&2	SR6R	CATTACCGAGTTA	552	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.35%		0	98%	9			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6281	ITS1&2	SR6R	TTACCTAAACGTT	506	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.02%		0	99%	10			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6282	ITS1&2	SR6R	CAACTCATCAACC	536	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.31%		0	98%	9			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6283	ITS1&2	SR6R	TTACCGAGTTATT	547	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.34%		0	98%	9			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6291	ITS1&2	SR6R	TTACCGAGTTATT	548	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43511	EF453110	98.34%		0	97%	9			O'Donnell et al 2007	CCGAGTTATTCAACTCAT
TU CIM 6292	ITS1&2	SR6R	TTACCGAGTTATT	542	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.34%		0	100%	9			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6197	ITS1&2	SR6R	CAACTCCCAAACC	542	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	98.88%		0	99%	6	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6198	ITS1&2	SR6R	TACCTTTTGTTGC	504	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	98.21%		0	100%	9	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6199	ITS1&2	SR6R	CCCCTGTGAACAT	528	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.42%		0	97%	3	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6201	ITS1&2	SR6R	CATTACCGAGTCT	626	*Campylocarpon fasciculare*	Campylocarpc	Hypocreales	Sordariomyce	*Campylocarpon fasciculare*	MBAi45CL	KJ573392	96.41%		0	90%	19	*Vitis vinifera*	Turkey: Salihl	Akgul et al 2014	TTGGAAGTAAAAATCGT
TU CIM 6218	ITS1&2	SR6R	ATCAACTCCCAAA	544	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.07%		0	99%	5	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6224	ITS1&2	SR6R	TTATCAACTCCCA	540	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.43%		0	98%	3	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6225	ITS1&2	SR6R	CAACTCCCAAACC	543	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	99.07%		0	99%	5	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6234	ITS1&2	SR6R	TCAACTCATCAAC	529	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.31%		0	100%	11			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6272	ITS1&2	SR6R	TTACCGAGTTTAC	537	*Paracremonium inflatum*	Paracremoniu	Hypocreales	Sordariomyce	*Paracremonium inflatum*	CBS 482.78	KM231830	99.06%		0	98%	5	soil	Colombia	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6274	ITS1&2	SR6R	CTCCCAAACCCCT	532	*Paracremonium inflatum*	Paracremoniu	Hypocreales	Sordariomyce	*Paracremonium inflatum*	CBS 482.78	KM231830	98.67%		0	99%	7	soil	Colombia	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6279	ITS1&2	SR6R	ATTACCGAGTTTA	541	*Paracremonium inflatum*	Paracremoniu	Hypocreales	Sordariomyce	*Paracremonium inflatum*	CBS 482.78	KM231830	98.52%		0	100%	8	soil	Colombia	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6302	ITS1&2	SR6R	CATTACCGAGTCT	861	*Campylocarpon fasciculare*	Campylocarpc	Hypocreales	Sordariomyce	*Campylocarpon fasciculare*	MBAi45CL	KJ573392	97.16%		0	94%	15	*Vitis vinifera*	Turkey: Salihl	Akgul et al 2014	TTGGAAGTAAAAATCGT
TU CIM 6322	ITS1&2	SR6R	CAACTCATCAACC	537	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.31%		0	98%	9			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6323	ITS1&2	SR6R	TTCAACTCATCAA	539	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.31%		0	98%	9			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6324	ITS1&2	SR6R	TTACCTAAACGTT	511	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	97.06%		0	99%	15			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6325	ITS1&2	SR6R	CAACTCCCAAACC	530	*Paracremonium inflatum*	Paracremoniu	Hypocreales	Sordariomyce	*Paracremonium inflatum*	CBS 482.78	KM231830	99.03%		0	97%	5	soil	Colombia	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6326	ITS1&2	SR6R	ATTACCGAGTTAT	548	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.34%		0	98%	9			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6328	ITS1&2	SR6R	TTACCGAGTTATT	542	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	MICMW-30.1	MG838039	98.34%		0	100%	11			Santillan-Mendoza et al 2	CATTACCGAGTTATTCAA
TU CIM 6331	ITS1&2	SR6R	TTCAACTCATCAA	536	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.14%		0	99%	10			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6334	ITS1&2	SR6R	TTACCGAGTTATT	556	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43511	EF453110	98.19%		0	98%	10			O'Donnell et al 2007	CCGAGTTATTCAACTCAT
TU CIM 6335	ITS1&2	SR6R	ATTCAACTCATCA	541	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	98.32%		0	98%	9			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6336	ITS1&2	SR6R	TTCAACTCATCAA	540	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43873	EF453216	97.98%		0	100%	11			O'Donnell et al 2007	TTATTCAACTCATCAACC
TU CIM 6337	ITS1&2	SR6R	TTACCGAGTTATT	550	*Fusarium* sp	Fusarium	Hypocreales	Sordariomyce	*Fusarium* sp	NRRL 43511	EF453110	97.82%		0	99%	12			O'Donnell et al 2007	CCGAGTTATTCAACTCAT
TU CIM 7008	ITS1&2	SR6R	TTACCGAGTTATC	553	*Xenoacremonium recifei*	Xenoacremon	Hypocreales	Sordariomyce	*Xenoacremonium recifei*	CBS 541.89	KM231834	98.55%		0	99%	8	soil	Brazil	Lombard et al 2015	CGTAACAAGGTCTCCGTT
TU CIM 6332	ITS1&2	SR6R	TTACCGAGTTATC	571	*Tolypocladium album*	Tolypocladiun	Hypocreales	Sordariomyce	*Tolypocladium album*	BH-06	LC386577	96.37%		0	96%	20	soil	South Korea	Das et al 2018	TGCGGAGGGATCATTAC
TU CIM 5717	ITS1&2	SR6R	CGAGTACAGGGG	584	*Anhellia nectandrae*	Anhellia	Myriangiales	Dothideomyce	*Anhellia nectandrae*	VIC 31767	NR_111700	82.62%	1e-124	93%		97	*Nectandra re*	Brazil	Schoch et al 2014	TCGTAACAAGGTTTCCGTA
TU CIM 5773	ITS1&2	SR6R	CTGAGTTCTAAAA	964	*Annulohypoxylon viridistratun*	Annulohypoxy	Xylariales	Sordariomyce	*Annulohypoxylon viridistratun*	EK14010	KX376325	99.68%		0	95%	3		Thailand	Kuhnert et al 2017	CAGCGGAGGGATCATTA
TU CIM 5779	ITS1&2	SR6R	GAGTTATACAACT	805	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	TMS-2011	HQ630967	96.72%		0	99%	19	*Miscanthus giganteus*		Shrestha et al 2011	TCTTGGTCATTTAGAGGA
TU CIM 5780	ITS1&2	SR6R	ATACCATTTGTCA	648	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	TMS-2011	HQ630967	96.63%		0	97%	19	*Miscanthus giganteus*		Shrestha et al 2011	TCTTGGTCATTTAGAGGA
TU CIM 5781	ITS1&2	SR6R	GAGTTATACAACT	813	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	SL6	KP689231	99.82%		0	95%	1	*Huperzia serr*	China	Wang et al 2016	GAACGGGCTTTACACTCC
TU CIM 5797	ITS1&2	SR6R	CTACTTCAAACCA	548	*Coniochaeta angustispora*	Coniochaeta	Coniochaetale	Sordariomyce	*Coniochaeta angustisporaArth*	CBS 872.73	MH860817	100%		0	94%	0		Suriname	Vu et al 2019	AACAAGGTCTCCGTTGG
TU CIM 5798	ITS1&2	SR6R	TACCATTTGTCAA	646	*Arthrinium marii*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium marii*	CBS:200.57	KF144900	97.90%		0	99%	11	*Beta vulgaris*	Netherlands	Crous et al 2013	TTTGTACACACCGCCCGT
TU CIM 5799	ITS1&2	SR6R	GAGTTATACAACT	587	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	wb558	AF455414	97.47%		0	95%	12			Buzina et al2003	AGTCGTAACAAGGTCTC
TU CIM 5807	ITS1&2	SR6R	TACAACTCCCATA	580	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	HKU41	LC158595	98.13%		0	95%	9	toenail	Hong Kong	Tsang et al 2019	AGGGATCATTACAGAGT
TU CIM 5809	ITS1&2	SR6R	TACAACTCCCATA	894	*Arthrinium marii*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium marii*	CBS:200.57	KF144900	98.51%		0	99%	9	*Beta vulgaris*	Netherlands	Crous et al 2013	TTTGTACACACCGCCCGT

TU CIM 5813	ITS1&2	SR6R	TTACAGAGTTATA	591	*Arthrinium phragmites*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium phragmites*	CPC 18900	NR_111873	90.85%	0	98%	54	*Phragmites a*	Italy	Schoch et al 2014	GCGGAGGGATCATTACA
TU CIM 5816	ITS1&2	SR6R	NCATTATAGAGTT	551	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	RM3.30.06	MH397130	99.81%	0	94%	1			Hamzah et al 2018	AAGTCGTAACAAGGTCT
TU CIM 5817	ITS1&2	SR6R	ATTATAGAGTTTA	552	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	RM3.30.06	MH397130	99.81%	0	94%	1			Hamzah et al 2018	AAGTCGTAACAAGGTCT
TU CIM 5818	ITS1&2	SR6R	TACAACTCCCATA	756	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	wb558	AF455414	97.25%	0	97%	13			Buzina et al2003	AGTCGTAACAAGGTCTC
TU CIM 5822	ITS1&2	SR6R	GAGTTATACAACT	583	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	wb559	AF455415	97.25%	0	96%	13			Buzina et al2003	AGTCGTAACAAGGTCTC
TU CIM 5823	ITS1&2	SR6R	TACAACTCCCATA	894	*Arthrinium marii*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium marii*	CBS:200.57	KF144900	99.16%	0	99%	5	*Beta vulgaris*	Netherlands	Crous et al 2013	TTTGTACACACCGCCCGT
TU CIM 5827	ITS1&2	SR6R	TACAACTCCCATA	555	*Arthrinium sp.*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium* sp.	HKU41	LC158595	97.93%	0	95%	10	toenail	Hong Kong	Tsang et al 2019	AGGGATCATTACAGAGT
TU CIM 5803	ITS1&2	SR6R	ACTCCCATACCAT	597	*Arthrinium marii*	Arthrinium	Xylariales	Sordariomyce	*Arthrinium marii*	BS 497.90	MH873913	98.64%	0	98%	8		Spain	Vu et al 2019	ATGGCTCAGTGAGGCTT
TU CIM 5814	ITS1&2	SR6R	ATTATAGAGTTTA	544	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	ERS017	KY413701	89.96%	0	100%		*Virola surinan*	Panama	Spear,E.R 2017	ATCATTATAGAGTTTTCT
TU CIM 5840	ITS1&2	SR6R	TTATAGAGTTTTC	814	*Castanediella couratarii*	Castanediella	Xylariales	Sordariomyce	*Castanediella couratarii*	CBS 579.71	NR_145250	90.31%	▯e-173	100%	47			Hernandez-Restrepo et a	GGAGGGATCATTATAGA
TU CIM 6009	ITS1&2	SR6R	CTACTTCAAACCA	548	*Coniochaeta* sp.	Coniochaeta	Coniochaetale	Sordariomyce	*Coniochaeta* sp.	1M35	MF942883	98.87%	0	97%	6	*Dicranum sco*	USA: Duke Fo	Chen et al 2018	GCGGRGGATCATTACAA
TU CIM 6008	ITS1&2	SR6R	TTACTGAGTTTAC	552	*Colletotrichum gloeosporioide*	Colletotrichun	Glomerellales	Sordariomyce	*Colletotrichum gloeosporioide*	TW4	MH930406	99.09%	0	99%	5			Leung et al 2018	GGAAGTAAAAGTCGTAA
TU CIM 6006	ITS1&2	SR6R	TTACAAGAAGCCC	552	*Coniochaeta* sp.	Coniochaeta	Coniochaetale	Sordariomyce	*Coniochaeta* sp.	1M35	MF942883	98.91%	0	100%	6	*Dicranum sco*	USA: Duke Fo	Chen et al 2018	GCGGRGGATCATTACAA
TU CIM 6022	ITS1&2	SR6R	ATTACAAGCCGAA	547	*Coniochaeta* sp.	Coniochaeta	Coniochaetale	Sordariomyce	*Coniochaeta* sp.	BRO-2013	KF367562	98.91%	0	100%	6	untreated dri	Portugal	Oliveira et al 2013	CTATCCAAACTCGGTCAT
TU CIM 6023	ITS1&2	SR6R	ATTATTACAAGCC	563	*Coniochaeta* sp.	Coniochaeta	Coniochaetale	Sordariomyce	*Coniochaeta* sp.	BRO-2013	KF367562	98.58%	0	99%	8	untreated dri	Portugal	Oliveira et al 2013	CTATCCAAACTCGGTCAT
TU CIM 6026	ITS1&2	SR6R	CATTACTGAGTTA	836	*Daldinia eschscholtzii*	Daldinia	Xylariales	Sordariomyce	*Daldinia eschscholtzii*	JMRC:SF:11930	KU304335	99.64%	0	100%	2	Paphiopedilu	Thailand: Chi	Barnes et al 2016	AGGGATGGAACCGTGAC
TU CIM 6030	ITS1&2	SR6R	ATTCAGTGAATCA	295	*Phomopsis* sp.	Phomopsis	Diaporthales	Sordariomyce	*Phomopsis* sp.	TW24	MH930425	100%	7e-151▯	100%	0			Leung et al 2018	GGAAGTAAAAGTCGTAA
TU CIM 6034	ITS1&2	SR6R	CATTGCTGGACTG	597	*Sordariomycetes sp.*			Sordariomyce	*Sordariomycetes sp.*	JMUR-2016	KX908495	86.72%	0	99%	81	*Quercus mon*	USA	U'Ren et al 2016	GGATCATTGCTGGAACT
TU CIM 5776	ITS1&2	SR6R	AGATACCCTATGT	379	*Chrysomorbus lagerstroemiae*	Chrysomorbu	Diaporthales	Sordariomyce	*Chrysomorbus lagerstroemiae*	CERC 8812	KY929339	86.24%	4,00E-109	96%	52	*Lagerstroemi*	China	Chen et al 2018	ATCATTGCTGGAACTGTG
TU CIM 6177	ITS1&2	SR6R	NNNATTGCTGGA	602	*Sordariomycetes sp.*			Sordariomyce	*Sordariomycetes sp.*	JMUR-2016	KX908495	86.37%	0	99%	83	*Quercus mon*	USA	U'Ren et al 2016	GGATCATTGCTGGAACT
TU CIM 6017	ITS1&2	SR6R	CGAGTACAGGGG	584	*Anhellia nectandrae*	Anhellia	Myriangiales	Dothideomyc	Anhellia nectandrae	VIC 31767	NR_111700	82.62%	1,00E-124	93%	97	*Nectandra re*	Brazil	Schoch et al 2014	TCGTAACAAGGTTTCCGT
TU CIM 6990	ITS1&2	SR6R	CATTAGAGAGTCT	556	*Nemania cf. Bipapillata*	Nemania	Xylariales	Sordariomyce	*Nemania cf. Bipapillata*	BCC 20944	AB625438	100%	0	94%	0	*leaf of Schizo*	Thailand	Okane et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 7016	ITS1&2	SR6R	CATTAGAGAGAG	534	*Nemania bipapillata*	Nemania	Xylariales	Sordariomyce	*Nemania bipapillata*	5100	JQ862661	99.02%	0	95%	5			Chen et al 2013	TTGCGTACGCGCTAGAG
TU CIM 5811	ITS1&2	SR6R	ACTGAGTACTACA	529	*Plectosphaerella cucumerina*	Plectosphaere	Glomerellales	Sordariomyce	*Plectosphaerella cucumerina*	2014_1556	MN523140	99.81%	0	97%	1	*cucurbita ster*	USA	Rivedal et al 2019	TTACTGAGTACTACACTC
TU CIM 6185	ITS1&2	SR6R	GNCATTACTGAGT	541	*Plectosphaerella cucumerina*	Plectosphaere	Glomerellales	Sordariomyce	*Plectosphaerella cucumerina*	380408	AJ492873	99.62%	0	97%	2	*potato cyst ne*	Jersey	Atkins et al 2013	GGAAGTAAAAGTCGTAA
TU CIM 6007	ITS1&2	SR6R	TTTCTACAACTCC	546	*Nemania primolutea*	Nemania	Xylariales	Sordariomyce	*Nemania primolutea*	91102001	EF026121	95.42%	9	99%	25	dead trunk	Taiwan	Hsieh et al 2010	TCCGTAGGTGAACCTGC
TU CIM 6014	ITS1&2	SR6R	AACTCCCAAACCC	537	*Nemania cf. Bipapillata*	Nemania	Xylariales	Sordariomyce	*Nemania cf. Bipapillata*	BCC 20944	AB625438	100%	0	94%	0	*leaf of Schizo*	Thailand	Okane et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 6018	ITS1&2	SR6R	TTAGAGAGTCTAA	556	*Nemania cf. Bipapillata*	Nemania	Xylariales	Sordariomyce	*Nemania cf. Bipapillata*	BCC 20944	AB625438	100%	0	94%	0	*leaf of Schizo*	Thailand	Okane et al 2014	TCTCCGTTGGTGAACCAG
TU CIM 6020	ITS1&2	SR6R	TTACAGAGTTGCA	560	*Neurospora calospora*	Neurospora	Sordariales	Sordariomyce	*Neurospora calospora*	CBS 265.51	MH856849	99.82%	0	100%	1		USA	Vu et al 2019	ATGGCTCAGTGAGGCTT
TU CIM 6024	ITS1&2	SR6R	GAGTTTTTTCAAC	575	*Cordyceps javanica*	Cordyceps	Hypocreales	Sordariomyce	*Cordyceps javanica*	MY02949	JN942618	100%	0	92%	0			Schoch et al 2012	TCCGTTGGTGAACCAGC
TU CIM 6025	ITS1&2	SR6R	GTTATACAACTCC	575	*Purpureocillium lilacinum*	Purpureocilliu	Hypocreales	Sordariomyce	*Purpureocillium lilacinum*	Kw 3411	FR822391	100%	0	98%	0			Khan et al 2012	TCCGTAGGTGAACCTGC
TU CIM 6027	ITS1&2	SR6R	CTCCCTAACCCTT	546	*Cordyceps javanica*	Cordyceps	Hypocreales	Sordariomyce	*Cordyceps javanica*	MY02949	JN942618	99.81%	0	95%	1			Schoch et al 2012	TCCGTTGGTGAACCAGC
TU CIM 6056	ITS1&2	SR6R	ATTATAGAGTTTT	560	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	ERS031	KY413714	99.37%	0	97%	3	*Trichilia tuber*	Panama	Spear,E.R 2017	GGATCATTATAGAGTTTT
TU CIM 5771	ITS1&2	SR6R	TTATAGAGTTTTC	578	*Pseudopestalotiopsis theae*	Pseudopestal	Xylariales	Sordariomyce	*Pseudopestalotiopsis theae*	P156	EF423553	100%	0	91%	0	*Faramea occi*	Panama	Gilbert et al 2007	GGACATTATAGAGTTTTC
TU CIM 5969	ITS1&2	SR6R	TTATAGAGTTTTC	811	*Neopestalotiopsis piceana*	Neopestalotio	Xylariales	Sordariomyce	*Neopestalotiopsis piceana*	CBS 225.30	MH855130	100%	0	98%	0			Vu et al 2019	GTCGTAACAAGGTCTCC
TU CIM 5971	ITS1&2	SR6R	NCATTATAGAGTT	829	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	AE-2013	KF746154	100%	0	97%	0	*Bradypus vari*	Panama	Higginbotham et al 2014	TTATAGAGTTTTCTAAAC
TU CIM 6004	ITS1&2	SR6R	ATTATAGAGTTTT	828	*Pseudopestalotiopsis theae*	Pseudopestal	Xylariales	Sordariomyce	*Pseudopestalotiopsis theae*	P156	EF423553	99.62%	0	99%	2	*Faramea occi*	Panama	Gilbert et al 2007	GGACATTATAGAGTTTTC
TU CIM 5495	ITS1&2	SR6R	TTATAGAGTTTTC	529	*Pseudopestalotiopsis* sp	Pseudopestal	Xylariales	Sordariomyce	*Pseudopestalotiopsis* sp	3-KW-2016	LC114037	99.02%	0	96%	5			Nozawa et al 2017	TCTCCGTTGGTGAACCAG
TU CIM 5496	ITS1&2	SR6R	TATAGAGTTTTCT	885	*Neopestalotiopsis clavispora*	Neopestalotio	Xylariales	Sordariomyce	*Neopestalotiopsis clavispora*		JX875595	100%	0	97%	0	*Mangifera indica*		Ismail et al 2013	CTGCGGAGGGATCATTA
TU CIM 5498	ITS1&2	SR6R	GAGTTTTCTAAAC	827	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	AE-2013	KF746154	100%	0	97%	0	*Bradypus vari*	Panama	Higginbotham et al 2014	TTATAGAGTTTTCTAAAC
TU CIM 5499	ITS1&2	SR6R	TATAGAGTTTTCT	533	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	AE-2013	KF746095	100%	0	95%	0	*Bradypus vari*	Panama	Higginbotham et al 2015	GTAACAAGGTCTCCGTT
TU CIM 5572	ITS1&2	SR6R	ATTATAGAGTTTT	537	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	ATT035	HQ607806	100%	0	97%	0	*Atta texana* r	USA: Texas	Rodrigues et al 2011	TGGAAGTAAAAGGTCGT
TU CIM 5632	ITS1&2	SR6R	GGGNCATTATAG	818	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	100%	0	97%	0	*Odontodenia*	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG
TU CIM 5636	ITS1&2	SR6R	TTATAGAGTTTTC	803	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	100%	0	97%	0	*Odontodenia*	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG
TU CIM 5644	ITS1&2	SR6R	ATTATAGAGTTTT	838	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	AE-2013	KF746095	100%	0	95%	0	*Bradypus vari*	Panama	Higginbotham et al 2015	GTAACAAGGTCTCCGTT
TU CIM 5645	ITS1&2	SR6R	NTTATAGAGTTTT	773	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	100%	0	97%	0	*Odontodenia*	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG
TU CIM 5777	ITS1&2	SR6R	ATTATAGAGTTTT	853	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	99.81%	0	98%	1	*Odontodenia*	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG
TU CIM 5783	ITS1&2	SR6R	GWWCATTATAGA	543	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	100%	0	96%	0	*Odontodenia*	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG
TU CIM 5784	ITS1&2	SR6R	TTATAGAGTTTTC	537	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	100%	0	97%	0	*Odontodenia*	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG
TU CIM 5788	ITS1&2	SR6R	ACTCCCAACCCAT	522	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	99.80%	0	97%	1	*Odontodenia*	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG

TU CIM 5829	ITS1&2	SR6R	CATTATAGAGTTT	549	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	ERS017	KY413701	99.45%	0	99%	3	*Virola surinan*	Panama	Spear,E.R 2017	ATCATTATAGAGTTTTCT
TU CIM 5837	ITS1&2	SR6R	ATTATAGAGTTTT	700	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	AE-2013	KF746095	100%	0	97%	0	*Bradypus vari*	Panama	Higginbotham et al 2015	GTAACAAGGTCTCCGTT
TU CIM 6015	ITS1&2	SR6R	ATTATAGAGTTTT	853	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	P089	EF423541	99.81%	0	98%	1	*Odontodenia* ,	Panama	Gilbert et al 2007	TCTGGAAGTAAAAGTCG
TU CIM 6028	ITS1&2	SR6R	TTACAGAGTTTCG	587	*Phaeoacremonium scolyti*	Phaeoacremo	Togniniales	Sordariomyce	*Phaeoacremonium scolyti*	STE-U 5955	EU128034	98.55%	0	93%	8			Damm et al 2008	AGGGATCATTAACGAGT
TU CIM 6035	ITS1&2	SR6R	AGAGTTTCGTACT	579	*Phaeoacremonium tardicresce*	Phaeoacremo	Togniniales	Sordariomyce	*Phaeoacremonium tardicresce*	CBS 110573	MH862865	98.24%	0	97%	10		USA: Texas	Vu et al 2019	GAGGTCTCCGTTGGTGA
TU CIM 6038	ITS1&2	SR6R	AGTTGCAAAACTC	535	*Phialemonium* sp.	Phialemonium	Sordariales	Sordariomyce	*Phialemonium* sp.	BRO-2013	KF367530	95.54%	0	99%	24	untreated dri	Portugal	Oliveira et al 2013	GATGGCTCAGTGAGGCT
TU CIM 6055	ITS1&2	SR6R	TTAAAGAGTTGCA	536	*Phialemonium* sp.	Phialemonium	Sordariales	Sordariomyce	*Phialemonium* sp.	BRO-2013	KF367530	95.86%	0	98%	21	untreated dri	Portugal	Oliveira et al 2013	GATGGCTCAGTGAGGCT
TU CIM 6057	ITS1&2	SR6R	GAGTTGCAAAACT	528	*Phialemoniopsis curvata*	Phialemonium	Sordariales	Sordariomyce	*Phialemoniopsis curvata*	UTHSC 06-4324	EU035984	97.71%	0	98%	12	poodle pleural fluid		Sutton et al 2008	AAAGTTATATTTCTCGCT
TU CIM 7081	ITS1&2	SR6R	TTTTCTAAACTCC	539	*Pestalotiopsis* sp.	Pestalotiopsis	Xylariales	Sordariomyce	*Pestalotiopsis* sp.	2 AE-2013	KF746122	99.06%	0	99%	5	*Bradypus vari*	Panama	Higginbotham et al 2014	GATCATTATAGAGTTTTC
TU CIM 6065	ITS1&2	SR6R	GCAAAACTCCCAA	525	*Phialemoniopsis pluriloculosa*	Phialemoniop	Xylariales	Sordariomyce	*Phialemoniopsis pluriloculosa*	CBS 131712	MH865904	99.21%	0	96%	4		USA	Vu et al 2019	AACAAGGTTTCCGTTGGT
TU CIM 6207	ITS1&2	SR6R	TTAAAGAGTTGCA	541	*Phialemoniopsis pluriloculosa*	Phialemoniop	Xylariales	Sordariomyce	*Phialemoniopsis pluriloculosa*	CBS 131712	MH865904	99.22%	0	95%	4		USA	Vu et al 2019	AACAAGGTTTCCGTTGGT
TU CIM 5635	ITS1&2	SR6R	ATTACCGAGTTAT	560	*Tolypocladium* sp.	Tolypocladium	Hypocreales	Sordariomyce	*Tolypocladium* sp.	DS10	KY432313	96.81%	0	95%	17	*Dendrobium sinense* roots		Wang et al 2017	TGTCATTGAGTTCACTCC
TU CIM 5646	ITS1&2	SR6R	GNCATTACTGAGT	541	*Plectosphaerella cucumerina*	Plectosphaere	Glomerellales	Sordariomyce	*Plectosphaerella cucumerina*	380408	AJ492873	99.62%	0	97%	2	*potato cyst ne*	Jersey	Atkins et al 2013	GGAAGTAAAAGTCGTAA
TU CIM 5711	ITS1&2	SR6R	ACTGAGTACTACA	529	*Plectosphaerella* sp.	Plectosphaere	Glomerellales	Sordariomyce	*Plectosphaerella* sp.	MH727	FJ430715	99.62%	0	100%	2			Hujslova et al 2010	ATTACAAAGCGAAACTG
TU CIM 5712	ITS1&2	SR6R	AGAGTTTATCATA	559	*Xylaria* sp	Xylaria	Xylariales	Sordariomyce	*Xylaria* sp.	1a0283EM2CC38	KP306964	99.08%	0	97%	5	marine sponge		Bolanos et al 2015	AACTCCCAAACCCATGTG
TU CIM 5714	ITS1&2	SR6R	NGTAAACTCCCCC	499	*Valsaceae* sp.	Valsaceae	Diaporthales	Sordariomyce	*Valsaceae* sp.	GS52	100%	96.48%	0	96%	17		Japan	Osono et al 2008	AGTAAAGTCGTAACAAG
TU CIM 5715	ITS1&2	SR6R	TTGCTGGAGCGTC	590	*Valsaceae* sp.	Valsaceae	Diaporthales	Sordariomyce	*Valsaceae* sp.	GS52	AB334109	96.65%	0	95%	19		Japan	Osono et al 2008	AGTAAAGTCGTAACAAG
TU CIM 7080	ITS1&2	SR6R	NCATTAGAGAGTC	565	*Nemania* sp.	Nemania	Xylariales	Sordariomyce	*Nemania* sp.	F1982	KU747850	99.44%	0	95%	13	*Campyloneuri*	Panama	Del Olmo-Ruiz et al 2017	CTCCCAACCCACTGTGAA
TU CIM 5992	ITS1&2	SR6R	TTGCTGGAGCGTC	597	*Valsaceae* sp.	Valsaceae	Diaporthales	Sordariomyce	*Valsaceae* sp.	GS52	AB334109	96.65%	0	96%	19		Japan	Osono et al 2008	AGTAAAGTCGTAACAAG
TU CIM 6029	ITS1&2	SR6R	GCTGGAGCGTCTC	591	*Valsaceae* sp.	Valsaceae	Diaporthales	Sordariomyce	*Valsaceae* sp.	GS52	AB334109	96.64%	0	95%	19		Japan	Osono et al 2008	AGTAAAGTCGTAACAAG
TU CIM 6070	ITS1&2	SR6R	ATTACAGAGTTTT	551	*Seiridium sp.*	Seiridium *sp.*	Xylariales	Sordariomyce	*Seiridium* sp.	2 Z28	JN198507	98.54%	0	98%	8			Wu et al 2013	GCGGTAATGAGACGCCG
TU CIM 6074	ITS1&2	SR6R	GAGTTGCAAAACT	528	*Phialemoniopsis pluriloculosa*	Phialemoniop	Xylariales	Sordariomyce	*Phialemoniopsis pluriloculosa*	CBS 131712	MH865904	99.22%	0	98%	4		USA	Vu et al 2019	AACAAGGTTTCCGTTGGT
TU CIM 6075	ITS1&2	SR6R	CATTGCTGGAAGC	592	*Valsaceae* sp.	Valsaceae	Diaporthales	Sordariomyce	*Valsaceae* sp.	GS52	AB334109	91.24%	0	94%	50		Japan	Osono et al 2008	AGTAAAGTCGTAACAAG
TU CIM 6077	ITS1&2	SR6R	GAGTTTATAAAAC	543	*Wardomyces* sp.	Wardomyces	Microascales	Sordariomyce	*Wardomyces* sp.	AHB16_5A	MH268155	99.62%	0	97%	2	*Hevea paucifl*	Peru	Skaltsas et al 2019	GTAAAAAGTCGTAACAA
TU CIM 6080	ITS1&2	SR6R	AGAGTTTATCATA	559	*Xylaria* sp	Xylaria	Xylariales	Sordariomyce	*Xylaria* sp.	1a0283EM2CC38	KP306964	99.08%	0	97%	5	marine sponge		Bolanos et al 2015	AACTCCCAAACCCATGTG
TU CIM 5995	ITS1&2	SR6R	AAGAGTTCTATAA	550	*Xylaria* sp	Xylaria	Xylariales	Sordariomyce	*Xylaria* sp.	NR-2006-A59	DQ480344	99.62%	0	95%	2			Phongpaichit et al 2006	GGTAACAAGGTCTCCGT
TU CIM 5506	ITS1&2	SR6R	ATTACTGAGTGAG	541	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	KSM-F532	LC315644	98.34%	0	100%	9			Shibata et al 2017	GGAAGTAAAAGTCGTAA
TU CIM 5507	ITS1&2	SR6R	TTNCTGAGTGAGC	561	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	CGMCC 3.18178	KX961214	95.89%	0	99%	3			Shibata et al 2017	GGAAGTAAAAGTCGTAA
TU CIM 5626	ITS1&2	SR6R	CATTACCGAGTGA	561	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	F731	KM249071	100%	0	99%	0	*Beta vulgaris*	USA: Idaho	Strausbaugh et al 2015	TCCGTAGGTGAACCTGC
TU CIM 5627	ITS1&2	SR6R	ATTACCGAGTGAC	560	*Penicillium expansum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium expansum*	ATCC 7861	NR_077154	100%	0	99%	0			Schoch et al 2014	TCCGTAGGTGAACCTGC
TU CIM 5647	ITS1&2	SR6R	CATTACCGAGTGA	561	*Penicillium polonicum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium polonicum*	25R-4-F02	KX958077	100%	0	100%	0	sediment bel	Japan	Liu et al 2016	CATTACCGAGTGAGGGC
TU CIM 5648	ITS1&2	SR6R	ATTACCGAGTGAC	568	*Penicillium expansum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium expansum*	ATCC 7861	NR_077154	99.82%	0	99%	1			Schoch et al 2014	TCCGTAGGTGAACCTGC
TU CIM 5650	ITS1&2	SR6R	GGCCCTCTGGGTC	540	*Penicillium glabrum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium glabrum*	CBS 125543	MH863551	100%	0	99%	0			Vu et 2019	TTACTGAGTGAGGGCCC
TU CIM 5651	ITS1&2	SR6R	TTACTGAGTGAGC	561	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	BRO-2013	KF367536	99.29	0	100%	4	untreated dri	Portugal	Oliveira et al 2013	TGATGGCTCAGTGAGGC
TU CIM 5750	ITS1&2	SR6R	GAGTGAGGGCCCT	556	*Penicillium echinulatum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium echinulatum*	NBPen2013A12	KM115166	100%	0	100%	0	Wensleydale cheese		Banjara et al 2015	TTACCGAGTGAGGGCCC
TU CIM 5713	ITS1&2	SR6R	NCATTACCGAGTG	563	*Penicillium expansum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium expansum*	ATCC 7861	NR_077154	100%	0	99%	0			Schoch et al 2014	TCCGTAGGTGAACCTGC
TU CIM 5718	ITS1&2	SR6R	TTACTGAGTGAGC	566	*Penicillium cairnsense*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium cairnsense*	CBS 124325	NR_121508	99.82%	0	99%	1			Schoch et al 2014	ACCCCCCAGAGCCGGAA
TU CIM 5764	ITS1&2	SR6R	GNGTTTATTTACC	521	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	BRO-2013	KF367506	92.15%	0	99%	11	untreated dri	Portugal	Oliveira et al 2013	TGCATTGATGGCTCAGT
TU CIM 5766	ITS1&2	SR6R	CGAGTGAGGGCC	567	*Penicillium polonicum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium polonicum*	25R-4-F02	KX958077	99.82%	0	99%	1	sediment bel	Japan	Liu et al 2016	CATTACCGAGTGAGGGC
TU CIM 5767	ITS1&2	SR6R	TGAGTGAGGGCC	551	*Penicillium rudallense*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium rudallense*	DI16-90	LT558912	100%	0	99%	0			Guevara-Suarez et al 201	AAGTAAAAAGTCTAACA
TU CIM 5768	ITS1&2	SR6R	NCATTACCGAGTG	562	*Penicillium expansum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium expansum*	ATCC 7861	NR_077154	100%	0	99%	0			Schoch et al 2014	TCCGTAGGTGAACCTGC
TU CIM 5770	ITS1&2	SR6R	GTGAGGGCCCTCT	547	*Penicillium rudallense*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium rudallense*	DI16-90	LT558912	100%	0	100%	0			Guevara-Suarez et al 201	AAGTAAAAAGTCTAACA
TU CIM 5810	ITS1&2	SR6R	TTACCGAGTGAGC	577	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	5H1-P0-P5-3	KM232463	99.30%	0	99%	4			Redou et al 2015	GTAACAAGGTTTCCGTA
TU CIM 5825	ITS1&2	SR6R	GNCATTACCGAGT	547	*Aspergillus creber*	Aspergillus	Eurotiales	Eurotiomycete	*Aspergillus creber*	UTHSC 10-639	LN898690	100%	0	99%	0			Siqueira et al 2016	AAGTCGTAACAAGGTTT
TU CIM 5830	ITS1&2	SR6R	ATTACCGAGTGAC	572	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	5H1-P0-P5-3	KM232463	99.30%	0	100%	4			Redou et al 2015	GTAACAAGGTTTCCGTA
TU CIM 5831	ITS1&2	SR6R	AGTGAGGGCCCTT	566	*Penicillium robsamsonii*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium robsamsonii*	CBS 140573	NR_144866	98.58%	0	99%	8	mouse dung	Denmark	Houbraken et al 2016	CTTGGGATTGGCTTAGG
TU CIM 5959	ITS1&2	SR6R	GNCATTACCGAGT	589	*Talaromyces wortmannii*	Talaromyces	Eurotiales	Eurotiomycete	*Talaromyces wortmannii*	CBS 391.48	MH856412	99.83%	0	98%	1		Denmark	Vu et al 2019	TCAGGGAGGTTGGCAAC
TU CIM 5966	ITS1&2	SR6R	GNCATTACCGAGT	568	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	FF7	FJ379813	97.54%	0	99%	14	oak forest soi	Czech Republ	Baldrian et al 2011	TGCGGAGGATCATTACC
TU CIM 5973	ITS1&2	SR6R	GAGTGAGGGCCCT	558	*Penicillium cinnamopurpureum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium cinnamopurpureum*	NRRL 162	NR_121327	99.82%	0	98%	1			Schoch et al 2014	AAGGATCATTACCGAGT
TU CIM 5994	ITS1&2	SR6R	CATTACCGAGTGA	627	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	5H1-P0-P5-3	KM232463	99.82%	0	97%	1			Redou et al 2015	GTAACAAGGTTTCCGTA

TU CIM 5996	ITS1&2	SR6R	GGGCCCTCTGGGT	556	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	P17	JN246044	98.72%	0	98%	7	field soil	Australia	Daynes et al 2012	TCCGTAGGTGAACCTGC
TU CIM 6001	ITS1&2	SR6R	GAGCCCGCCTCAC	495	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	P17	JN246044	98.78%	0	99%	6	field soil	Australia	Daynes et al 2012	TCCGTAGGTGAACCTGC
TU CIM 6078	ITS1&2	SR6R	GNCATTACTGAGT	564	*Penicillium glabrum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium glabrum*	CBS 125543	MH863551	99.82%	0	99%	1			Vu et 2019	TTACTGAGTGAGGGCCC
TU CIM 6079	ITS1&2	SR6R	ATTACTGAGTGAG	568	*Penicillium glabrum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium glabrum*	CBS 125543	MH863551	99.47%	0	98%	3			Vu et 2019	TTACTGAGTGAGGGCCC
TU CIM 6081	ITS1&2	SR6R	TTACTGAGTGAGC	563	*Penicillium glabrum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium glabrum*	CBS 125543	MH863551	99.82%	0	99%	1			Vu et 2019	TTACTGAGTGAGGGCCC
TU CIM 6084	ITS1&2	SR6R	GNCATTACTGAGT	582	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	CLJ-3	LC373146	99.65%	0	98%	2	*Cinchona ledg*	Japan	Maehara et al 2019	
TU CIM 6090	ITS1&2	SR6R	CATTACTGAGTGA	571	*Penicillium glabrum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium glabrum*	CBS 125543	MH863551	99.82%	0	98%	1			Vu et 2019	TTACTGAGTGAGGGCCC
TU CIM 6173	ITS1&2	SR6R	NCATTACTGAGTG	571	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.47%	0	98%	3			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6188	ITS1&2	SR6R	CTGAGTTCTAAAA	964	*Annulohypoxylon viridistratun*	Annulohypoxy	Xylariales	Sordariomyce	*Annulohypoxylon viridistratun*	EK14010	KX376325	99.68%	0	95%	3		Thailand	Kuhnert et al 2017	CAGCGGAGGGATCATTA
TU CIM 6209	ITS1&2	SR6R	NCATTACCGAGTG	542	*Penicillium citrinum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium citrinum*	OR1	MH427065	100%	0	97%	0	orange natural infection		Shie et al 2019	CCTGCGGAAGGATCATT
TU CIM 6216	ITS1&2	SR6R	CATTACCGAGTGA	570	*Penicillium chrysogenum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium chrysogenum*	DI16-54	LT558876	99.82%	0	99%	1			Guevara-Suarez et al 201	GTAAAAATCGTAACAAG
TU CIM 6217	ITS1&2	SR6R	GNCATTACCGAGT	564	*Penicillium expansum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium expansum*	ATCC 7861	NR_077154	100%	0	99%				Schoch et al 2014	TCCGTAGGTGAACCTGC
TU CIM 6219	ITS1&2	SR6R	NCATTACCGAGTG	570	*Penicillium chrysogenum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium chrysogenum*	DI16-54	LT558876	99.65%	0	99%	0			Guevara-Suarez et al 201	GTAAAAATCGTAACAAG
TU CIM 6226	ITS1&2	SR6R	CATTACCGAGTGA	579	*Penicillium simplicissimum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium simplicissimum*	KUC5153	HM469430	99.82%	0	98%	1			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6227	ITS1&2	SR6R	ATTACCGAGTGAC	587	*Paecilomyces* sp.	Paecilomyces	Eurotiales	Eurotiomycete	*Paecilomyces* sp.	JCM 12546	AB217858	99.66%	0	98%	2			Nitta et al 2005	GGAAGTAAAAGTCGTAA
TU CIM 6228	ITS1&2	SR6R	NCATTACCGAGTG	576	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	JJK-2011	HM469409	99.48%	0	99%	3			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6229	ITS1&2	SR6R	ATTACTGAGTGAG	572	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.30%	0	99%	4			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6232	ITS1&2	SR6R	CATTACTGAGTGA	96	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	KSM-F532	LC315644	100%	3e-39	97%	0			Shibata et al 2017	GGAAGTAAAAGTCGTAA
TU CIM 6288	ITS1&2	SR6R	CATTACTGAGTGA	570	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.47%	0	98%	3			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6293	ITS1&2	SR6R	CATTACTGAGTGA	576	*Penicillium meleagrinum var. *	Penicillium	Eurotiales	Eurotiomycete	*Penicillium meleagrinum var. *	KUC1678	HM469412	99.65%	0	100%	2			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6300	ITS1&2	SR6R	GCGCGATGGACG	1020	*Penicillium pulvillorum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium pulvillorum*	WSF 239	AF178527	97.01%	0	97%	30			Tuthill et al 2001	TAATGCGTCCTTCCGCAG
TU CIM 6303	ITS1&2	SR6R	CATTACTGAGTGA	562	*Penicillium adametzioides*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium adametzioides*	F25-01	KX664354	99.82%	0	99%	1	floor surface	USA	Mayer et al 2016	AGGATCATTACTGAGTG
TU CIM 6313	ITS1&2	SR6R	NCATTACCGAGTG	587	*Aspergillus niger*	Aspergillus	Eurotiales	Eurotiomycete	*Aspergillus niger*	F48-02	KX664417	99.66%	0	99%	2	floor surface	USA	Mayer et al 2016	GTGACCTGCGGAGGATC
TU CIM 6315	ITS1&2	SR6R	CGGGNTCCAACCT	563	*Penicillium meleagrinum var. *	Penicillium	Eurotiales	Eurotiomycete	*Penicillium meleagrinum var. *	KUC1678	HM469412	98.76%	0	100%	7			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6316	ITS1&2	SR6R	GNCATTACTGAGT	564	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.64%	0	98%	2			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6318	ITS1&2	SR6R	ATTACTGAGTGAG	566	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.46%	0	98%	3			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6319	ITS1&2	SR6R	ATTACTGAGTGAG	570	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycete	*Penicillium* sp.	CGMCC 3.18178	KX961214	95.80%	0	99%	24			Shibata et al 2017	GGAAGTAAAAGTCGTAA
TU CIM 6320	ITS1&2	SR6R	NCATTACTGAGTG	533	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.81%	0	99%	1			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6327	ITS1&2	SR6R	CATTACTGAGTGA	566	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.46%	0	98%	3			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6329	ITS1&2	SR6R	GNCATTACTGAGT	575	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.30%	0	98%	4			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6330	ITS1&2	SR6R	NCATTACTGAGTG	573	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	99.30%	0	98%	4			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 7007	ITS1&2	SR6R	NCATTACCGAGTG	578	*Penicillium rubens*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium rubens*	DI16-52	LT558874	99.83%	0	98%	1			Guevara-Suarez et al 201	ATGGAAGTAAAAAATCG
TU CIM 7014	ITS1&2	SR6R	GNCATTACCGAGT	546	*Penicillium citrinum*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium citrinum*	CBS 117.64	MH858380	99.63%	0	99%	2			Vu et al 2019	GGCTCAGTGAGGCCTTC
TU CIM 7035	ITS1&2	SR6R	GNCATTACTGAGT	562	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1626	HM469407	98.93%	0	99%	6			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 7036	ITS1&2	SR6R	NCATTACTGAGTG	569	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1627	HM469408	99.11%	0	98%	5			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 9319	ITS1&2	SR6R	ATTACTGAGTGAG	570	*Penicillium multicolor*	Penicillium	Eurotiales	Eurotiomycete	*Penicillium multicolor*	KUC1627	HM469408	99.30%	0	99%	4			Jang et al 2011	TCCGTAGGTGAACCTGC
TU CIM 6180	ITS1&2	SR6R	ATTACCGAGTTAG	612	*Cyphellophora reptans*	Cyphellophora	Chaetothyriale	Eurotiomycete	*Cyphellophora reptans*	CBS 113.85	NR_121346	89.56%	0	99%	64			Schoch et al 2014	GGATCATTACCGAGTTA
TU CIM 5967	ITS1&2	SR6R	NCATTAACGAGTT	608	*Cladophialophora chaetospira*	Cladophialopl	Chaetothyriale	Eurotiomycete	*Cladophialophora chaetospira*	CBS 114747	EU035403	93.09%	0	99%	42	*Phyllostachys*	China	Crous et al 2007	AGAGGAAGTAAAAGTCG
TU CIM 5988	ITS1&2	SR6R	NNCATTACCGAGT	605	*Exophiala* sp	Exophiala	Chaetothyriale	Eurotiomycete	*Exophiala* sp	2H5-S0-P7-3	KM232445	87.54%	0	98%	78			Redou et al 2015	AACAAGGTCTTCGTAGG
TU CIM 6182	ITS1&2	SR6R	CATTAACGAGTTA	615	*Cladophialophora immunda*	Cladophialopl	Chaetothyriale	Eurotiomycete	*Cladophialophora immunda*	CBS 126871	MH864253	97.23%	0	98%	17		Brazil	Vu et al 2019	TCACACCTGTGTCCCTAG
TU CIM 6200	ITS1&2	SR6R	NCATTAACGAGTT	609	*Fonsecaea minima*	Fonsecaea	Chaetothyriale	Eurotiomycete	*Fonsecaea minima*	CBS 126022	MH863890	92.03%	0	98%	49		Brazil	Vu et al 2019	GCTTTGTACACACCGCCC
TU CIM 6205	ITS1&2	SR6R	CATTACCGAGTTA	621	*Chaetothyriales* sp.	Chaetothyriale	Chaetothyriale	Eurotiomycete	*Chaetothyriales* sp.	CBS 128948	KX822492	86.78%	0	99%	83	*Tetrathylacium macrophyllu*		Vasse et al 2017	CTAAGTATAAGCAATCAT
TU CIM 5820	ITS1&2	SR6R	NCATTACCGAGTG	561	*Talaromyces stollii*	Talaromyces	Eurotiales	Eurotiomycete	*Talaromyces stollii*	CBS 408.93	NR_111781	99.82%	0	99%	1			Schoch et al 2014	AAGGATCATTACCGAGT
TU CIM 5821	ITS1&2	SR6R	NCATTACCGAGTG	567	*Talaromyces stollii*	Talaromyces	Eurotiales	Eurotiomycete	*Talaromyces stollii*	CBS 408.93	NR_111781	99.65%	0	99%	2			Schoch et al 2014	AAGGATCATTACCGAGT
TU CIM 6991	ITS1&2	SR6R	NCATTAACGAGTT	618	*Cladophialophora immunda*	Cladophialopl	Chaetothyriale	Eurotiomycete	*Cladophialophora immunda*	CBS 126871	MH864253	91.59%	0	99%	53		Brazil	Vu et al 2019	TCACACCTGTGTCCCTAG
TU CIM 6995	ITS1&2	SR6R	TCTTTTGGCCCAA	569	*Chaetothyriales* sp.	Chaetothyriale	Chaetothyriale	Eurotiomycete	*Chaetothyriales* sp.	KhNk2-2b	HQ634648	99.65%	0	99%	2	*Crematogaster* sp. ant don		Voglmayer et al 2011	CATTATCGAGTTAGGGTC
TU CIM 6996	ITS1&2	SR6R	ATTATCGAGTTAG	583	*Chaetothyriales* sp.	Chaetothyriale	Chaetothyriale	Eurotiomycete	*Chaetothyriales* sp.	MACP1	HQ634653	98.11%	0	98%	11	*Cladomyrma petalae* ant d		Voglmayer et al 2011	CACACCGCCCGTCGCTAC
TU CIM 6997	ITS1&2	SR6R	CATTATCGAGTTA	585	*Chaetothyriales* sp.	Chaetothyriale	Chaetothyriale	Eurotiomycete	*Chaetothyriales* sp.	MACP1	HQ634653	98.11%	0	99%	1	*Cladomyrma petalae* ant d		Voglmayer et al 2011	CACACCGCCCGTCGCTAC
TU CIM 7002	ITS1&2	SR6R	AGCCTATTTCCTG	646	*Chaetothyriales* sp.	Chaetothyriale	Chaetothyriale	Eurotiomycete	*Chaetothyriales* sp.	MACP1	HQ634653	90.98%	0	93%	15	*Cladomyrma petalae* ant d		Voglmayer et al 2011	CACACCGCCCGTCGCTAC
TU CIM 5631	ITS1&2	SR6R	NCATTACCGAGTT	520	*Lasiodiplodia theobromae*	Lasiodiplodia	Botryosphaeri	Dothideomyce	*Lasiodiplodia theobromae*	CBS 111530	FJ150695	98.46%	0	99%	8	*Leucospermu*	USA: Hawaii	Marincowitz et al 2008	ATGGCTTAGTGAGGCCT

TU CIM 6037	ITS1&2	SR6R	GNCATTACCGAGT	824	*Lasiodiplodia pseudotheobrom*	Lasiodiplodia	Botryosphaer	Dothideomyc	*Lasiodiplodia pseudotheobrom*	CMM4008	JX464090	99.42%	0	99%	3	*Mangifera inc*	Brazil	Marques et al 2014	TGAACCTGCGGAAGGAT
TU CIM 6045	ITS1&2	SR6R	GNCATTACCGAGT	570	*Lasiodiplodia parva*	Lasiodiplodia	Botryosphaer	Dothideomyc	*Lasiodiplodia parva*	CBS 456.78	MH861166	99.05%	0	92%	5			Vu et al 2019	ATAACAAGGTTTCCGTA
TU CIM 6047	ITS1&2	SR6R	GNCATTACCGAGT	821	*Lasiodiplodia parva*	Lasiodiplodia	Botryosphaer	Dothideomyc	*Lasiodiplodia parva*	CBS 456.78	MH861166	99.05%	0	99%	5			Vu et al 2019	ATAACAAGGTTTCCGTA
TU CIM 6052	ITS1&2	SR6R	NGNCATTACCGAC	536	*Lasiodiplodia parva*	Lasiodiplodia	Botryosphaer	Dothideomyc	*Lasiodiplodia parva*	CBS 456.78	MH861166	98.87%	0	98%	6			Vu et al 2019	ATAACAAGGTTTCCGTA
TU CIM 6095	ITS1&2	SR6R	ATTACTGAGTTAC	573	*Endomelanconiopsis* sp.	Endomelanco	Botryosphaer	Dothideomyc	*Endomelanconiopsis* sp.	F1133	KU747730	97.86%	0	97%	12	*Campyloneur*	Panama	Del Olmo-Ruiz et al 2017	CGAGTTTTGGGGGCTCT
TU CIM 6179	ITS1&2	SR6R	ATTACTGAGTTAC	569	*Endomelanconiopsis microspo*	Endomelanco	Botryosphaer	Dothideomyc	*Endomelanconiopsis microspo*	CBS 353.97	KF766165	96.45%	0	98%	20			Slippers et al 2013	AACAAGGTTTCCGTAGG
TU CIM 6186	ITS1&2	SR6R	NCTCNTCACACCC	542	*Endomelanconiopsis* sp.	Endomelanco	Botryosphaer	Dothideomyc	*Endomelanconiopsis* sp.	F1133	KU747730	97.98%	0	99%	11	*Campyloneur*	Panama	Del Olmo-Ruiz et al 2017	CGAGTTTTGGGGGCTCT
TU CIM 6187	ITS1&2	SR6R	TCACACCCTATGT	535	*Endomelanconiopsis* sp.	Endomelanco	Botryosphaer	Dothideomyc	*Endomelanconiopsis* sp.	F1133	KU747730	98.68%	0	98%	7	*Campyloneur*	Panama	Del Olmo-Ruiz et al 2017	CGAGTTTTGGGGGCTCT
TU CIM 6183	ITS1&2	SR6R	CCTCCGTGGCCCG	506	*Capnodium* sp.	Capnodium	Capnodiales	Dothideomyc	*Capnodium* sp.	SC11d10p11-8	HQ631045	95.27%	0	99%	24	*Saccharum officinarum*		Shrestha et al 2011	TCTTGGTCATTTAGAGGA
TU CIM 7015	ITS1&2	SR6R	ATTANGAGCGAA	558	*Scorias spongiosa*	Scorias	Capnodiales	Dothideomyc	*Scorias spongiosa*	CBS:325.33	GU214696	83.70%	3,00E-134	96%	90	aphid		Crous et al 2009	AAGTATAAGCAATCTATA
TU CIM 7077	ITS1&2	SR6R	ATTAACGAGCGAA	558	*Scorias spongiosa*	Scorias	Capnodiales	Dothideomyc	*Scorias spongiosa*	CBS:325.33	GU214696	83.69%	5,00E-137	96%	90	aphid		Crous et al 2009	AAGTATAAGCAATCTATA
TU CIM 5719	ITS1&2	SR6R	CCCCGGTCTAACC	526	*Cladosporium tenuissimum*	Cladosporium	Capnodiales	Dothideomyc	*Cladosporium tenuissimum*	DTO:324-C6	MF473304	99.81%	0	98%	1	Indoor air	China	Bensch et al 2018	ATTGAATGGCTCGGTGA
TU CIM 6286	ITS1&2	SR6R	CCCGGTTTACCAC	513	*Cladosporium* sp.	Cladosporium	Capnodiales	Dothideomyc	*Cladosporium* sp.	LD-N5	EF424419	99.42%	0	100%	3			Ding et al 2018	TCCGTAGGTGAACCTGC
TU CIM 6082	ITS1&2	SR6R	ACTACGGAAGCC	912	*Corynespora smithii*	Corynespora	Pleosporales	Dothideomyc	*Corynespora smithii*	L133	KY984299	81.36%	0	98%	176	*Fagus sylvatic*	Austria	Voglmayer et al 2017	CTACCGATTGAATGGCTC
TU CIM 6181	ITS1&2	SR6R	CCTTATGGATGGC	1005	*Hermatomyces krabiensis*	Hermatomyce	Pleosporales	Dothideomyc	*Hermatomyces krabiensis*	MFLUCC:160249I	KX525750	90.36%	1,00E-147	40%	40	forest soil	Thailand	Tibpromma et al 2016	CCGCGAGGTTGGGTTGA
TU CIM 5836	ITS1&2	SR6R	CCTTATGGATGGC	1005	*Hermatomyces krabiensis*	Hermatomyce	Pleosporales	Dothideomyc	*Hermatomyces krabiensis*	MFLUCC:160249I	KX525750	90.36%	1,00E-147	40%	40	forest soil	Thailand	Tibpromma et al 2016	CCGCGAGGTTGGGTTGA
TU CIM 5839	ITS1&2	SR6R	CATTACAGTTGGG	544	*Lophiotrema mucilaginosis*	Lophiotrema	Pleosporales	Dothideomyc	Lophiotrema mucilaginosis	HMAS 255437	NR_164039	100%	0	95%	0	dead wood	China	Phookamsak et al. 2018	CCTTCCGTAGGGTGACCT
TU CIM 5785	ITS1&2	SR6R	TTACAACAAGGCT	567	*Periconia byssoides*	Periconia	Pleosporales	Dothideomyc	*Periconia byssoides*	50338	KC954157	99.10%	0	97%	5	*Angelica sylv*	Lithuania	Markovskaja et al 2014	GGAAGTAAAAGTCGTAA
TU CIM 5815	ITS1&2	SR6R	TACTGAGTGAGG	516	*Pseudocercosporella fraxini*	Pseudocercos	Capnodiales	Dothideomyc	*Pseudocercosporella fraxini*	MUT<ITA>:4372	KC339227	99,59%	0	95%	2		Italy: Ligury, F	Panno et al 2013	AAAAGTCGTAACAAGGT
TU CIM 5819	ITS1&2	SR6R	CATTACTGAGTGA	518	*Pseudocercosporella fraxini*	Pseudocercos	Capnodiales	Dothideomyc	*Pseudocercosporella fraxini*	3R-3-F01	KX958044	99,02%	0	98%	5		Japan: Shimo	Liu et al 2016	CCGAAGTGAGGGCCTCG
TU CIM 5838	ITS1&2	SR6R	CATTACTGAGTGA	526	*Pseudocercosporella fraxini*	Pseudocercos	Capnodiales	Dothideomyc	*Pseudocercosporella fraxini*	3R-3-F01	KX958044	99,02%	0	96%	5		Japan: Shimo	Liu et al 2016	CCGAAGTGAGGGCCTCG
TU CIM 5951	ITS1&2	SR6R	NCATTACTGAGTG	531	*Acrodontium crateriforme*	Acrodontium	Capnodiales	Dothideomyc	*Acrodontium crateriforme*	CPC 11509	GU214682	99,81%	0	98%	1		South Korea	Crous et al 2009	GCAACTATACGGTGAAA
TU CIM 5965	ITS1&2	SR6R	NCATTACTGAGAA	526	*Readeriella guyanensis*	Readeriella	Capnodiales	Dothideomyc	*Readeriella guyanensis*	CBS 117550	EU707900	98,85%	0	99%	6	leaf litter	French Guian	Crous et al 2018	ATGGCTCAGTGAGGCCT
TU CIM 5968	ITS1&2	SR6R	NNCATTACTGAGT	526	*Readeriella guyanensis*	Readeriella	Capnodiales	Dothideomyc	*Readeriella guyanensis*	CBS 117550	EU707900	98,85%	0	99%	6	leaf litter	French Guian	Crous et al 2018	ATGGCTCAGTGAGGCCT
TU CIM 5970	ITS1&2	SR6R	GNCATTACTGAGT	535	*Readeriella patrickii*	Readeriella	Capnodiales	Dothideomyc	*Readeriella patrickii*	CBS 124987	MH863439	91,02%	0	94%	46		Australia	Vu et al 2019	ACAAGGTCTCCGTAGGT
TU CIM 5982	ITS1&2	SR6R	GNCATTACTGAGT	521	*Readeriella patrickii*	Readeriella	Capnodiales	Dothideomyc	*Readeriella patrickii*	CBS 124987	MH863439	91,02%	0	97%	46		Australia	Vu et al 2019	ACAAGGTCTCCGTAGGT
TU CIM 6000	ITS1&2	SR6R	CTGAGTGAGGGC	538	*Readeriella nontingens*	Readeriella	Capnodiales	Dothideomyc	*Readeriella nontingens*	CPC:14444	GQ852786	90,58%	0	96%	49	*Eucalyptus ob*	Australia	Crous,P.W., 2009	GGGCCGGAAAGTTCGTC
TU CIM 6021	ITS1&2	SR6R	GNCATTACTGAGT	538	*Readeriella nontingens*	Readeriella	Capnodiales	Dothideomyc	*Readeriella nontingens*	CPC:14444	GQ852786	90,58%	0	96%	49	*Eucalyptus ob*	Australia	Crous,P.W., 2009	GGGCCGGAAAGTTCGTC
TU CIM 6093	ITS1&2	SR6R	CTGAGTGAGGGC	525	*Readeriella patrickii*	Readeriella	Capnodiales	Dothideomyc	*Readeriella patrickii*	CBS 124987	MH863439	91,12%	0	95%	45	type material	Australia	Vu et al2019	ACAAGGTCTCCGTAGGT
TU CIM 6094	ITS1&2	SR6R	AAGGGCCTTCGG	508	*Readeriella guyanensis*	Readeriella	Capnodiales	Dothideomyc	*Readeriella guyanensis*	CBS 117550	EU707900	100,00%	0	100%	0	leaf litter	French Guian	Crous et al 2008	ATGGCTCAGTGAGGCCT
TU CIM 6096	ITS1&2	SR6R	GGGCCTTCGGGT	507	*Readeriella guyanensis*	Readeriella	Capnodiales	Dothideomyc	*Readeriella guyanensis*	CBS 117550	EU707900	99,60%	0	99%	2	leaf litter	French Guian	Crous et al 2008	ATGGCTCAGTGAGGCCT
TU CIM 6184	ITS1&2	SR6R	NCATTACTGAGAA	526	*Readeriella guyanensis*	Readeriella	Capnodiales	Dothideomyc	*Readeriella guyanensis*	CBS 117550	EU707900	99,81%	0	98%	1	leaf litter	French Guian	Crous et al 2008	ATGGCTCAGTGAGGCCT
TU CIM 6998	ITS1&2	SR6R	CATTACTGAGTGA	524	*Neophaeothecoidea proteae*	Neophaeothe	Capnodiales	Dothideomyc	*Neophaeothecoidea proteae*	CBS 114129	EU707898	87.36%	6,00E-166	99%	68	*Protea repens*	South Africa	Crous et al 2008	ATGGCTCAGTGAGGCCT
TU CIM 6999	ITS1&2	SR6R	NNCATTATCGAGT	560	*Fumiglobus pieridicola*	Fumiglobus	Capnodiales	Dothideomyc	*Fumiglobus pieridicola*	UBC F23788	NR_153985	83.82%	1e-133	96%	88	*Pieris japonic*	Canada	Bose et al 2014	CCGTAGGTGAACCTGCG
TU CIM 5786	ITS1&2	SR6R	ATTAAATTTCTTG	563	*Setophoma yingyisheniae*	Setophoma	Pleosporales	Dothideomyc	*Setophoma yingyisheniae*	CGMCC 3.19527	NR_164602	100%	0	90%	0	*Camellia sine*	China	Liu et al 2019	GGGTCGTGTGTCATAAC
TU CIM 5806	ITS1&2	SR6R	ATTAAATTTCTTG	563	*Setophoma yingyisheniae*	Setophoma	Pleosporales	Dothideomyc	*Setophoma yingyisheniae*	CGMCC 3.19527	NR_164602	100%	0	90%	0	*Camellia sine*	China	Liu et al 2019	GGGTCGTGTGTCATAAC
TU CIM 5808	ITS1&2	SR6R	TTAAATTTCTTGG	564	*Setophoma yingyisheniae*	Setophoma	Pleosporales	Dothideomyc	*Setophoma yingyisheniae*	CGMCC 3.19527	NR_164602	100%	0	90%	0	*Camellia sine*	China	Liu et al 2019	GGGTCGTGTGTCATAAC
TU CIM 6089	ITS1&2	SR6R	AATTTCTTGGGCG	569	*Setophoma yingyisheniae*	Setophoma	Pleosporales	Dothideomyc	*Setophoma yingyisheniae*	CGMCC 3.19527	NR_164602	100%	0	89%	0	*Camellia sine*	China	Liu et al 2019	GGGTCGTGTGTCATAAC
TU CIM 6164	ITS1&2	SR6R	AGCTCGTCCGCGA	1041	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	90.98%	0	50%	48	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6170	ITS1&2	SR6R	NGCTCGTCCGCGA	1047	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.34%	0	50%	46	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6167	ITS1&2	SR6R	TCGTCCGCGAGGT	1048	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.53%	0	50%	45	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6172	ITS1&2	SR6R	NNGCTCGTCCGCC	1041	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.46%	0	50%	46	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6192	ITS1&2	SR6R	GCTCGTCCGCGAC	1048	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.53%	0	50%	45	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6193	ITS1&2	SR6R	NNGCTCGTCCGCC	1056	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.38%	0	51%	47	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6194	ITS1&2	SR6R	NGCTCGTCCGCGA	1043	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.17%	0	50%	47	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGC
TU CIM 6206	ITS1&2	SR6R	GGGAMAGCTCGT	1059	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.36%	0	51%	47	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6233	ITS1&2	SR6R	GCTCGTCCGCGAC	1050	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.45%	0	50%	40	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6269	ITS1&2	SR6R	TCGAGATGATCCT	1040	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.36%	0	52%	47	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6277	ITS1&2	SR6R	CGNGGTCGAGAT	1041	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.62%	0	51%	45	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6278	ITS1&2	SR6R	GGTCGAGATGAT	1036	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.43%	0	51%	45	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG

TU CIM 6301	ITS1&2	SR6R	CTCGTCCGCGAG(	1049	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.48%	0	51%	46	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6310	ITS1&2	SR6R	ATGATCCTTCCGC	799	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	P1130	KT268448	89.00%	3,00E-129	86%	43	*Microthlaspi*	France	Glynou et al 2016	TCGACCGCAAGGTCGAG
TU CIM 6311	ITS1&2	SR6R	TCGTCCGCGAGG1	1048	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.31%	0	51%	47	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6312	ITS1&2	SR6R	GCTCGTCCGCGA(	1045	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.23%	0	51%	46	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6321	ITS1&2	SR6R	GCTCGTCCGCGA(	1049	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.31%	0	51%	47	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 5956	ITS1&2	SR6R	GCTCGTCCGCGA(	1054	*Pleosporales* sp		Pleosporales	Dothideomyc	*Pleosporales* sp	REF117	JN859337	91.36%	0	51%	47	*Juniperus con*	Hungary	Knapp et al 2012	TCTTGGTCCATTTAGAGG
TU CIM 6237	ITS1&2	SR6R	TTAAAGAGTAAG(	566	*Aureobasidium melanogenum*	Aureobasidiu	Dothideales	Dothideomyc	*Aureobasidium melanogenum*	KAS5840	KY659501	100%	0	98%	0	house dust		Humphries et al 2017	AGTGAGGCCTTCGGACT
TU CIM 5972	ITS1&2	SR6R	AGTAAGGGTGCT(	561	*Aureobasidium melanogenum*	Aureobasidiu	Dothideales	Dothideomyc	*Aureobasidium melanogenum*	KAS5840	KY659501	99.82%	0	98%	1	house dust		Humphries et al 2017	AGTGAGGCCTTCGGACT
TU CIM 5991	ITS1&2	SR6R	TTAAAGAGTAAG(	566	*Aureobasidium melanogenum*	Aureobasidiu	Dothideales	Dothideomyc	*Aureobasidium melanogenum*	KAS5840	KY659501	100%	0	98%	0	house dust		Humphries et al 2017	AGTGAGGCCTTCGGACT
TU CIM 7029	ITS1&2	SR6R	TATCGTGGGGGC1	520	*Preussia* sp.	Preussia	Pleosporales	Dothideomyc	*Preussia* sp.	CF279773	KX710256	88.65%	4,00E-173	98%	59	*Retama sphae*	Spain	Gonzalez-Menendez et a	GGATCATTATCGTGGGG
TU CIM 7032	ITS1&2	SR6R	GCGCAACACTTG(	967	*Teichospora quercus*	Teichospora	Pleosporales	Dothideomyc	*Teichospora quercus*	CBS:143396	NR_159069	90.33%	e-175	52%	47	*Quercus* sp. l	France	Crous et al 2018	GTAACAAGGTTTCCGTA
TU CIM 5801	ITS1&2	SR6R	ATTATAGAGAATA	538	*Infundichalara microchona*	Infundichalara	Helotiales	Leotiomycetes	*Infundichalara microchona*	CBS:175.74	NR_154074	89.23%	3e-179	95%	56	*Pinus sylvestr*	Netherlands	Chen et al 2016	GTAACAAGGTTTCCGTA
TU CIM 5802	ITS1&2	SR6R	ATACCGCCCTCCG	518	*Infundichalara microchona*	Infundichalara	Helotiales	Leotiomycetes	*Infundichalara microchona*	CBS:175.74	NR_154074	89.53%	2e-176	96%	53	*Pinus sylvestr*	Netherlands	Chen et al 2016	GTAACAAGGTTTCCGTA
TU CIM 5804	ITS1&2	SR6R	ATTATAGAGAATA	529	*Infundichalara microchona*	Infundichalara	Helotiales	Leotiomycetes	*Infundichalara microchona*	CBS:175.74	NR_154074	89.23%	3e-179	97%	56	*Pinus sylvestr*	Netherlands	Chen et al 2016	GTAACAAGGTTTCCGTA
TU CIM 5716	ITS1&2	SR6R	AGAGTTCATGCC(	519	*Sclerotinia sclerotiorum*	Sclerotinia	Helotiales	Leotiomycetes	*Sclerotinia sclerotiorum*	ATCC 46762	JX648201	97.30%	0	99%	14	*Brassica olerc*	Australia	Naumann et al 2013	AGTTCATGCCCGAAAGG
TU CIM 5774	ITS1&2	SR6R	GAGTTCATGCCCG	510	*Sclerotinia sclerotiorum*	Sclerotinia	Helotiales	Leotiomycetes	*Sclerotinia sclerotiorum*	ATCC 46762	JX648201	97.45%	0	99%	13	*Brassica olerc*	Australia	Naumann et al 2013	AGTTCATGCCCGAAAGG
TU CIM 5824 NE	ITS1&2	SR6R	ATTACAGAATTCC	505	*Incrucipulum pseudosulphureli*	Incrucipulum	Helotiales	Leotiomycetes	*Incrucipulum pseudosulphureli*	TNS:F-81441	LC438570	86.98%	3e-154	99%	66	*Myrica gale v*	Japan	Tochihara et al 2019	TCTTGGTCATTTAGAGGA
TU CIM 5841 NE	ITS1&2	SR6R	ACAGTAGCTCAG(	1128	*Paraphaeosphaeria neglecta*	Paraphaeosph	Pleosporales	Dothideomyc	*Paraphaeosphaeria neglecta*	CBS:627.94	JX496101	80.24%	4,00E-73	35%	81		Canada	Verkley et al 2014	GCCTTTGCAGCTGGAGA
TU CIM 6983	ITS1&2	SR6R	ACCTCCTTTCTAA(	951	*Unclear*														
TU CIM 7001	ITS1&2	SR6R	CACGCTCTGCGG(	586	*Anthopsis catenata*	Anthopsis	Chaetothyrial	Eurotiomycet	*Anthopsis catenata*	CBS 492.81	NR_159623	84.44%	2e-141	90%	84		Germany	Vu et al 2019	GTAACAAGGTTTCCGTA
TU CIM 5494	ITS1&2	SR6R	TTACTGAGTGAG(	560	*Penicillium* sp.	Penicillium	Eurotiales	Eurotiomycet	*Penicillium* sp.	KSM-F532	LC315644	98.92%	0	99%	6			Shibata et al 2017	GGAAGTAAAAGTCGTAA
TU CIM 5710	ITS1&2	SR6R	GAGTGAGGGCCC	556	*Penicillium echinulatum*	Penicillium	Eurotiales	Eurotiomycet	*Penicillium echinulatum*	NBPen2013A12	KM115166	100%	0	100%	0	Wensleydale cheese		Banjara et al 2015	TTACCGAGTGAGGGCCC
TU CIM 5508	ITS1&2	SR6R	TTACAGTATTCTT	616	*Debaryomyces fabryi*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces fabryi*	Y-17914	KJ705004	100%	0	99%	0			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 5567	ITS1&2	SR6R	TTCTTTTTGCCAG(	616	*Debaryomyces fabryi*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces fabryi*	Y-17914	KJ705004	99.51%	0	100%	3			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 5568	ITS1&2	SR6R	TTACAGAATGAAA	488	*Candida orthopsilosis*	Candida	Saccharomyce	Saccharomyce	*Candida orthopsilosis*	MCO456	AY391846	100%	0	99%	0			Rycovska et al 2004	GTCGTAACAAGGTTTCC
TU CIM 5812	ITS1&2	SR6R	TACAGTATTCTTT	581	*Meyerozyma guilliermondii*	Meyerozyma	Saccharomyce	Saccharomyce	*Meyerozyma guilliermondii*	CBS:12037	KY104257	100%	0	100%	0			Vu et al 2016	TTTAAGTCCCCTGCCCTT
TU CIM 5566	ITS1&2	SR6R	TTCTTTTTGCCAG(	607	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS 2334	KJ705003	99.50%	0	99%	3			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 5826	ITS1&2	SR6R	TACAGTATTCTTT	620	*Debaryomyces fabryi*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces fabryi*	Y-17914	KJ705004	100%	0	98%	0			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 5979	ITS1&2	SR6R	CATTACCGAGTTT	536	*Fusarium* sp	Fusarium	Hypocreales	sordariomyce	*Fusarium* sp	EML-GYP3	HM560021	99.81%	0	100%	1			Lee et al 2012	GGTCTGTGACGCGGAGG
TU CIM 6245	ITS1&2	SR6R	GTATTCTTTTTGC(	609	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS 2334	KJ705003	100%	0	100%	0			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 6239	ITS1&2	SR6R	AGTATTCTTTTTG(	614	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS 2334	KJ705003	100%	0	99%	4			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 6244	ITS1&2	SR6R	ACAGTATTCTTTT	627	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS:12037	KJ705003	99.20%	0	99%	5			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 6235	ITS1&2	SR6R	TTACAGTATTCTT	587	*Meyerozyma guilliermondii*	Meyerozyma	Saccharomyce	Saccharomyce	*Meyerozyma guilliermondii*	CBS:12037	KY104257	100%	0	98%				Vu et al 2016	TTTAAGTCCCCTGCCCTT
TU CIM 6236	ITS1&2	SR6R	GNCATTACAGTTT	538	*Candida cylindracea*	Candida	Saccharomyce	Saccharomyce	*Candida cylindracea*	CBS:7869	KY102039	93.73%	0	96%	33	food	Portugal	Vu et al 2016	TTTGTACACACCGCCCGT
TU CIM 6238	ITS1&2	SR6R	GAATGAAAAGTG(	498	*Candida parapsilosis*	Candida	Saccharomyce	Saccharomyce	*Candida parapsilosis*	CBS:2193	KY102320	100%	0	98%	0			Vu et al 2016	CTGCCCTTTGTACACACC
TU CIM 6240	ITS1&2	SR6R	ATAATATTCTTAC	381	*Kodamaea ohmeri*	Kodamaea	Saccharomyce	Saccharomyce	*Kodamaea ohmeri*	PMM10-1288L	KP132356	100%	0	99%	0		France	Irinyi et al 2015	GAGGCATCGGGATGGAA
TU CIM 6068	ITS1&2	SR6R	TTTGCTTAATTGC	508	*Candida tropicalis*	Candida	Saccharomyce	Saccharomyce	*Candida tropicalis*		EU288196	99.60%	0	99%	2			Desnos-Ollivier et al 2008	GGGGGCAACTCCATTCT
TU CIM 6071	ITS1&2	SR6R	AGTTTAGGCGTG1	522	*Candida cylindracea*	Candida	Saccharomyce	Saccharomyce	*Candida cylindracea*	CBS:6330	KY102038	99.42%	0	96%	3	soil		Vu et al 2016	TCGTAACAAGGTTTCCGT
TU CIM 5955	ITS1&2	SR6R	GTATTCTTCGGTG	597	*Candida* sp	Candida	Saccharomyce	Saccharomyce	*Candida* sp	VN11-F0569	LC076104	90.40%	0	99%	58	leaf of *Melas*	Vietnam	Luong et al 2015	AAGGATCATTAAAGTATT
TU CIM 5958	ITS1&2	SR6R	ACAGCAAACAATA	327	*Geotrichum candidum*	Galactomyces	Saccharomyce	Saccharomyce	*Galactomyces candidum*	TOM_YEAST	KF112070	96.94%	1e-155	100%	10	*Solanum lyco*	USA	Bourret et al 2013	TCCCTTTGTACACACCGC
TU CIM 5993	ITS1&2	SR6R	AATATTTGTGAAA	344	*Geotrichum candidum*	Galactomyces	Saccharomyce	Saccharomyce	*Galactomyces candidum*	TOM_YEAST	KF112071	99.42%	3e-176	100%	2	*Solanum lyco*	USA	Bourret et al 2013	TCCCTTTGTACACACCGC
TU CIM 5977	ITS1&2	SR6R	TTAAGAATTGATA	347	*Geotrichum candidum*	Galactomyces	Saccharomyce	Saccharomyce	*Galactomyces candidum*	TOM_YEAST	KF112072	99.14%	1e-175	99%	3	*Solanum lyco*	USA	Bourret et al 2013	TCCCTTTGTACACACCGC
TU CIM 5985	ITS1&2	SR6R	TAATATTTGTGAA	336	*Geotrichum candidum*	Galactomyces	Saccharomyce	Saccharomyce	*Galactomyces candidum*	TOM_YEAST	KF112073	99.40%	9e-172	100%	2	*Solanum lyco*	USA	Bourret et al 2013	TCCCTTTGTACACACCGC
TU CIM 5974	ITS1&2	SR6R	CNANTTTTTTAAT(	289	*Galactomyces pseudocandidus*	Galactomyces	Saccharomyce	Saccharomyce	*Galactomyces pseudocandidus*	CBS:10073	KY103458	92.88%	2,00E-117	96%	20	soil		Vu et al 2016	GTACACACCGCCCGTCG
TU CIM 5980	ITS1&2	SR6R	TATTGATATTTAT	344	*Galactomyces* sp.	Galactomyces	Saccharomyce	Saccharomyce	*Galactomyces* sp.	JFMG-CM- Y317	MG599261	92.80%	3,00E-137	99%	25	rotting wood	Brazil	Lopes et al 2018	TATTGATATTTATTATTT
TU CIM 5987	ITS1&2	SR6R	TATTGATATTTAT	344	*Galactomyces* sp.	Galactomyces	Saccharomyce	Saccharomyce	*Galactomyces* sp.	JFMG-CM- Y317	MG599261	92.80%	3,00E-137	99%	25	rotting wood	Brazil	Lopes et al 2018	TATTGATATTTATTATTT
TU CIM 6260	ITS1&2	SR6R	ATTACAGTATTCT	630	*Schwanniomyces vanrijiae var*	Schwanniomy	Saccharomyce	Saccharomyce	*Schwanniomyces vanrijiae var*	CBS:3024	KY105408	100%	0	96%	0	soil	South Africa	Vu et al 2016	CGTAACAAGGTTTCCGTA
TU CIM 6261	ITS1&2	SR6R	GTATTCTTTTTGC(	618	*Schwanniomyces vanrijiae var*	Schwanniomy	Saccharomyce	Saccharomyce	*Schwanniomyces vanrijiae var*	CBS:3024	KY105408	100%	0	97%	0	soil	South Africa	Vu et al 2016	CGTAACAAGGTTTCCGTA
TU CIM 6262	ITS1&2	SR6R	AGTATTCTTTTTG(	613	*Schwanniomyces vanrijiae var*	Schwanniomy	Saccharomyce	Saccharomyce	*Schwanniomyces vanrijiae var*	CBS:3024	KY105408	100%	0	98%	0	soil	South Africa	Vu et al 2016	CGTAACAAGGTTTCCGTA
TU CIM 6263	ITS1&2	SR6R	TTACAGTATTCTT	628	*Schwanniomyces vanrijiae var*	Schwanniomy	Saccharomyce	Saccharomyce	*Schwanniomyces vanrijiae var*	CBS:3024	KY105408	100%	0	96%	0	soil	South Africa	Vu et al 2016	CGTAACAAGGTTTCCGTA

TU CIM 6242	ITS1&2	SR6R	CAGTATTCTTTTG(	586	*Meyerozyma guilliermondii*	Meyerozyma	Saccharomyce	Saccharomyce	*Meyerozyma guilliermondii*	CBS:12037	KY104257	99.83%	0	99%	1			Vu et al 2016	TTTAAGTCCCCTGCCCTT
TU CIM 6289	ITS1&2	SR6R	NGTTTTTTTACAA(	360	*Kodamaea ohmeri*	Kodamaea	Saccharomyce	Saccharomyce	*Kodamaea ohmeri*	CBS:2038	KY103876	99.72%	0	99%	1	food		Vu et al 2016	TCGTAACAAGGTTTCCGT
TU CIM 6246	ITS1&2	SR6R	GNCATTACAGTAT	626	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS 2334	KJ705003	99.68%	0	99%	2			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 6249	ITS1&2	SR6R	GTATTCTTTTTGC(	610	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS 2334	KJ705003	100%	0	100%	0			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 6251	ITS1&2	SR6R	ACAGTATTCTTTT	623	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS 2334	KJ705003	99.84%	0	99%	1			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 6984	ITS1&2	SR6R	AGTATTCTTTTTG(	616	*Schwanniomyces vanrijiae var*	Schwanniomy	Saccharomyce	Saccharomyce	*Schwanniomyces vanrijiae var*	CBS:3024	KY105408	100%	0	98%	0	soil	South Africa	Vu et al 2016	CGTAACAAGGTTTCCGTA
TU CIM 6985	ITS1&2	SR6R	AGTATTCTTTTTG(	622	*Schwanniomyces vanrijiae var*	Schwanniomy	Saccharomyce	Saccharomyce	*Schwanniomyces vanrijiae var*	CBS:3024	KY105408	100%	0	97%	0	soil	South Africa	Vu et al 2016	CGTAACAAGGTTTCCGTA
TU CIM 6986	ITS1&2	SR6R	AGGGNCATTACA(	555	*Chloridium virescens var. Chla*	Chloridium	Chaetosphaer	Sordariomyce	Chloridium virescens var. Chla	CBS 126074	MH864069	99.06%	0	95%	5			Vu et al 2019	GTTGTACACACCGCCCGT
TU CIM 6989	ITS1&2	SR6R	TTACAGAGTTACT	607	*Pseudallescheria apiosperma*	Pseudallesche	Microascales	Sordariomyce	*Pseudallescheria apiosperma*	WM 06.471	EF639871	99.17%	0	99%	5		Australia	Delhaes et al 2008	TAACAAGGTCTCCGTTG
TU CIM 6990	ITS1&2	SR6R	ACTCCCAACCCTG	535	*Hawksworthiomyces crousii*	Hawksworthic	Ophiostomata	Sordariomyce	*Hawksworthiomyces crousii*	CMW37531	KX396551	94.02%	0	89%	29			de Beer et al 2016	TGAACCAGCGGAGGGAT
TU CIM 7009	ITS1&2	SR6R	CATTACAGTATTC	631	*Debaryomyces nepalensis*	Debaryomyce	Saccharomyce	Saccharomyce	*Debaryomyces nepalensis*	CBS 2334	KJ705003	99.36%	0	98%	4			Feng et al 2014	AAGGATCATTACAGTATT
TU CIM 6298	*tef1- α*	EF1 728f	ATCCTCGTACCCT	1117	*Trichoderma* sp	Trichoderma	Hypocreales	Sordariomyce	Trichoderma sp	TC278	MF371223	91.71%	0	82%	81			Chen et al 2017	CTTTTTGCATCAATCTCTT
TU CIM 6178	*tef1- α*	EF1 728f	CATCCTCGTACCC	1193	*Trichoderma* sp	Trichoderma	Hypocreales	Sordariomyce	Trichoderma sp	TC278	MF371223	91.42%	0	82%	85			Chen et al 2017	CTTTTTGCATCAATCTCTT
TU CIM 6295	*tef1- α*	EF1 728f	TTTCCTAGGCGCC	1176	*Trichoderma* sp	Trichoderma	Hypocreales	Sordariomyce	Trichoderma sp	TC278	MF371223	90.68%	0	83%	93			Chen et al 2017	CTTTTTGCATCAATCTCTT
TU CIM 5845	*tef1- α*	EF1 728f	ACATTCAATTGTG	1145	*Trichoderma atrobrunneum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma atrobrunneum*	S414	KJ665393	100%	0	100%	0		Spain	Jaklitsch et al 2015	CTCGATTCTTCCTCCTTCA
TU CIM 5596	*tef1- α*	EF1 728f	AGCCGGCACCGA(	1090	*Trichoderma simmonsii*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma simmonsii*	S86	KJ665721	97.60%	0	99%	26		Italy	Jaklitsch et al 2015	TCGATTCTCCTCCACATT
TU CIM 6058	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1151	*Trichoderma simmonsii*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma simmonsii*	S314	KJ665714	97.91%	0	100%	24		Crotia	Jaklitsch et al 2015	TCGGATTCTCCCTCCACA
TU CIM 5643	*tef1- α*	EF1 728f	ATTGTGNCCGAC/	162	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	LESF343	KT279021	93.17%	1,00E-56	96%	11	*Atta capiguar*	Brazil: Fazenc	Montoya et al 2016	CAACGAAATCTCCCTCCT
TU CIM 6033	*tef1- α*	EF1 728f	CCGACAATTCTGC	597	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	PPRC S23	FJ577790	91.12%	0	100%	53			Druzhinina et al 2010	GCCCGACAATTCTGCAG
TU CIM 6215	*tef1- α*	EF1 728f	CGTTCATTGTGCC	1186	*Trichoderma simmonsii*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma simmonsii*	S86	KJ665721	96.22%	0	99%	45		Italy	Jaklitsch et al 2015	TCGATTCTCCTCCACATT
TU CIM 5629	*tef1- α*	EF1 728f	GCAACGTACTGA(	1000	*Beauveria bassiana*	Beauveria	Hypocreales	Sordariomyce	*Beauveria bassiana*	2922	AY531920	90.58%	0	96%	93			Rehner et al 2005	AGGACAAGACTCACATC
TU CIM 5794	*tef1- α*	EF1 728f	ATTTTCCCTACGA	1158	*Fusarium oxysporum f. sp. vas*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum f. sp. vas*	AuSeed14	KT323873	97,86%	0	100%	25			Ortiz,C.S., et al 2017	GGCCACGTCGACTCTGG
TU CIM 5796	*tef1- α*	EF1 728f	CATCGATTTTCCC(	1176	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	MS15	MH828020	96,96%	0	100%	36	wilted cotton	plant	Bell,A.A., et al 2019	GGCCACGTCGACTCTGG
TU CIM 5795	*tef1- α*	EF1 728f	CGTGCCCGCTACC	1139	*Fusarium oxysporum f. sp. vas*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum f. sp. vas*	AuK24232	KT323874	97,82%	0	100%	25			Ortiz,C.S., et al 2017	GGCCACGTCGACTCTGG
TU CIM 5769	*tef1- α*	EF1 728f	CNATTTTCCCTAC(	1107	*Fusarium oxysporum f. sp. vas*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum f. sp. vas*	AuK24232	KT323874	97,84%	0	99%	24			Ortiz,C.S., et al 2017	GGCCACGTCGACTCTGG
TU CIM 5772	*tef1- α*	EF1 728f	GATNTTCCCTACG	1160	*Fusarium oxysporum f. sp. vas*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum f. sp. vas*	AuSeed14	KT323873	97,60%	0	100%	28			Ortiz,C.S., et al 2017	GGCCACGTCGACTCTGG
TU CIM 5792	*tef1- α*	EF1 728f	GATTTTCCCTACG.	1106	*Fusarium oxysporum f. sp. vas*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum f. sp. vas*	CDR1072	KT323869	97,67%	0	100%	26			Ortiz,C.S., et al 2017	GGCCACGTCGACTCTGG
TU CIM 5762	*tef1- α*	EF1 728f	NATNTTCCCCTAC	1154	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	MS15	MH828020	97,07%	0	99%	34	wilted cotton	plant	Bell,A.A., et al 2019	GGCCACGTCGACTCTGG
TU CIM 5759	*tef1- α*	EF1 728f	TCGATTTTCCCCT/	1125	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	MS15	MH828020	97,18%	0	100%	32	wilted cotton	plant	Bell,A.A., et al 2019	GGCCACGTCGACTCTGG
TU CIM 5760	*tef1- α*	EF1 728f	TCGATTTTCCCCT/	1159	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	MS15	MH828020	97,09%	0	100%	34	wilted cotton	plant	Bell,A.A., et al 2019	GGCCACGTCGACTCTGG
TU CIM 5763	*tef1- α*	EF1 728f	TCGNAACGTGCC(	1146	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	MS15	MH828020	97,06%	0	100%	34	wilted cotton	plant	Bell,A.A., et al 2019	GGCCACGTCGACTCTGG
TU CIM 5761	*tef1- α*	EF1 728f	TTCCCCTACGACT(	1167	*Fusarium oxysporum*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum*	MS15	MH828020	97,28%	0	100%	32	wilted cotton	plant	Bell,A.A., et al 2019	GGCCACGTCGACTCTGG
TU CIM 5787	*tef1- α*	EF1 728f	TTGGTGGGGCATT	1084	*Fusarium oxysporum f. sp. vas*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum f. sp. vas*	AuSeed14	KT323873	97,99%	0	100%	22			Ortiz,C.S., et al 2017	GGCCACGTCGACTCTGG
TU CIM 5793	*tef1- α*	EF1 728f	TTTTCCCTACGAT	1149	*Fusarium oxysporum f. sp. vas*	Fusarium	Hypocreales	Sordariomyce	*Fusarium oxysporum f. sp. vas*	AuSeed14	KT323873	97,84%	0	100%	25			Ortiz,C.S., et al 2017	GGCCACGTCGACTCTGG
TU CIM 6040	*tef1- α*	EF1 728f	ACCGACCTGTCCA	1095	*Trichoderma barbatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma barbatum*	TC700	MF095877	90,96%	0	90%	90			Chen,K., et al 2017	ATCTCTTCTTCGCACTCA
TU CIM 5841	*tef1- α*	EF1 728f	CTCGCAGGATCTG	1143	*Atrocalyx asturiensis*	Atrocalyx	Pleosporales	Dothideomyc	*Atrocalyx asturiensis*	OF	MG912916	93,63%	0	99%	73		Spain	Jaklitsch,W.M., et al 2018	TGAGCGCACACGTTTCCT
TU CIM 5824	*tef1- α*	EF1 728f	GGATTTTCCCCTC.	1088	*Glarea lozoyensis*	Glarea	Helotiales	Leotiomycete	*Glarea lozoyensis*	ATCC 20868	XM_0080874!	93,07%	0	79%		pond water f	Spain	Chen,L., et al 2019	ATGCACATTAACGTGGTC
TU CIM 5491	*tef1- α*	EF1 728f	TCTGGTCACTAGC	1156	*Metarhizium guizhouense (Me*	Metarhizium	Hypocreales	Sordariomyce	*Metarhizium guizhouense (Me*	CBS:258.90	EU248862	89,88%	0	77%	92	Lepidoptera	China	Bischoff,J.F., et al 2009	TATCGTAAGTCGCCTGCC
TU CIM 5644	*tef1- α*	EF1 728f	AGCGTCATGATTT	1135	*Neopestalotiopsis clavispora*	Neopestalotio	Xylariales	Sordariomyce	*Neopestalotiopsis clavispora*	MFLUCC12-028(	JX399044	99,06%	0	75%	8	dead plant m	China	Maharachchikumbura,S.S	CTTGATCTACAAGTGCG
TU CIM 5755	*tef1- α*	EF1 728f	CATTCAATTGTGC	1125	*Trichoderma aggregatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma aggregatum*	HMAS:248863	KY688062	95,91%	0	100%	46			Chen,K., et al 2017	CCTGATTCTCCCTCCACA
TU CIM 5754	*tef1- α*	EF1 728f	CATTCAATTGTGC	1051	*Trichoderma aggregatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma aggregatum*	HMAS:248863	KY688062	96,19%	0	100%	40			Chen,K., et al 2017	CCTGATTCTCCCTCCACA
TU CIM 5753	*tef1- α*	EF1 728f	WTCAATTGTGCT(	1132	*Trichoderma aggregatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma aggregatum*	HMAS:248863	KY688062	95,23%	0	99%	54			Chen,K., et al 2017	CCTGATTCTCCCTCCACA
TU CIM 5640	*tef1- α*	EF1 728f	ATTCAATTGTGCT	1059	*Trichoderma aggregatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma aggregatum*	HMAS:248863	KY688062	94,52%	0	100%	58			Chen,K., et al 2017	CCTGATTCTCCCTCCACA
TU CIM 5641	*tef1- α*	EF1 728f	CYCCGCTTTCCAT	1077	*Trichoderma aggregatum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma aggregatum*	HMAS:248863	KY688062	95,72%	0	99%	46			Chen,K., et al 2017	CCTGATTCTCCCTCCACA
TU CIM 5752	*tef1- α*	EF1 728f	AATTGTGCCCGAC	1126	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,36%	0	93%	28		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5619	*tef1- α*	EF1 728f	AATTTTCGCGTCG	1101	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,49%	0	93%	26		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5625	*tef1- α*	EF1 728f	ACATTCAATTGTG	1338	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,84%	0	92%	23		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5733	*tef1- α*	EF1 728f	ACATTCAATTGTG	1133	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,03%	0	94%	21		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5652	*tef1- α*	EF1 728f	ACGTTCAATTGTG	1132	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,03%	0	94%	21		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5748	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1125	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,38%	0	94%	28		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA

TU CIM 5724	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1124	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,66%	0	94%	25		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5728	*tef1- α*	EF1 728f	ATTCAATTGTGCC	262	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypo*	CFAM-422	MG986725	96,60%	8,00E-118	100%	9	Amazon fore:	Brazil	Fernandes de Souza,M., e	TAAGCTTCAACTCATTTT
TU CIM 5750	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1129	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,46%	0	94%	27		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5617	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1134	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,74%	0	93%	24		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5607	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1135	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,31%	0	93%	18		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5613	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1119	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,40%	0	95%	17		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5615	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1135	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,31%	0	93%	18		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5729	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1162	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,22%	0	91%	19		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5738	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1125	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,22%	0	94%	19		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5739	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1162	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,22%	0	91%	19		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5618	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1130	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,65%	0	93%	25		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5734	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1120	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,03%	0	95%	21		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5731	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1123	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,84%	0	94%	23		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5505	*tef1- α*	EF1 728f	ATTCAATTGTGCC	1045	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,19%	0	100%	19		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5599	*tef1- α*	EF1 728f	ATTGTGNCCGACN	1127	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,21%	0	94%	19		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5594	*tef1- α*	EF1 728f	CAATTGTGCCCGA	1134	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,11%	0	93%	20		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5609	*tef1- α*	EF1 728f	CANATTTTTTTTG	903	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,77%	0	99%	20		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5736	*tef1- α*	EF1 728f	CATTCAATTGTGC	1160	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,46%	0	91%	27		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5741	*tef1- α*	EF1 728f	CATTCAATTGTGC	1051	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,91%	0	100%	21		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5749	*tef1- α*	EF1 728f	CATTCAATTGTGC	1119	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	96,91%	0	95%	33		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5725	*tef1- α*	EF1 728f	CATTCAATTGTGC	1126	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,13%	0	94%	20		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5726	*tef1- α*	EF1 728f	CATTCAATTGTGC	1126	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,94%	0	94%	22		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5740	*tef1- α*	EF1 728f	CATTCAATTGTGC	1061	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,64%	0	100%	25		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5727	*tef1- α*	EF1 728f	CATTCAATTGTGC	890	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,42%	0	100%	23		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5758	*tef1- α*	EF1 728f	CATTCAATTGTGC	261	*Trichoderma harzianum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum*	Th203	AB558912	97,70%	4,00E-121	100%	6		Colombia	Smith,A., et al 2013	TTATCCCTTCTTCACGTT
TU CIM 5606	*tef1- α*	EF1 728f	CATTCAATTGTGC	1137	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,31%	0	93%	18		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5616	*tef1- α*	EF1 728f	CATTCAATTGTGC	1109	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,31%	0	96%	18		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5722	*tef1- α*	EF1 728f	CATTCAATTGTGC	1152	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	97,31%	0	100%	31		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5723	*tef1- α*	EF1 728f	CATTCAATTGTGC	1156	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	97,06%	0	100%	33		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5742	*tef1- α*	EF1 728f	CATTCAATTGTGC	1147	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	97,04%	0	100%	34		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5743	*tef1- α*	EF1 728f	CATTCAATTGTGC	1137	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	97,19%	0	100%	32		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5637	*tef1- α*	EF1 728f	CATTCAATTGTGC	1161	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,14%	0	100%	45		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5497	*tef1- α*	EF1 728f	CATTCAATTGTGC	1134	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,84%	0	100%	36		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5735	*tef1- α*	EF1 728f	CATTCAATTGTGC	1119	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,70%	0	100%	37		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5730	*tef1- α*	EF1 728f	CATTCAATTGTGC	1136	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,57%	0	100%	39		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5488	*tef1- α*	EF1 728f	CATTCAATTGTGC	1150	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,88%	0	99%	36		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5756	*tef1- α*	EF1 728f	CATTCAATTGTGC	1150	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,53%	0	100%	26		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5569	*tef1- α*	EF1 728f	CATTCAATTGTGC	1156	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	97,06%	0	100%	34		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5614	*tef1- α*	EF1 728f	CKMGTCGACAAT	1092	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,79%	0	99%	35		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5639	*tef1- α*	EF1 728f	CTTGWGMACCCC	815	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	99,36%	0	96%	5		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5622	*tef1- α*	EF1 728f	CWNMCCGCTTTG	1071	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,72%	0	99%	35		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5624	*tef1- α*	EF1 728f	GTTTGNTTTTAGT	1008	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	95,54%	0	100%	45		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5598	*tef1- α*	EF1 728f	KCNNCCCGCTTTG	993	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,48%	0	99%	15		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5638	*tef1- α*	EF1 728f	MCCGCTTTGCATT	1064	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,53%	0	99%	37		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5611	*tef1- α*	EF1 728f	NCGACNATTCTGC	1113	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,41%	0	99%	40		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5642	*tef1- α*	EF1 728f	TCCACTCTCACTG	1064	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,53%	0	99%	37		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5612	*tef1- α*	EF1 728f	TCGACAAYTTTTC	1010	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	98,22%	0	100%	18		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5653	*tef1- α*	EF1 728f	TCNCGTTCAATTG	1153	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,79%	0	99%	37		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5608	*tef1- α*	EF1 728f	TCRACAATTTTTC	1095	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,72%	0	100%	36		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5737	*tef1- α*	EF1 728f	TTCAATTGTGCCC	1044	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,42%	0	100%	27		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA

TU CIM 5751	*tef1- α*	EF1 728f	TTCAATTGTGCCC	1133	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,13%	0	100%	44		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5595	*tef1- α*	EF1 728f	TTCAATTGTGCCC	1130	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,73%	0	100%	37		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5732	*tef1- α*	EF1 728f	TTCAATTGTGCCC	1123	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,62%	0	100%	38		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5500	*tef1- α*	EF1 728f	TTCAATTGTGCCC	1148	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,96%	0	100%	35		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5757	*tef1- α*	EF1 728f	TTCAATTGTGCCC	1106	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,37%	0	96%	28		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5597	*tef1- α*	EF1 728f	TTGTGNCCGACNA	1135	*Trichoderma sp. S610*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sp. S610*	CBS:135585	KJ665737	96,65%	0	99%	38		Greece	Jaklitsch,W.M.,et al 2015	GATTCTCTTCACATTCAA
TU CIM 5623	*tef1- α*	EF1 728f	TTTTTTTTGCTGTC	918	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,69%	0	98%	21		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5610	*tef1- α*	EF1 728f	YCCCGCTTTGCAT	926	*Trichoderma harzianum (Hypo*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma harzianum (Hypocrea lixii)*		KF923284	97,95%	0	99%	19		China	Zhu,Z.X. et al 2015	CTCGATTCTCCCTCCACA
TU CIM 5571	*tef1- α*	EF1 728f	CACAATCGTGTCC	1126	*Trichoderma koningiopsis (Hyp*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis (Hyp*	S359	KJ665546	97,70%	0	100%	26		France	Jaklitsch,W.M.,et al 2015	TTTTTCACACGCTTGGCA
TU CIM 5745	*tef1- α*	EF1 728f	ACAATCGTGTCCG	1167	*Trichoderma koningiopsis (Hyp*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis (Hyp*	S359	KJ665546	95,30%	0	100%	55		France	Jaklitsch,W.M.,et al 2015	TTTTTCACACGCTTGGCA
TU CIM 5746	*tef1- α*	EF1 728f	CAATCGTGTCCGA	1141	*Trichoderma koningiopsis (Hyp*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis (Hyp*	S359	KJ665546	95,10%	0	99%	56		France	Jaklitsch,W.M.,et al 2015	TTTTTCACACGCTTGGCA
TU CIM 5744	*tef1- α*	EF1 728f	GGCACAATCGTGT	1179	*Trichoderma koningiopsis (Hyp*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma koningiopsis (Hyp*	S359	KJ665546	95,10%	0	100%	58		France	Jaklitsch,W.M.,et al 2015	TTTTTCACACGCTTGGCA
TU CIM 5621	*tef1- α*	EF1 728f	AAATTTTTTTTTGN	708	*Trichoderma reesei*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma reesei*	CBS 881.96	GQ354369	91,81%	0	100%	58			Druzhinina,I.S., et al 2010	CAATCTTCCTTTGCCCAT
TU CIM 5620	*tef1- α*	EF1 728f	TGTGCCGACACGA	707	*Trichoderma reesei*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma reesei*	CBS 881.96	GQ354369	94,80%	0	100%	37			Druzhinina,I.S., et al 2010	CAATCTTCCTTTGCCCAT
TU CIM 5570	*tef1- α*	EF1 728f	TNTTTCCCGCTCA	1106	*Trichoderma sinuosum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sinuosum*	HMAS 252541	KF729983	98,03%	0	99%	22		China	Zhu,Z.X. et al 2015	TAAGCTCAATCAACTGAT
TU CIM 5502	*tef1- α*	EF1 728f	CCTTTGGACACAA	1137	*Trichoderma sparsum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma sparsum*	10122	KU529136	97,01%	0	99%	34		China	Qin,W.T., et al 2016	TTTTTTCGTTACACCTTTC
TU CIM 5501	*tef1- α*	EF1 728f	CTCTTGCCCGACT	904	*Trichoderma paraviridescens*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma paraviridescens*	S36	KC285678	86,86%	0	98%	120		Italy	Jaklitsch,W.M.,et al 2013	TACGCTTTCTTGACACAA
TU CIM 5649	*tef1- α*	EF1 728f	AATCGTGTCCGAC	460	*Trichoderma ovalisporum*	Trichoderma	Hypocreales	Sordariomyce	*Trichoderma ovalisporum*	DAOM 232078	EU280004	93,29%	0	100%	31		Brazil	Hoyos-Carvajal,L., et al 2(	GAGAAGACTCACATCAA