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PROGRAMA DE PÓS-GRADUAÇÃO EM BIOLOGIA MICROBIANA

JEFFERSON BRENDON ALMEIDA DOS REIS

MICOBIOTA ENDOFÍTICA DE SEIS ESPÉCIES LENHOSAS DO CERRADO: EFEITOS DA PLANTA HOSPEDEIRA E DA ADIÇÃO DE NUTRIENTES AO SOLO

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Coorientadora: Dra. Adriana Sturion Lorenzi

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Dissertação de Mestrado

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MICOBIOTA ENDOFÍTICA DE SEIS ESPÉCIES LENHOSAS DO CERRADO: EFEITOS DA PLANTA HOSPEDEIRA E DA ADIÇÃO DE NUTRIENTES AO SOLO

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BRASILIA
2022

"Em algum lugar, algo incrível está
esperando para ser descoberto."
Carl Sagan

AGRADECIMENTOS

Somos filhos de nossas histórias e trajetórias, e ao longo dos meus breves anos de vida fui abençoado com pessoas incríveis, que transformaram meu mundo e me mostraram perspectivas que jamais poderia ter sozinho. A estas pessoas dedico os meus mais sinceros, verdadeiros e profundos agradecimentos.

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Resumo geral

O Cerrado é a maior savana tropical seca da América do Sul e um dos lugares mais biodiversos do mundo. Grande parte da biodiversidade desse bioma está na fitofisionomia, que abriga mais de 7.000 espécies de plantas endêmicas. As plantas do Cerrado, por sua vez, representam um importante nicho para fungos endofíticos. Os fungos endofíticos são micro-organismos que, durante parte ou todo o seu ciclo de vida, colonizam o interior do tecido vegetal sem causar sintomas de doença. Esses micro-organismos estão intimamente relacionados com seus hospedeiros, de modo que a colonização não é acidental, mas um processo especializado que evoluiu ao longo de milhões de anos e depende de uma complexa rede de interações entre fungo-planta, fungo-fungo, planta-ambiente e fungo-ambiente. O conhecimento sobre a diversidade de espécies de fungos endofíticos do Cerrado é limitado. Deve-se considerar que estudos cujo foco foi descrever a diversidade de fungos endofíticos relacionados às espécies vegetais deste bioma utilizaram métodos dependentes de cultivo, limitando a fração de fungos facilmente cultivados nas condições testadas. Tomando essas questões como ponto de partida, testamos como os fatores de identidade da planta hospedeira e o tipo de fenologia foliar (fatores bióticos) influenciam a diversidade de espécies fúngicas do micobioma endofítico foliar das hospedeiras *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperma* e *Styrax ferrugineus;* e o efeito da adição de nutrientes ao solo a longo prazo (fatores abióticos) sobre a micobiota endofítica foliar de *C. brasiliense* e *O. hexasperma* utilizando métodos dependentes e independentes de cultivo (*metabarcoding*). Em ambas as metodologias, foram observadas diferenças entre o micobioma endofítico dos hospedeiros para todos os experimentos. *Metabarcoding* e cultivo mostraram que *Ascomycota* é o filo dominante. No entanto, o *metabarcoding* mostrou que, embora os ascomicetos sejam mais abundantes, eles não são o único filo presente na micobiota endofítica desses hospedeiros. Outros filos como *Basidiomycota* e filos recentemente propostos foram relatados em mais de um hospedeiro em ambos os três experimentos. Uma porcentagem considerável das sequências *metabarcoding* foram classificadas apenas ao nível de reino Fungi, sugerindo que o micobioma endofítico desses hospedeiros pode abrigar grupos taxonômicos ainda não conhecidos. Os fatores de identidade e fenologia foram importantes determinantes da diversidade e abundância relativa de cada espécie no micobioma endofítico. No experimento de adição de nutrientes ao solo as maiores diferenças quanto à composição taxonômica do micobioma endofítico foram observadas nos tratamentos com calagem, com fósforo e com nitrogênio. Em relação ao cultivo, mais da metade dos isolados pertencem ao gênero *Diaporthe* e a maioria das espécies não são compartilhadas entre hospedeiros/tratamentos. Os resultados apresentados demonstram como o micobioma endofítico foliar de espécies lenhosas do Cerrado é dinâmico, complexo e moldado por fatores bióticos e abióticos. Além disso, este estudo evidencia a enorme diversidade de espécies de fungos endofíticos e reforça ainda mais a importância do estudo deste nicho tão importante e diversificado.

Keywords: Fungos; *Illumina MiSeq*; Savana tropical; DNA *metabarcoding; Diaporthe*; *Ascomycota*.

General abstract

The Cerrado is the largest dry tropical savanna in South America and one of the most biodiverse places in the world. Much of the biodiversity of this biome is in phytophysiognomy, that host more than 7.000 endemic plant species. Cerrado plants, in turn, represent an important niche for endophytic fungi. Endophytic fungi are microorganisms that, during part or all of their life cycle, colonize the interior of plant tissue without causing symptoms of the disease. These microorganisms are closely related to their hosts, so colonization is not an accidental process but a specialized one that has evolved over millions of years and depends on a complex network of interactions between fungus-plant, fungus-fungus, plant-environment, and fungus-environment. There is limited knowledge about the diversity of endophytic fungi species in Cerrado plant species. It should also be considered that studies whose focus was to describe the diversity of endophytic fungi related to plant species of this biome used cultivation-dependent methods, limiting the fraction of fungi easily cultivated under the conditions tested. Taking these questions as a starting point, we tested how the factors of host plant identity and type of leaf phenology (biotic factors) influence the diversity of fungal species in the leaf endophytic mycobiome of the host species *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperma,* and *Styrax ferrugineus*; and the effect of long-term addition of nutrients to the soil (abiotic factors) on the leaf endophytic mycobiota of *C. brasiliense* and *O. hexasperma* using cultivation-dependent and independent methods (*metabarcoding*). In both methodologies, dissimilarities between the endophytic mycobiome of the hosts were observed for all experiments. *Metabarcoding* and cultivation showed that *Ascomycota* was the dominant phylum. However, *metabarcoding* showed that although ascomycetes are more abundant, they are not the only phyla present in the endophytic mycobiota of these hosts. Other phyla such as *Basidiomycota* and recently proposed phyla were reported in more than one host in both three experiments. A considerable percentage of the metabarcoding sequences were classified only at the fungi kingdom level, suggesting that the endophytic mycobiome of these hosts may harbor taxonomic groups not yet known. The identity and phenology factors were important determinants of the diversity and relative abundance of each species in the endophytic mycobiome. In the soil nutrient addition experiment, the greatest differences regarding the taxonomic composition of the endophytic mycobiome were observed in the liming, nitrogen and phosphorus treatments. Regarding cultivation, more than half of the isolates belong to the genus *Diaporthe* and most species are not shared between hosts/treatments. The results presented show how the leaf endophytic mycobiome of Cerrado woody species is dynamic, complex and shaped by biotic and abiotic factors. In addition, this study shows the enormous diversity of endophytic fungal species and further reinforces the importance of studying this very important and diverse niche.

Keywords: Fungal; *Illumina MiSeq*; Tropical Savanna; DNA *metabarcoding; Diaporthe*.

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INTRODUÇÃO GERAL

O Cerrado é a maior savana tropical da América do Sul e o segundo maior bioma brasileiro, ocupando uma área de mais de dois milhões de quilômetros quadrados (cerca de 25% do território do país), que estão continuamente distribuídos em todos os estados da região Centro-Oeste (Figura 1), partes dos estados do Norte, Nordeste e Sudeste, e pequenos pontos isolados nos estados da região Sul do país. Esse bioma também é conhecido como uma das savanas tropicais mais biodiversas do mundo, com destaque para a sua flora, conhecida pelo elevado grau de endêmica e heterogeneidade. Estima-se que este bioma abriga mais de 7.000 espécies vegetais endêmicas, que se distribuem em diferentes gradientes de fitossionomias ao longo de sua extensão.

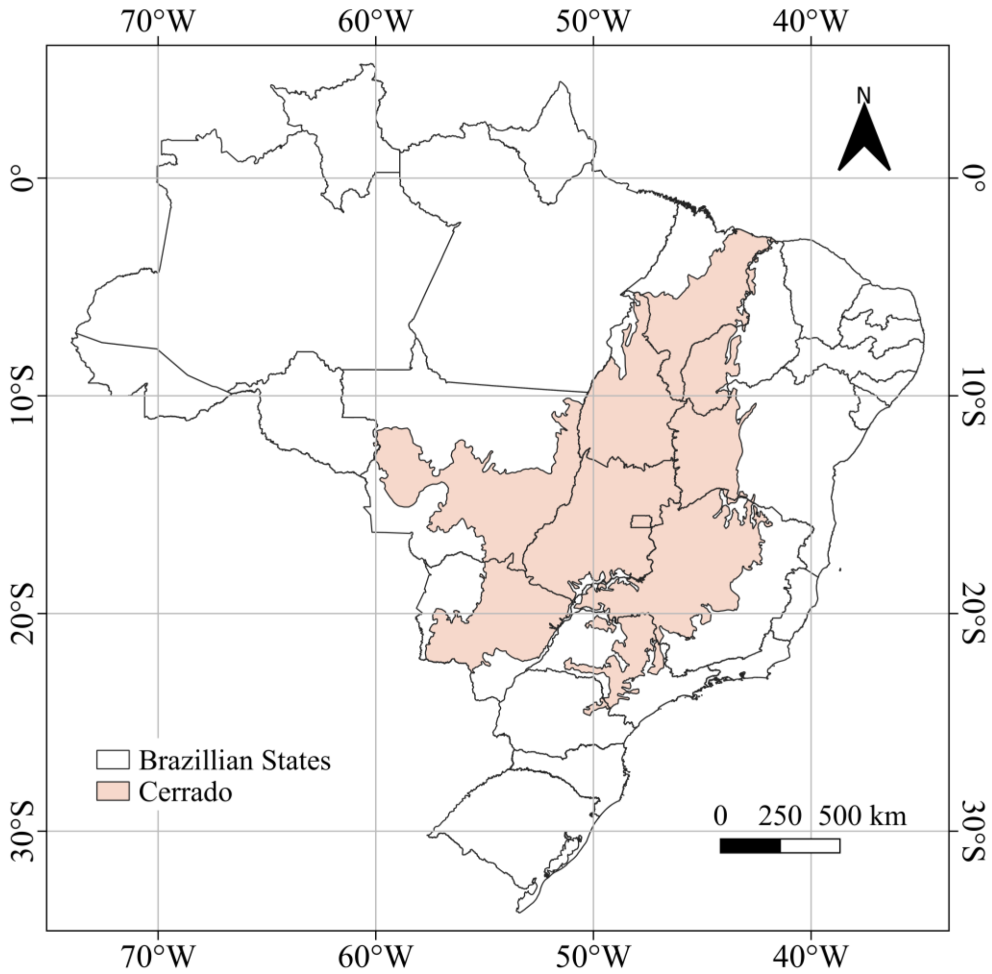


Figura 1. Distribuição geoespacial do bioma Cerrado no Brasil. Fonte: Mapa obtido no software Qgis, com base em dados fornecidos pelo Instituto Nacional de Pesquisas Espaciais.

As inúmeras espécies vegetais do Cerrado, por sua vez, representam um importante nicho ecológico para espécies microbianas, especialmente para fungos endofíticos. Os fungos endofíticos são micro-organismos que, durante parte ou todo o seu ciclo de vida, colonizam o interior do tecido vegetal em espaços intra ou extracelulares sem causar manifestação aparente de doença. Esses micro-organismos estão intimamente relacionados com suas hospedeiras vegetais, de maneira que a colonização não é um processo acidental provocado por quimiotaxia, mas uma relação complexa, estabelecida entre planta-fungo ao longo de milhares de anos de coevolução, que envolvem a inúmeros mecanismos genéticos e moleculares presentes em ambos os reinos que interagem entre si e entre o ambiente. Por tanto, a estrutura taxonômica, ocorrência, diversidade, equidade de espécies do micobioma endofítico é determinado por um conjunto de fatores, que incluem a identidade da hospedeira, fatores genéticos em ambos os grupos (Filtragem ambiental biótica) e variáveis ambientais (Filtragem ambiental abiótica).

No Cerrado brasileiro, estudos com a premissa de avaliar a diversidade de fungos endofíticos associados a plantas nativas desse bioma evidenciam que esse nicho é altamente diverso e um ponto quente para descrição de espécimes novas. No entanto, embora essas pesquisas tragam contribuições notáveis para mapeamento da diversidade de fungos endofíticos que ocorrem neste bioma, esses trabalhos, em sua maioria, não contemplam os efeitos do filtro ecológico exercido pela hospedeira e pelo ambiente sobre essas comunidades, se restringindo basicamente a avaliação do micobioma endofítico de uma única espécie hospedeira e em uma única condição ambiental. Por tanto, a dinâmica da estrutura taxonômica do micobioma endofítico de espécies vegetais do Cerrado em resposta a variações ambientais e em diferentes hospedeiras permanece desconhecido.

Ainda de forma problemática, essas pesquisas utilizam métodos dependentes de cultivo, se limitando a fração de fungos endofíticos cultiváveis nas condições prepostas, excluindo aqueles micro-organismos que não são possíveis de serem cultiváveis nessas condições. Além disso, outros problemas encontrados na utilização de métodos dependentes de cultivos incluem maior risco de contaminação com espécies de fungos sopróﬁtas; tipo de substrato utilizado que pode favorecer determinado grupo, que tende a se sobressair e inibir outros grupos; dificuldade de isolamento; alto esforço amostral para cobrir uma maior diversidade; e métodos trabalhosos e que demandam tempo, reagentes e espaço. Uma alternativa diante das limitações dos métodos dependentes de cultivo para estudar diversidade microbiana é a utilização conjunta destes com metodologias independentes de cultivo, uma vez que os métodos dependentes de cultivo fornecem táxons cultiváveis que podem ser explorados biotecnologicamente enquanto os métodos independentes fornecem um panorama mais amplo da real diversidade.

As metodologias independentes de cultivo vêm sendo consideradas ferramentas poderosas para estudos de comunidades microbianas, sobretudo para avaliação de efeitos de variáveis bióticas e abióticas sobre a estrutura taxonômica dessas comunidades. O *metabarcoding*, por exemplo, vem sendo empregado para estudar o micobioma endofítico de espécies vegetais sobre diferentes gradientes de variáveis ambientais e para evidenciar o efeito de filtro ecológico exercido pela identidade da planta hospedeira. Essa ferramenta tem possibilitado a descrição da diversidade em termos de ocorrência, abundância equidade e dinâmica espaço-temporal.

Considerando todos os aspectos discutidos, o presente estudo possui os seguintes objetivos: **a)** relatar a diversidade de fungos endofíticos foliares associados a seis espécies lenhosas nativas do Cerrado, **b)** utilizando ferramentas dependentes e independentes de cultivo, sendo elas *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperna* e *Styrax ferrugineus;* **c)** avaliar o efeito do processo de filtragem ambiental exercida pela identidade taxonômica da hospedeira sobre a comunidade de fungos endofíticos entre as hospedeiras; **d)** avaliar o efeito da fenologia foliar sobre a diversidade de espécies fúngicas que ocorrem entre as fenologias decíduas, brevídeciduous e sempre verdes; **e)** relatar a diversidade de fungos endofíticos foliares que ocorrem em *C. brasiliense* e *O. hexasperma* em condições de antropização do solo provocadas pela adição de fertilizantes minerais a longo prazo; e **f)** correlacionar os efeitos da adição de fertilizantes minerais ao solo com alterações na estrutura taxonômica da comunidade de fungos endofíticos foliares nessas duas hospedeiras.

TÍTULOS DOS CAPÍTULOS

Capítulo 1- ***ENDOPHYTIC FUNGI AND SELECTION OF PLANT HOSTS***.

Capítulo 2- ***DIVERSITY, STRUCTURE AND SPECIES-SHARING NETWORK OF THE ENDOPHYTIC MYCOBIOME OF SIX WOODY SPECIES FROM THE BRAZILIAN NEOTROPICAL SAVANNA***.

Capítulo 3- ***THE TYPE OF LEAF PHENOLOGY HAS AN EFFECT ON THE DIVERSITY OF THE ENDOPHYTIC MYCOBIOME IN A NEOTROPICAL SAVANNA ECOSYSTEM***.

Capítulo 4- ***DIFFERENT RESPONSES OF THE LEAF ENDOPHYTIC MYCOBIOME OF TWO PLANT SPECIES OF A NEOTROPICAL SAVANNA ECOSYSTEM TO LONG-TERM MINERAL FERTILIZATION***.

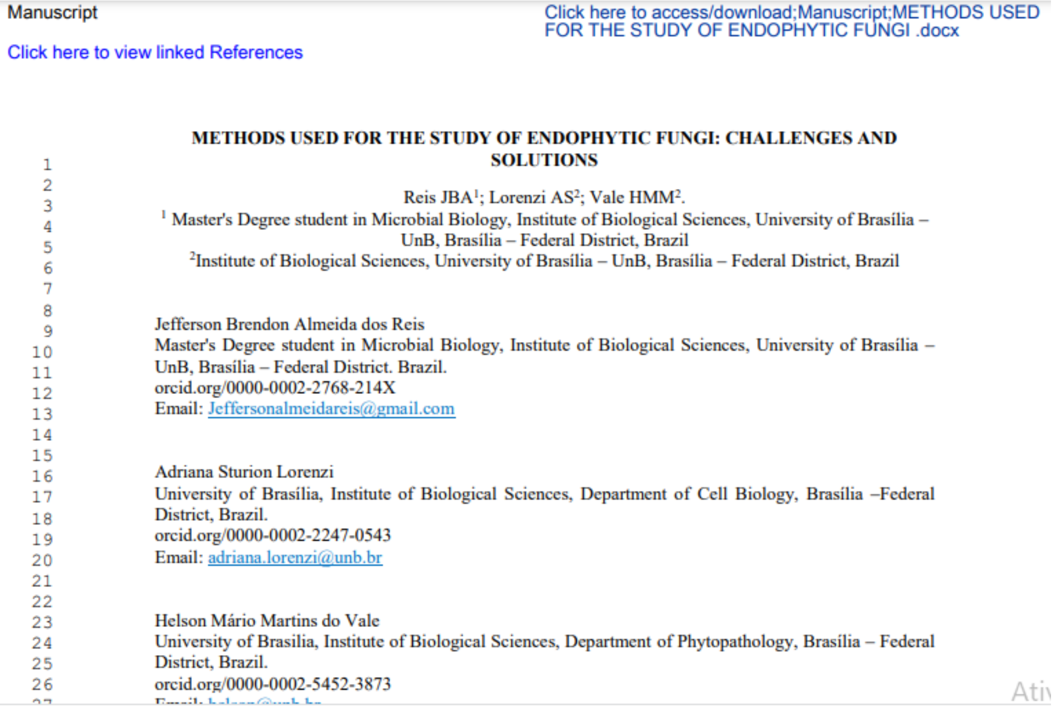
OBJETIVOS E HIPÓTESES

Tabela 1. Organização dos capítulos, objetivos gerais e hipóteses

CAPÍTULOS	PROPÓSITO GERAL	HIPÓTESE
Capítulo 1	Discutir sobre as variáveis que influenciam na composição taxonômica do micobioma endofítico, bem como descrever os papéis ecológicos dessa comunidade, diversidade, mecanismos de interação com seus hospedeiros e colonização. Este capítulo também fornecerá as justificativas para a escolha das metodologias e espécies de plantas hospedeiras.	***Exclusivo para revisão de literatura***. Esse capítulo resultou em duas revisões bibliográficas que foram submetidas para publicação, uma envolvendo métodos utilizados para estudo de fungos endofíticos que recebeu o título "*Methods used for the study of endophytic fungi: challenges and solutions*", que está sobre consideração para publicação na revista *Archives of microbiology* (Figura 2); e a outra sobre diversidade taxonômica de fungos endofíticos relacionados a espécies vegetais do Cerrado brasileiro, denominada "*Insights into taxonomic diversity and bioprospecting potential of cerrado endophytic fungi: a review exploring an unique brazilian biome and methodological limitations*" que foi enviado para publicação na revista *Environmental Earth Sciences* e se encontra em revisão por pares (figura 3). - O micobioma endofíticos das seis espécies hospedeiras será diverso em espécies;

Capítulo 2	Avalair o micobioma endofítico foliar em seis espécies vegetais nativas do Cerrado utilizando abordagens dependentes e independentes de cultivo, visando caracterizar a estrutura taxonômica dessa comunidade em termos de ocorrência, abundância e riqueza de espécies; e evidenciar o efeito de filtragem ambiental exercida pela identidade da planta hospedeira sobre o *pool* de espécies fúngicas que as colonizam.	- O número de espécies observadas pelos *metabarcoding* será maior que os observados nos métodos dependentes de cultivo; - O fator hospedeiro será decisivo para a estruturação da comunidade fúngica endofítica foliar na mesma região geográfica; - A abordagem cultivo-dependente indicará uma prevalência > 90% de fungos do filo *Ascomycota*; - Fungos do filo *Basidiomycota* representarão < 10% dos isolados na metodologia cultivo-dependente.
Capítulo 3	Avaliar o efeito da fenologia foliar sobre a comunidade de fungos endofíticos agrupando diferentes espécies vegetais de uma mesma fenologia foliar e comparando-as com grupos de fenologia distintas;	- O micobioma das espécies sempre-verdes será mais diverso em espécies do que o micobioma das espécies decíduas e brevídeciduas; - O micobioma das espécies decíduas será o menos diverso; - Ascomycota será dominante em ambas as fenologias; - Basidiomycota será mais abundante em espécies de fenologia sempre-verdes.
		-A comunidade de fungos endofíticos irá diferir nas diferentes condições de antropização do solo quando comparadas com o grupo controle (sem

		adição de nutrientes ao solo) para ambas as espécies hospedeiras;
Capítulo 4	Descrever a estrutura taxonômica do micobioma endofítico foliar de duas espécies vegetais nativas do Cerrado em diferentes tratamentos de adição de nutrientes ao solo a longo prazo, utilizando abordagens dependentes e independentes de cultivo	-Os efeitos mais notáveis de dissimilaridade da comunidade de fungos endofíticos, entre os diferentes tratamentos, serão observados na hospedeira *Ouratea hexasperma*. -Dissimilaridades entre ocorrência de táxons não será observada na abordagem dependente de cultivo; - As comunidades presentes nos tratamentos com nitrogênio e calagem serão os menos diversos em espécies.



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METHODS USED FOR THE STUDY OF ENDOPHYTIC FUNGI: CHALLENGES AND SOLUTIONS

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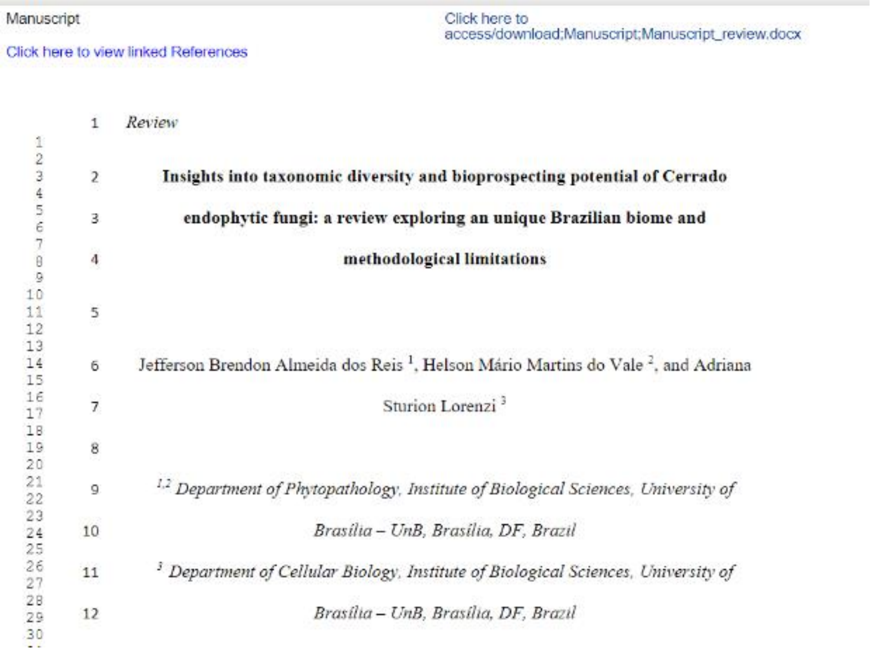
Figura 2. Revisão de literatura intitulada *"Methods used for the study of endophytic fungi: challenges and solutions"* considerada para publicação, com correções, na revista *Archives in Microbiology.*



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Review

Insights into taxonomic diversity and bioprospecting potential of Cerrado endophytic fungi: a review exploring an unique Brazilian biome and methodological limitations

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Figura 3. Revisão de literatura intitulada “*Insights into taxonomic diversity and bioprospecting potential of cerrado endophytic fungi: a review exploring an unique brazilian biome and methodological limitations*" submetida para publicação na revista Environmental Earth Sciences.

CHAPTER 1: ENDOPHYTIC FUNGI AND SELECTION OF PLANT HOSTS

Abstract: Cerrado plant species can be considered an reservoir of microbial species, especially endophytic fungi. Endophytic fungi are microorganisms that colonize the interior of plant tissue (leaves, fruits, flowers, seeds, stems, roots etc.) without causing any apparent symptoms of disease in their host. These microorganisms evolved together with their plant hosts so that over time, the relationship between endophytic fungus and host became specialized to the point that colonization depends on numerous genetic and molecular factors present in both groups, together with interactions with environmental factors. Thus the taxonomic structure of the endophytic mycobiome in terms of species diversity and equity is complex and varies depending on host identity and environmental and edaphic conditions. In the Cerrado, there are many efforts aimed at understanding the diversity of endophytic fungi species related to native plant species and the factors that shape these communities as well as for biotechnology exploration of these microorganisms. However, studies involving the description of the diversity of endophytic fungi in native species of the Cerrado are limited to the fraction of cultivable taxa, which does not reflect the true diversity. Bearing in mind all these issues, this chapter brings a bibliographic survey on a) the ecology and biology of endophytic fungi; b) biotic and abiotic factors that influence the taxonomic structuring of the endophytic mycobiome; c) culture-dependent and independent methods used to study this microbial community; d) challenges encountered and perspectives; e) an inventory of the taxonomic diversity of endophytic fungi associated with endemic species of the Cerrado; as well as the justification for the f) choice of host species to have the endophytic mycobiome analyzed.

Keywords: Mycobioma; *Ascomycota*; Symbiosis; *Metabarcoding*; ITS; *Sordariomycetes; Dothideomycetes; Diaporthe*; Tropical Savannah; Woody species.

1. BRAZILIAN CERRADO AND MICROBIAL DIVERSITY

The Cerrado is the largest tropical savanna in South America and the second largest biome in Brazil, surpassed only by the Amazon Forest, with an area of more than two million square kilometers (24% of the Brazilian territory) that is continuously distributed. in all states of the Midwest region; parts of the North, Northeast, Southeast; and small isolated points in the south of the country (Machado et al., 2005; Machado et al., 2008).

Due to its enormous territorial extension, the Cerrado varies greatly in its abiotic and biotic characteristics. In general, the Cerrado has a seasonal tropical climate, characterized by a rainy period, which lasts from October to March, and a dry period, which lasts from April to September (Nimer & Brandão, 1989). The soils in this biome are old, sandy, deep, and poor in organic matter and mineral salts, but have high aluminum concentrations (Klink & Machado, 2005). Its plant physiognomy is characterized by having xeromorphic vegetation, basically composed of grasses, trees, and sparse shrubs, adapted to climatic and edaphic conditions (Sano et al., 2010; Roitman et al., 2018).

The Cerrado's high degree of environmental heterogeneity makes its vegetation one of the most diverse in species (Roitman et al., 2018) with a high degree of endemicity (Klink et al., 2005). It is estimated that there are more than 7.000 species of native plants that are distributed among vegetation of the sensu stricto type, savanna, intercalations of fields and dense forests (Klink et al., 2005). This enormous phytophysiognomic variety, together with the high degree of endemicity of the native plant species of this biome, drew the attention of pioneers in the investigation of Cerrado vegetation and was highlighted in the work of Warming (1908), which brought an instigating description of the phenology of numerous plant species in this biome.

In addition to the vast diversity of plants, the Cerrado is home to a great diversity of microorganisms (Araújo et al., 2012), especially fungi (de Castro et al., 2016; Vieira et al., 2020; Coelho et al., 2020) (Figure 4). Research carried out in the Department of Phytopathology of the University of Brasília, in the last 20 years, showed that the biodiversity of Cerrado fungi is still a little-explored field and with a vast wealth of microorganisms, many of which have not yet been cataloged (Hernandez- Gutierrez et al., 2015; Souza et al., 2015; Santos et al., 2016; Velez-Zambrano et al., 2017). These researches aimed at identifying fungi from the Cerrado resulted in the implementation of the UnB Mycological Collection (Herbarium UB/Micrological Collection), where more than 23,000 specimens of fungi from the Federal District, Goiás, Mato Grosso, Mato Grosso do Sul were incorporated, Minas Gerais, Rondônia, Tocantins, South of Piauí, among which 73 new species were identified, nine of them type-species of new genera.

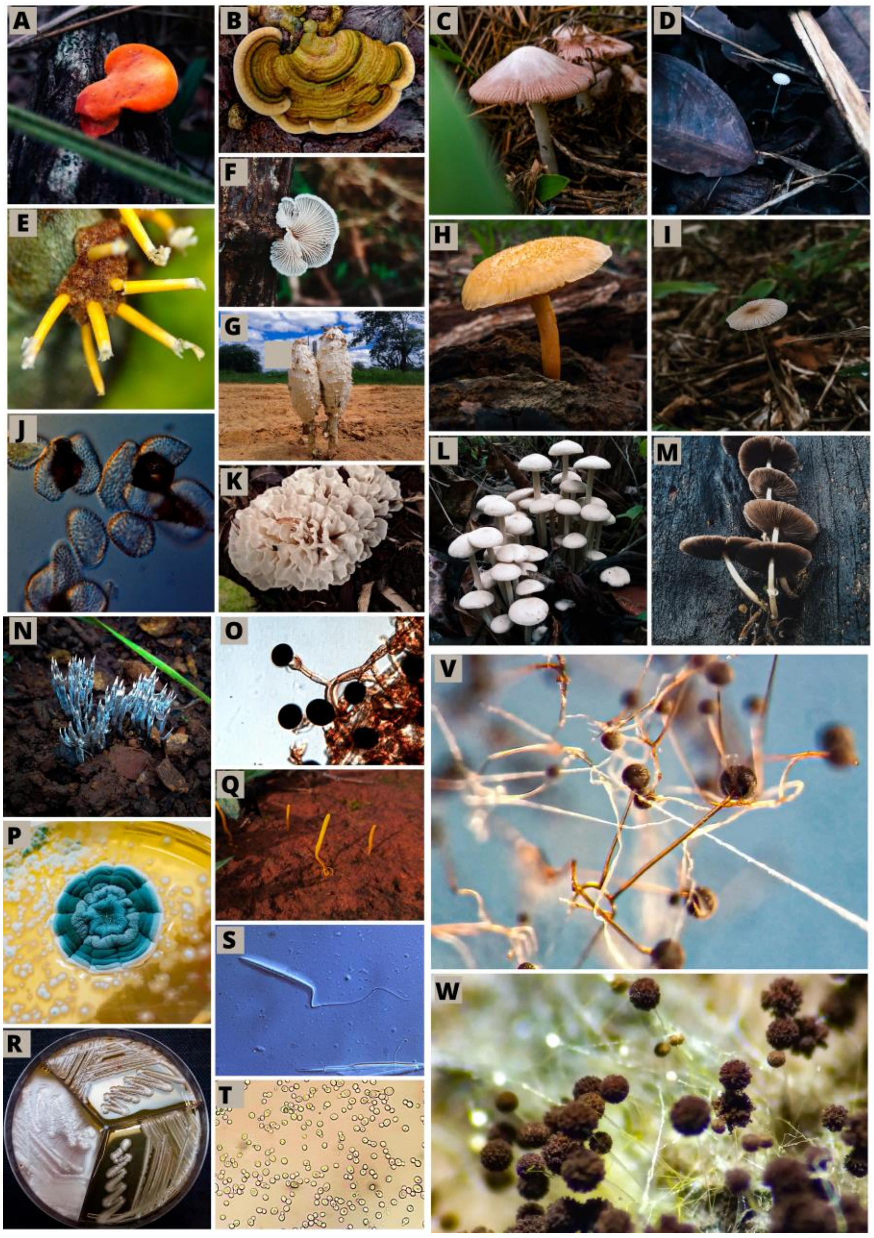


Figure 4. Fungal diversity in the Cerrado. A-M, N and Q *Basidiomycota*; O, P-T *Ascomycota*; V and W *Mucoromycotina*. A) *Pycnoporus* sp.; B-D, F-I, K-N and Q *Agaromycetes* spp; E) *Aecium* of *Pucciniaceae* sp. in *Phthirusa* sp. leaf; J) *Pucciniaceae* sp. urediniospore; O) *Nigrospora* sp. P) *Penicillium* sp.; R) *Eremotecium* spp.; S) ascospore of *Eremotecium* sp. endophytic; T) fresh

microscopy of *Pichia* sp, where it is possible to observe oval/elliptical yeast cells. V) *Gilbertela* sp; W) *Rhizopus* sp. All photographs are of fungi found in the Cerrado of the Federal District region, Brazil (*15°47'42.79” S 48°8'40.98”*), except for G and S, which were found in the Municipality of Tabocas do Brejo Velho, Bahia, Brazil (*12° 41' 51" S 44° 0' 9"*). Source: author's collection.

During the last decades, fungi related to native plates of the Cerrado have been studied by numerous groups of researchers at the University of Brasília, resulting in the description of 15 new genera and more than 100 species (Armando et al., 2015; Hernandez-Gutierrez et al., 2015; Souza et al., 2015; Santos et al., 2016; Velez-Zambrano et al., 2017). However, most of these works aimed to study the epiphytic microbiota, limiting themselves to only the fungi present in the phylloplane. Research aimed at evaluating the community of endophytic fungi in plant species from the Cerrado, although few, showed that this niche is extremely diverse in species (Detmann et al., 2008; Vieira et al., 2012; Vieira et al., 2014; Noriler et al., 2018), but little explored.

Studies carried out in recent decades show that the communities of endophytic fungi that occur in plant species in the Cerrado are highly biodiverse (Table 2) (Vieira et al., 2014) and have potential for biotechnological applications (Silva et al., 2010). As an example, Noriller et al. (2018) retrieve more than 1.100 endophytic fungi isolates from two Cerrado species, which were distributed in more than 20 genera, including possible new genera. In addition, these researchers reported antifungal, antiphytopathogenic, antibacterial and antioxidant activity that some of these isolates had, further reinforcing the importance of studying these microorganisms.

Table 2. Inventory of endophytic fungi isolated from host plants in the Cerrado biome

Host plant species	Geographic location of the host	Plant tissue analyzed	Taxonomic classification of isolated fungal endophytes	Author
(**1**) *Arrabidaea samydoides* (**2**) *Casearia sylvestris* (**3**) *Cassia spectabilis,* (**4**) *Cupania vernalis* (**5**) *Ocotea corymbosa* (**6**) *Rudgea viburnioides* (**7**) *Styrax camporum* (**8**) *Styrax ferrugineus*	São Paulo, Brazil (Geographical coordinates not informed)	Leaves	(**1**) *Xylaria sp.* (**2**) *Xylaria sp.* (**3**) *Phomopsis cassiae* (**3**) *Acremonium sp.* (**4**) *Phoma Herbarum* (**4**) *Minitans Coniothyrium* (**4**) *Ustilaginoidea sp.* (**4**) *Xylaria sp*. (**5**) *Trichoderma viridae*	Joly et al., 2010

(**9**) *Xylopia aromática*			(**6**) *Chaetonium sp.* (**7**) *Phomopsis stipata* (**8**) *Paecilomyces sp*. (**9**) *Periconia atropurpurea*	
Anacardium othonianum	Montes Claros de Goiás, Goiás, Brazil (16°08'S 51º17' W)	Roots	*Agaricomycetes* sp. *Bionectria ochroleuca* *Cladosporium cladosporioide* *Diaporthe* sp. *Eupenicillium shearii* *Fusarium oxysporum* *Paecilomyces lilacinus* *Periconia macrospinosa* *Phomopsis asparagi* *Phomopsis lagerstroemiae*	Alberto, 2013
Annona squamosa	Grande Dourados Mato Grasso do Sul, Brazil (22°14'16" S e 54°48'02" W)	Fruits	*Pichia* spp.	Araújo, 2014
Baccharis trimera	Serra do Ouro Branco, Minas Gerais, Brazil (20°30 369' S, 43°37'837'W)	Leaves	*Alternaria* sp. *Chaetomium* sp. *Cochliobolus lunatus* *Diaporthe* spp. *Diaporthe phaseolorum* *Epicoccum nigrum* *Epicoccum* sp. *Guignardia* sp. *Nigrospora* spp. *Pestalotiopsis* spp. *Phomopsis* spp. *Phoma* spp. *Podospora* sp. *Preussia pseudominima* *Preussia* spp. *Preussia africana* *Sporormiella* sp. *Xylaria* sp.	Vieira et al., 2014
Baccharis dracunculifolia	Belo Horizonte, Minas Gerais, Brazil (19 ° 52 ′ S 43 ° 58 ′ W)	Leaves and Branches	*Cladosporium halotolerans* *Coriolopsis rígida* *Preussia africana* *Preussia* sp. *Xylaria apiculata* *Xylaria venulosa* *Xylaria* sp. *Mycelia sterilia*	Fernandes et al., 2018
Butia purpurascens	Rio Verde, Goiás, Brazil (17° 35' 10.51" S 50° 59' 13.06" W)	Roots	*Aspergillus tubingensis* *Bionectria ochroleuca* *Codinaeopsis* spp. *Diaporthe* spp. *Gibberella moniliformis* *Fusarium concentricum* *Fusarium oxysporum* *Fusarium proliferatum* *Hamigera insecticol* *Penicillium purpurogenum* *Periconia macrospinosa* *Phomopsis* sp. *Talaromyces amestolkiae*	da Silva et al., 2018
	Brasília, Brasil	Fruits	*Candida cylindracea*	Coelho et

Caryocar brasiliense			*Candida* sp. *Hanseniaspora uvarum* *Hanseniaspora* sp.	al., 2020
Cassia spectabilis	São Paulo, Brazil (Geographical coordinates not informed)	Leaves	*Phomopis cassiae*	Silva et al., 2006
Campomanesia adamantium .	Grande Dourados Mato Grosso do Sul, Brazil (22°14’16” S e 54°48’02” W)	Fruits	*Candida* spp. *Saccharomyces* sp.	Araújo, 2014
Guapira graciliflora	Brasília, Brazil	Fruits	*Aureobasidium leucospermi* *Cryptococcus cuniculi* *Hannaella pagnoccae* *Hannaella* sp *Sirobasidium* sp	Coelho et al., 2020
Hancornia Speciosa	Recife, Pernambuco, Brazil (08º24'334 ”S, 34º94'384” W)	Tree bark	*Aspergillus flavus* *Aspergillus niger Tiegh* *Cladosporium cladosporioides* *Colletotrichum gloeosporioides* *Fusarium lateritium Nees* *Fusarium solani* *Lasiodiplodia theobromae* *Mariannaea elegans* *Mycelia sterilia* *Nigrospora sphaerica* *Penicillium fellutanum* *Phoma cava Schulzer* *Phomopsis archeri* *Trichoderma harzianum* *Tritirachium oryzae*	Chagas et al., 2017
Hyptis marrubioides	Três Barras em Lavras, Minas Gerais, Brazil (Geographical coordinates not informed)	Roots	*Trichoderma* sp *Papulaspora* sp. *Fusarium* sp.	Januário & Vitorino, 2013
Inga edulis	Grande Dourados Mato Grosso do Sul, Brazil (22°14’16” S e 54°48’02” W)	Fruits	*Candida spp.*	Araújo, 2014
Ocotea corymbosa	São Paulo, Brazil (Geographical coordinates not informed)	Leaves	*Thichoderma viridae*	Lisboa et al., 2013
Ocotea corymbosa	Araraquara, São Paulo, Brazil (Geographical coordinates not informed)	Leaves	*Curvularia* spp.	Teles et al., 2005
Rudgea viburnioides	São Paulo, Brazil (Geographical coordinates not	Leaves	*Chaetonium* sp.	Lisboa et al., 2013

	informed)			
Schinus terebinthifolia	Geographical coordinates not informed	Leaves	*Diaporthe terebinthifolii*	Tonial et al., 2017
Styrax camporum	São Paulo, Brazil (Geographical coordinates not informed)	Leaves	*Phomopsis stipata*	Lisboa et al., 2013
S. ferrugineus	São Paulo, Brazil (Geographical coordinates not informed)	Leaves	*Paecilomyces* sp.	Lisboa et al., 2013
Stryphnodendron adstringens	Miranda, Mato Grosso do Sul, Brazil (20 ° 18′10,8 ″ S 56 ° 15′44,3 ″ W)	Leaves and petiole	*Acrocalymma medigans* *Alternaria alternata* *Bjerkandera* sp *Coniochaeta nepalica* *Corynespora cambrensis* *Colletotrichum* spp. *Colletotrichum siamense* *Curvularia* sp. *Diatrypaceae* sp. *Diaporthe cf. heveae* *Diaporthe* spp. *D. ocoteae* *D. Schini* *Didymella* sp. *Epicoccum* sp. *Efibula* sp. *Fusarium* sp. *F. pseudocircinatum* *Hypoxylon* sp. *Lasiodiplodia* spp. *Neofusicoccum brasiliense* *Neopestalotiopsis* sp *Nigrospora hainanensis* *Paraphaeosphaeria* spp. *Pestalotiopsis* spp. *Phaeophleospora* sp. *Phyllosticta* spp. *Pseudofusicoccum* sp. *P. stromaticcum* *Xylariacea* spp	Noriler et al., 2018
Stryphnodendron adstringens *Solanum lycocarpum*	São Carlos, São Paulo, Brazil (21°58’, 47°52’W)	Leaves and branches	*Colletotrichum* sp. *Curvalaria* sp *Diaporthe* spp. *Phomopsis* spp *Nigrospora* spp *Neofusicoccum* spp. *Pseudofusicoccum* spp. *Paraconiothrium* spp. *Phlebiopsis* spp. *Phomopsis* spp. *Neurospora* sp. *Phomopsis* spp. *Neopestalotiopsis* spp. *Schizophyllum* spp. *Xenoacremonium* spp.	Santos, 2014

Stryphnodendron adstringens	Serra do Cipó e Serra de São José, Minas Gerais, Brazil	Leaves	*Alternaria alternata,* *Arthrobotrys foliicola* *Aspergillus ustus* *A. flavipes* *Botryosphaeria dothidea* *Cladosporium cladosporioides* *Colletotrichum boninense* *C. gloeosporioides* *Coniochaeta discoidea* *Cytospora* sp. *Diaporthe* sp. *D. phaseolorum* *Guignardia camelliae* *G. mangiferae* *Muscodor vitigenus* *Neofusicoccum ribis* *Nigrospora oryzae* *Paraconiothyrium brasiliense* *Penicillium glabrum* *P. minioluteum* *Pestalotiopsis clavispora* *P. cocculi* *P. microspora* *Phyllosticta theicola* *Phomopsis* sp. *Preussia* sp. *Pseudofusicoccum stromaticum* *Sarcosomataceous* sp. *Sordaria fimicola* *S. tomento-alba* *Sporormiella* sp. *Trichoderma* sp. *Xylaria* sp.	Carvalho et al., 2012
Vellozia gigantea	Parque Nacional da Serra do Cipó, Minas Gerais, Brazil (19 ° 14′874 ″ S; 043 ° 30′574 ″ W)	Leaves and roots	*Bipolaris drechsleri* *Botryosphaeriales* sp. *Camarosporium aloes* *Candida michaelii* *Candida parapsilosis* *Candida* spp. *Cladophialophora boppii* *Clonostachys rosea* *Coccomyces proteae* *Colletotrichum aeschynomenes* *Colletotrichum cymbidiicola* *Colletotrichum gigasporum* *Colletotrichum karstii* *Colletotrichum* spp. *Coniochaetales* sp. *Crucellisporiopsis marquesiae* *Daldinia loculata* *Diaporthe acaciarum* *Diaporthe acaciigena* *Diaporthe anacardii* *Diaporthe arengae* *Diaporthe citri*	Ferreira et al., 2017

	Diaporthe diospyricola
	Diaporthe eucalyptorum
	Diaporthe foeniculina
	Diaporthe hickoriae
	Diaporthe inconspicua
	Diaporthe kongii
	Diaporthe masirevicii
	Diaporthe maytenicola
	Diaporthe miriciae
	Diaporthe nothofagi
	Diaporthe saccarata
	Diaporthe sackstonii
	Diaporthe schini
	Diaporthe sclerotioides
	Diaporthe sojae
	Diaporthe spp.
	Diaporthe terebinthifolii
	Dothideomycetes sp.
	Fusarium bulbicola
	Fusarium circinatum
	Fusarium inflexum
	Fusarium oxysporum
	Fusarium spp.
	Geotrichum vulgare
	Guignardia mangiferae
	Harpophora oryzae
	Herpotrichiellaceae sp.
	Hyaloscyphaceae sp.
	Hypoxylon liviae
	Kabatiella lini
	Lecythophora
	Lecythophora decumbens
	Lodderomyces (Candida) parapsilosis
	Magnaporthaceae spp.
	Massarinaceae spp.
	Medicopsis romeroi
	Muscodor equiseti
	Muscodor oryzae
	Muscodor spp.
	Muscodor suthepensis
	Mycoleptodiscus terrestris
	Mycosphaerella stramenti
	Myxotrichum arcticum
	Myxotrichum sp.
	Nemania abortivo
	Neofusicoccum parvum
	Neopestalotiopsis surinamensis
	Nigrospora oryzae
	Ochrocladosporium adansoniae
	Pallidocercospora ventilago
	Paraconiothyrium estuarinum
	Paraconiothyrium sp.
	Paraphaeosphaeria parmeliae
	Penicillium citrinum
	Penicillium herquei

			Penicillium quebecense *Pestalotiopsis australasiae* *Peyronellaea prosopidis* *Peyronellaea* sp. *Pezicula sporulosa* *Phaeophleospora stramenti* *Phialocephala scopiformis* *Pleosporineae* sp. *Pseudobotrytis bisbyi* *Pseudocercospora norchiensis* *Pseudolachnea fraxini* *Pseudophialophora schizachyrii* *Quadricrura meridionalis* *Sordariomycetes* sp. *Stagonospora perfecta* *Stagonospora pseudocaricis* *Trematosphaeriaceae* sp. *Trichoderma effusum* *Trichoderma viride* *Xylaria arbuscula* *Xylaria berteri* *Xylariaceae* spp. *Yamadazyma michaelii* *Yamadazyma riverae*	
Vellozia compacta	Mateiros, Tocantins, Brazil (10 ° 36′ 043″ S; 046 ° 35′ 836″ W)	Leaves and Roots	*Acarospora* sp. *Chaetomium* sp. *Diaporthe* sp. *Dothideomycetes* sp. *Gelasinospora seminuda* *Fusarium oxysporum* *Penicillium* spp. *Pestalotiopsis herbarum* *Pestalotiopsis* sp. *Phomopsis* spp. *Xylariacea* sp	Rodrigues et al., 2010
Viguiera arenaria	Geographical coordinates not informed	Leaves	*Glomerella cigulata* *Fusarium* spp.	Guimarães et al., 2010
Viguiera robusta	Geographical coordinates not informed	Leaves	*Colletotrichum gloeosporioides* *Penicillium crustosum*	Guimarães et al., 2010
Xylopia aromática	Araraquara, São Paulo, Brazil (Geographical coordinates not informed)	Leaves	*Periconia atropurpurea*	Teles et al., 2006
Xylopia aromática	São Paulo, Brasil (Geographical coordinates not informed)	Leaves	*Periconia atropurpure*	Lisboa et al., 2013

Legend: The numbers in parentheses correlate fungus with host plant for those studies with isolates from different host species.

Despite the enormous diversity of plant and microbial species that occur in the Cerrado and the numerous ecological roles played by these organisms for the maintenance of this biome, in recent decades, the Cerrado has suffered a brutal loss of its native area (Klink et al., 2020). It is estimated that almost 50% of the original area of this biome has already been deforested and replaced for agricultural activities (De Mattos Scaramuzza et al., 2017; Beuchle et al., 2019; Souza et al., 2020) and more than 80% of its native vegetation is threatened by the advance of these practices (Myers et al., 2000). This process of degradation of the Cerrado biome intensified after 1960, with the strong performance of the Brazilian economy and together with the policy of occupation of “empty” spaces in the Cerrado, thus creating an environment conducive to investment (Klink, 2014; Mueller). et al., 2016; Klein et al., 2019) so that the Cerrado is currently the largest soybean and pasture producing region in Brazil and an important producer of sugarcane and cotton (Klink et al., 2020).

Decisions on Cerrado lands are mainly focused on soil management. As stated at the beginning, the Cerrado soil is considered poor in nutrients and rich in aluminum, but with the correct management, it can be considered great for production (Vieira et al., 2011). From the point of view of income generation, the benefits of soil management in the Cerrado, mainly focused on agriculture, are a success and fundamental for the country's economy and socioeconomic development (Soterroni et al., 2019). However, these practices significantly threaten the species of this biome.

An article published in Nature in mid-2000 classified the Cerrado as one of the 25 world *hotspots* extremely threatened by exacerbated human exploratory activities, mainly reinforcing the threat to plant species endemic to this biome (Purvis et al., 2000). Furthermore, Zalles et al. (2019) demonstrated that after the year 2000 there was an intensification of land use in the Cerrado, which resulted in a loss of habitat for native plant species by more than 50% in some states whose predominant biome is the Cerrado. Other researchers reinforce the importance of preserving plant species in this biome, demonstrating that soil management activities do not only result in the loss of plant diversity but also impact the biogeochemical cycles of water (Spera et al., 2016; Nóbrega et al., 2017; Nóbrega et al., 2018).

Decisions about land use in the Cerrado, especially activities that involve soil management, in addition to resulting in the loss of habitat for native plant species, also impact the diversity of microorganisms that coexist in this biome

(Silveira et al., 2021). Souza et al. (2016) demonstrated that soil management (fertilization and type of cultivar) impacted the diversity of microorganisms present in the Cerrado soil, resulting in the loss of microbial biomass and a decrease in species diversity. Rampelotto et al. (2013) demonstrated that activities involving land use in the Cerrado are capable of modifying the structure of the microbial assemblage so that some species try to outperform others, causing a dysbiosis condition.

Research carried out in the Cerrado evaluating the impact of the addition of nutrients to the soil on the community of symbiotic fungi in plants involves exclusively mycorrhizal fungi (Miranda et al., 1997; Miranda et al., 2005; Cordeiro et al., 2005; Miranda et al., 2008; Moura, 2015). For example, Ferreira et al. (2012) demonstrated that the diversity and population density of mycorrhizal fungi tend to differ between the type of fertilizer and cultivar used in soil management. Although there are studies that evaluate the effect of soil management practices on mycorrhizal fungi, no studies were found that aim to assess the short or long term impact that the addition of nutrients to the soil can have on the taxonomic structuring of the leaf endophytic mycobiota of native plant species from this biome.

Understanding the importance of the Cerrado as a reservoir of species and its varied environmental and phytophysiognomic conditions, studying the endophytic mycobiota is extremely necessary, both to know the taxonomic structure of this community, as well as to shed light on its ecological and evolutionary roles. In addition, because the biodiversity of this biome is threatened by human exploratory practices, to study the diversity of endophytic fungi and the effect that practices involving soil management, such as fertilization, impact on these micro-organisms, it is extremely necessary, since such researchs can reinforce the urgent need to implement public policies for the preservation of this biome.

2. BIOLOGY AND ECOLOGY OF ENDOPHYTIC FUNGI

Endophytic fungi are a group of polyphyletic microorganisms that reside asymptomatically in the most diverse plant tissues (stem, flowers, leaves, fruits, roots, seeds etc.) apparent manifestation of disease in colonized tissues (Bacon

& White, 2000; Zhou et al., 2019). These microorganisms were first described in the early 19th century as latent plant pathogens, they remained unexplored for a long time and neglected regarding their ecological role and their interactions with their hosts (Azevedo, 1996). It was only at the end of the 20th century, with the isolation of the endophytic Taxomyces andreanae (Stierle et al., 1993), that these microorganisms received attention from the scientific community.

Initially, it was postulated that fungi with an endophytic lifestyle colonized specific species, but over the years it was discovered that all vascular plant species in the most varied natural environments are colonized by at least one species of endophytic fungus (Strobel et al., 2003; Strobel et al., 2004; Ferrara, 2006; Sun et al., 2012). In addition, there is a great diversity of fungal species that have an endophytic lifestyle, with an estimate of approximately two million species (Hawksworth et al., 2017; see review Rashmi et al., 2019), occurring mainly in temperate and tropical regions (Lia et al., 2016), but there are also reports of endophytic fungi in species from regions with hostile environments, such as Arctic (Zhang et al., 2015), Andean (Vidal et al., 2020) and desert regions. (Li et al., 2020).

Endophytic fungi come from the environment where their hosts occur, which include soil fungi, airborne spores and from the feeding processes of herbivores (Rodriguez et al., 2009; Manzotti et al., 2020). The transmission of endophytic fungi generally occurs by two main patterns, vertical transmission and horizontal transmission (Rodriguez et al., 2009).

Vertical transmission of endophytic fungi occurs when maternal plants transmit these microorganisms to their seeds (Compat et al., 2010; Gagic et al., 2018; Vandana et al., 2021). When the seeds germinate, the fungal spores or fragments of hyphae present enter the interior of the tissue, thus carrying out the transmission between the mother plant and the offspring (Jordaan et al., 2006; Shen et al., 2014; Vandana et al., 2021). Infection mediated by this process occurs mainly in the roots (Compant et al., 2010), which is considered by some authors to be the main entry route for endophytic fungi (Tyburska-Woś et al., 2019; Ori et al., 2020).

Horizontal transmission of endophytic fungi usually occurs in aboveground tissues via inoculation of spores and/or hyphae fragments by biotic or abiotic dispersal agents, from plant to plant or from environment to plant (Vorholt, 2012; Li et al., 2012; Park et al., 2012; Park et al., 2015). Horizontally transmitted endophytic fungi use natural openings or those caused by biotic and abiotic agents to enter and colonize the internal tissue of their hosts (Singh et al., 2018; Yao et al., 2019; Alibrandi et al., 2020).

The process of colonization by endophytic fungi involves a complex relationship between these microorganisms and their hosts (Kaul et al., 2012; Li et al., 2012; Pan et al., 2020; Yang et al., 2020). Unlike epiphytic fungi, which are in contact with the external environment and basically depend on nutrients deposited in leaves and on abiotic factors to colonize a plant (Inácio et al., 2002), endophytic fungi are closely related to their plant hosts and, therefore, they mainly depend on plant characteristics to establish colonization (Table 3) (Clay et al., 2002; Yao et al., 2019).

Table 3. Determining factors for the taxonomic structuring of the endophytic mycobiota in different host species

Host Botanical Family	Plant tissue	Type of climate (Habitat)	Factor that influences the assembly of the community	Author
Myrsinaceae *Verbenaceae* *Rhizophoraceae* *Euphorbiaceae*	Leaf	Tropical	Host Identity^A	Yao et al., 2019
Crassulaceae	Rhizome	Semi-arid	Host Identity^A	Cui et al., 2015
Paeoniaceae	Uninformed	Tempered	Environmental Factors^A	Yang et al., 2018
Oleaceae	Leaves	Mediterranean	Environmental Factors^A	Gomes et al., 2018
Oleaceae	Leaves	Mediterranean	Host Identity + Environmental Factors^A	Materatski et al., 2019
Ulmaceae	Leaves, Xylem Tissue, Shoots	Tempered	Host Identity^A	Martín et al., 2013
Chenopodiaceae *Poaceae* *Tamaricaceae* *Asteraceae* *Zygophyllaceae*	Twigs and Roots	Tempered arid	Host Identity^A	Li et al., 2020
Zygophyllaceae *Simmondsiaceae* *Fabaceae*	Leaves and Branches	Arid	Host Identity + Seasonality^A	Massino et al., 2015

Cactaceae				
Polygonaceae *Potamogetonaceae* *Hydrocharitaceae* *Haloragaceae*	Stem and Leaves	Semi-arid	Host Identity[A]	Sandberg et al., 2014
Poaceae	Stem and Leaves	Tropical	Host Identity[A]	David et al., 2016
Cupressaceae	Stem and Leaves	Semi-arid	Host Identity + Environmental Factors[A]	Hoffman et al., 2008
Lycopodiaceae *Pinaceae* *Rosaceae*	Stem and Leaves	Arctic	Host Identity[A]	Higgins et al., 2007

A: cultivation dependent techniques

Environmental filtering (niche process) is a fundamental process in the taxonomic structuring of any biotic community (Cottenie, 2005). The effect of environmental filtering by host plants, for example host identity, has already been widely documented as a key and determining factor for the taxonomic structuring of the community of endophytic and mycorrhizal fungi (Ványi et al., 2015; Ciccolini et al., 2016; Van Geel et al., 2018; Šmilauer et al., 2020). Likewise, host phylogeny also strongly predicts the communities of microorganisms that will colonize the plant (Van Geel et al., 2018; Šmilauer et al., 2020). According to phylogenetic niche conservatism, closely related plant species are more similar in morphological and physiological characteristics than distantly related ones (Losos, 2008), and perhaps tend to have more similar microbial communities to each other (Figure 5).

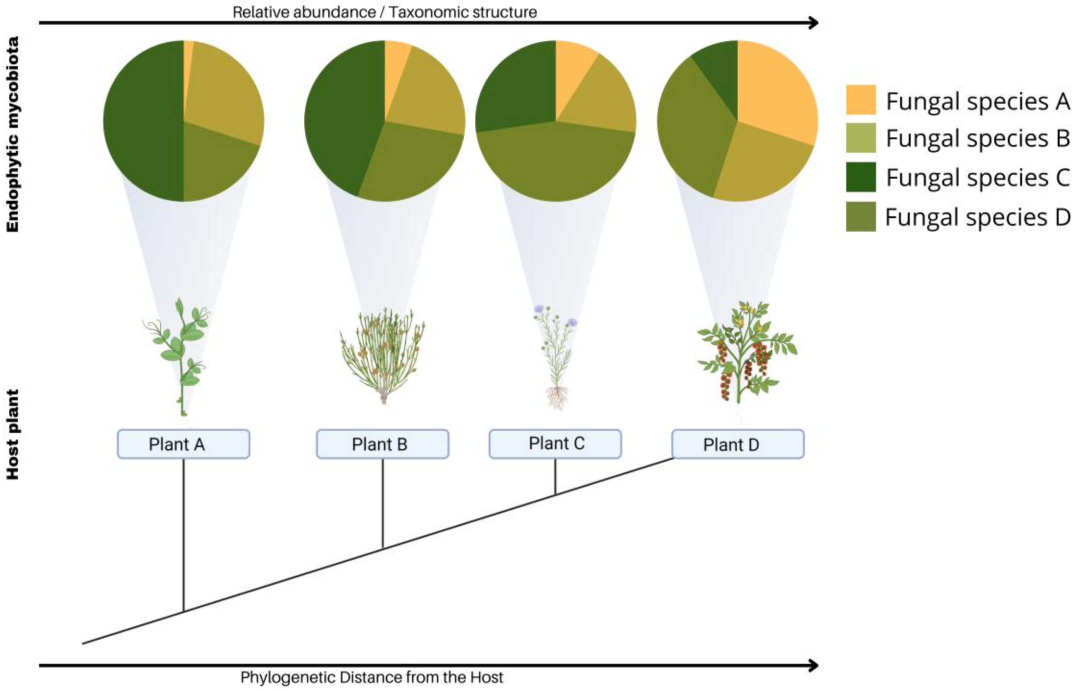


Figure 5. Overview of the phyletic niche conservatism theory applied to the endophytic fungal community. Phylogenetically close plant species may present endophytic fungal communities that are more similar to each other than when compared to phylogenetically more distant plant species. For example, the composition of the mycobiome community that occurs in plant A is more similar to that of plant B, which is phylogene0tically closer, than to plants C and D, which are phylogenetically more distant. Likewise, the endophytic mycobiome community of plant D is more similar to that of plant C, which is phylogenetically close, than to plants A and B, which are more phylogenetically distant. Created with BioRender.com and Canva.

The identity of the host plant exerts control over the composition of the fungal community that will endophytically colonize it (Sandberg et al., 2014; David et al., 2016). However, in addition to the host factor to determine the endophytic fungal community, abiotic factors, such as moisture, seasonality, and availability of nutrients in the soil, can act in this process of colonization selection indirectly (Ulrich et al., 2008; Dennis et al., 2010; Hardoim et al., 2015; Mereque et al., 2018), since the abiotic characteristics of a given region can influence the nutritional and chemical composition of the plant (Yang et al., 2020), which directly impacts the selection of fungi that will colonize it (Paul et al., 2019; Chen et al., 2019; Windisch et al., 2021; Heijo et al., 2021). In a simplified way, it should be considered that the taxonomic structuring of the community of endophytic microorganisms in the different tissues of the plant host is dynamic and occurs in real-time, instead of remaining static (Carvalho et al., 2016), therefore both the factors, host identity, and abiotic factors, interact to control the endophytic fungal assemblage.

The taxonomic structure of the endophytic fungal community also varies depending on the type of tissue colonized within the same host. Xing et al. (2011) isolated 39 species of endophytic fungi in five different species and found different colonization rates depending on the tissue analyzed, with colonization rates by these microorganisms ranging from 12.5 to 41.7% in the roots, from 8.0 to 54.0% in the stem and from 12.5 to 25.1% in the leaves. In short, other studies reinforce these findings, demonstrating how not only the host factor is decisive for the assembly of the endophytic fungal community, but also the type of organ and tissue colonized (Sun et al., 2012; Li et al., 2016a; Li et al., 2016b).

The difference between endophytic colonization and diversity between different tissues can be attributed mainly to biotic factors, such as the different phytochemical composition of microenvironments within plant tissues, which act as a selection factor; the degree of specialization of endophytic fungi in colonizing these tissues (Herrera et al., 2010; Larkin et al., 2012; Vincent et al., 2016; Põlme et al., 2018). For example, species of the genus Alternaria, with an endophytic lifestyle, are more dominant in aerial tissues, such as stems, flowers, leaves, and fruits when compared to roots, evidencing the tissue sealing effect and the degre2 of specialization and preference of this genus. for specific tissues (Muhsin et al., 1987; Sun et al., 2011b; Porras-Alfaro et al., 2014; Bezerra et al., 2015; Li et al., 2020).

Endophytic fungi have been isolated from the most diverse plant hosts in the most varied habitats on the planet (Mandyam et al., 2005) and the interaction between these two groups of organisms, in many cases, presents a high degree of specificity and specialization (Kaul et al., 2012; Li et al., 2012; Sandberg et al., 2014; David et al., 2016). Therefore, the colonization of the plant host by endophytic fungi is not a merely accidental process, caused by chemotaxis (Jia et al., 2016; Liu et al., 2020), but an evolutionarily complex symbiotic relationship that has been shaped according to these two groups of organisms coexisted during their evolutionary processes (Figure 6), and that, as a consequence of the degree of specialization, depends on a series of intrinsic factors present in both groups for colonization to occur (Read et al., 2000; Sieber, 2007; Lanfranco et al., 2018; Rimington et al., 2018; Liu et al., 2020; Savary et al., 2020; Latz et al., 2021).

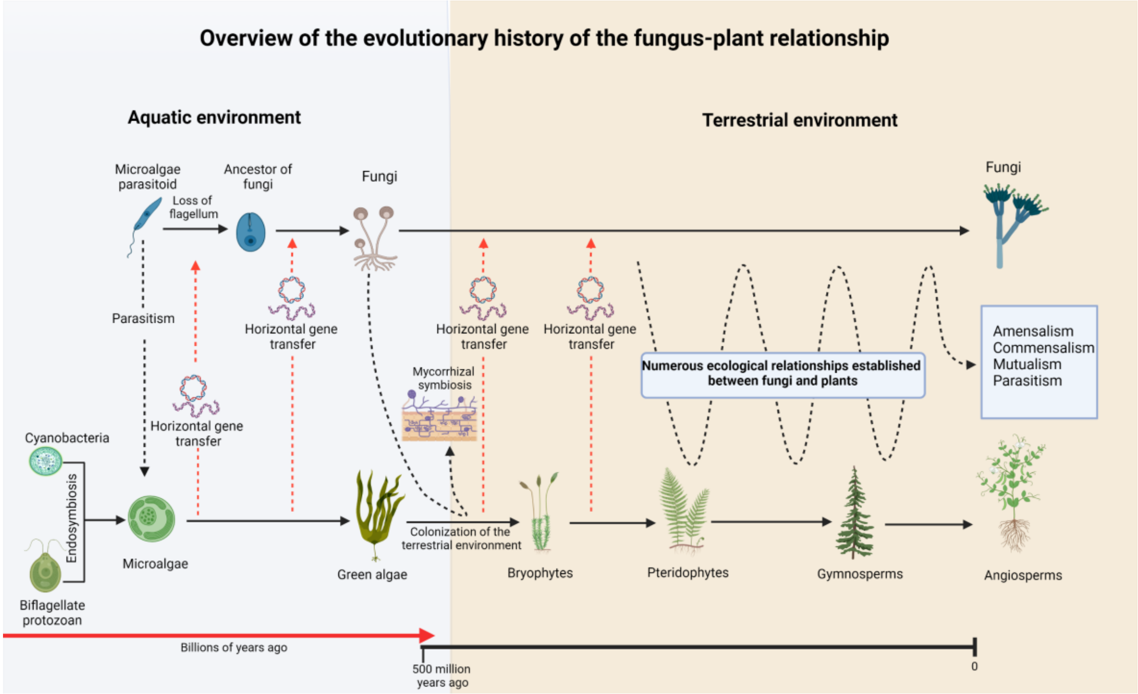


Figure 6. Hypothesis of the evolution of the ecological relationships established between fungi and plants. Throughout the evolutionary processes of fungi and plants, numerous ecological relationships were established (Amensalisms, Commensalism, Parasitism, Mutualism etc.) colonization of the terrestrial environment by plants. Furthermore, as the evolutionary process progressed, the ecological relationships between fungi and plants became increasingly specialized, including the exchange of genetic material via horizontal gene transfer. A classic example of these narrow and specialized ecological relationships between fungi and plants is the case of endophytic fungi, which evolved together with their hosts and exert fundamental functions for their aptitude, adaptations and survival, especially under stress conditions. (Badawy et al., 2021). The elaboration of the image was based on information provided by Richards et al., 2009; Lyu et al., 2021; Naranjo-Ortiz et al., 2021. Created with BioRender.com and Canva.

The mechanisms of interaction between endophyte and host plant have not yet been fully elucidated. Comparative genomic insights demonstrate that this relationship is extremely heterogeneous, differing between endophytic fungi and host plant species (Knapp et al., 2018). In general, it is theorized that different types of secondary metabolites produced by plants in conjunction with host defense mechanisms act as resistance mechanisms against phytopathogenic fungi and possibly against endophytic fungi (Pang et al., 2021). Therefore, to overcome this, endophytic fungi must be able to go unnoticed or evade these mechanisms to colonize their plant hosts (Figure 7) (Ohm et al., 2012).

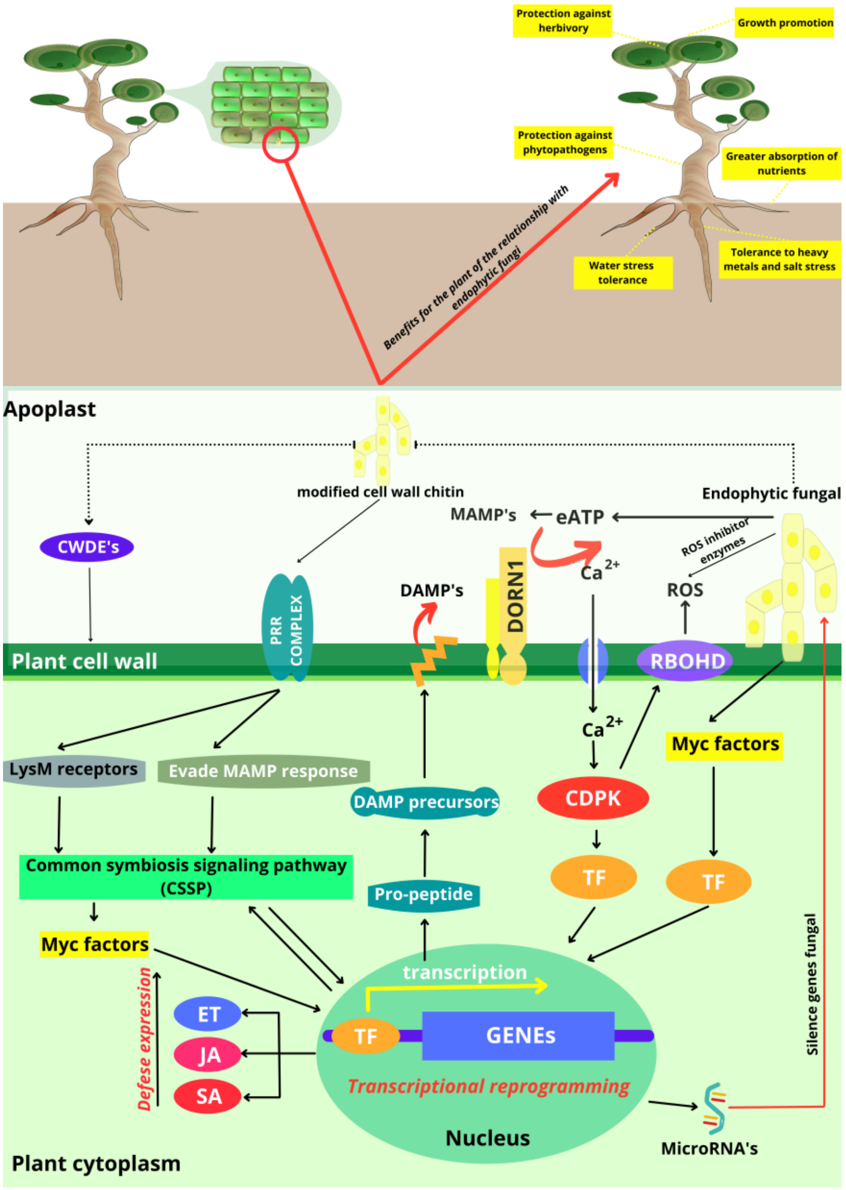


Figure 7. Communication between endophytic fungi and host plant, and the benefits behind this relationship. To colonize plant tissues, endophytic fungi need to disrupt and/or modify the cell wall of plant cells and, for this purpose, secrete cell wall degrading enzymes (CWDEs) (Chow et al., 2019). Once invaded by the fungus, plants have an innate defense system that responds to molecular patterns associated with microbes or pathogens (MAMP and/or PAMP) (Wu et al., 2018) through pattern recognition receptors (PRR) (Tang et al., 2017). Recognition of these molecules or damage-associated molecular patterns (DAMP) induces pattern-triggered immunity (PTI) (Saijo et al., 2018). In addition, plants have a second line of defense known as effector-triggered immunity (ETI) (Yu et al., 2017; Tian et al., 2019). Activation of PTI and ETI causes a cascade of intracellular signal transduction in the plant cell, which involves the signaling of Ca 2+, Ca 2+ -dependent protein kinase (CDPK) and a series of transcriptional

factors (TF) that modify transcription patterns in the plant and alter the flow of ions through the membrane, causing an increase in apoplastic reactive oxygen species (ROS), production of phytohormones such as ethylene (ET), jasmonic acid (JA) and salicylic acid (SA), and release of microRNA's that act by silencing virulence genes of microorganisms in an attempt to eliminate the invading agent (Chanclud et al., 2016; Rutter et al., 2018). Therefore, to colonize plant tissue, the endophytic fungus needs a series of adaptations capable of circumventing the plant defense system. For example, endophytic fungi may present alterations in the cell wall that prevent recognition by PRR's or lipochitooligosaccharide (LCO) signaling derived from the microbial cell wall, also known as Myc factors, may be recognized by lysine-motif receptors (LysM) in the plant cell, which are involved in the activation of a common symbiosis signaling pathway (CSSP), thus allowing the endophytic fungi to establish a symbiotic relationship with its host and colonize the interior of the plant tissue (Gough et al., 2011; Genre et al., 2013). As a result of this relationship between fungal endophyte and host plant, both organisms benefit: the fungi offers the plant protection against phytopathogens and herbivory, greater tolerance to water and saline stress while the plant offers the fungi a habitat with low fluctuations in the supply of available nutrients (sugars, amino acids etc.) and protection against abiotic stresses etc. (Hardoim et al., 2015). Source: author's collection.

Plants have different defense mechanisms capable of recognizing microbial signaling molecules, which results in different responses (Sanabria et al., 2010; Dubery et al., 2012; Abdul et al., 2020). One of these mechanisms occurs through the recognition of pathogen-associated molecular patterns (PAMPs) through receptors that recognize these patterns on the cell surface, the so-called pattern recognition receptors (RRPs) (Imam et al., 2016; Abdul et al., 2020), triggering the MTI (Triggered Immunity) type response (Tang et al., 2017). Another mechanism is the recognition of effector molecules produced by fungi and identified through intracellular receptors located in plant cells, triggering the effector-mediated defense response (ITE) (Saijo et al., 2018; Nishad et al., 2020). The establishment of colonization of endophytic fungi in their hosts requires that these mechanisms be circumvented.

To evade the MTI-type response, it is hypothesized that endophytic fungi can adapt their interaction behavior with their hosts in a way that maximizes their fitness, such as through structural modifications and alteration of the recognition sites of plant defense mechanisms (Vandenkoornhuyse et al., 2015; Jacobs et al., 2016). As an example of one of these modifications, *Fusarium solani* has alterations in specific amino acids at the binding site of camptothecin, an alkaloid produced by plant species to inhibit the DNA topoisomerase I enzyme of possible phytopathogens (Kusari et al., 2012); and *Piriformospora indicates* that it can modify the structural composition of its cell wall so that it goes unnoticed by the RRPs of the plant defense system (Wawra et al. 2016; Wawra et al., 2019).

Regarding the ITE-type defense, Ma et al. (2017) demonstrated that the *Phytophthora sojae* isolate can encode a protein without catalytic activity but which is capable of binding to plant defense system proteins that aim to neutralize fungal effectors, blocking them and allowing colonization to occur. Other mechanisms that plant symbiotic fungi possess that can “cheat” the defense mechanisms of their host plant(s) have been reported and proposed (Jacobs et al., 2011; Handoin et al., 2015) but the knowledge we have about these is limited, remaining largely unknown.

The beneficial and non-pathogenic properties between endophytic fungi and their hosts depend on a balanced interaction between endophytic fungal virulence factors and host plant defense (Figure 8) (Schulz et al., 2005; Schulz et al., 2015). The mechanisms behind this relationship have not yet been fully elucidated and remain unknown in the vast majority of cases as previously stated.

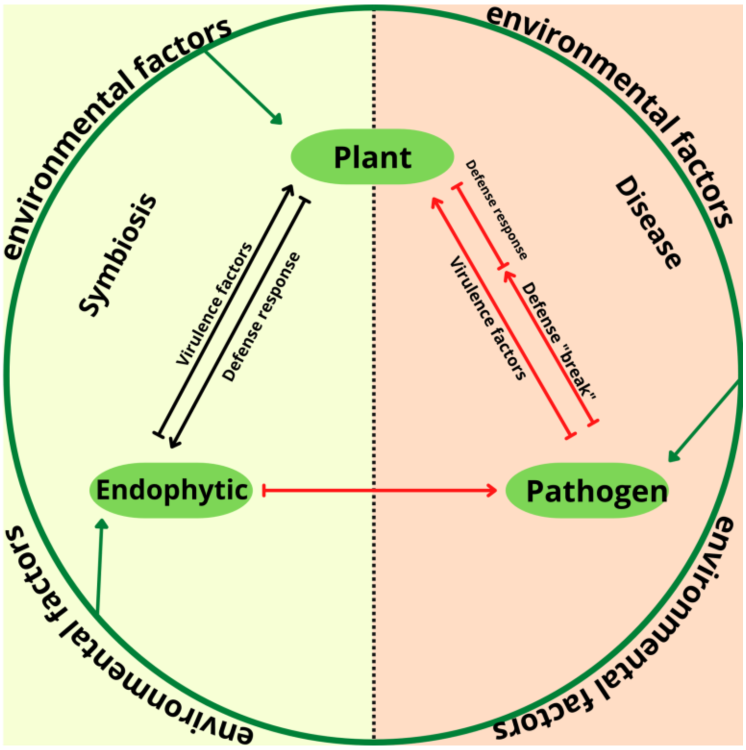


Figure 8. Interaction between endophytic fungus and plant host. The balanced antagonism hypothesis postulates that there is a balance between the host plant's defense in response to endophytic fungi and the effect of the virulence mechanisms of these microorganisms on their hosts. In this relationship,

endophytic fungi are able to resist or evade plant defense mechanisms and coexist inside their tissues without causing symptoms or disease. In this way, the interaction between plant-endophytic is asymptomatic, as long as there is a balance between host defense and virulence of the endophytic fungus. If this balance is disrupted, endophytes will die or become pathogenic. Figure inspired by Schulz (2005), Schulz (2015) and Yan et al. (2018). Source: author's collection.

The community of endophytic fungi is predominantly composed of ascomycetes and to a lesser extent basidiomycetes (Ikeda et al., 2014; Chagnon et al., 2014; Chagnon et al., 2016; Coleman-Derr et al., 2016; Gashgare et al., 2016; Fang et al., 2019; Rashmi et al., 2019). However, it is important to highlight that, depending on the methodology used to study the taxonomic diversity of endophytic fungi in their hosts, there may be variations in the findings regarding the taxonomic composition of this community (Table 4) (Sun et al., 2012). Traditional methods, which depend on cultivation, show the prevalence of more than 90% of species of the phylum *Ascomycota* and to a lesser extent the phylum *Basidiomycota* (Guo et al., 2000; Osono, 2007), while, in contrast, independent methods of cultivation, such as high-throughput DNA sequencing, provide a more complete picture of the endophytic fungal community, showing that, although Ascomycota is the predominant phylum, the abundance of basidiomycetes tends to be higher (Ikeda et al., 2014; Chagnon et al., 2016). In addition, the use of metabarcoding, for example, to study the composition of the community of endophytic fungi has been reporting the occurrence of other phyla (Durán et al., 2021), not previously reported in studies with traditional methods.

Table 4. Dominant phylum of endophytic fungi, corresponding host plants and methodology used for the study.

Major endophytic fungal phylum found	Host plant	Botanical Family	Methodology used in the study	Author
Ascomycota e Basidiomycota	*Dalbergia odorífera*	*Fabaceae*	Cultivation dependent methods	Sun t al., 2015
Ascomycota	*Zanthoxylum bungeanum*	*Rutaceae*	Cultivation dependent methods	Li et al., 2016C
Ascomycota	*Polygonum acuminatum* *Aeschynomene fluminensis*	*Polygonaceae* *Leguminosae*	Cultivation dependent methods	Pietro-Souza et al., 2017
Ascomycota, Basidiomycota e Zigomycota	*Dipsacus asperoides*	*Dipsacaceae*	Cultivation dependent methods	Gong et al., 2019
Ascomycota	*Camélia oleifera*	*Theaceae*	Cultivation dependent methods	Yu et al., 2018
Ascomycota	*Teucrium polium*	*Lamiaceae*	Cultivation dependent methods	Hassa et al., 2017
Ascomycota	*Monarda citriodora*	*Lamiaceae*	Cultivation dependent methods	Katoch et al., 2017A
Ascomycota	*Asparagus racemosus* *Hemidesmus indicus*	*Liliaceae* *Asclepiadaceae*	Cultivation dependent methods	Em Vez de RA et al., 2018
Ascomycota	*Viola odorata*	*Violaceae*	Cultivation dependent methods	Katooh et al., 2017B

Ascomycota	*Paeonia ostii*	*Paeoniaceae*	Cultivation dependent methods	Yang et al., 2018
Ascomycota	*Phoenix dactylifera*	*Arecaceae*	Cultivation dependent methods	Mefteh et al., 2017
Ascomycota e Basidiomycota	*Huperzia serrata*	*Lycopodiaceae*	Independent cultivation methods	Fan et al., 2020
Ascomycota e Basidiomycota	*Dendrobium huoshanense*	Orchidaceae	Independent cultivation methods	Chan et al., 2020
Ascomycota e Basidiomycota	*Theobroma Cacao*	*Malvaceae*	Independent cultivation methods	Wemheuer et al., 2020
Ascomycota e Basidiomycota	*Dactylis glomerata* *Festuca rubra* *Lolium perenne*	*Poaceae* *Poaceae* *Poaceae*	Independent cultivation methods	Wemheuer et al., 2019
Ascomycota e Basidiomycota	*Ageratina adenophora*	*Asteraceae*	Independent cultivation methods + Cultivation dependent methods	Fang et al., 2019
Ascomycota e Basidiomycota	*Aegiceras corniculatum* *Avicennia marina* *Bruguiera gymnorrhiza,* *Kandelia candel* *Rhizophora stylosa* *Excoecaria agallocha*	*Myrsinaceae* *Verbenaceae* *Verbenaceae* *Verbenaceae* *Rhizophoraceae* *Euphorbiaceae*	Independent cultivation methods	Gashgare et al., 2016

The interaction relationship between endophytic and host plant is still considered a hermetic process, however it is known that both the plant and the symbiont fungus benefit to some degree from this relationship (Kaul et al., 2012). Plants provide photoassimilates, mainly carbon sources, and nutrients to endophytic fungi (Buscto et al., 2000), contributing to their survival and reproduction; in turn, these microorganisms play important physiological and ecological roles in the niche they colonize, resulting in mechanisms that contribute to the protection and survival of their hosts (Figure 9) (Ateba et al., 2018).

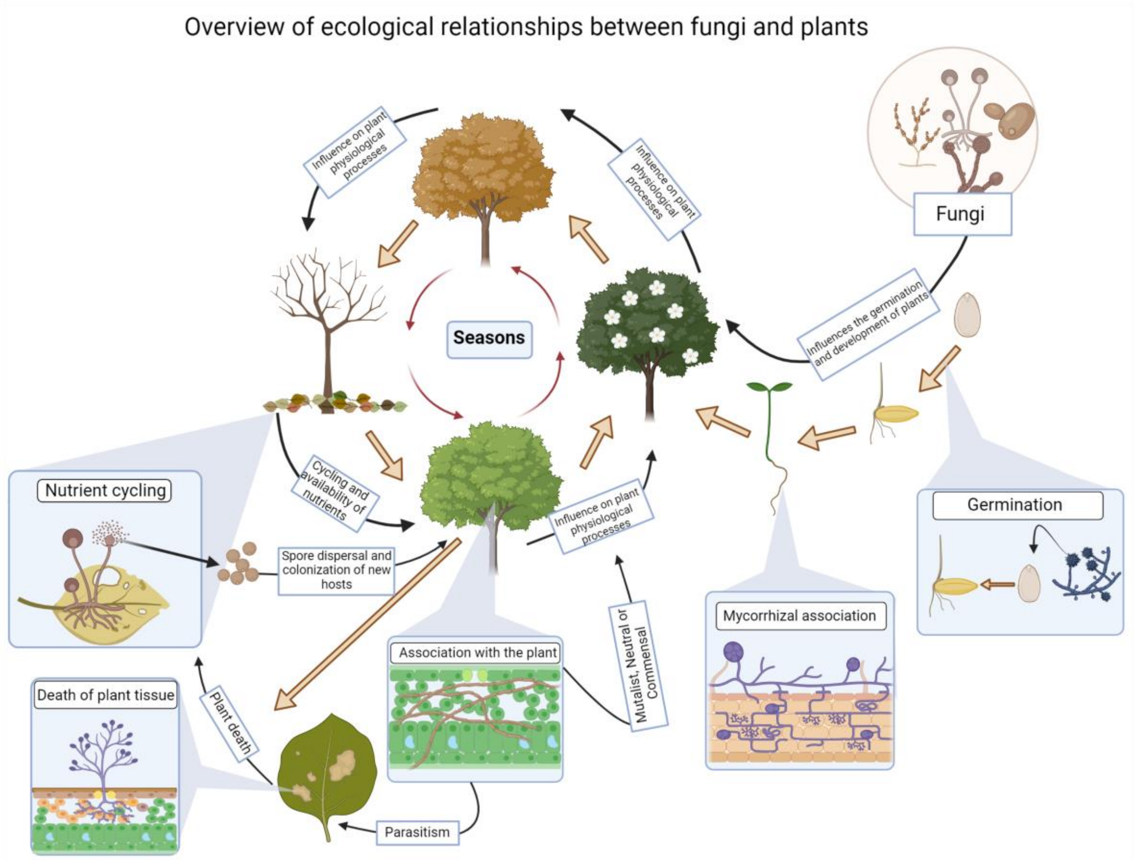


Figure 9. Overview of fungal-plant interactions and effects of these interactions on different plant phenophases. Fungi interact directly or indirectly in plant phenophases. For example, fungi can influence seed germination (Li et al., 2019); plant development (Li et al., 2019); flowering (Lu et al., 2018); shelf life of leaves (Were et al., 2021). Source: author's collection.

Endophytic fungi can promote plant growth (Oses-Pedraza et al., 2020), protect their hosts against abiotic stress under water deficit and high salinity conditions (Ripa et al., 2019), and protect against herbivory (Ripa et al., 2019). Ateba et al., 2018). In addition, endophytic fungi can prevent the invasion of phytopathogens through the production of secondary metabolites (Yao et al., 2017).

Endophytic fungi with potential for plant growth have already been reported in different host species (See review Nisa et al., 2015; Jin et al., 2016; Turbat et al., 2020; Dang et al., 2021). Khalil et al. (2021) isolated 15 species of endophytic fungi from the host Ephedra pachyclada, which were distributed among the genera *Penicillium, Alternaria,* and *Aspergillus*, among which some species were able to produce indole acetic acid (IAA) and solubilize phosphate, characteristics that positively influence the growth of plants. Similarly Hassan et al. (2017), reported endophytic *Penicillium* species with the ability to induce plant growth through the availability of phosphate and production of IAA.

Regarding protection against abiotic stresses, Gul Jan et al. (2019) demonstrated that plants in association with arbuscular mycorrhizal fungi showed greater tolerance to saline and water stress conditions when compared to those that did not show this association. More in-depth, a meta-analysis performed by Dastogeer et al. (2020) showed that in many cases the interaction between fungus and plant is not only capable of inducing tolerance to salt and water stress, but can also induce an increase in leaf, stem, and root biomass of their hosts under these conditions.

Endophytic fungi are also known to synthesize a wide range of secondary metabolites (see reviews Uzma et al., 2018; Zheng et al., 2021), which are primarily responsible for the beneficial characteristics of the relationship they establish with their hosts (Sun et al., 2012). These metabolites produced by these microorganisms received special attention from the scientific community after the 1990s with the isolation of the endophytic *Taxomyces andreanae*, from yew, and its enormous potential for the production of taxol, a compound used in the treatment of several types of cancers (Stierle et al., 1993).

Over time, many compounds with therapeutic potential and/or biotechnological application were discovered from cultivable endophytic fungi, as reviewed by Manganyi et al. (2020). Among these compounds, we can mention camptothecin (Satish et al., 2005), deoxypodophyllotoxin (Kusari et al., 2009), and several others with a wide and diversified activity (Table 5).

Table 5. Biotechnological application of endophytic fungi isolated from different hosts

Endophytic fungi	Host plant	Atividade	Author
Penicillium chrysogenum	*Alhagi graecorum,* *Cressa cretica* *Citrullus colocynthis* *Tamarix nilotica* *Achillea fragrantissima* *Artemisia sieberi* *Nitraria retusa*	Antimicrobial	Gashgari et al., 2016
Penicillium commune *Penicillium glabrum*	*Bauhinia forficate*	Antimicrobial	Bezerra et al., 2017
Xylaria sp	*Opuntia ícus-indica*	Hydrolytic activity (cellulase)	Bezerra et al., 2012
Alternaria sp. *Cladosporium funiculosum* *Paraconiothyrium* sp.	*Opuntia humifusa*	Antifungal	Silva-Hughes et al., 2015
Phomopsis sp *Curvularia* sp *Mycoleptodiscus* sp	*Clerodendrum inerme*	Antifungal	Gong et al., 2015
Tritirachium oryzae Truncatella spadicea Fusarium larvarum	*Pinus wallichiana*	Antifungal	Quadri et al., 2014
Fusarium oxysporum *Aspergillus fumigatus* *Cladosporium tenuissimum* *Fusarium* sp. *Fusarium. Oxysporum*	*Monarda citriodora*	Anticancer	Katoch et al., 2017
Fusarium oxysporum *Fusarium redolens*	*Monarda citriodora*	Biocontrol of phytopathogens and anti-food activity	Katoch et al., 2017
Aspergillus fumigatus	*Melia azedarach*	Biocontrol of phytopathogens and anti-food activity	Li et al., 2012
Botryosphaeria dothidea	*Melia azedarach*	Antimicrobial, antioxidant, anticancer activity	Xião et al., 2014
Penicillium spp.	*Symphonia globulifera*	Antiparasitic	Ateba et al., 2018
Penicillium oxalicum	*Gymnema sylvestre*	Antidiabetic	Parthasarathy et al., 2014
Penicillium oxalicum	*Limonia acidíssima*	larvicidal activity	Seetharaman et al., 2017

Based on what has been exposed, endophytic fungi represent a wide source for the discovery of new species and numerous compounds not yet known and because of this, studies involving the characterization of the composition of the endophytic fungi community have been carried out with plants from the most varied habitats (see Table 3). These studies describe species with an endophytic lifestyle not previously reported (Su et al. 2011; Sun et al. 2012; Li et al. 2016a; Li et al., 2016b; Yao et al., 2019), new species (Su et al., 2016; Zhou et al., 2019; Tazik et al., 2020; Del Carmen et al., 2021) and new genera (Bezerra et al., 2019). However, most of these works use culture-dependent methods to identify and describe these species, limiting themselves to only the species that can be cultivated, which represent a minimal fraction of the real diversity (Alteio et al., 2020).

2.1. Factors that influence the taxonomic structure of the endophytic mycobiota: host identity and environment

Endophytic fungi are present in plant species from the most varied regions (Table 3) and of all categories, are already reported in angiosperms (Coelho et al., 2020), bryophytes (Desiro et al., 2013; Carella et al., 2018), gymnosperms (Stierle et al., 1993) and pteridophytes (Olmo-Ruiz, 2014). Furthermore, it is known that the interactions between endophytic microorganisms and host plants are highly dynamic (Figure 10), and their colonization by these microorganisms depends on several factors, such as age, phenotype, and genotype of the host together with environmental factors and inter or intraspecies interactions within the microphytobiome (Douanla-Meli et al. 2013; Carvalho et al., 2016).

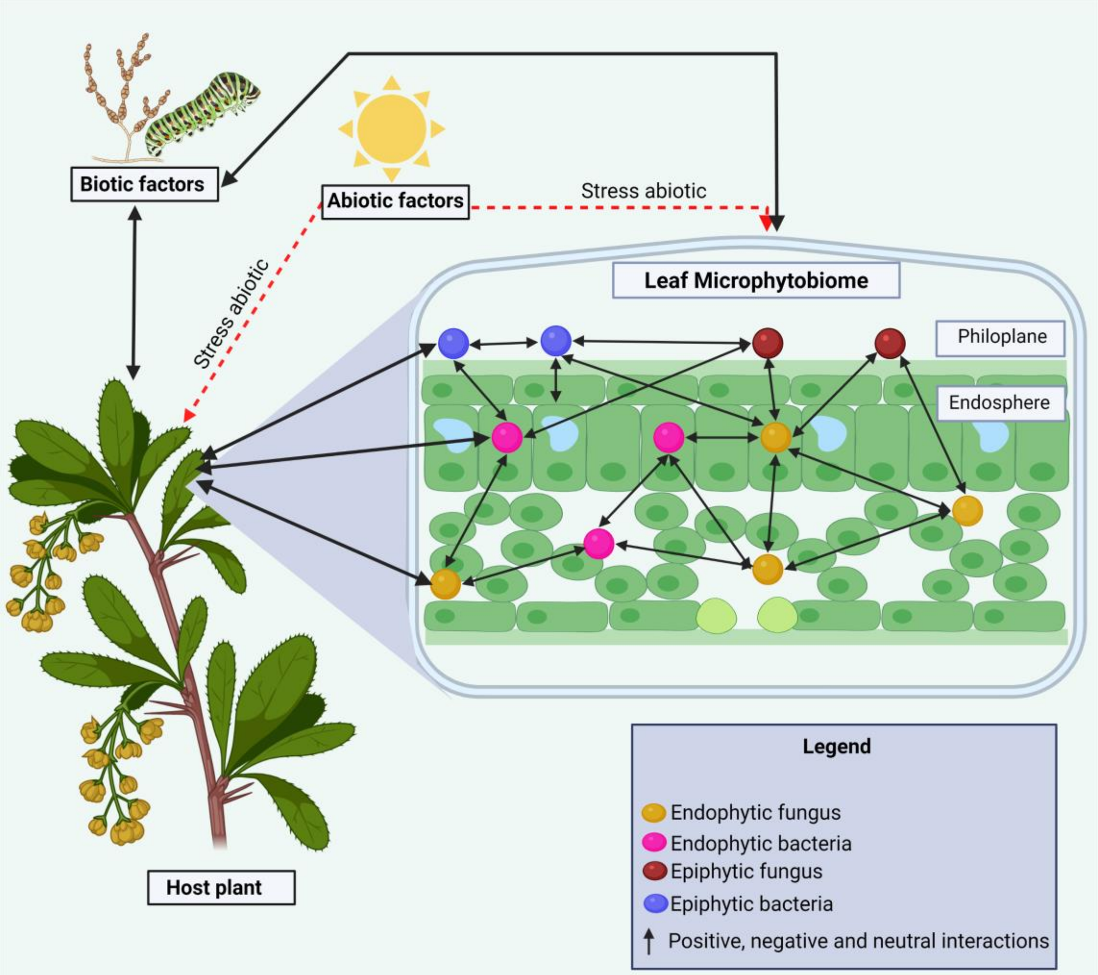


Figure 10. Interactive dynamics of the leaf microphytobiome. The leaf microbiome is not composed of a single species of organism, but of a set of microorganisms intraspecies, interspecies and between distinct kingdoms, which interact with each other and between the host plant, so that the result of these interactions shape the leaf microphytobiome. Therefore, the establishment of colonization and the abundance of each species within the leaf microbiome and its distinct effects on the host, whether commensal, mutualistic or pathogenic, are the result of these numerous interactive processes. These processes are, in turn, influenced by the environment, the host genotype, and the microorganisms that enter and leave the leaf habitat. Created with BioRender.com. Source: author's collection

Analyzes of host plant genotypes and the expression of the fungal symbiont lifestyle show that fungal-plant relationships are flexible, the directionality of which is determined by controlling the expression of host genes in response to the fungi, or conversely (Redman et al., 2001; Saikkonen et al., 2004; Paszkowski et al., 2006; Kogel et al., 2006; Provorov 2009; Unterseher & Schnittler, 2010; Oono et al., 2015; Rai & Agarkar, 2016). Therefore, small genetic differences in the genome of both partners control this interaction, so that population structure, taxonomic diversity and abundance of endophytic fungal taxa largely depend on host fitness, suggesting that host plants are able to modulate distribution of endophytic fungi in their tissues based on their genetic history and expressed genes (Saikkonen et al., 2004; Paszkowski et al., 2006; Kogel et al., 2006; Provorov 2009; Rai & Agarkar, 2016). This process of modulating the endophytic mycobiota by the plant can be called environmental filtering.

The environmental filtering process exerted by the host in the taxonomic structuring of the endophytic fungal community has been observed in the most diverse habitats (Table 3) and some authors suggest that this is the main factor for the structuration of the endophytic mycobiome (Arfi et al., 2012; Costa et al., 2012; Martín et al., 2013; Sandberg et al., 2014). For example, some studies show that different plant species from the same biogeographic region have endophytic fungal communities that are divergent from each other while sharing the closest epiphytic mycobiota (Osono et al., 2007; Fonseca-García et al., 2016; Yao et al., 2019). These findings are particularly important, as they demonstrate that the distribution of endophytic fungi does not occur randomly, as in the epiphytic mycobiota, but are the result of the characteristics of the host plant in interaction with endophytic fungi (Saikkonen et al., 2004).

In addition to the genotype, the phenological characteristics of the host plant are also capable of modulating the endophytic fungal community. Studies performed with endophytic fungi and the effects of plant phenology demonstrate that host species with distinct phenologies have distant endophytic fungal communities (Fuchs & Haselwandter, 2004; Bueno de Mesquita et al., 2018a; Bueno de Mesquita et al., 2018b; Kowal et al., 2018b; Kowal et al., 2018b; Kowal et al. al., 2020), suggesting that plant phenology is one of the subfactors within the host factor that shapes the endophytic mycobiome. As an example of the effect of phenology, Bueno de Mesquita et al (2018a) demonstrated that colonization by endophytic fungi of root tissue presents structural and density differences depending on the phenology and phenological phase of the host plants.

In general, there is extensive literature on the effect of host phenology on the endophytic fungal community in roots and arbuscular mycorrhizae (Bohrer et al., 2004; Escudero et al., 2005; Mandyam et al., 2008; Lugo et al., 2008; Lugo et al., 2004; Escudero et al., 2005; al., 2018; Kowal et al., 2020). However, studies involving the effect of plant phenology on the structure of the endophytic community that occur in areas of plants are rare (Arnold et al., 2003; Vincent et al., 2016), but provide important data.

It is known that different leaf phenologies have different endophytic fungal communities (Christian et al., 2020), since they have different nutritional characteristics and senescence processes (Panchen et al., 2015), and it is known that leaf endophytic fungi they present specificity for certain types of nutrients (Rodriguez, 1994) and vary in density and diversity depending on the leaf senescence phase (Bezerra et al., 2013). Therefore, the facts suggest that leaf phenology is one of the factors that predict the assembly of the endophytic mycobiome. These facts are reinforced by Arnold et al. (2003), who showed that leaf chemistry and its senescence process determine the diversity and density of fungal endophytes.

The diversity and equity of endophytic mycobiome species are also influenced by abiotic factors, such as seasonality, dry periods, fires, and humidity variations, which can increase or decrease the diversity of species in this Community (Higgins et al., 2007; Hoffman et al., 2008; McGuire et al., 2012; Oita et al., 2021). For example, the particular conditions of a geographic region, such as rainfall levels and soil characteristics, determine the distribution ranges of host plants, which in turn, determine the endophytic fungal species and their germination, growth, reproduction, and metabolism.

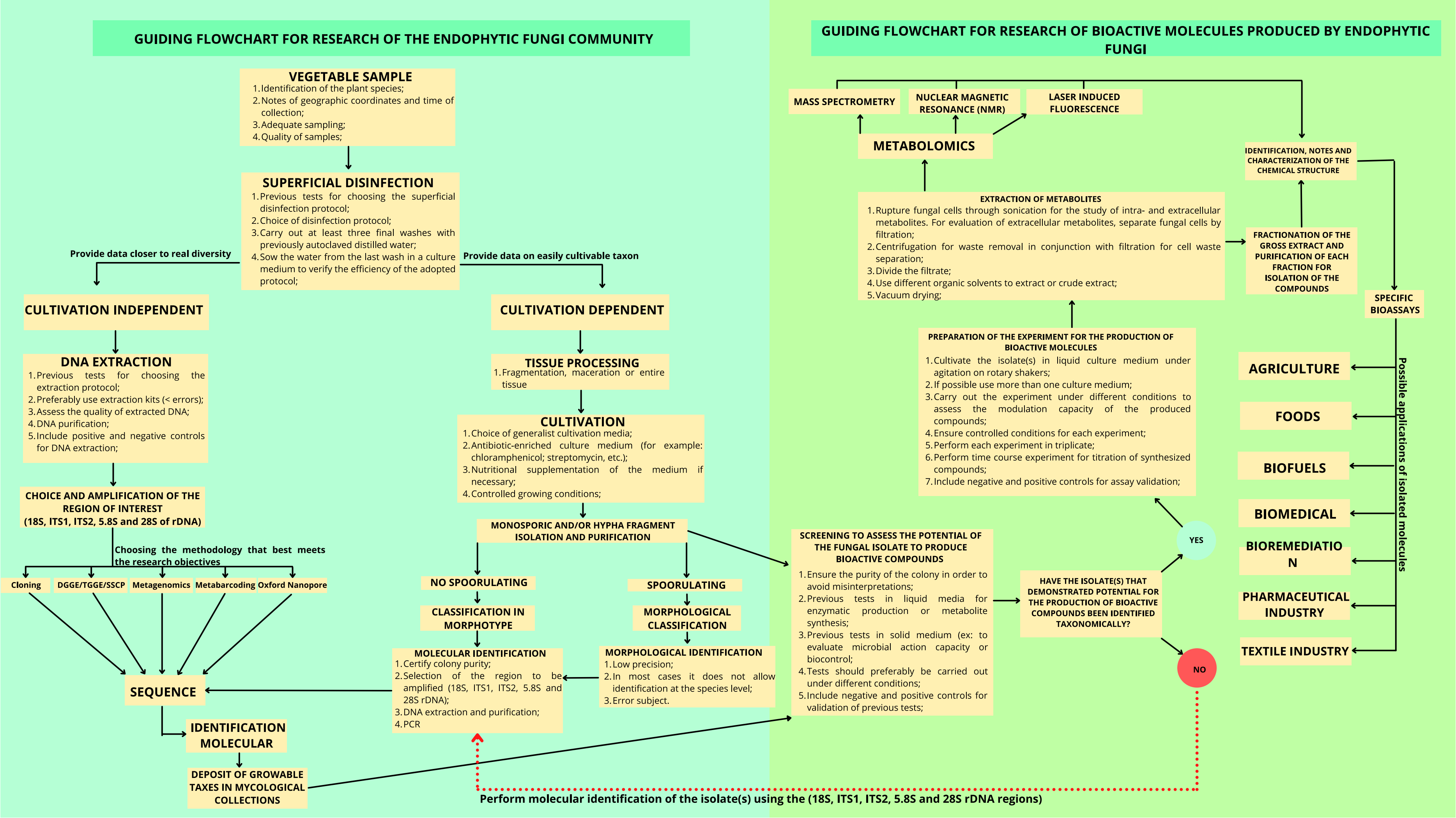
Climate and seasonality can modulate the edophytic mycobiome in several ways (U'Ren et al., 2012; Huang et al., 2016; Oita et al., 2021). As an example, severe dry seasons can impose a strong physiological filter on horizontally transmitted endophytic fungi, potentially leading to a lower richness of the *pool* of endophytic species that will colonize their hosts (Arnold et al., 2007).

To a lesser extent, the nutritional composition of the soil and the type of management employed affect the taxonomic structure of the endophytic fungal community (Bengtsson et al., 2000; Chen et al., 2014; Xiang et al., 2016; Chen et al., 2020; Soonvald et al., 2020). This fact is exposed by Liu et al. (2020), demonstrating that long-term fertilization, especially using phosphorus, was able to change the diversity of endophytic fungi associated with the root tissue of the host Zea mays. Xiang et al. (2016) demonstrated that soil treatments with nitrogen, phosphorus, and nitrogen+phosphorus were able to significantly change the diversity and population density of arbuscular mycorrhizal fungi.

The taxonomic structuring of the endophytobiome depends on several factors, such as host identity (genotype and phenology) in conjunction with environmental factors and genetic factors of endophytic fungi, which interact together to orchestrate a highly heterogeneous and sophisticated symbiosis process, the result of millions of years of evolution. Therefore, understanding this process is extremely important, because, in addition to providing data on the diversity of endophytic fungi, it is possible to elucidate the mechanisms behind this relationship and provide alternatives for the preservation and maintenance of microorganisms and their plant hosts.

3. METHODS FOR STUDYING THE DIVERSITY OF ENDOPHYTIC FUNGI

The protocols used to study endophytes, in general, are relatively simple but involve complex steps that must be strictly followed to avoid misinterpretation (Figure 11). The first step after plant material collection is the superficial disinfection of the sampled tissue to eliminate the epiphytic microbiota (Li et al., 2016a; Li et al., 2016b; Yao et al., 2017); then it can be subjected to dependent (Szűcs et al., 2018; Yao et al., 2019; Du et al., 2020; Fan et al., 2020) and culture-independent techniques (Yao et al., 2019) to study these microorganisms.



GUIDING FLOWCHART FOR RESEARCH OF THE ENDOPHYTIC FUNGI COMMUNITY

VEGETABLE SAMPLE

1. Identification of the plant species;
2. Notes of geographic coordinates and time of collection;
3. Adequate sampling;
4. Quality of samples;

SUPERFICIAL DISINFECTION

1. Previous tests for choosing the superficial disinfection protocol;
2. Choice of disinfection protocol;
3. Carry out at least three final washes with previously autoclaved distilled water;
4. Sow the water from the last wash in a culture medium to verify the efficiency of the adopted protocol;

Provide data closer to real diversity

CULTIVATION INDEPENDENT

DNA EXTRACTION

1. Previous tests for choosing the extraction protocol;
2. Preferably use extraction kits (< errors);
3. Assess the quality of extracted DNA;
4. DNA purification;
5. Include positive and negative controls for DNA extraction;

CHOICE AND AMPLIFICATION OF THE REGION OF INTEREST (18S, ITS1, ITS2, 5.8S and 28S of rDNA)

Choosing the methodology that best meets the research objectives

Cloning

DGGE/TGGE/SSCP

Metagenomics

Metabarcoding

Oxford Nanopore

SEQUENCE

IDENTIFICATION MOLECULAR

DEPOSIT OF GROWABLE TAXES IN MYCOLOGICAL COLLECTIONS

Provide data on easily cultivable taxon

CULTIVATION DEPENDENT

TISSUE PROCESSING

1. Fragmentation, maceration or entire tissue

CULTIVATION

1. Choice of generalist cultivation media;
2. Antibiotic-enriched culture medium (for example: chloramphenicol; streptomycin, etc.);
3. Nutritional supplementation of the medium if necessary;
4. Controlled growing conditions;

MONOSPORIC AND/OR HYPHA FRAGMENT ISOLATION AND PURIFICATION

NO SPOORULATING

CLASSIFICATION IN MORPHOTYPE

MOLECULAR IDENTIFICATION

1. Certify colony purity;
2. Selection of the region to be amplified (18S, ITS1, ITS2, 5.8S and 28S rDNA);
3. DNA extraction and purification;
4. PCR

SPOORULATING

MORPHOLOGICAL CLASSIFICATION

MORPHOLOGICAL IDENTIFICATION

1. Low precision;
2. In most cases it does not allow identification at the species level;
3. Error subject.

Perform molecular identification of the isolate(s) using the (18S, ITS1, ITS2, 5.8S and 28S rDNA regions)

GUIDING FLOWCHART FOR RESEARCH OF BIOACTIVE MOLECULES PRODUCED BY ENDOPHYTIC FUNGI

SCREENING TO ASSESS THE POTENTIAL OF THE FUNGAL ISOLATE TO PRODUCE BIOACTIVE COMPOUNDS

1. Ensure the purity of the colony in order to avoid misinterpretations;
2. Previous tests in liquid media for enzymatic production or metabolite synthesis;
3. Previous tests in solid medium (ex: to evaluate microbial action capacity or biocontrol;
4. Tests should preferably be carried out under different conditions;
5. Include negative and positive controls for validation of previous tests;

HAVE THE ISOLATE(S) THAT DEMONSTRATED POTENTIAL FOR THE PRODUCTION OF BIOACTIVE COMPOUNDS BEEN IDENTIFIED TAXONOMICALLY?

YES

NO

PREPARATION OF THE EXPERIMENT FOR THE PRODUCTION OF BIOACTIVE MOLECULES

1. Cultivate the isolate(s) in liquid culture medium under agitation on rotary shakers;
2. If possible use more than one culture medium;
3. Carry out the experiment under different conditions to assess the modulation capacity of the produced compounds;
4. Ensure controlled conditions for each experiment;
5. Perform each experiment in triplicate;
6. Perform time course experiment for titration of synthesized compounds;
7. Include negative and positive controls for assay validation;

EXTRACTION OF METABOLITES

1. Rupture fungal cells through sonication for the study of intra- and extracellular metabolites. For evaluation of extracellular metabolites, separate fungal cells by filtration;
2. Centrifugation for waste removal in conjunction with filtration for cell waste separation;
3. Divide the filtrate;
4. Use different organic solvents to extract or crude extract;
5. Vacuum drying;

METABOLOMICS

MASS SPECTROMETRY

NUCLEAR MAGNETIC RESONANCE (NMR)

LASER INDUCED FLUORESCENCE

FRACTIONATION OF THE GROSS EXTRACT AND PURIFICATION OF EACH FRACTION FOR ISOLATION OF THE COMPOUNDS

IDENTIFICATION, NOTES AND CHARACTERIZATION OF THE CHEMICAL STRUCTURE

SPECIFIC BIOASSAYS

Possible applications of isolated molecules

AGRICULTURE

FOODS

BIOFUELS

BIOMEDICAL

BIOREMEDIATION

PHARMACEUTICAL INDUSTRY

TEXTILE INDUSTRY

Figura 11. Flowchart for studying the diversity of endophytic fungi and their potential for producing bioactive compounds.

Over the decades, the identification of endophytic fungi was based on culture-dependent methodologies (Szűcs et al., 2018; Hamzah et al., 2018; Gong et al., 2019). For this, the plant samples are fragmented and distributed in a culture medium, incubated and after the fungi grow, the colonies are purified and identified based on morphological characteristics or by molecular analysis (Ibrahim et al., 2017; Pietro-Souza et al., 2017; Yao et al., 2017).

It is known that culture-based methods do not reflect the real diversity of fungi in a given niche (Fan et al., 2017; Lücking et al., 2020), since some of these microorganisms cannot be cultivated under laboratory conditions (Fan et al., 2017; al., 2017; Wu et al., 2019). Furthermore, the use of phenotypic methods based on morphological characteristics to identify fungal species can generate incorrect identification, since fungi of different species only have one type of structure (such as hyphae) (Lücking et al., 2020). Both of these methods require modifications, such as enriching the culture medium with a certain substrate to increase the diversity of species that will grow in it (Mourad et al., 2018) together with the use of molecular methods to identify the isolates (Noriler et al., 2018).

Despite the improvement of the methodologies adopted to study endophytic fungi, several obstacles arise at all stages of commonly used protocols, requiring several modifications to avoid misinterpretation. Therefore, this review aims to discuss the protocols used to study endophytic fungi, pointing out the main limitations and proposing alternatives to circumvent and/or minimize them.

3.1. Collection and sampling

The first step to study endophytic microorganisms is the collection of plant material. However, there is no universal consensus on the adequate value of sampled individuals and the number of samples per individual, but it is recommended that the sampling be representative according to the objectives proposed by the study. For example, Yao et al. (2019) evaluated the diversity of endophytic fungi in different species of tropical mangroves considering the geographic factor, being chosen eight individuals per plant species and recommended that the minimum distance between each plant species analyzed should be at least 50 meters. Wang et al. (2016) aimed to describe the three-year-old mycobiota of *Zanthoxylum bungeanum* and for this ten specimens were sampled excluding spatial criteria. Fan et al. (2017) aimed to study the endophytic mycobiome of cultivated *Huperzia serrata* and three specimens were randomly chosen. Based on the above, the number of plant individuals sampled must meet the objective of the research, but the quantity, quality of sampling, and the biotic and abiotic factors that can interfere with the endophytic mycobiota must be considered (Figure 12).

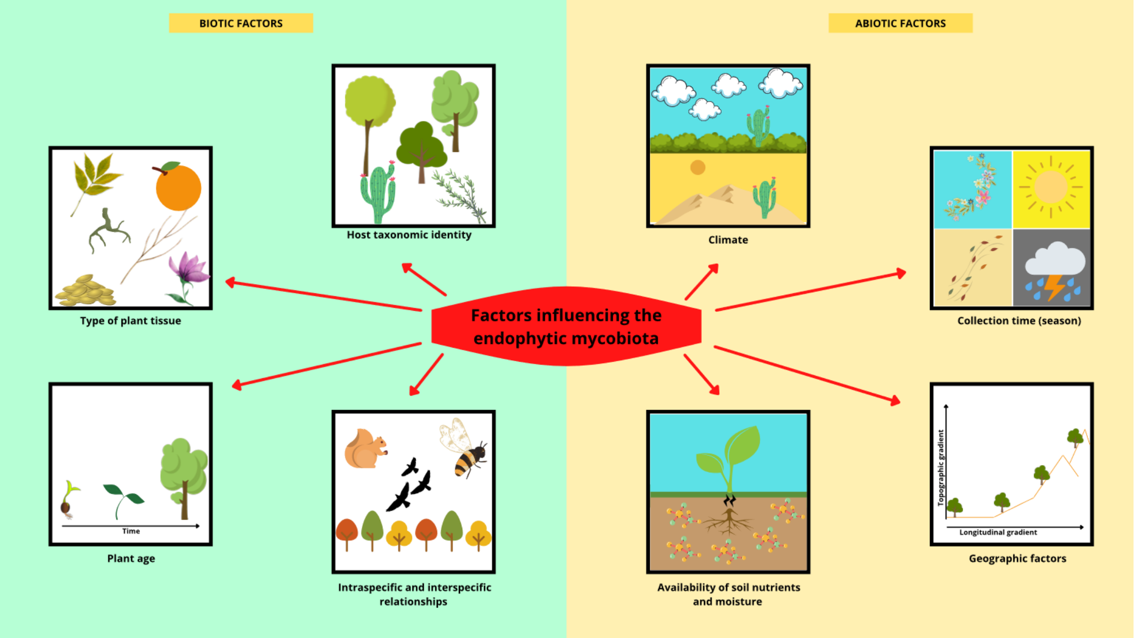


Figure 12. Factors influencing the assembly of the endophytic mycobiota. The community of endophytic fungi within the same plant species is highly dynamic and its richness and diversity of taxa can be influenced and determined by several factors, which include biotic factors such as host identity and age, tissue type, and relationships interspecific and intraspecific established between the host and other species; and abiotic, such as soil nutrient availability, moisture, time of year (season), longitudinal and topographic gradients, climate, and fire. Image based on findings by David et al. (2016), Fernandes et al. (2018), Chi et al. (2019), Yao et al. (2019) and Wu et al. (2020). Source: author's collection.

Regarding sampling by the individual, the literature suggests that the number of individuals should be > 5 / per individual (Li et al., 2016a; Li et al., 2016b; Yao et al., 2017; Szűcs et al., 2018; Yao et al., 2019; Du et al., 2020; Fan et al., 2020), but extraordinary cases should be considered. Still, on sampling by the individual, it is important to consider the various biological and abiotic factors that can interfere with the endophytic fungi community within an individual to be sampled, being necessary to consider to have a composite and representative sample (Figure 13).

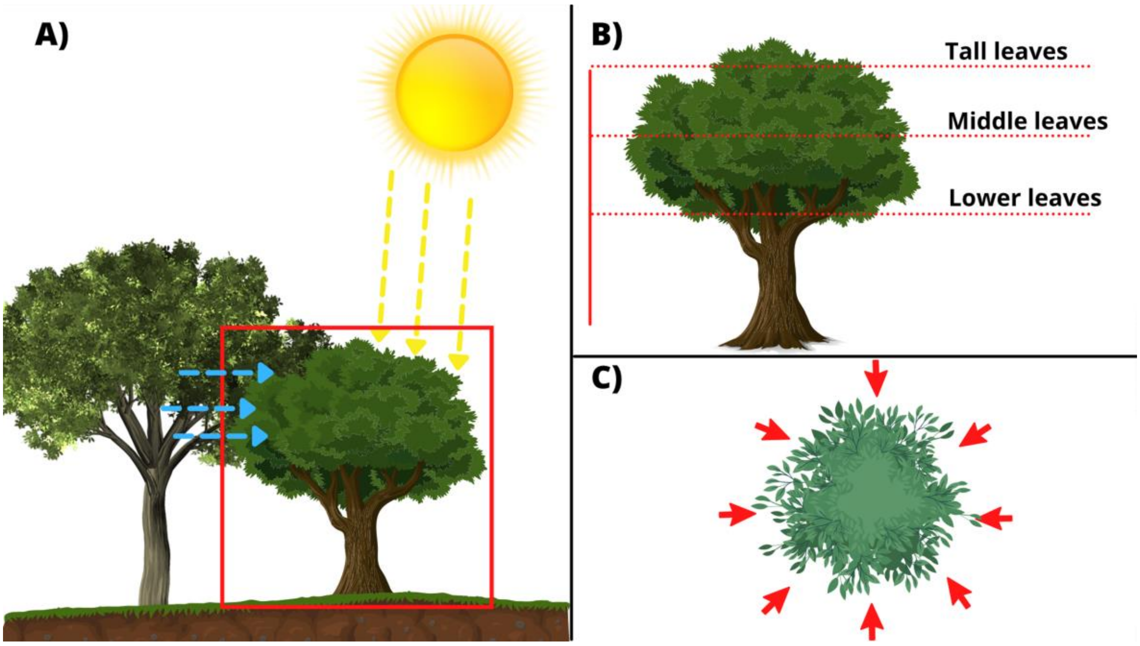


Figure 13. Strategy for leaf sampling to study endophytic fungi. A) the red square refers to the specimen to be sampled, the blue arrows indicate the influence of biotic factors (interaction with another species) that results in a lower incidence of sunlight on the region, while the yellow arrows indicate a greater number of light solar over the corresponding area. Environmental conditions vary in species distribution not only on a macroscale but also on a microscale, as within a local site exemplified here as the specimen to be sampled. These variations within microenvironments expose natural populations, such as fungi, to mosaics of resource availability, different abiotic conditions (temperature, humidity, light, availability of nutrients.), and biotic (interaction with nodes of the same species and other species.) (Kluting et al., 2019; Denney et al., 2020; Hurtado-McCormick et al., 2021); therefore, these factors must be taken into account during leaf sampling for the study of endophytic fungi. B) The red dotted lines indicate leaf tissue sampling to study fungal endophytes, demonstrating that lower, middle, and upper leaves should be collected to obtain a greater representation of the real diversity of these microorganisms in the niche in question; while in C) the top view of the sampled plant specimen is exemplified and the red arrows indicate that the collection must be made in different regions. Image inspired by the collection strategy chosen by Wu et al. (2020) and in the findings of Kluting et al (2019), Denney et al. (2020), and Hurtado-McCormick et al. (2021) on population variations in microenvironments. Source: author's collection.

After collecting the plant material, it must be placed in a sterile plastic container or bag and placed in a cool box at a controlled temperature, and preferably processed within 24 hours after collection (Lundberg et al., 2012; Sharma et al., 2016; Li et al., 2016a; Li et al., 2016b; Ibrahim et al., 2017; Pietro-Souza et al., 2017; Yao et al., 2017; Szűcs et al., 2018; Hamzah et al., 2018; Gong et al., 2019; Yao et al., 2019; Dhayanithy et al., 2019; Thi et al., 2019; Jayatilake et al., 2020; Du et al., 2020; Fan et al., 2020; Chowdappa et al., 2020; Ibrahim et al., 2021).

3.2. Surface disinfection

Since the discovery of taxol in an endophytic fungus associated with *Taxus* spp (Stierle et al., 1993), endophytic fungi have been drawing the attention of the scientific community both in terms of species diversity and their capacity to synthesize bioactive molecules. However, several methodological obstacles arise when studying endophytes, which include the complete removal of the microorganisms that make up the epiphytic microbiota. The surface disinfection methods adopted to remove the epiphytic microbiota are the mandatory first step for the study of endophytic microorganisms and can be chemical or physical.

Chemical sterilization of the surface is the most used method for removing microorganisms from the rhizoplane and there are many protocols available (Table 6), but in most cases, it consists of three basic steps: 1st) submersion of the tissue in ethanol; → 2nd) immersion of the tissue in the main sterilizing agent; 3rd) → successive washing with distilled water previously autoclaved. The main sterilizing agents used in rhizoplane disinfection are sodium hypochlorite (NaOCl) (Yao et al., 2019) and mercury chloride (HgCl2) (Du et al., 2020). Other sterilizing agents can also be used, such as hydrogen peroxide (H2O2), paraquat, or 1% peroxyacetic acid (CH3COOOH) in 30% ethanol (Sieber, 2002). Here again, it is worth mentioning that some authors recommend that before carrying out the surface disinfection method, the samples are washed in running tap water for some time to remove debris, dust, other particles, and main epiphytes, thus enhancing the superficial disinfection process that will be carried out next (Píetro-Souza et al., 2017; Ibrahim et al., 2021).

Table 6. Botanical species, tissue type, methods used for surface disinfection, and culture medium used to study endophytic fungi

Plant species(s) and botanical family	Tissue	Surface disinfection methods	Procedure for validating the effectiveness of surface disinfection	Diameter of the fragment used for recovery of endophytic fungi	Culture medium used for recovery of endophytic fungi	Author
Aegiceras corniculatum (Myrsinaceae) *Avicennia marina* (Verbenaceae) *Bruguiera gymnorrhiza* (Rhizophoraceae) *Excoecaria agallocha* (Euphorbiaceae) *Kandelia candel* Rhizophoraceae) *Rhizophora stylosa* (Rhizophoraceae)	Leaves	Consecutive immersion in 75% ethanol for 1 min, 3.25% sodium hypochlorite for 3 minutes, 75% ethanol for 30 s and three rinses in sterile distilled water	Not informed by authors	Whole leaves	Independent cultivation method	Yao et al., 2019
Securinega suffruticosa (Euphorbiaceae)	Stem, leaves, and roots	Repeated washing with running tap water to remove dirt and facilitate the surface disinfection process. Surface disinfection was performed according to the following procedures: i) rinse with 75% ethanol for 2–3 min; ii) washing with sterile water 4–6 times; superficial disinfection with 0.1% mercury chloride for 3–5 min; and rinse with sterile water four to six times.	Fabric printing on Potato Dextrose Agar	Fragments with 5 mm x 5 mm	Potato dextrose agar with penicillin	Du et al., 2020

Zanthoxylum bungeanum (Rutaceae)	Stem, flowers, leaves, fruits, thorns, and roots	The samples of each tissue were disinfected by immersion in 75% ethanol for 2 min, then soaked in 0.2% mercury chloride solution for 10 min, and finally washed three times with autoclaved distilled water	Not informed by authors	Fragments with 1 cm x 1cm	Potato Dextrose Agar	Li et al., 2016b
Sophora tonkinensis (Fabaceae)	Roots	The root segments were washed in running water for 30 min and rinsed with double-distilled water for 10 min. The samples were sterilized with 75% ethanol for 1 min, 1% sodium hypochlorite for 2 min, 75% ethanol for 30 s, and rinsed three times with sterile double-distilled water	Not informed by authors	Fragments with 1 cm x 1 cm	Potato Dextrose Agar with chloramphenicol	Yao et al., 2017
Armoracia rusticana (Brassicaceae)	Roots	The samples were sterilized using commercial bleaching solution diluted 4 times, followed by washing with sterile distilled water	Printing the sterilized tissue and seeding an aliquot of the last rinse in Sabouraud Dextrose culture medium	Fragments with 1 - 2 cm	Sabouraud dextrose agar	Szűcs et al., 2018
Huperzia serrata (Lycopodiaceae)	Stem, leaves, and roots	The samples were submerged in 70% ethanol for 1 min, in a sodium hypochlorite solution for 3 min, 2.5% 3% sodium thiosulfate for 5 min, and finally, they were rinsed five times with sterile water	Not informed by authors	Whole leaves	Independent cultivation method	Fan et al., 2020

Acalypha ornata (Euphorbiaceae) *Albizia zygia* (Fabaceae) *Alchornea cordifolia* (Euphorbiaceae) *Chrysophyllum albidum* (Sapotaceae) *Ficus exasperata* (Moraceae) *Gomphrena celosioides* (Amaranthaceae) *Millettia thonningii* (Fabaceae) *Newbouldia laevis* (Bignoniaceae)	Leaves	The samples were washed under running tap water to remove dust and debris, followed by consecutive washes with distilled water. Surface disinfection was performed by sequential immersion in 70% ethanol for 60 s, 0.5% sodium hypochlorite for 5 min, 70% ethanol for 30 s, followed by a final rinse in sterilized distilled water for 5 min.	Fabric printing on Potato Dextrose Agar	Fragments with 2–4 mm	Potato Dextrose Agar with gentamicin	Ibrahim et al., 2021
Cymbidium aloifolium (Orchidaceae)	Leaves, Flowers, and Roots	Surface sterilization of samples was performed with 0.2% sodium hypochlorite, followed by three washes with sterile distilled water.	Fabric printing on Potato Dextrose Agar	Not informed by authors	Potato Dextrose Agar with tetracycline	Chowdappa et al., 2020
Polygonum acuminatum (Polygonaceae) *Aeschynomene fluminensis* (Fabaceae)	Roots	The roots were initially washed with neutral detergent (Ype® Neutral Detergent) to remove debris. Surface disinfection was performed with immersion in 70% ethanol for 1 min, 2.5% sodium hypochlorite for 5 min, followed by five rinses in sterile distilled water.	Not informed by authors	Fragments with 5 mm x 5 mm	Potato Dextrose Agar supplemented with chloramphenicol, streptomycin and tetracycline	Pietro-Souza et al., 2017

Cupressus torulosa (Cupressaceae)	Leaves (*needles*)	The leaf fragments were surface sterilized by consecutive immersion for 1 min in 75% ethanol, followed by immersion in 0.1% mercury chloride for 1 min and several consecutive washing steps with autoclaved distilled water.	Sowing aliquots of the water from the last rinse in Potato Dextrose Agar	Fragments with 5 mm x 5 mm	Potato Dextrose Agar supplemented with chloramphenicol	Sharma et al., 2016
Markhamia tomentosa (Chrysobalanaceae)	Leaves	The plant samples were washed in running water to remove residues and debris. Surface sterilization was performed with sequential immersion in 70% ethanol for 60 s, 10% sodium hypochlorite for 5 min, 70% ethanol for 30 s, followed by a final rinse in sterilized distilled water for 5 min.	Not informed by authors	Fragments with 1 cm x 1 cm	Malt Extract Agar and Potato Dextrose Agar with streptomycin	Ibrahim et al., 2017

Catharanthus roseus (Apocynaceae)	Stem, Bark, Leaves, and Roots	The samples were washed with running water to remove dirt present on the fabrics and then they were washed in a sterilizing solution for two minutes in each solution: 70% ethanol, 0.1% sodium hypochlorite, and finally autoclaved distilled water	Fabric printing on Potato Dextrose Agar	Fragments with 5mm x 5mm	Potato Dextrose Agar supplemented with, streptomycin	Dhayanithy et al., 2019
Mikania cordata (Asteraceae)	Stems, Leaves, Branches, and Roots	The samples were washed under running water to remove adhered soil particles and other debris. The disinfection procedure was performed in two steps: i) immersion of the samples in 5% sodium hypochlorite for 3 min, followed by washing with sterile distilled water for 1 min (3 times). ii) Immersion of samples in 70% ethanol for 1 min and washing with distilled water for 1 min. The last step was repeated three times.	Fabric printing on Potato Dextrose Agar	Fragments with 1 cm x 1 cm	Potato Dextrose Agar supplemented with chloramphenicol	Jayatilake et al., 2020
Huperzia serrata (Lycopodiaceae)	Stems, Leaves, and Roots	The samples were washed with tap water and sequentially sterilized by washing with 75% ethanol for 5 min, 10% sodium hypochlorite for 10 min, and 0.1% mercury chloride for 2 min, and finally they were rinsed with four washes with sterile distilled water	Sowing aliquots of the water from the last rinse in ´Potato Dextrose Agar	Fragments with 2-5mm	Potato Dextrose Agar with streptomycin and penicillin	Thi et al., 2019
		The samples were washed in running water, immersed in 70% ethanol for 2	Sowing aliquots of the water from the last	Fragments with	Medium A (bacteriological agar, malt	Hamzah et

Rhizophora mucronata (Rhizophoraceae)	Leaves	min, followed by immersion in 4% hypochlorite for 1 min, and rinsed several times in sterile distilled water.	rinse in ´Potato Dextrose Agar	2 cm x 2 cm	extract, artificial sea salt, and sterile distilled water) with chloramphenicol	al., 2018
Arabidopsis thaliana (Brassicaceae)	Seeds	The seeds were superficially sterilized by immersion in 70% ethanol with 0.1% Triton-X100 for 1min, followed by 12 min in 10% A-1 bleach with 0.1% Triton-X100, followed by three washes in sterile distilled water.	Printing the sterilized tissue and seeding an aliquot of the last rinse in different culture medium.	Whole leaves	Agar containing Murashige & Skoog (MS) vitamins and sucrose	Lundberg et al., 2012
Dipsacus asperoides	Roots	The surface of the plant material was sterilized by immersion in 0.1% mercury chloride for 5 min, then in 75% ethanol for 3 min. Finally, the material was rinsed three times with sterile water.	Not informed by authors	Fragments with 5 mm x 5 mm	Potato Dextrose Agar, Tryptone Soy Agar, Tryptone Bovine Extract Agar, and Luria-Bertani culture medium.	Gong et al., 2019
Aegiceras corniculatum (Myrsinaceae) *Avicennia marina* (Verbenaceae) *Bruguiera gymnorrhiza* (Rhizophoraceae)	Leaves and Branches	The segments were surface sterilized by consecutive immersion for 1 min in 75% ethanol, 3 min in 3.25% sodium hypochlorite and 30 s in 75% ethanol.	Not informed by authors	Fragments 5 mm long and about 8 mm cm in diameter	Malt Extract Agar with Sodium Benzylpenicillin	Li et al., 2016

Physical surface disinfection methods can be mediated by sonication or ultraviolet (UV) light. In the case of sonication, the plant tissue must be previously washed in tap water and then immersed in a buffer solution (sonicator or sonication bath) where the sound waves will be propagated to cause the removal and lysis of microbial cells (Guzmán et al. 2020). This method is considered a great method for removing epiphytes present in plant tissue (Lundberg et al., 2012), but the sound frequency used, application time and tissue characteristics should be considered when choosing it as the method of superficial disinfection. Surface disinfection mediated by UV light also requires that the plant sample be washed repeatedly in tap water beforehand to remove as much dirt as possible from the plant tissue and then the plant tissue must be exposed to UV rays for 20 min (Sarsaiya et al., 2020). Another physical method used to remove epiphytes is plant tissue buckling (Saldierna et al., 2020), but this methodology is not widely used due to the various biases inherent to it.

The choice of the disinfection protocol is a critical step to study endophytic microorganisms and the methodology used must be able to completely remove the epiphytic microbiota without interfering with the endophytic microbiota. Therefore, the method should be chosen based on the characteristics of the analyzed tissue/plant species. For example, Burgdorf, et al., (2014), evaluated the effectiveness of two methods of surface disinfection, one chemical, and one physical, on leaves of *Triticum aestivum*. For this, the leaves were artificially sprayed with *Saccharomyces cerevisiae* and then individually submitted to both treatments to remove the epiphytes. Physical treatment was mediated by sonication for 5 min in a Biosonic sonication bath (Colténe / Whaledent, Altstätten, Switzerland) and successive washings with sterile distilled water; while for chemical treatment the samples were consecutively immersed in 95% ethanol for 5 s, 0.5% sodium hypochlorite for 2 min, 70% ethanol for 2 min and successive washings with sterile distilled water. The rinse of the last wash in both methodologies was seeded in Potato Dextrose Agar (PDA) and analyzed by PCR, and as a result, these authors demonstrated that the physical treatment, in addition to being more reproducible, was the most consistent and effective for removal of microorganisms present on the plant surface of this host when compared to the chemical treatment analyzed.

Guzmán et al. (2020) evaluated the effectiveness of four methods of surface disinfection in different tissues of two different plant species, namely *Pinus* *contorta* and *Populus fremontti*. The evaluated protocols consisted of three chemical methods using different sterilizing agents individually (1st - 100% ethanol for 1 min; 2nd - 8.25% sodium hypochlorite for 5 Mim; and 3rd - 30% hydrogen peroxide for 1 min) and one physical (4th - sonication at 40 kHz for 10 min). At the end of each procedure, the samples were successively washed with sterile distilled water and the final rinse was recovered for further evaluation. PCR amplification using the final rinses and seeding by printing the tissues analyzed in Lysogeny Broth culture medium after superficial disinfection were negative for all treatments, showing that all were efficient in removing the epiphytic microbiota. However, scanning electron microscopy analysis demonstrated the presence of hyphae, yeast, and bacteria on the leaf surface of both species in the sonication treatment. In addition, *P. fremontti* leaves were not damaged by chemical treatments, but in contrast, treatments with hydrogen peroxide and sodium hypochlorite caused severe damage to *P. contorta* leaves, which may interfere with the endophytic mycobioma. Therefore, these authors demonstrate that different species require different methodologies to remove the rhizoplane microbiota.

Some authors suggest new methods of superficial disinfection in addition to those commonly used. For example, Waheeda & Shyam (2017) proposed a disinfection method that includes washing in 3.15% calcium hypochlorite for 10 min, followed by washing in 10% sodium hydrogen carbonate for 15 minutes and finally washing in sodium azide 1% for 2 min.

Similar to plant tissue, fungal species are also not equally sensitive to sterilizing agents, and this fact should be considered when choosing the method of surface disinfection. For example, Reissinger et al. (2001) demonstrated that ethanol and hypochlorite concentrations, as well as the time commonly used in surface disinfection protocols, are ineffective for the removal and unfeasibility of *Chaetomium globosum* ascospores present in *Hordeum vulgare* leaves. Similarly, Holdenrieder (1989) tested a three-step protocol (i-immersion in ethanol; ii-immersion in hypochlorite; iii-washing with sterile distilled water) for superficial disinfection of *Picea abies* roots artificially contaminated with conidia of *Penicillium* sp. or *Cylindrocarpon destructans* and demonstrated that the spores of *C. destructans* were eliminated after 60 min, while those of *Penicillium* remained viable for more than two hours. *Penicillium* conidia were only killed when hydrogen peroxide was used without prior submersion in ethanol.

The effectiveness of the disinfection method adopted must also be evaluated when studying endophytic microorganisms and this step must be performed properly to validate the adopted procedure. Some authors use the sowing in culture medium, usually in PDA, of water recovered from the last rinse to validate the effectiveness of the chosen disinfection method (Yao et al., 2017; Szűcs et al., 2018; Fan et al., 2020; Ibrahim et al., 2021). In this case, centrifugation can be used to concentrate any microorganisms present in the last rinse water, discard the supernatant, and sow the centrifuged sediment in a culture medium (Sierbe, 2002). Another alternative is to print the tissue in the culture medium after surface disinfection (Szűcs et al., 2018; Dhayanithy et al., 2019; Jayatilake et al., 2020).

Verification of the effectiveness of the disinfection method can also be performed by screening nucleic acids, for example using PCR, from the water recovered from the last rinse (Burgdorf et al., 2014; Guzmán et al., 2020). However, depending on the disinfection method used, it is important to highlight that there may be false-positive results since sterilizing agents can cause cell death of epiphytic microorganisms, but not the degradation of their nucleic acids (Burgdorf et al., 2014). The combination of two or more techniques to assess the effectiveness of the surface disinfection method can ensure greater security regarding its effectiveness, such as the use of scanning electron microscopy (Guzmán et al., 2020) with seeding of the water from the latter rinsing in culture medium may be an alternative.

In general and based on what was discussed, the characteristics of the analyzed tissue, the composition of the epiphytic microbiota, the toxicity of the sterilizing agents, and the methods used to validate the surface disinfection protocol should be considered when studying fungal endophyte communities. Therefore, the performance of previous tests with different sterilization protocols, the previous description of the epiphytic microbiota, and the combination of two or more methodologies to validate the disinfection is extremely necessary to avoid misinterpretations about the composition of the culturable endophytic mycobiota.

3.3. Culture medium for endophytic fungi

There are many culture medium used to recover endophytic fungi, with PDA being the most used (see table 6). However, this is not the only culture medium used. Other medium such as Malt Extract Agar (Li et al., 2016), Agar containing Murashige & Skoog vitamins (MS) and sucrose (Lundberg et al., 2012), Hagem Minimal Medium (Khan et al., 2016), medium Czapek (Chand et al., 2020), Tryptone Soybean Agar, Tryptone Bovine Extract Agar, and Luria-Bertani (Gong et al., 2019) can be used to recover endophytic fungi from a plant sample. There are several culture medium used for the recovery and cultivation of endophytic fungi, but in general, these must have a slightly acidic pH range (5.8-6.0 pH) (Lundberg et al., 2012; Li et al., 2016; An et al., 2020). Depending on the purpose of the study and the characteristics of the habitat (host plant species), the medium commonly used can be nutritionally supplemented and/or replaced by specific medium to better achieve the study objectives (Pietro-Souza et al., 2017; Hamzah et al., 2017; Hamzah et al. al., 2018).

In the case of a study whose focus is on the description of the diversity of cultivable endophytic fungi, a single culture medium can be used, such as PDA agar (Ibrahim et al., 2021), or even this one together with two or more culture medium different to increase the number of retrieved taxon (Man et al., 2015; Gong et al., 2019). The supplementation of the culture medium with plant material from the host species can also be used for better recovery of endophytic fungi (Mourad et al., 2018), and in this case, the plant material must be properly processed and autoclaved in order to avoid contamination. The use of a water agar medium is also a great option to consider for the study of fungal endophyte diversity since this medium is poor in nutrients and prevents fast-growing fungal species from standing out over slower-growing ones (Stone et al., 2004).

The use of antibiotics to inhibit endophytic bacteria is essential when the objective of the study is to assess the diversity of cultivable fungal endophytes (Yao et al., 2017). In this case, the use of one or more broad-spectrum antibiotics is recommended, such as sodium benzylpenicillin (Li et al., 2016), chloramphenicol (Hamzah et al., 2018), streptomycin (Ibrahim et al., 2016), gentamicin (Ibrahim et al., 2021) and tetracycline (Chowdappa et al., 2020).

3.4. Conditions of cultivation, purification, morphological or morphotype grouping, and storage of endophytic fungi colonies

The cultivation conditions in artificial culture medium for endophytic fungi are adverse and will depend on the objectives of the study. The temperature commonly used for incubation of plates is usually 25º C (Li et al., 2016; Du et al., 2020) to 28º C (Yao et al., 2017), and the incubation time varies between 3 -20 days (Li et al., 2016; Yao et al., 2017; Du et al., 2020), which can be extended for up to six weeks if necessary (Yao et al., 2017). In the case of cultures that require a longer incubation period or that are kept in environmental conditions outside the greenhouse or BOD, it is recommended that the plates be sealed with pvc plastic to minimize the risks of contamination and drying of the culture medium (Szűcs et al., 2018; Ababutain et al., 2021). Cultivation can also be carried out with or without incidence of light (Duan et al., 2019; Agbessenou et al., 2020) and for this, the circadian clocks of these microorganisms and their capacities for adaptation and survival depending on the incidence or not of light (Dunlap et al., 2017).

Plates seeded with plant tissue should be monitored daily and as fungal growth is evident from the edges of the inoculated plant tissue, isolation is recommended by collecting the hyphae from the edges of the fungal colonies and seeding them in culture medium fresh with or without antibiotics (Li et al., 2016; Ibrahim et al., 2017; Yao et al., 2017; Ababutain et al., 2021). This step must be repeated several times until a pure endophytic fungus strain with a uniform colony is reached (Ibrahim et al., 2017) and only then the monosporic and/or hypha tip purification must be performed (Supaphon et al., 2013; Duan et al., 2019) for later deposit in a mycological collection and/or molecular identification of the isolate(s).

After the purification process of the fungal isolates, they can be grouped based on their macro and micromorphological characteristics (Dhayanithy et al., 2019; Jayatilake et al., 2020). For this, macroscopic vegetative characteristics must be considered, which include color, texture, topography, diffuse pigmentation, color and topography of the colony's dorsum; and also for their microscopic reproductive structures, using microculture and/or sporulation methods (Dos Banhos et al., 2014). The macroscopic classification allows the grouping of isolates into morphotypes, while the microscopic classification allows the morphological classification of the isolates. However, the arrangement in morphotypes and/or morphological does not reflect the real phylogeny, and even more when considering non-sporulating fungal endophyte species (Li et al., 2016; Yao et al., 2017; Du et al., 2020), which then requires the use of more robust tools to identify the isolates, such as the use of molecular methods for taxonomic classification.

To avoid losses of isolated colonies caused by contamination, re-isolation in cryotubes with inclined PDAB under sterile mineral oil and subsequent storage in a cold chamber at 4 º C and freezer -80 º C is recommended (Li et al., 2016; Wang et al., 2016; Wang et al. al., 2019). For long-term preservation of cultures, mycelia and spores can be transferred to 20% glycerol in ultrapure distilled water and stored at -80°C (Wang et al., 2019). Another alternative for long-term preservation of pure colonies is to transfer small pieces of the medium to sterile Eppendorfs containing 30% glycerol (v/v) and sterile rice medium, incubate at 25ºC, and after observing the fungal growth transfer to a freezer at – 20 º C and cold room at 4 º C, respectively (Ibrahim et al., 2017).

3.5. Molecular identification of isolated endophytic fungi

Despite the development of different methods to promote fungal sporulation (Taylor et al., 1999; Sun et al., 2008a) more than 50% of endophytic fungal isolates do not sporulate in cultures (*Mycelia sterilia*) (Wang et al., 2008a) 2007; Sun et al., 2008b; Sun et al., 2011), making the conventional classification that depends on the observation of the reproductive structures of fungi impossible. Furthermore, even for those isolates capable of sporulating, some taxonomists do not consider the identification of fungi only in the observation of reproductive structures (Sun & Gun, 2012). Therefore, it is necessary to use molecular methods to identify these isolates.

There are many protocols used for molecular identification of endophytic fungal isolates (Table 7), but briefly, these methods require the following steps: I) extraction of the genomic DNA of the isolate from a purified colony; II) amplification (PCR) of conserved DNA sequences (rDNA) using specific or universal primers; III) sequencing of amplified products; IV) editing and comparing sequences with sequences deposited in gene sequence databases; V) interpretation of data and construction of a phylogenetic tree (Hamzah et al., 2018; Thi et al., 2019; Jayatilake et al., 2020). Here it is worth mentioning that other methods can be used to study and identify endophytic fungi, such as the use of cloning vectors to amplify a gene region of interest (Atsatt et al., 2014).

Table 7. Main steps and reagents used for molecular identification of endophytic fungi using culture-dependent methods

DNA extraction protocol	Primers used for amplification	Amplified genomic region	Reagents used in PCR	Amplification conditions	Amplicon size	Database used to search for homologous sequences	Author
Genomic DNA extraction was performed using the CTAB method according to the extraction kit instructions of Biotech Bioengineering Co. Ltd.	ITS1 (5′-TCCG-TAGGTGAACCTGCGG-3′) and ITS4 (5′-TCCTCCGCTTATTGA TATGC-3′).	Internal transcribed spacer region (ITS)	▪ 12,5 μL of 2 × Pfu PCR Mix; ▪ 0,5 μL of ITS1; ▪ 0,5 μL of ITS4; ▪ 1,5 μL of DNA; ▪ 10 μL of ultrapure water.	Initial denaturation step at 94 °C for 5 min; followed by 35 cycles of 94 °C for 1 min, 54 °C for 1 min and 72 °C for 30 s; and final step at 72°C for 15 min.	400–800 bp	Genbank.	Du et al., 2020
The mycelia were macerated using liquid nitrogen and autoclaved mortar, then DNA extraction was performed using the TaKaRa MiniBEST Plant Genomic DNA Extraction kit (Takara Biotechnology Co., Ltd., Dalian, China, Code No. 9768).	ITS1 (5′-TCCG-TAGGTGAACCTGCGG-3 ′) and ITS4 (5′-TCCTCCGCTTATTGA-TATGC-3 ′).	Internal transcribed spacer region (ITS)	▪ 15 μL of Premix TaqTM (Takara Biotechnology Co., Ltd., Dalian, China No. RR003A); ▪ 0,5μL of DNA; ▪ 1,0 μL of primer ITS1; ▪ 1,0 μL of primer ITS4; ▪ 12,5 μL of ultrapure water.	Initial denaturation step at 94 °C for 3 min, followed for 34 cycles of 30 s at 94 °C, 30 s of primer annealing at 54 °C, 45 s of extension at 72 °C, and final elongation step of 10 min at 72 °C.	Not informed by authors	Genbank.	Li et al., 2016
The mycelia were previously macerated in liquid nitrogen, and then TaKaRa MiniBEST bacterial genomic DNA extraction kit (Dalian, China) was used for DNA extraction.	ITS1 (5′-TCCG-TAGGTGAACCTGCGG-3 ′) and ITS4 (5′-TCCTCCGCTTATTGA-TATGC-3 ′)	Internal transcribed spacer region (ITS)	▪ 5.0 μL of 10× Taq buffer; ▪ 4.0 μL of 200 mmol / L dNTPs; 2.0 μL of ITS1 to 10 μM; ▪ 2.0 μL of ITS4 at 10 μM; ▪ 0.5 μL Ex Taq enzyme (TaKaRa, Dalian); ▪ 5.0 μL of genomic DNA.	Initial denaturation step at 95 °C for one minute, followed by 35 cycles of 15 s at 95 °C, 30 s at 55 °C and 1 min at 72 °C; and a final extension of 10 m at 72 °C	Not informed by authors	Genbank	An et al., 2020
Fungal genomic DNA was extracted using the SDS method	ITS1 (5′-TCCG-TAGGTGAACCTGCGG-3 ′) and ITS4 (5′-	Internal transcribed spacer	Not informed by authors	Not informed by authors	500-750 bp	Genbank	Tang et al., 2020

	TCCTCCGCTTATTGATATGC-3 ′)	region (ITS)					
The adopted DNA extraction procedure was the standard phenol-chloroform method with modifications	ITS1 (5′-TCCGTAGGTGAACCTGCGG-3 ′) and ITS4 (5′-TCCTCCGCTTATTGATATGC-3 ′)	Internal transcribed spacer region (ITS)	▪ 2.5 µL of 10× PCR buffer; ▪ 0.5 µL of 1 mmol dNTPs ▪ 2.5 µL of 10 pmol ITS1 ▪ 2.5 µL of 10 pmol ITS4 ▪ 1 µL of 40 ng of DNA ▪ 0.25 µl of 5 units of Taq polymerase.	Initial denaturation step at 94 °C for 2 min; 35 cycles of 94 °C for 1 min, primer specific annealing temperature at 57 °C for 1.30 min and extension at 72 °C for 2 min; and a final extension at 72°C for 4 min	400-750 bp	Genbank	Ibrahim et al., 2017
Genomic DNA (gDNA) was extracted using a fungal genomic DNA extraction kit (Sangon, Shanghai, China)	ITS1 (5′-TCCGTAGGTGAACCTGCGG-3 ′) and ITS4 (5′-TCCTCCGCTTATTGATATGC-3 ′)	Internal transcribed spacer region (ITS)	▪ 5 µL of 10× PCR buffer (10 mM); ▪ 1 µL of dNTP mix (10 mM); ▪ 0.5 µL of Taq polymerase (5 U/µL); ▪ 2 µL of each primer (10 mM) ▪ 5 ng of Gdna; ▪ Double distilled water.	Initial denaturation step at 94 °C for 5 min; followed by 35 cycles of 94 °C for 1 min, 54 °C for 1 min and 72 °C for 30 s; and finally 72°C for 5 min	Not informed by authors	Genbank	Yu et al., 2018
Genomic DNA was extracted from endophytic fungi samples using the Genomic DNA Purification Kit (Promega, USA)	18S rRNA foward (5′-GCTTAATTTGACTCAACACGGGA-3 ′) and rRNA 18S reverse (5′-AGCTATCAATCTGTCAATCCTGTC-3’)	18S rDNA	Not informed by authors	Initial denaturation step at 95 °C for 10 min, followed by 35 cycles of 95 °C for 1 min, 67.7 °C for 1 min and 15 s and 72 °C for 2 min and finally an extension step at 72 °C for 5 min.	Not informed by authors	FungiDB	Ababutain et al., 2021

The process of extracting DNA from the isolates is a critical step for identifying the isolates and must be carried out from pure cultures (Li et al., 2016; Wang et al., 2019). Briefly, fungal DNA extraction begins with the lysis of fungal cells, and different techniques are used, such as maceration in liquid nitrogen (Li et al., 2016) or cell lysis kits (Ababutin et al., 2021). For the extraction of DNA from the compound from cell lysis, several protocols and kits can be used, ranging from the use of genomic DNA extraction kits (Du et al., 2020; Ababutin et al., 2021) to protocols artisans, such as the standard phenol-chloroform method (Ibrahim et al., 2017; Tang et al., 2020). In this sense, to avoid biases, it is recommended to use kits and the length of the extraction steps as recommended by the respective manufacturer (Ababutin et al., 2021), but these can be adapted to better meet the requirements that may eventually arise (Du et al., 2020). After extraction, the DNA must be purified and an aliquot observed, for example, on a 1% electrophoresis gel, to confirm that the DNA was extracted (Ibrahim et al., 2017; Tang et al., 2020).

The next step after DNA extraction is the amplification step of a particular gene sequence of interest and many methods fulfill this objective (Reller et al., 2007). However, the most used to study endophytic fungi from pure cultures is the generation of amplicons from PCR. To perform the PCR, some basic components and reagents are needed, such as primers specific to the region of interest (ITS and 18 rDNA), thermostable DNA polymerase, dNTP's, the DNA to be amplified, and cofactors (Table 7). All components must be in the proper concentrations as described in the previously chosen protocol. After the preparation of the PCR mix, that is, a mixture containing all the fundamental components for carrying out the PCR, this mix is then taken to the thermocycler, where the amplification will take place through numerous cycles of temperature variation. Briefly, the thermal cycles of PCR are double-stranded DNA denaturation, primer annealing, and amplification (Table 7) (Chowdappa et al., 2020; Ibrahim et al., 2021). Here again, it is worth noting that the cycling program should be based mainly on the characteristics of the used primers (Sarsaiya et al., 2020). Finally, the amplicons obtained are purified and usually visualized on gel electrophoresis to confirm amplification and purity, and then sequenced (Ibrahim et al., 2017; Tang et al., 2020; Du et al., 2020).

The sequencing of amplicons from the region(s) of the fungal endophyte genome can be performed by different methodologies, but the main technique used is Sanger sequencing (Li et al., 2016; Ibrahim et al., 2017; Yu et al., 2018; Du et al., 2020; An et al., 2020; Tang et al., 2020; Ababutain et al., 2021). After sequencing, the digital sequences are treated in software for noise removal and quality assessment, and only then are they submitted to digital sequence banks platforms to be compared with already deposited sequences and to arrive at a taxonomic identity (Ibrahim et al., 2017; Tang et al., 2020; Du et al., 2020), considering that sequence similarity of 94% allows classification at the genus level and >97% allows classification at the species level (Li et al., 2016). Normally, data from these sequences are submitted to BLASTn (Basic Local Alignment Search Tool) analysis via Nucleotide, both tools and database respectively from the NCBI (National Center for Biotechnology Information) (Li et al., 2016; Ibrahim et al., 2017; Yu et al., 2018; Du et al., 2020; An et al., 2020; Tang et al., 2020). Other tools and databases can also be used for the taxonomic identification of endophytic fungi (Ababutin et al., 2021). However, identification at the species level will not always be possible only using a single gene region, as observed in the study by Noriler et al. (2018), which requires the use of other regions (See next subtopic).

After the taxonomic identification of fungal isolates, in the case of studies of diversity of endophytic fungi, phylogenetic analyzes of these taxa are recommended to better understand their taxonomic diversity in their habitat (host plant). For this, several tools can be used to assess the phylogenetic relationships between isolated and identified taxa (Li et al., 2016a; Li et al., 2016b; Na et al., 2020).

3.6. Barcodes for identification of endophytic fungi and primers used

The nuclear ribosomal internal transcript (ITS) spacer region is considered to be the primary DNA marker used to identify fungi (Figure 14) (Schoch et al., 2012; Koljalg et al., 2013). Together with the 18S and 28s regions, the ITS region is present in thousands of copies in the genome of all fungi and other eukaryotes is commonly used as a barcode for identifying fungi taxons (Kiss, 2012). To better understand, it is necessary to know that barcode sequences are short universal and standardized DNA sequences that can be easily amplified (500-800bp) and that are common to a given taxonomic group, but that are divergent at the species level, enabling accurate and rapid identification (Blackwell et al., 2011). These sequences must still be unique and stable for each species (Schoch et al., 2012). Furthermore, to be considered a good barcode, the interspecific variation must exceed the intraspecific variation, generating a “break” in the distribution of distances (Hebert et al., 2003).

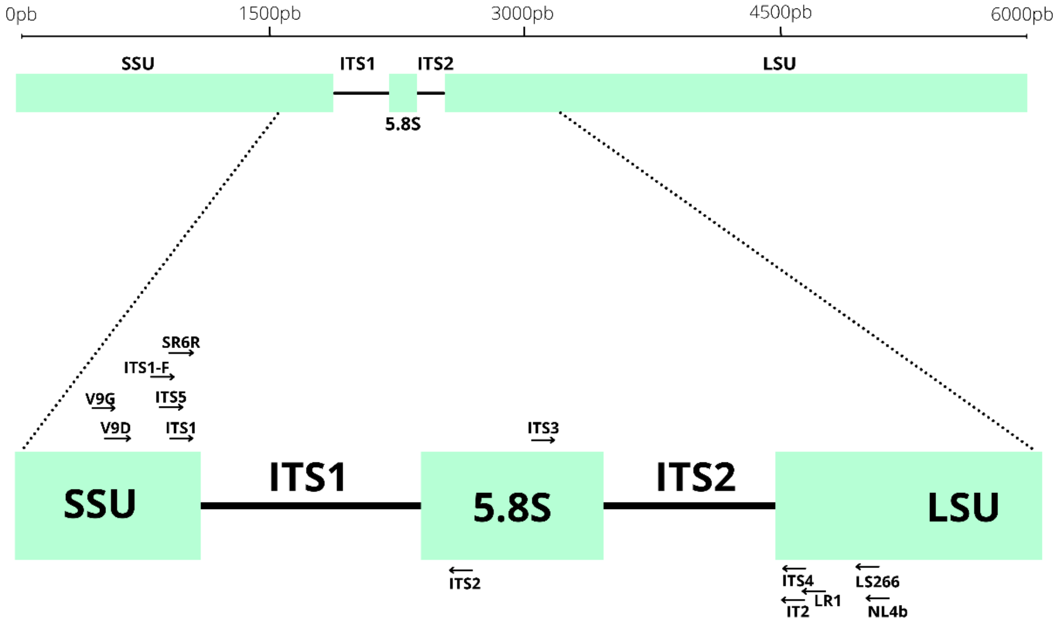


Figure 14. Ribosomal RNA nuclear genes and their ITS regions. The ITS region includes the ITS1 and ITS2 regions that are separated by the 5.8S gene and are between the 18S (SSU) and 28S (LSU) genes (Blackwell et al., 2011). This region is considered a primary barcode for identification of fungal taxon and for this several universal primers have been proposed (Lücking et al., 2020). The average size of amplicons generated from this region for either studies using Sanger sequencing or high-performance sequencing generally range from 450-800bp (Li et al., 2016; Ibrahim et al., 2017; Yu et al., 2018; Du et al., 2020; An et al., 2020). The small arrows observed from the magnification of the ITS region demonstrate the annealing position of the primers used for amplification of this region (White et al., 1990; Gardes & Hester, 1993; O'Donnell, 1993; Gerrits van den Ende and de Hoog, 1999; Beguin et al., 2012). Source: author's collection.

According to Schoch et al. (2012) in the vast majority of cases, the ITS region meets all the requirements mentioned above and when it comes to molecular identification of endophytic fungi this is the first and main region of choice (Li et al., 2016; Ibrahim et al., 2017; Yu et al., 2018; Du et al., 2020; An et al., 2020; Tang et al., 2020). However, the ITS region may not be sufficient for species-level identification of fungal isolates (Noriler et al., 2018), presenting a low resolution for taxonomic classification of *Aspergillus* spp., *Alternaria* spp., *Cladosporium* spp., *Colletotrichum* spp., *Fusarium* spp. and *Penicillium* spp for example (Lücking et al., 2020). An analysis of the accuracy of the ITS as a barcode showed that for 6% and 17% of yeast and filamentous fungi species respectively, classification at the species level from the ITS is not possible (Vu et al., 2016; Vu et al., 2019). Still in a problematic way, within the genome of a single fungal cell there may be thousands of copies of ITS (Kiss, 2012), and between these copies, there may be intergenomic variability (Smith et al., 2007; Weitemier et al., 2015). Such variations can interfere with the PCR and the identification of the studied isolates (Xu, 2016). Therefore, in cases where precise identification is not possible through the ITS region, it is necessary to choose other regions that allow the identification of taxons (Lücking et al., 2020). In this situation, it is recommended to use one or more regions, which are called secondary bar codes, to arrive at the precise identity; for example, the D1/D2 regions are commonly employed for species-level classification in yeast (Scorzetti et al., 2002).

Protein-coding genes can be used to identify fungal species and some authors consider them even more accurate than ITS (Frisvad et al., 2004; Seifert, 2009; Sarmiento-Ramirez et al., 2014). For the Ascomycota phylum, these genes are considered superior to the rDNA genes to resolve relationships at different taxonomic and phylogenetic levels (Schoch et al., 2009), for example, some authors use β-tubulin to classify at the species level for *Penicillium* spp. (Frisvad et al., 2004) and *Aspergillus* spp. (Samson et al., 2014); and TEF1 for *Fusarium* spp. (Short et al., 2013). Other protein-coding genes classified as secondary barcodes have been proposed, such as the β-tubulin II gene (TUB2); cytochrome c oxidase subunit I (COX1) and subunit II (COX2); DNA-directed subunits of the largest RNA polymerase II (RPB1) and the second-largest (RPB2); intergenic spacer (IGS); translational elongation factor 1α (TEF1); DNA topoisomerase I (TOP1) and phosphoglycerate kinase (PGK) (Lücking et al., 2020).

The primers available for amplification of these barcoded regions must be specific and capable of amplifying a sufficient length for the correct analysis (Lücking et al., 2020). The ITS1, ITS2, and ITS4 primers are commonly used to study endophytic fungi and these primers allow the amplification of 400-800bp (Li et al., 2016; Ibrahim et al., 2017; Yu et al., 2018; Du et al., 2020; An et al., 2020; Tang et al., 2020). However, these primers are not the only ones desired for this region. Other specific primers were designed for the ITS region to avoid cross-reactions with animal and/or plant DNA, such as ITS1F (Gardes & Hester, 1993), IT2 (Beguin et al., 2012), NL4b (O'Donnell, 1993), V9D, V9G and LS266 (Gerrits van den Ende and de Hoog, 1999).

As discussed above, in some cases these amplified sequences do not always present sufficient resolution to classify some fungal strains and for this, secondary bar code regions are used (Frisvad et al., 2004). Primers designed for these regions must be universal and must be able to amplify a region that allows for accurate analysis, enabling the identification of the fungal strain (Stielow et al., 2015); for example, the EF1-1018F (Al33F) / EF1-1620R (Al33R), EF1-1002F (Al34F) / EF1-1688R (Al34R) primers designed for TEF1α (Stielow et al., 2015). However, these are not the only proposed primers, there are others designed for this region and other loci (Table 8).

Table 8. Primers designed for universal fungal barcodes used for taxonomic identification

Barcode	Primer name	Primer Sequence	Target gene loci	Author
Primary barcode	ITS1	5 ′ TCCGTAGGTGAACCTGCGG 3 ′	ITS1-5.8S-ITS2 do rDNA	White et al., 1990
Primary barcode	ITS2	5 ′ GCTGCGTTCTTCATCGATGC 3 ′	ITS1-5.8S-ITS2 do rDNA	White et al., 1990
Primary barcode	ITS3	5 ′ GCATCGATGAAGAACGCAGC 3 ′	ITS1-5.8S-ITS2 do rDNA	White et al., 1990
Primary barcode	ITS4	5 ′ TCCTCCGCTTATTGATATGC 3 ′	ITS1-5.8S-ITS2 do rDNA	White et al., 1990
Primary barcode	ITS5	5 ′ GGAAGTAAAAGTCGTAACAAGG 3 ′	ITS1-5.8S-ITS2 do rDNA	White et al., 1990
Primary barcode	ITS1-F	5 ′ CTTGGTCATTTAGAGGAAGTAA 3 ′	ITS1-5.8S-ITS2 do rDNA	Gardes & Hester, 1993
Primary barcode	ITS4-B	5 ′ CAGGAGACTTGTACACGGTCCAG 3 ′	ITS1-5.8S-ITS2 do rDNA	Gardes & Hester, 1993
Primary barcode	IT2	5 ′ CCTCCGCTTATTGATATGCTTAGG 3 ′	ITS1-5.8S-ITS2 do rDNA	Beguin et al., 2012
Primary barcode	NL4b	5 ′ GGATTCTCACCCTCTATGAC 3 ′	ITS1-5.8S-ITS2 do rDNA	O'Donnell, 1993
Primary barcode	SR6R	5 ′ AAGTATAAGTCGTAACAAGG 3 ′	ITS1-5.8S-ITS2 do rDNA	Vilgalys e Hester, 1990
Primary barcode	LR1	5 ′ GGTTGGTTTCTTTCCT 3 ′	ITS1-5.8S-ITS2 do rDNA	Vilgalys e Hester, 1990
Primary barcode	V9D	5 ′ TTAAGTCCCTGCCCTTTGTA 3 ′	ITS1-5.8S-ITS2 do rDNA	Gerrits van den Ende e de Hoog, 1999
Primary barcode	V9G	5 ′ TACGTCCCTGCCCTTTGTA 3 ′	ITS1-5.8S-ITS2 do rDNA	Gerrits van den Ende e de Hoog, 1999
Primary barcode	LS266	5 ′ GCATTCCCAAACAACTCGACTC 3	ITS1-5.8S-ITS2 do rDNA	Masclaux et al. 1995
Primary barcode	18SrRNA F	5 ′ GCTTAATTTGACTCAACACGGGA-3 ′	18S rDNA (SSU)	Ababutain et al., 2021
Primary barcode	18S rRNA R	5 ’ AG-AGCTATCAATCTGTCAATCCTGTC 3’	18S rDNA (SSU)	Ababutain et al., 2021
Primary barcode	NS1	5 ′ GTAGTCATATGCTTGTCTC 3’	18S rDNA (SSU)	White et al. 1990
Primary barcode	NS4	5 ′ CTTCCGTCAATTCCTTTAAG 3’	18S rDNA (SSU)	White et al. 1990
Primary barcode	LROR	5 ′ ACCCGCTGAACTTAAGC 3’	28S rDNA (LSU)	Vilgalys & Sun 1994
Primary barcode	LR5	5 ′ TCCTGAGGGAAACTTCG 3’	28S rDNA (LSU)	Vilgalys & Sun 1994
Secondary barcode	EF1-1002F	5 ′ TTCATCAAGAACATGAT 3 ′	TEF1α	Stielow et al., 2015

Secondary barcode	EF1-1018F	5 ′ GAYTTCATCAAGAACATGAT 3 ′	TEF1α	Stielow et al., 2015
Secondary barcode	EF1-1620R	5 ′ GACGTTGAADCCRACRTTGTC 3 ′	TEF1α	Stielow et al., 2015
Secondary barcode	EF1-1688R	5 ′ GCTATCATCACAATGGACGTTCTTGGAG 3 ′	TEF1α	Stielow et al., 2015
Secondary barcode	EF1	5 ' ATGGGTAAGGA (A / G) GACAAGAC 3 '	TEF1*α*	O’Donnell et al., 1998
Secondary barcode	EF2	5 ' GGA (G/A) GTACCAGT (G / C) ATCATGTT 3 '	TEF1*α*	O’Donnell et al., 1998
Secondary barcode	NL11	5 ' CTGAACGCCTCTAAGTCAG 3 '	IGS	Aoki et al., 2003
Secondary barcode	CNS1	5 ' GAGACAAGCATATGACTAC 3 '	IGS	Aoki et al., 2003
Secondary barcode	Bt 2 a	5 ' GGTAACCAAATCGGTGCTGCTTTC 3 '	β-tubulin II	Glass & Donaldson 1995
Secondary barcode	Bt 2 b	5 ' ACCCTCAGTGTAGTGACCCTTGGC 3 '	β-tubulin II	Glass & Donaldson 1995
Secondary barcode	CMD5	5 ' CCGAGTACAAGGARGCCTTC 3 '	Calmodulin (CaM)	Hong et al. 2005
Secondary barcode	CMD6	5 ' CCGATRGAGGTCATRACGTGG 3 '	Calmodulin (CaM)	Hong et al. 2005
Secondary barcode	CF1	5 ' GCCGACTCTTTGACYGARGAR 3 '	Calmodulin (CaM)	Peterson et al. 2005
Secondary barcode	CF4	5 ' TTTYTGCATRAGYTGGAC 3 '	Calmodulin (CaM)	Peterson et al. 2005
Secondary barcode	5F	5 ' GAYGAYMGWGATCAYTTYGG 3 '	RNA polymerase II (RPB2)	Liu et al., 1999
Secondary barcode	7CR	5 ' CCCATRGCTTGYTTRCCCAT 3 '	RNA polymerase II (RPB2)	Liu et al., 1999
Secondary barcode	5Feur	5 ' GAYGAYCGKGAYCAYTTCGG 3 '	RNA polymerase II (RPB2)	Houbraken et al., 2012
Secondary barcode	7CReur	5 ' CCCATRGCYTGYTTRCCCAT 3 '	RNA polymerase II (RPB2)	Houbraken et al., 2012

3.7. Methods for studying the chemical diversity of endophytic fungi

Endophytic fungi are known to synthesize a wide range of bioactive molecules with the most diverse applications, as reviewed by Toghueo et al. (2020), Sagita et al. (2021) and Zheng et al. (2021). There are many methods used for the evaluation, characterization and isolation of compounds produced by endophytic fungi and the choice of methodology will depend on the objectives of the study. For example, for the study of secondary metabolites, usually purified isolates are subcultured in liquid medium and incubated for a time course of 7-14 days at 25-28 º C, under constant agitation (160-180 rpm/min) (Li et al., 2016; An et al., 2020; Tang et al., 2020; Wei et al., 2020). Then, the fermented broth can be treated to cause cell lysis, filtered and washed one or more times with different organic solvents, vacuum volatized or in a water bath to obtain the metabolites and then they are separated, identified and tested according to the premise of study (Li et al., 2016; Tang et al., 2020). It is noteworthy that guided prior tests can guide and help in the selection of fungal endophytes to be investigated as to their potential for producing metabolites are indispensable (Luo et al., 2015; Sagita et al., 2021).

The identification of metabolites produced by endophytic fungi can be performed by different methods, but with the advent of metabolomics, the most indicated and performed nowadays is the use of high-performance gas or liquid chromatography (GC and LC, respectively) coupled with spectrometry mass (MS) and nuclear magnetic resonance (NMR) spectroscopy (chromatographic profile guided experiment) (Silva et al., 2018; Teimoori-Boghsani et al., 2019; Wei et al., 2020; Sagita et al., 2021).

3.8. Independent cultivation methods for the study of endophytic fungi

The advent of the development of culture-independent tools has allowed the study of microbial communities in a more comprehensive way (Rojas et al., 2019; Ruiz Gómez et al., 2019), since these methods allow a closer description of the real diversity of microorganisms from environmental samples, enabling the description of taxa that are not possible to be isolated and identified when using conventional methods dependent on cultivation under artificial conditions (Forbes et al., 2017). For the analysis of fungal communities, independent cultivation methods have been widely used to study fungal diversity in the most varied habitats, such as soil (Pang et al., 2019), plants (Chi et al., 2019), and hospital environment (Donovan et al., 2018).

For the study of endophytic fungal communities, culture-independent methodologies are being considered a great option to better understand the genetic and functional diversity of species (Chi et al., 2019) of these microorganisms (Staniek et al., 2009; Sagita et al., 2009; Sagita et al., 2009; al., 2021). Chi et al. (2019) used culture-dependent methods in combination with culture-independent methods (metabarcoding) to describe the diversity of fungal taxa in *Acanthus ilicifolius*, and for the culture-dependent method, 203 fungal strains were isolated and classified into 30 different species; while for the metabarcoding, 111 operational taxonomic units (OTU's) were identified, showing the efficiency of the cultivation-independent method in relation to the cultivation-dependent method for the study of microbial diversity in a given habitat. Staniek et al. (2009) designed specific primers to study taxol-coding genes in endophytic fungi, dispensing with elaborate screening procedures that depend on culture and are subject to methodological and observational biases.

There are many culture-independent methodologies that can be used to study endophytic microbial diversity, such as DDGE (Bogas et al., 2015), metabarcoding (Chi et al., 2018). But in general, to study fungi from environmental DNA, these methodologies are based on rDNA ITS1-5.8S-ITS2 PCR amplification (Chi et al., 2018) using specific primers that exclude non-fungal DNA (O' Donnell, 1993). For analysis of the generated amplicons and correct identification of species, several pipelines were developed from ITS data, such as Plutof, Clotu, PIPITS and CloVR-ITS (Abarenkov et al., 2010; Kumar et al., 2011; White et al., 2013 Gweon et al., 2015). But these are not the only ones, others such as BioMaS, Mothur and Qiime have also been used to analyze fungal ITS amplicons (Schloss et al., 2009; Caporaso et al., 2010; Fosso et al., 2015).

Despite advances in independent cultivation techniques for studying microbial communities, these techniques are still in the “kindergarten” and have several methodological limitations. For example, metabarconding usually generates short (~250bp) DNA fragments, making it impossible to classify the taxa at the level of species, genus or even family, as observed in Chi et al. (2019). Therefore, these limitations must be considered when choosing the method that will best meet the objective of the study.

3.9. Considerations about the different methodology adopted for the study of endophytic fungi

As discussed throughout this topic, there are many methodological biases and limitations in studies with endophytic fungi, ranging from field collection to processing the data generated in the case of molecular identification of isolates. For example, some authors consider the methods dependent on imprecise and sparse cultivation to study microbial communities (Taylor et al., 2016; Wu et al., 2019). Some fungal taxonomists, on the other hand, consider cultivation-independent approaches taxonomically unfruitful due to the absence of supporting physical specimens (Lücking et al., 2020). In addition, these techniques cover a high diversity of higher taxa, making it impossible to identify species for all lineages (Chi et al., 2019). Therefore, to minimize this, it is recommended to combine culture-independent and culture-dependent methods. Other alternatives and solutions for possible limitations of the methods adopted to study endophytes are exemplified in Table 9.

Table 9. Possible errors when working with endophytic fungi and suggestions for preventive measures

Experimental steps in studies with endophytic fungi	Error risks and/or methodological limitations	Preventive measures	Author
Identification of plant host(s) and geographic location	Misidentifications of the plant species(s) to be analyzed	- Previous knowledge of the morphological characteristics of the species(s) to be analyzed; - Collect sampling for deposit in herbarium; - Document the sampling location and the deposit slip sample; - Photographic records of the species(s) to be collected, as well as the geographic region.	Silva et al., 2004
Collection and processing of plant tissue	Low sampling, sampling of tissues with herbivory or with symptoms of disease can give erroneous results regarding the diversity of endophytic fungi. Processing time and post-collection storage conditions can also interfere with the diversity of these microorganisms.	- Carry out adequate sampling to obtain the greatest possible representation; - Collect tissue without apparent manifestations of herbivory or disease symptoms; - After collection, the plant tissue must be stored in a temperature-controlled container and taken to the laboratory as soon as possible; - The surface disinfection process of samples should preferably be carried out within 24 hours after collection.	Verma et al., 2007
surface disinfection method	The inappropriate choice of the superficial disinfection protocol may result in the non-elimination of the epiphytic mycobiota or loss of the endophytic mycobiota, thus generating erroneous results	- Conducting previous pilots using different superficial disinfection protocols to find the most suitable for the species and type of tissue analyzed; - Carry out at least three successive washes with distilled water; - Collect water from the last wash to certify the effectiveness of the surface disinfection method;	Saldierna et al., 2020
Plant tissue sampling	Tissue size and number of plant samples sampled may affect observed fungal diversity	- Fragmentation of the fabric to obtain greater coverage; - Fragments must be 2mm-5mm in diameter; - The fabric can be ground or macerated.	Gamboa et al., 2002

Culture médium used and cultivation	The antibiotic-free culture medium can result in the growth of bacteria that protrude over the fungi. The period and temperature of culture can also interfere with the diversity of fungi that will grow under laboratory conditions. Culture-dependent methods are not able to identify fungal taxons not cultivable under laboratory conditions.	- Use of antibiotics and colony limiters in the culture medium to prevent bacterial growth; - pH adjustment of the culture medium; - Choice and control of the appropriate temperature for incubation; - Nutritional enrichment/limitation of the culture medium; - Use culture medium that meet the research objective(s); - Longer incubation time to meet fungal taxons that demand longer growth time; - Use of independent cultivation methods for a description closer to reality of the diversity of endophytic fungi.	Mishra et al., 2012; Sun & Guo, 2012; Verma et al., 2014;
Phenotypic identification of isolates	Identification based only on morphological characteristics of the isolates is not sufficient to classify the táxons	- Use morphological characteristics for prior targeting; - Use methods for sporulation for prior targeting; - Use molecular tools, such as sanger sequencing, together or/not with phenotypic techniques to identify the isolates.	Sun & Guo, 2012; Lindahl et al., 2013
Molecular identification of isolates	Contamination of extracted DNA with DNA from other microorganisms, contamination of reagents used and inappropriate choice of primers can result in inaccurate data	- Ensure culture purity; -Use negative and positive control to perform the PCR; - Choose regions known as barcodes for fungal identification, for example 18S, ITS1, ITS2, 5.8S and 28S regions of rDNA. -Properly choose the primers that will be used; - Use more than one gene region to identify the isolates when a single gene region is not enough for taxonomic classification at the species level.	Sun & Guo, 2012; Lindahl et al., 2013
Observation of the distribution of endophytic fungi in plant tissue	If the tissue is not treated and stained correctly, there may be misinterpretations	- Selection of the appropriate clarification method for the species and plant tissue analyzed; - Choice of colorant to be used; - Use of fluorescent probes.	Detmann et al., 2008
Identification of endophytic fungi from DNA	- Depending on the technique used, the taxonomic classification may be restricted to higher	- Choosing the methodology that best meets the research objectives: metabarcoding; Denaturing gradient gel electrophoresis (DGGE); single sequence repeat (SSR); analysis of randomly amplified polymorphic DNA (RAPD),	Sun & Guo,

extracted from plant tissue (independent methods of cultivation)	taxa, such as phylum, class, order, family. - Depends on the method used, more abundant species may stand out over less abundant ones, making it impossible to describe these	metagenomics; - Combination of different methods; - Use independent and cultivation-dependent methods together.	2012; Verma et al., 2019
Identification and measurement of secondary metabolites in cultivable endophytic fungi	Unpurified cultures and inadequate screening processes can lead to contamination by metabolites or enzymes from the host plant and/or other microorganisms, which can generate false positive results	- Purification of isolates and cultivation under controlled conditions; - Extraction of metabolites to be tested using different organic solvents; - Purification of molecules with biological activity to be tested; - Include negative control with antifungal agents to detect any transport of secondary metabolites or enzymes from the plant or other contaminating sources that result in the synthesis of secondary metabolites; - Carrying out screening experiments using several specific activity bioassays for each isolated metabolite; - Conduct time course experiments to observe if there is an increase in the titration of secondary metabolites as there is an increase in fungal biomass; - Include assays under different culture conditions to modulate the production of secondary metabolites (this case should only be considered when there is solid evidence of metabolite production by the isolate in question); - Use of molecular approaches for screening or amplification of genes responsible for the synthesis of secondary metabolites.	Vasundhara et al., 2016; Sagita et al., 2021

4. TAXONOMIC DIVERSITY OF ENDOPHYTIC FUNGI IN THE CERRADO AND METHODOLOGICAL LIMITATIONS

A huge diversity of endophytic fungi can be found in plant species from tropical regions (Saucedo-García et al., 2014; Li et al., 2016 Yao et al., 2019; Du et al., 2020), so that estimates that up to 100% of the leaves of tropical forest plant species contain endophytic fungi, with each leaf individually harboring up to one isolate every 2mm^2 (Gamboa et al., 2002). As an example of this vast colonization, some studies show that visibly healthy leaves from the same individual (host plant species) from tropical regions can be colonized by different fungal species instead of a single species with systemic growth or hyphae extension (Arnold & Herre, 2003; David et al., 2016; Yao et al., 2019).

Although the endophytic fungi community from tropical regions is highly diverse and valuable, in the Brazilian Cerrado it is still little explored and remains largely unknown. The few studies that have focused on the description of endophytic fungi (Table 2) in native Cerrado hosts, especially the most recent ones that use molecular tools to identify the isolates, show the enormous diversity of fungal endophyte species in this niche (Ferreira et al., 2017; Noriler et al., 2018), including its potential for describing new species and with potential for biotechnological applications (Vieira et al., 2012). For example, Ferreira et al. (2017) reported the occurrence of almost 100 species of endophytic fungi belonging to 27 genera in the host *Vellozia gigantea*; Vieira et al., (2017) recovered 179 isolates of endophytic fungi from leaves of the host species *Baccharis trimera* that were classified into 25 taxon; while Noriler et al. (2018) reported 48 taxon, including three possible new genera, in the host *Stryphnodendron adstringens*. Santos et al. (2014) and Carvalho et al. (2012) also evaluated the diversity of fungal endophytes in *S. astringes* and reported that it is dynamic and diverse. However, due to methodological limitations in the studies carried out by these authors, most fungal taxa were classified only at the genus level.

The reviewed works demonstrate that the taxa belong exclusively to the phylum *Ascomycota* and *Basidiomycota*, with a predominance of species from the phylum *Ascomycota* (96,7%) (Carvalho et al., 2012; Santos et al., 2014; Ferreira et al., 2017; Noriler et al., 2017; Noriler et al., 2017; Noriler et al., 2017; al., 2018; da Silva et al., 2018; Coelho et al., 2020), which coincides with the findings of other authors on the diversity of endophytic fungi in plant species from tropical regions throughout the world (Yang et al., 2018; Yao et al., 2019; Du et al., 2020). More than 75% of the taxa described belong to the classes *Dothiodeomycetes* (24.9%) and *Sordariomycetes* (54.3%) (Figure 15). *Dothiodeomycetes* is the largest and most diverse class in *Ascomycota*, having more than 19,000 described species, which are distributed on all continents and have the most varied lifestyles (Kirk et al., 2008; Lumbsch et al., 2009). Some strains in this class are known to establish a symbiotic relationship with plants, such as mycorrhizae (Spatafora et al., 2012). *Sordariomycetes*, on the other hand, is the second-largest class in *Ascomycota* and includes three subclasses, 28 orders, 90 families, 1,344 genera, approximately 900 uncertain genera, and more than 10,000 described species (Zhang et al., 2006; Fonseca-García et al., 2016; Maharachchikumbura et al., 2016; Réblová et al., 2016; Zhang et al., 2021), being also the dominant class in the endophytic fungi community of several plants (Fonseca-García et al., 2016). Furthermore, *Sordaryomycetes* include important taxa with an endophytic lifestyle that are used as biological control agents, such as *Trichoderma* spp. (Pedrero-Méndez et al., 2021).

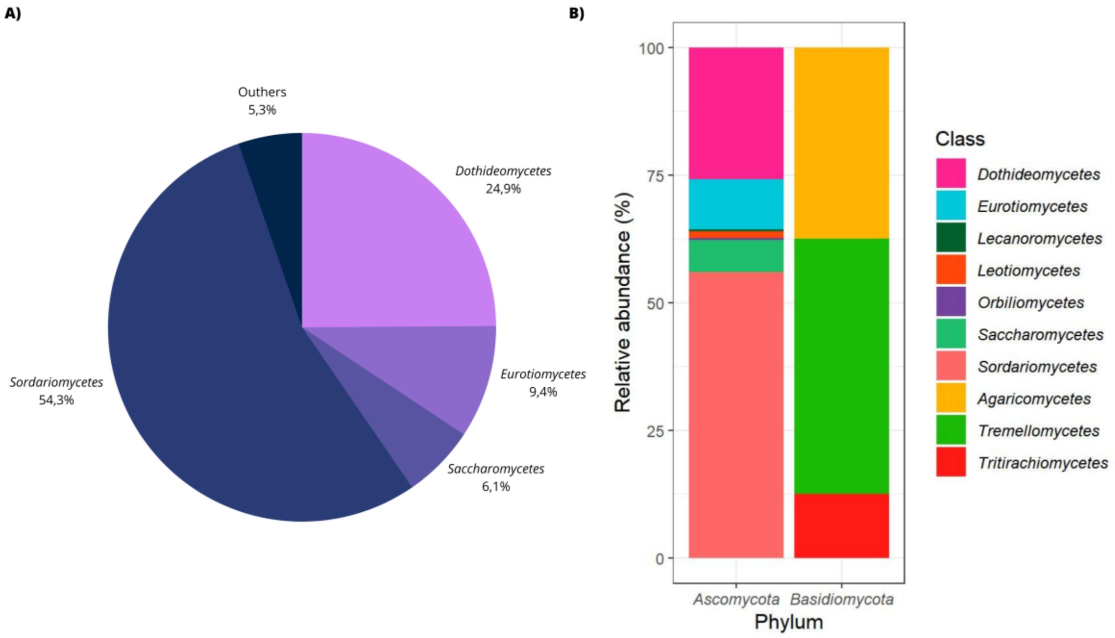


Figure 15. Class-level taxonomic composition of endophytic fungi isolated from Cerrado plant species: **A)** Relative occurrence rate of each class; **B)** Relative abundance (%) of each class in its respective phylum. The data used to prepare the figure are available in Table 2. The taxonomic hierarchy of the taxa was checked in the Mycobank and IndexFungorum databases.

The most prevalent orders are *Diaportheales, Pleoporales, Hypocreales* and *Eurotiales* (Figure 16) In total, 96 genera belonging to 52 families were described in the studies presented in Table 2, the most frequent being *Diaporthe, Fusarium, Colletotrichum, Trichoderma, Penicillium, Pestalotiopsis, Candida* and *Xylaria* (Figure 17). The total number of described species was >100 and this number may be even higher, as some works present taxa classified only at the genus and/or family level (Teles et al., 2005; Rodriguez, 2010; Carvalho et al., 2012; Januário & Vitorino, 2013; Lisboa et al., 2013; Araújo, 2014; Santos, 2014; Vieira et al., 2014; Ferreira, 2017; Noriler et al., 2018). In addition to the enormous diversity of endophytic fungi found, Cerrado plants may also represent an important niche for the description of new species of fungi, including potential for bioprospecting (Noriler et al., 2018; Noriler et al., 2019; Savi et al., 2020).

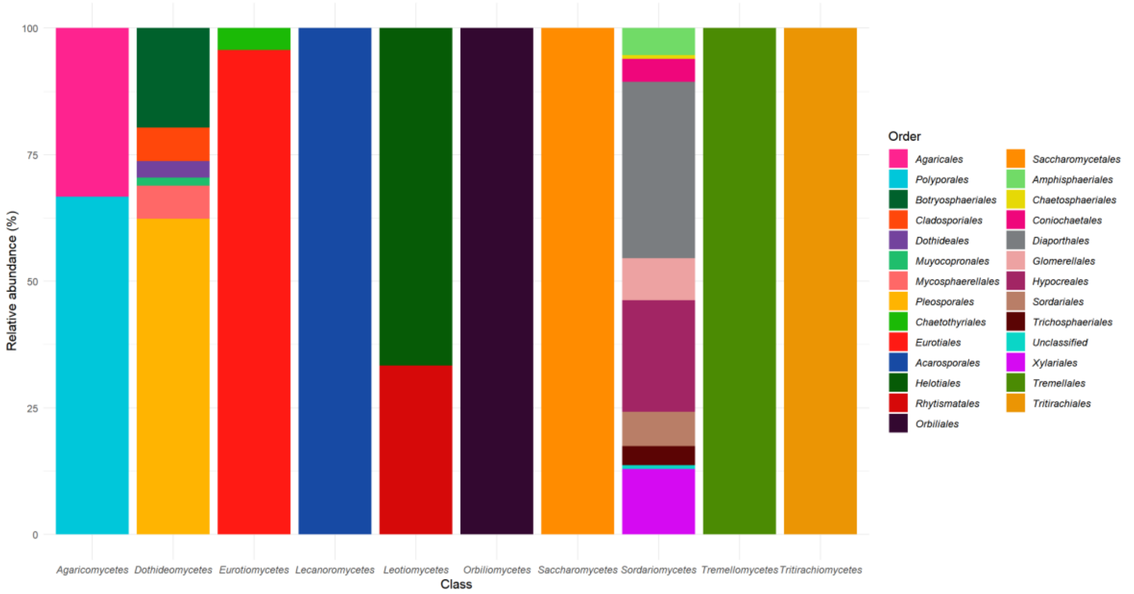


Figure 16. Relative abundances (%) of orders of endophytic fungi of Cerrado plant species. The taxonomic hierarchy of the taxa was checked in the Mycobank and Indexfungorum databases. The data used to prepare the figure are available in Table 2. Taxons with unresolved taxonomic classifications, or only at the phylum level, were not considered.

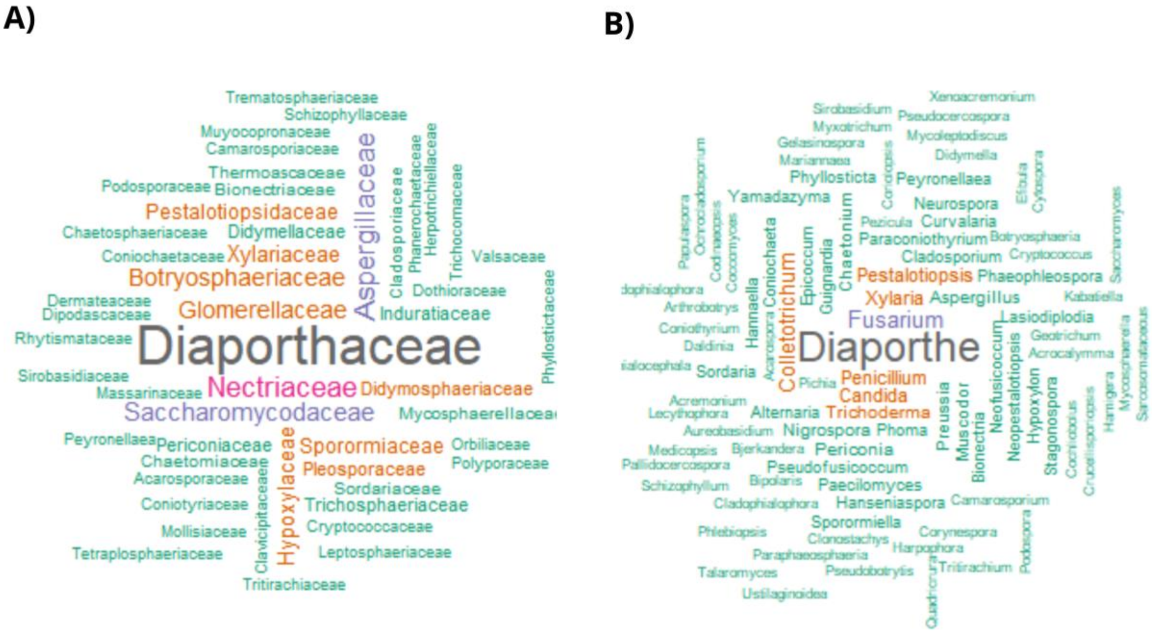


Figure 17. Word cloud illustrates the frequency of **A)** Families and **B)** fungal genera that occur endophytically in Cerrado plant species. The more frequent a family or genera, the greater its representation in the cloud. The data used to prepare the figure are available in Table 2. Taxons with unresolved taxonomic classifications, or only at the phylum level, were not considered

The endophytic mycobiota of plant species from the Cerrado have proved to be quite diverse and complex. However, it is important to emphasize that most studies carried out with endophytic fungi of plant species from the Cerrado use culture-based methods (Teles et al., 2006; Santos, 2014; da Silva et al., 2018; Coelho et al., 2020), limiting itself to only the fraction of fungi that can be cultivated under laboratory conditions, which does not allow knowledge of the real diversity (Pudasaini et al., 2017; Wu et al., 2019). Also problematically, the identification of isolates based on phenotypic characteristics (colony characteristics, cell morphology, etc.), as in the study by Araújo (2014), can generate erroneous identifications and are not indicated to define taxa (Koch et al. al., 2017). An alternative to cover the fungal endophyte community more comprehensively is the joint use of independent methods of cultivation with those that are dependent on the culture, since the independent techniques of cultivation provide data closer to the real diversity, while the dependent ones provide information on the fungal taxa easily cultivable (Lücking et al., 2019; Wen et al., 2020).

Another bias that can generate erroneous results regarding the diversity of fungal endophytes in plant species is the choice of the superficial disinfection method (Saldierna et al., 2020). Briefly and in general, the works reviewed here used mostly 70% alcohol, sodium hypochlorite, and distilled water to remove the epiphytic microbiota. Saldierna et al. (2020) demonstrated that the choice of the superficial disinfection protocol is crucial to avoid misinterpretations, as depending on the protocol used, the integrity of the plant tissue can be compromised, which can result in the loss of part of the endophytic mycobiota. These authors also reinforce the premise that different plant species may require different protocols and/or adaptations of these superficial disinfection protocols, therefore, the performance of previous tests to choose the surface disinfection method becomes necessary.

The choice of recovery and isolation method for endophytic fungi is also crucial for determining the diversity of cultivable taxon. Traditionally, the methods used to describe the endophytic fungi community consist of fragmenting the plant tissue to be analyzed and printing it on a culture medium (Figure 18) (Rodriguez, 2010; Carvalho et al., 2012; Januário & Vitorino, 2013; Lisbon et al., 2013). Despite being efficient, this methodology tends to favor the isolation of filamentous fungi about yeasts, since they present mycelial growth. The choice of isolation methodology for the works reviewed here may be related to the low occurrence of yeast-like fungal species (< 15%), since some studies that used the plant tissue maceration method and successive serial dilutions for later seeding in culture medium have demonstrated that plant species from the Cerrado are a rich habitat for yeast species (Coelho et al., 2020; Vale et al., 2021).

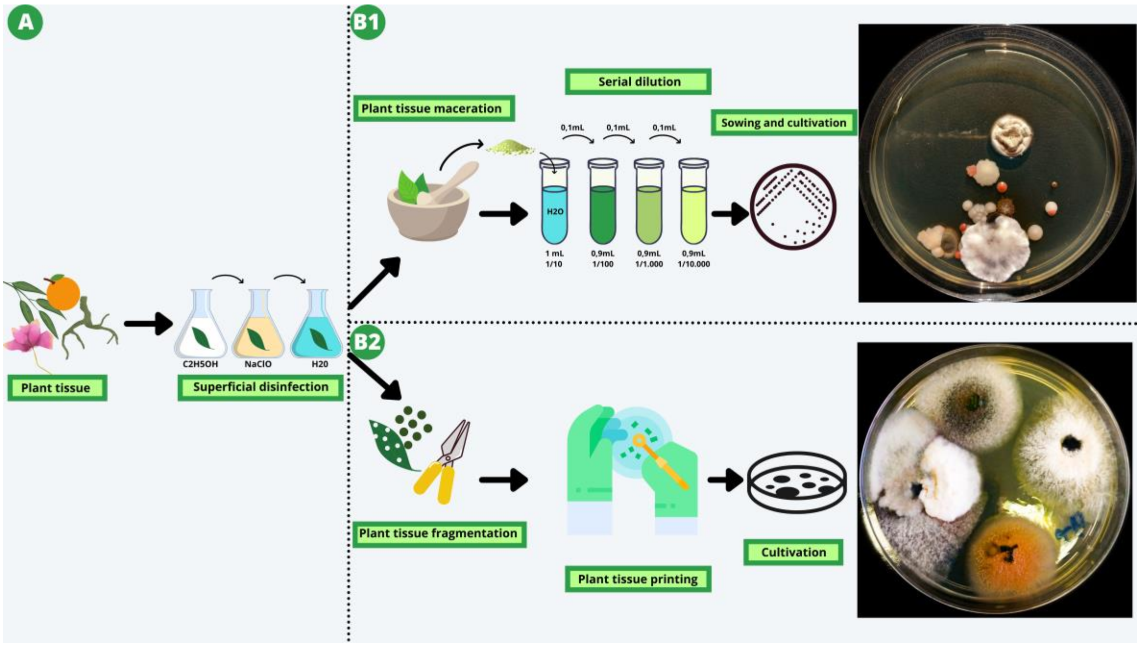


Figure 18. Main methodologies for recovery and isolation of endophytic fungi. After the process of **A)** surface disinfection, which consists of submerging the tissue in 70% ethanol (C_2H_5OH), sodium hypochlorite (NaClO) for respective periods of time, and, finally, successive washing with sterile distilled water (H_2O), the plant tissue can be processed in different ways: **B1)** This can be weighed, macerated with the aid of a crucible and pestle, then a fraction of the macerate is added to sterile distilled water or 1% peptone, vigorously vortexed or incubated under agitation for a time course, to later be diluted in series and seeded in culture medium; or even **B2)** the plant tissue can be fragmented with the aid of a scalpel, eyelet pliers or scissors to be printed on a culture medium and incubated.

Other factors such as host identity (Arfi et al., 2012; Costa et al., 2012), tissue type, host age (Arnold & Herre, 2003), seasonality and geographic (Sandberg et al., 2014; David et al., 2014; David et al., 2016) may influence the composition of the endophytic mycobiota, and, therefore, should be considered when evaluating these communities in plant species from the Cerrado, since this biome is known for its heterogeneous characteristics.

The findings presented here, despite methodological limitations, demonstrate that the endophytic mycobiota of Cerrado plants are rich in species. However, the findings presented here reinforce the need to use more comprehensive methods to study these communities, such as the joint use of dependent and independent methods of cultivation (Chi et al., 2019), as well as methodological adaptations in techniques commonly used to study this community to minimize errors.

5. HOSTS ANALYZED

Cerrado plant species have developed a wide variety of phenological strategies to deal with seasonal variations throughout the year (Figure 19). Some tree species have deep root systems, capable of reaching the moist layers, which allows them to produce leaves and maintain the transpiration process during the dry season (Batalha et al., 1997; Oliveira et al., 2005), and these species are known as evergreen (Sarmiento et al. 1985, Franco et al. 2005; Oliveira et al., 2005; Oliveira 2008). On the other extreme, some species completely shed their leaves during a period in the dry season to minimize water loss, and for this reason, they are classified as brevideciduous or deciduous (Sarmiento et al. 1985, Franco et al. 2005, Lenza & Klink 2006; Lenza & Klink, 2006; Carvalho et al., 2007; Silverio & Lenza, 2010).

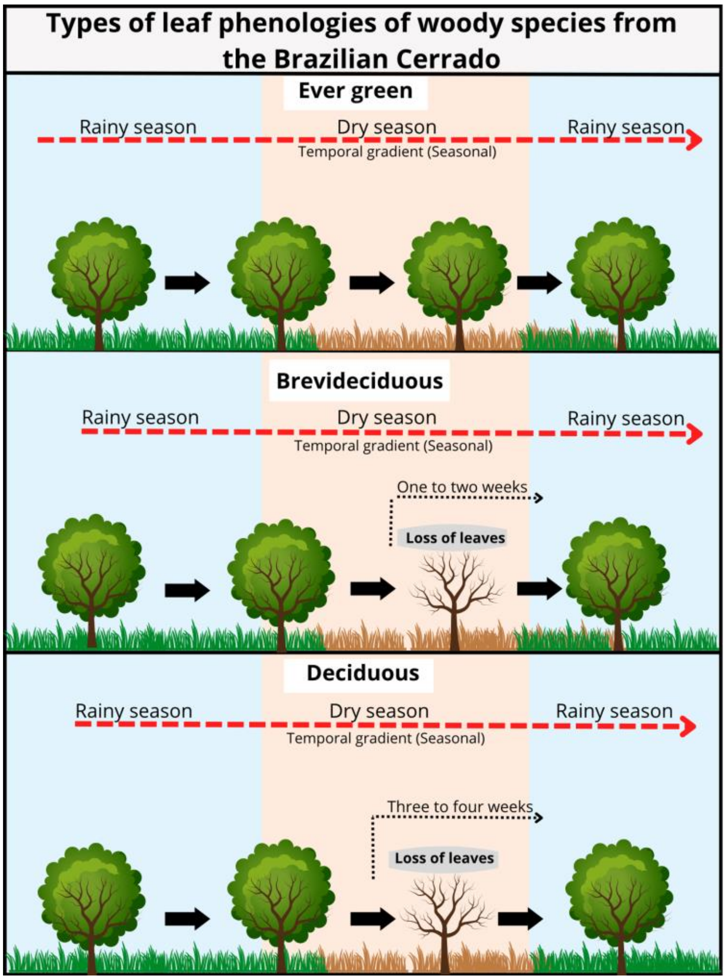


Figure 19. Leaf phenology of Cerrado woody species. The Cerrado, a savanna with a seasonal tropical climate, is characterized by having two well-defined seasons, a rainy period, which lasts from October to March, and a dry period, which lasts from April to September (Nimer & Brandão, 1989), the plant

species have developed numerous mechanisms to deal with this contrasting seasonal gradient, which include different types of phenomenological strategies (Figure 35) (Oliveira, 2008). For example, some tree species have a developed root system, capable of reaching the deepest and wetter layers of the soil, which allows them to absorb water and maintain leaf cover during the dry season (Batalha et al., 1997). These species are called evergreens. Other species, during a period of the dry season, completely lose their leaves and are classified as brevideciduous or deciduous (Silverio et al., 2010).

Based on these characteristics, six different species were selected, two for each phenology (Figure 20), being *Caryocar brasiliense* and *Dalbergia miscolobium* for brevideciduous, *Leptolobium dasycarpum* and *Qualea parviflora* for deciduous, and *Ouratea hexasperna* and *Styrax ferrugineus* for evergreen, with the objective to assess whether host identity and phenology types can shape the taxonomic structure of leaf endophytic mycobiota.

Caryocar brasiliense

Taxonomic hierarchy
Kingdom: Plantae
Phylum: Magnoliophyta
Class: Magnoliopsida
Order: Malpighiales
Family: *Caryocaraceae*
Genus: *Caryocar*
Species: *C. brasilense*
Leaf Phenology: **Brevideciduous**

Dalbergia miscolobium

Taxonomic hierarchy
Kingdom: Plantae
Phylum: Tracheophyta
Class: Magnoliopsida
Order: Fabales
Family: *Fabaceae*
Genus: *Dalbergia*
Species: *D. miscolobium*
Leaf Phenology: **Brevideciduous**

Leptolobium dasycarpum

Taxonomic hierarchy
Kingdom: Plantae
Phylum: Magnoliophyta
Class: Magnoliopsida
Order: Fabales
Family: *Fabaceae*
Genus: *Leptolobium*
Species: *L. dasycarpum*
Leaf Phenology: **Deciduous**

Qualea parviflora

Taxonomic hierarchy
Kingdom: Plantae
Phylum: Tracheophyta
Class: Magnoliopsida
Order: Myrtales
Family: *Vochysiaceae*
Genus: *Qualea*
Species: *Q. parviflora*
Leaf Phenology: **Deciduous**

Ouratea hexasperma

Taxonomic hierarchy
Kingdom: Plantae
Phylum: Tracheophyta
Class: Magnoliopsida
Order: Malpighiales
Family: *Ochnaceae*
Genus: *Ouratea*
Species: *O. hexasperma*
Leaf Phenology: **Ever green**

Styrax ferrugineus

Taxonomic hierarchy
Kingdom: Plantae
Phylum: Tracheophyta
Class: Magnoliopsida
Order: Ericales
Family: *Styracaceae*
Genus: *Styrax*
Species: *S. ferrugineus*
Leaf Phenology: **Ever green**

Figure 20. Taxonomic and phenological classification of the analyzed species

The *Caryocar brasiliense* Camb (Caryocaraceae), popularly known as pequi, is a brevideciduous, neotropical tree species with crooked, thick trunks with grayish bark (Chase et al., 2016; Nunes et al., 2020). Its leaves are compound, trifoliate, and opposite; the leaflets are serrated, oboval with an obtuse apex, hairy, with protruding abaxial veins that can measure up to 20 cm in length and 15 cm in width, and fall off at the end of the rainy season (Chase et al., 2016). This species is very popular in Central Brazil, given the use of its fruits in cooking and its socio-economic importance, being considered one of the candidates for native Cerrado plants to be incorporated into cropping systems (Nunes et al., 2019; Nunes et al., 2019; Nunes et al., 2019; Nunes et al. al., 2020). Regarding the endophytic microbial community, there are descriptions of bacteria isolated from its leaves (Assis, 2018) and of yeasts from fruits (Coelho et al, 2020), identified through cultivation-dependent techniques. However, no studies were found that evaluated the community of endophytic fungi in this species using more robust tools, which allow a closer description of the real diversity of endophytic fungi, in this symbol species of the Cerrado.

Dalbergia miscolobium Benth. (Fabaceae) is a woody, brevideciduous species widely distributed in the Cerrado (Novaes et al., 2013), with bluish-green leaves and dark spots caused by a fungus of the genus *Phoma* (Braz et al., 2000). Studies involving fungi related to this species have described a new species (Dianese et al., 1994) and fungi belonging to its epiphytic microbiota (Mendes et al., 1998). However, recent studies were not found that evaluate the real diversity of the endophytic mycobiota that occurs in the leaves of this species using the combination of dependent and independent techniques of cultivation to know the real diversity.

Leptolobium dasycarpum Vogel Yakovlev (*Fabaceae*) is a deciduous species exclusive to the cerrado and cerradões, restricted to the central and northeastern regions of Brazil, occurring between the states of Bahia, Goiás, Minas Gerais, Mato Grosso and São Paulo (Bridgewater & Stirton, 1997; Silva et al., 2015). Its height varies between 4 and 6 m, with a small crown, and a tortuous trunk with suberous bark (Silva et al., 2015). Regarding its endophytic mycobiota, no studies were found that described the diversity of fungal taxa, so this work is the first to describe the endophytic fungal community associated with the leaf tissue of this species.

Qualea parviflora Mart. (*Vochysiaceae*) is a deciduous species found in the Cerrado, mainly in cerrado stritu sensu, campo sujo and cerradão (Gonçalvez-Alves et al., 2004; de Mesquita et al., 2015; Ariano et al., 2016). There are reports of its gastroprotective, antidiarrheal, antihemorrhagic, and mutagenic potential in compounds found in this species (Mazzolin et al., 2013). Concerning microorganisms that colonize its leaves endophytically, no studies were found. So, taking as a starting point its gastroprotective effects and the lack of studies involving its endophytic mycobiota, this species has enormous potential to harbor endophytes with potential for pharmacological application, as already reported by

Stierle et al. (1993), who isolated an endophytic fungus capable of producing compounds analogous to its host.

The *Ouratea hexasperma* (A.St.-Hil.) Baill. (*Ochnaceae*) is an evergreen species, found in forest edges, Cerradão, and typical Cerrado, popularly called witch's broom (Silverio & Leza, 2010). Studies involving this plant species, in most cases, aim to describe its phytochemistry and possible biotechnological and pharmaceutical applications of its secondary metabolites (Moreira et al., 1999; Estevam et al., 2005; Carvalho, 2008; Silverio et al., 2010; Pires et al., 2020). When it comes to research aimed at studying fungi associated with *O. hexasperma*, Coelho et al (2020) evidenced the presence of endophytic yeasts in their fruits. However, there is no robust data on the diversity of fungi, especially endophytic fungi, in this plant species.

Finally, *Styrax ferrugineus* Nees & Mart. (*Styracaceae*), an evergreen tree species found mainly in the typical Cerrado and Cerradão (Oliveira, 2005). Similar to *Ouratea hexasperma*, studies involving this species are mainly focused on phytochemical characterization (Silva et al., 2016; Silva et al., 2017). Research involving the interaction of *S. ferrugineus* with microorganisms is limited to the study of the interaction that this species has with *Parmularia styracis*, a species of epiphytic fungus responsible for causing black spots on its leaves (Guatimosim et al., 2015; de Souza, 2017).

BIBLIOGRAPHIC REFERENCES

1. Ababutain IM et al. Identification and Antibacterial Characterization of Endophytic Fungi from *Artemisia sieberi. International Journal of Microbiology*. 2021: 6651020.
2. Abarenkov K, Tedersoo L, Nilsson RK, Vellak K, Saar I, Veldre V, et al. PlutoF—a Web Based Workbench for Ecological and Taxonomic Research, with an Online Implementation for Fungal ITS Sequences. *Evol Bioinformatic Online*. 2010. 6: 189–96.
3. Abdul Malik NA, Kumar IS, Nadarajah K. Elicitor and Receptor Molecules: Orchestrators of Plant Defense and Immunity. *International Journal Molecular Sci*ence. 2020; 21 (3): 963.
4. Agbessenou A, Akutse KS, Yusuf AA, Ekesi S, Subramanian S, Khamis FM. Endophytic fungi protect tomato and nightshade plants against *Tuta absoluta* (Lepidoptera: Gelechiidae) through a hidden friendship and cryptic battl . *Scientific Report*. 2020; 10 (1): 22195.
5. Alberto PS. Diversidade de fungos endofíticos de *Anacardium othonianum* Rizzini e seu potencial biotecnológico. Dissertação (Mestrado em Ciências Agrárias-Agronomia) Instituto Federal de Educação, Ciência e Tecnologia Goiano, Rio Verde, Goiás, Brasil. 2013.
6. Alibrandi P, Schnell S, Perotto S, Cardinale M. Diversity and structure of endophytic bacterial communities associated with three terrestrial orchid species, as revealed by 16S rRNA Gene Metabarcoding. *Frontiers Microbiology*. 2020; vol 11: 604964.
7. Almendras K, García J, Carú M, Orlando J. Nitrogen-Fixing Bacteria Associated with *Peltigera cyanolichens* and *Cladonia chlorolichens*. *Molecules*. 2018; 23(12): 3077.
8. Alteio LV, Schulz F, Seshadri R, et al. Complementary Metagenomics Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. *mSystems*. 2020; 5 (2): e00768-19.
9. An C, Ma S, Shi X, Xue W, Liu C, Ding H (2020). Diversity and Antimicrobial Activity of Endophytic Fungi Isolated from *Chloranthus japonicus* Sieb in Qinling Mountains, China. *International Journal of Microbiology*. 21 (17): 5958.
10. An C, Ma S, Shi X, Xue W, Liu C, Ding H. Isolation, diversity and antimicrobial activity of fungal endophytes of *Rohdea chinensis* (Baker) N.Tanaka (synonymous with *Tupistra chinensis* Baker) from the Qinling Mountains, China. *PeerJ*. 2020; 8: e9342.
11. Anguita-Maeso M, Olivares-García C, Haro C, Imperial J, Navas-Cortés JA, Landa BB. Culture-dependent and culture-independent characterization of olive xylem microbiota: effect of sap extraction methods. *Frontier in Plant Science*. 2020; 10: 1708.
12. Aoki T, O'Donnell K, Homma Y, Lattanzi AR. Sudden-death syndrome of soybean is caused by two morphologically and phylogenetically distinct species within the *Fusarium solani* species complex--*F. virguliforme* in North America and *F. tucumaniae* in South America. *Mycology.* 2003; 95: 660-684.
13. Araujo JF, de Castro AP, Costa MM, Togawa RC, Júnior GJ, Quirino BF, Bustamante MM, Williamson L, Handelsman J, Krüger RH. Characterization

of soil bacterial assemblies in Brazilian savanna-like vegetation reveals acidobacteria dominance. *Microbial Ecology*. 2012; 64(3):760-70.

14. Araújo MAM. Isolamento e seleção de leveduras para produção de enzimas de interesse industrial a partir de frutos do Cerrado. Dissertação (Mestrado em Biotecnologia) Universidade Católica Dom Bosco, Mato Grosso do Sul, Brasil. 2014.
15. Arfi Y, Buée M, Marchand C, Levasseur A, Record E. Multiple marker pyrosequencing reveals highly diverse and host-specific fungal communities in *Avicennia marina* and *Rhizophora stylosa* mangrove trees. *FEMS Microbiology Ecology*. 2012; 79: 433–444.
16. Ariano APR, Silva IV. Leaf anatomy of *Qualea parviflora* (Vochysiaceae) in three phytophysiognomies of the Mato Grosso State, Brazil. *Acta Amazonica*. 2016; 46 (2): 119-126.
17. Arnold AE, Herre EA. Canopy cover and leaf age affect colonization by tropical fungal endophytes: Ecological pattern and process in *Theobroma cacao* (Malvaceae). *Mycologia*. 2003; 95(3): 388-398.
18. Ateba JET, Toghueo RMK, Awantu AF, et al. Antiplasmodial Properties and Cytotoxicity of Endophytic Fungi from *Symphonia globulifera* (Clusiaceae). *Journal Fungi (Basel)*. 2018; 4(2): 70.
19. Atsatt PR, Whiteside MD. Novel Symbiotic Protoplasts Formed by Endophytic Fungi Explain Their Hidden Existence, Lifestyle Switching, and Diversity within the Plant Kingdom. *Plos One*. 2014; 9 (4): e95266.
20. Azevedo JL. Endophytic fungi andtheir rolesmainly in tropical plants. In International Symposium On Microbial Ecology. 1996; 7.
21. Bacon CW, White J. Microbial endophytes. New York, NY: CRC. 2000.
22. Badawy AA, Alotaibi MO, Abdelaziz AM, Osman MS, Khalil AMA, Saleh AM, Mohammed AE, Hashem AH. Enhancement of Seawater Stress Tolerance in Barley by the Endophytic Fungus *Aspergillus ochraceus. Metabolites*. 2021 29;11(7):428.
23. Barreto RW, Johnston PR, Crous PW, Evans HC. A new species of the lenticella fungus genus *Claviradulomyces* (Ostropales) from the Brazilian Atlantic Forest tree *Xylopia sericea* (Annonaceae). *IMA Fungus*. 2012; 3 (2): 135-41. doi: 10.5598 / imafungus.2012.03.02.05.
24. Barth Reller L, Melvin P, Weinstein CA. Petti, Detection and Identification of Microorganisms by Gene Amplification and Sequencing. *Clinical Infectious Diseases*. 2007; 44(8): 1108–1114.
25. Batalha MA & Martins FR. The vascular flora of the cerrado in Emas National Park 427 (Central Brazil): a savanna flora summarized. *Brazilian Archives of Biology and Technology*. 2007; 50(2): 269–277.
26. Batalha MA et al. Variações fenológicas das espécies do cerrado em Emas - Pirassununga, SP. *Acta Botanica Brasilica.* 1997; 11 (1): 61-78.
27. Beguin H, Pyck N, Hendrickx M, Planard C, Stubbe D, Detandt M. The taxonomic status of *Trichophyton quinckeanum* and *T. interdigitale* revisited: a multigene phylogenetic approach. *Medical Mycology*. 2012; 50 (8): 871-82.
28. Bengtsson J, Ahnström J, Weibull AC. The effects of organic agriculture on biodiversity and abundance: a meta-analysis. *Journal of Applied Ecology*. 2005; 42: 261–269.
29. Bengtsson-Palme J, Ryberg M, et al. Enhanced software detection and col lection of ITS1 and ITS2 of ribosomal ITS sequences from fungi and other

eukaryotes for environmental sequencing data. *Methods Ecology*. 2013; 4: 919.

30. Benítez-Páez A, Portune KJ, Sanz Y. Species-level resolution of 16S rRNA gene amplicons sequenced through the MinION™ portable nanopore sequencer. *Gigascience*. 2016; 5:4.
31. Benítez-Páez A, Sanz Y. Multi-locus sequencing approach and long amplicons to study microbial diversity at the species level using the MinION™ portable nanopore sequencer. *Gigascience*. 2017; 6 (7): 1-12.
32. Beuchle R, Grecchi RC, Shimabukuro YE, Seliger R, Eva HD, Sano E, et al. Land cover changes in the Brazilian Cerrado and Caatinga biomes from 1990 to 2010 based on a systematic remote sensing sampling approach. *Applied Geography*. 2015; 58: 116–127.
33. Bezerra JD, Nascimento CC, Barbosa Rdo N, et al. Endophytic fungi from medicinal plant *Bauhinia forficata*: Diversity and biotechnological potential. *Brazilian Journal Microbiology*. 2015; 46(1): 49-57.
34. Bezerra JD, Nascimento CC, Barbosa Rdo N, et al. Endophytic fungi of the medicinal plant *Bauhinia forficata*: Diversity and biotechnological potential. *Brazilian Journal Microbiology*. 2015; 46 (1): 49-57.
35. Bezerra JD, Santos MG, Svedese VM, et al. Richness of endophytic fungi isolated from *Opuntia ficus-indica* Mill. (Cactaceae) and preliminary screening for enzyme production. *World of Journal Microbiology and Biotechnology*. 2012; 28(5): 1989-1995.
36. Bezerra JDP, et al. Fungal endophytes from cactus *Cereus jamacaru* in brazilian tropical dry forest: a first study. *Symbiosis*. 2013; 60: 53-63.
37. Bezerra JDP, Oliveira RJV, Paiva LM *et al. Bezerromycetales* and *Wiesneriomycetales* ord. nov. (classe *Dothideomycetes*), with two new genera to accommodate endophytic fungi of Brazilian cacti. *Mycology Progress.* 2017; 16: 297–309.
38. Blackwell M. The fungi: 1, 2, 3... 5.1 million species?. *American Journal of Botanic*. 2011; 98(3):426-438.
39. Bogas AC, Ferreira AJ, Araújo WL, Astolfi-Filho S, Kitajima EW, Lacava PT, Azevedo JL. Endophytic bacterial diversity in the phyllosphere of Amazon *Paullinia cupana* associated with asymptomatic and symptomatic anthracnose. *Springerplus*. 2015; 13 (4):258.
40. Bohrer KE, Friese CF, Amon JP. Seasonal dynamics of arbuscular mycorrhizal fungi in differing wetland habitats. *Mycorrhiza*. 2004;14 (5): 329-337.
41. Brannstrom C, et al. Land change in the Brazilian Savanna (Cerrado), 1986-2002: Comparative analysis and implications for land-use policy. *Land Use Policy*. 2008; 25: 579-595.
42. Brasil. Ministério do Meio Ambiente, Mapeamento do Uso e Cobertura do Cerrado: Projeto TerraClass Cerrado 2013/MMA/sbf.Brasília:MMA. 2015; 67: 978-85.
43. Braz VS, Kanegae MF, & Franco AC. Estabelecimento e desenvolvimento de *Dalbergia miscolobium* Benth. em duas fitofisionomias típicas dos cerrados do Brasil Central. *Acta Botanica Brasilis*. 2000; 14.

44. Bridgewater SMG, and Stirton CH. “A Morphological and Biogeographic Study of the *Acosmium Dasycarpum* Complex (Leguminosae: Papilionoideae, Sophoreae).” *Kew Bulletin*. 1997; 52(2): 471–475.
45. Bueno de Mesquita CP, Martinez Del Río CM, Suding KN, Schmidt SK. Rapid temporal changes in root colonization by arbuscular mycorrhizal fungi and fine root endophytes, not dark septate endophytes, track plant activity and environment in an alpine ecosystem. *Mycorrhiza*. 2018a; 28(8): 717-726.
46. Bueno de Mesquita CP, Sartwell SA, Ordemann EV, Porazinska DL, Farrer EC, King AJ, Spasojevic MJ, Smith JG, Suding KN, Schmidt SK. Root colonization patterns by arbuscular mycorrhizal fungi and dark septate endophytes in a nearly unvegetated high-altitude landscape. *Fungal Ecology*. 2018b; 36: 63–74.
47. Bukovská P, Rozmoš M, Kotianová M, et al. Arbuscular Mycorrhiza Mediates Efficient Recycling From Soil to Plants of Nitrogen Bound in Chitin. *Frontiers Microbiology*. 2021; 12: 574060.
48. Bulgarelli D, Rott M, Schlaeppi K., Ver Loren van Themaat E, Ahmadinejad N., Assenza F, et al. Revealing structure and assembly tips for the bacterial microbiota inhabiting the root of *Arabidopsis*. *Nature*. 2012; 488 (7409): 91–5.
49. Burgdorf, RJ et al. A procedure to evaluate the efficiency of surface sterilization methods in culture-independent fungal endophyte studies. *Brazilian Journal of Microbiology*. 2014; 45 (3): 977-983.
50. Buschart A, Sachs S, Chen X, Herglotz J, Krause A, Reinhold-Hurek B. Flagella mediate endophytic competence rather than acting as MAMPs in rice - *Azoarcus* sp. BH72 strain interactions. *Molecular Plant-Microbe Interaciont.* 2012*;* 25: 191–199.
51. Buscot F, Munch JC, Charcosset JY, et al. Recent advances in exploring physiology and biodiversity of ectomycorrhizas highlight the functioning of these symbioses in ecosystems. *New Phytologist.* 2000; 24: 601–14.
52. Buzatti RSO, Pfeilsticker TR, de Magalhães RF, Bueno ML, Lemos-Filho JP, Lovato MB. Genetic and historical analyzes of the colonization of an endemic savanna tree, *Qualea grandiflora*, reveal ancient connections between Amazonian savannas and cerrado core. *Frontiers in Plant Sciences*. 2018; 9: 981.
53. Cafeu MC. et al. Substâncias antifúngicas de Xylaria sp., um fungo endofítico isolado de *Palicourea marcgravii* (Rubiaceae). *Química Nova*. 2005; 28(6): 991-995.
54. Camacho E, Niño-Vega GA. *Paracoccidioides* Spp.: Virulence Factors and Immune-Evasion Strategies. *Mediators Inflamm*. 2017; 2017: 5313691. doi: 10.1155/2017/5313691.
55. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, et al. QIIME allows analysis of high-throughput community sequencing data. *Nature Methods*. 2010; 7 (5): 335–336.
56. Carella P, Schornack S. Manipulation of Bryophyte Hosts by Pathogenic and Symbiotic Microbes. *Plant Cell Physiology*. 2018; 59 (4): 651-660.
57. Carvalho APF, Bustamante MMC, kozovits AR and Asner GP. Variações sazonais nas concentrações de pigmentos e nutrientes em folhas de espécies

de cerrado com diferentes estratégias fenológicas. *Revista Brasileira de Botânica.* 2007; 30, (1): 19-27.

58. Carvalho et al. The diversity, antimicrobial and anticancer activity of endophytic fungi associated with the medicinal plant Stryphnodendron adstringens (Mart.) Coville (Fabaceae) from the Brazilian savanna. *Symbiosis*. 2011; 57 (2): 95-107.
59. Carvalho MG. 2008. New Flavonoids and other Constituents *from Ouratea hexasperma* (Ochnaceae). *Journal Brazilian Chemical Society*. 2008; 19(7): 1423-1428.
60. Catão E, Castro AP, Barreto CC, Krüger RH, Kyaw CM. Diversity of Archaea in Brazilian savanna soils. *Archives of Microbiology*. 2013; 195(7): 507-512.
61. Catão EC, Lopes FA, Araújo JF, et al. Soil acidobacterial 16S rRNA gene sequences reveal differences in subgroup levels between the Savana-type Cerrado and Brazilian Atlantic Forest biomes. *International Journal Microbiology*. 2014; 2014: 156341.
62. Chagas MBO, Prazeres Dos Santos I, Nascimento da Silva LC, Correia MTDS, Magali de Araújo J, Cavalcanti MDS, Lima VLM. Antimicrobial Activity of Cultivable Endophytic Fungi Associated with *Hancornia Speciosa* Gomes Bark. *Microbiol Journal*. 2017; 21 (11):179-188. doi: 10.2174/1874285801711010179.
63. Chagnon PL, U'Ren JM, Miadlikowska J, Lutzoni F, Arnold AE. The type of interaction influences the structure of the ecological network more than the local abiotic conditions: evidence of endophytic and endolychenic fungi on a continental scale. *The Ecology.* 2016; 180: 181–191.
64. Chanclud E & Morel JB. Plant hormones: A fungal point of view. *Molecular Plant Pathology.* 2016; 17:1289–1297.
65. Chand K, Shah S, Sharma J, Paudel MR, Pant B. Isolation, characterization, and plant growth-promoting activities of endophytic fungi from a wild orchid Vanda cristata. *Plant Signal Behav*. 2020; 15 (5): 1744294.
66. Chen J, Akutse KS, Saqib HSA, et al. Fungal Endophyte Communities of Crucifer Crops Are Seasonally Dynamic and Structu; red by Plant Identity, Plant Tissue and Environmental Factors. *Frontiers Microbiology*. 2020; 11: 1519.
67. Chen S, Dai J, Song X, Jiang X, Zhao Q, Sun C, Chen C, Chen N, Han B. Endophytic Microbiota Comparison of *Dendrobium huoshanense* Root and Stem in Different Growth Years. *Planta Medicine*. 2020; 86(13-14): 967-975.
68. Chen, YL, Zhang X, Ye JS, Han HY, Wan SQ & Chen BD. Six-year fertilization modifies the biodiversity of arbuscular mycorrhizal fungi in a temperate steppe in Inner Mongolia. *Soil Biology & Biochemistry*. 2014; 69: 371–381.
69. Chi WC, Chen W, He CC, et al. A highly diverse fungal community associated with the leaves of the mangrove plant *Acanthus ilicifolius* var. xiamenensis revealed by isolation and metabocoding analyzes. *PeerJ*. 2019; 7: e7293.
70. Chow YY, Ting ASY. Influence of fungal infection on plant tissues: FTIR detects compositional changes to plant cell walls. *Fungal Ecololy.* 2019; 37:38–47.
71. Chowdappa S, Jagannath S, Konappa N, Udayashankar AC, Jogaiah S. Diversity and biological activities of endophytic fungi associated with *Catharanthus roseus*. 2020; 10 (10): 1412.

72. Christian N, Sedio BE, Florez-Buitrago X, et al. Host affinity of endophytic fungi and the potential for reciprocal interactions involving host secondary chemistry. *American Journal Botany*. 2020; 107(2): 219-228.
73. Ciccolini V, Ercoli L, Davison J, Vasar M, Öpik M, Pellegrino E. Land-use intensity and host plant simultaneously shape the composition of arbuscular mycorrhizal fungal communities in a Mediterranean drained peatland. *FEMS Microbiology Ecology*. 2016; 92(12): fiw186.
74. Clay K, Schardl C. Evolutionary origins and ecological consequences of endophytic symbiosis with grasses. *American Nature.* 2002; 160: S99 – S127.
75. Coelho L.GF., Moreira GAM., Bomfim, C.A, & Vale HMM. Structure of yeast communities in fruits of different native plant species from the Brazilian Cerrado. *Journal of Neotropical Biology*, 2020; *17*(1): 35–46.
76. Coleman-Derr D, Desgarennes D, Fonseca-Garcia C, Gross S, Clingenpeel S, Woyke T, et al. Plant compartment and biogeography affect microbiome composition in cultivated and native Agave species. *New Phytologist.* 2016; 209: 798–811.
77. Compant S., Clément C., Sessitsch A. Plant growth-promoting bacteria in the rhizome and endosphere of plants: their role, colonization, mechanisms involved and prospects for use. *Soil Biology and Biochemistry. 2010;* 42: 669–678.
78. Cordeiro MAS, Carneiro MAC, Paulino HB & Saggin Júnior OJ. Colonização e densidade de esporos de fungos micorrízicos em dois solos do cerrado sob diferentes sistemas de manejo. *Pesquisa Agropecuária Tropical*. 2005; 35: 147-153.
79. Costa I, Maia LC, Cavalcanti MA. Diversity of leaf endophytic fungi in mangrove plants in Northeast Brazil. *Brazilian Journal Microbiology*. 2012; 43: 1165–1173.
80. Coutinho BG, Licastro D, Mendonça-Previato L, Cámara M, Venturi V. Plant-influenced gene expression in the rice endophyte Burkholderia kururiensis M130. *Molecular Plant-Microbe Interaction.* 2015*;* 28: 10–21.
81. Crous PW, Carnegie AJ, Wingfield MJ, et al. Fungal Planet description sheets: 868-950. *Persoonia*. 2019; 42:291-473. doi:10.3767/persoonia.2019.42.11
82. Cui JL, Guo TT, Ren ZX, Zhang NS, Wang ML. Diversity and antioxidant activity of cultivable endophytic fungi from alpine plants of *Rhodiola crenulata, R. angusta* and *R. sachalinensis*. *Plos O*ne. 2015; 10 (3): e0118204.
83. Cummins M, Huitema E. Effector-Decoy Pairs: Another Countermeasure Emerging during Host-Microbe Co-evolutionary Arms Races?. *Molecular Plant*. 2017; 10(5): 662-664.
84. Currah RS, Van Dyk M. Um levantamento de algumas espécies de plantas vasculares perenes nativas de Alberta para a ocorrência de fungos micorrízicos. *Canadian Campo-Naturalist.* 1986*;* 100: 330 – 342.
85. da Silva CF, Vitorino LC, Soares MA, Souchie EL. Multifunctional potential of endophytic and rhizospheric microbial isolates associated with *Butia purpurascens* roots for promoting plant growth. *Antonie van Leeuwenhoek*. 2018; 111(11): 2157-2174.
86. Dang H, Zhang T, Wang Z, et al. Succession of endophytic fungi and arbuscular mycorrhizal fungi associated with the growth of plant and their

correlation with secondary metabolites in the roots of plants. *BMC Plant Biology*. 2021; 21(1): 165.

87. Dastogeer KMG, Zahan MI, Tahjib-Ul-Arif M, Akter MA, Okazaki S. Plant Salinity Tolerance Conferred by Arbuscular Mycorrhizal Fungi and Associated Mechanisms: A Meta-Analysis. *Frontiers in Plant Science.* 2020; 11:588550.
88. David AS, Seabloom EW, May G. Plant Host Species and Geographic Distance Affect the Structure of Aboveground Fungal Symbiont Communities, and Environmental Filtering Affects Belowground Communities in a Coastal Dune Ecosystem. *Microbial Ecology*. 2016; 71(4): 912-926.
89. Davies GL, Dibner DM, Battey FJ. Preparation of DNA from eukaryotic cells: general method In: Davis Leonard G, editor. *Basic methods in molecular biology*. New York: Elsevier. 1986; 44–46.
90. de Araujo AS, Bezerra WM, Dos Santos VM, et al. Distinct bacterial communities across a gradient of vegetation from a preserved Brazilian Cerrado. *Antonie Van Leeuwenhoek*. 2017; 110(4): 457-469.
91. de Castro AP, Sartori da Silva MR, Quirino BF, da Cunha Bustamante MM, Krüger RH. Microbial Diversity in Cerrado Biome (Neotropical Savanna) Soils. *Plos One*. 2016; 11(2): e0148785.
92. De Mattos Scaramuzza CA, Sano EE, Adami M., Bolfe EL, Coutinho AC, César J, Mora D, Eduardo L, Maurano P, Narvaes S, et al. Mapeamento do uso e cobertura da terra do Cerrado brasileiro com base principalmente em imagens do satélite LANDSAT-8. *Rev. Brasileira de Cartografia.* 2017; 69: 1041–1051.
93. de Medeiros AG, Savi DC, Mitra P, Shaaban KA, Jha AK, Thorson JS, Rohr J, Glienke C. Bioprospecting of *Diaporthe terebinthifolii* LGMF907 para compostos antimicrobianos. *Folia Microbiologica* (Praha). 2018; 63 (4): 499-505. doi: 10.1007 / s12223-018-0587-2.
94. de Mesquita, ML, Leão, WF, Ferreira, MR, de Paula, JE, Espindola, LS, & Soares, LA. Método de cromatografia líquida de fase reversa para separação e quantificação de ácido gálico de extratos hidroalcoólicos de *Qualea grandiflora* e *Qualea parviflora*. *Revista de farmacognosia*. 2015; *11* (Suplemento 2): S316 – S321.
95. Del Carmen H Rodríguez M, Evans HC, de Abreu LM, et al. New species and records of *Trichoderma* isolated as mycoparasites and endophytes from cultivated and wild coffee in Africa. *Scientific Reports*. 2021; 11(1): 5671.
96. Denney DA, Jameel MI, Bemmels JB, Rochford ME, Anderson JT. Small spaces, big impacts: contributions of micro-environmental variation to population persistence under climate change. AoB Plants. 2020 18;12(2):plaa005.
97. Desiro A., Duckett JG, Pressel S., Villarreal JC. Fungal symbioses in hornworts: a checkered history. *Proceedings of the Royal Society B: Biological Sciences*. 2013; 280: 20130207.
98. Detmann KSC, Delgado MN, Rebello VPA, Leite TD, Azevedo AA, Kasuya MCM, Almeida AM. Comparação de métodos para a observação de fungos micorrízicos arbusculares e endofíticos do tipo *dark septate* em espécies nativas de Cerrado*. Revista Brasileira de Ciência do Solo*. 2008; 32: 1883-1890.

99. Dhayanithy G, Subban K, Chelliah J. Diversity and biological activities of endophytic fungi associated with *Catharanthus roseus*. *BMC Microbiology*. 2019; 19 (1): 22.

100. Dianese JC, Santos LTP, Medeiros RB, Sanchez M. *Mimema venturae* sp. nov. on *Dalbergia miscolobium* in Brazil. *Mycological Research*. 1994; 98 (7): 786-788.

101. Ding T, Melcher U. Influences of Plant Species, Season and Location on Leaf Endophytic Bacterial Communities of Non-Cultivated Plants. *Plos One*. 2016; 11 (3): e0150895.

102. Donovan PD, Gonzalez G, Higgins DG, Butler G, Ito K. Identification of fungi in shotgun metagenomics datasets. *Plos One*. 2018; 14;13(2):e0192898.

103. Dos Banhos EF, de Souza AQ, de Andrade JC, de Souza AD, Koolen HH, Albuquerque PM. Endophytic fungi from *Myrcia guianensis* at the Brazilian Amazon: distribution and bioactivity. *Brazilian Journal of Microbiology*. 2014; 45 (1): 153-161.

104. Du W, Yao Z, Li J, Sun C, Xia J, Wang B, Shi D, Ren L. Diversity and antimicrobial activity of endophytic fungi isolated from *Securinega suffruticosa* in the Yellow River Delta. *Plos One*. 2020; 15(3): e0229589.

105. Duan X, Xu F, Qin D, Gao T, Shen W, Zuo S, Yu B, Xu J, Peng Y, Dong J. Diversity and bioactivities of fungal endophytes from *Distylium chinense*, a rare waterlogging tolerant plant endemic to the Three Gorges Reservoir. *BMC Microbiol*. 2019; 19(1): 278.

106. Dubery IA, Sanabria NM, Huang JC. Nonself perception in plant innate immunity. *Advances in Experimental Medicine and Biology*. 2012; 738: 79-107.

107. Dudeja S. S., Giri R. Beneficial properties, colonization, establishment and molecular diversity of endophytic bacteria in legume and non-legume. *Journal Microbiology Re*search. 2014; 8: 1562–1572.

108. Dunlap JC, Loros JJ. Making Time: conservation of biological clocks from fungi to animals. microbiol spectr. 2017; 5(3):10.1128/microbiolspec.

109. Edwards J, et al. Structure, variation and assembly of the microbiome associated with rice root. *Proceedings of the National Academy of Sciences.* 2015; 112 E911 – E920.

110. Edwards JE, Forster RJ, Callaghan TM, et al. PCR and Omics-based techniques to study the diversity, ecology and biology of anaerobic fungi: insights, challenges and opportunities. *Frontiers Microbiology*. 2017; 8: 1657.

111. Eiten G.The Cerrado vegetation of Brazil. *Botanical Review*. 1972; 38: 201-341.

112. El-Bondkly EAM, El-Bondkly AAM, El-Bondkly AAM. Marine endophytic fungal metabolites: A whole new world of pharmaceutical therapy exploration. Heliyon. 2021; 8;7 (3): e06362. doi: 10.1016/j.heliyon.2021.e06362.

113. El-Sayed ASA, El-Sayed MT, Rady A, et al. Exploiting the Biosynthetic Potency of Taxol from Fungal Endophytes of Conifers Plants; Genome Mining and Metabolic Manipulation. *Molecules*. 2020; 25(13): 3000.

114. de RA, Srinivasan V, Anwar M. Seasonal shift affects leaf endophyte assemblage and diversity in *Asparagus racemosus* and *Hemidesmus indicus*. *BMC Ecology*. 2018; 18 (1): 52.

115. Escudero V, Mendoza R. Seasonal variation of arbuscular mycorrhizal fungi in temperate grasslands along a wide hydrologic gradient. *Mycorrhiza*. 2005; 15(4): 291-299.
116. Espírito-Santo MM, Leite ME, Silva JO, et al. Understanding patterns of land-cover change in the Brazilian Cerrado from 2000 to 2015. *Philosophical Transactions of the Royal Society B: Bioogicall Sciences*. 2016; 371(1703): 20150435.
117. Estevam CS. et al. Constituintes químicos e avaliação preliminar in vivo da atividade antimalárica de *Ouratea nitida* Aubl (*Ochnaceae)*. *Revista Brasileira Farmacognosia.* 2005; 15 (3): 195-198.
118. Faeth SH & Fagan WF. Fungal endophytes: common host plant symbionts but uncommon mutualists. Integr Comp Biol. 2002 42(2):360-8. doi: 10.1093/icb/42.2.360. PMID: 21708729.
119. Fahey M, Rossetto M, Wilson PD, Ho SYW. Habitat preference differentiates Holocene dynamics, but not barrier effects on two sympatric and congeneric trees (*Tristaniopsis, Myrtaceae*). *Heredity (Edinb)*. 2019; 123 (4): 532-548.
120. Fan S, Miao L, Li H, Lin A, Song F, & Zhang P. Illumina-based analysis yields new insights into the diversity and composition of endophytic fungi in cultivated *Huperzia serrata*. *Plos one*. 2020; 15 (11), e0242258.
121. Fang K, Miao YF, Chen L, et al. Tissue-Specific and Geographic Variation in Endophytic Fungi of Ageratin adenophora and Fungal Associations with the Environment. *Frontiers Microbiology*. 2019; 10: 2919.
122. Farias GC, Nunes KG, Soares MA, et al. Dark-septate endophytic fungi attenuate the effects of salt stress in cowpea plants. *Brazilian Journal of Microbiology.* 2020; *51* (1), 243–253.
123. Fernandes GW, Oki Y, Belmiro MS. et al. Multitrophic interactions among fungal endophytes, bees, and *Baccharis dracunculifolia*: resin tapering for propolis production leads to endophyte infection. *Arthropod-Plant Interactions*. 2018; 12: 329–337.
124. Ferrara MA. Fungos Endofíticos: Potencial para a produção de substâncias bioativas. Revista Fitos. 2006; 2(1): 73-79.
125. Ferreira CA. Estudo fitoquímico e ensaios da atividade antioxidante dos extratos de *Acosmium dasycarpum* (vogel) yakovlev (fabaceae) e croton antisyphiliticus mart. (euphorbiaceae). Dissertação de mestrado, Universidade Federal dos Vales do Jequitinhonha e Mucuri, Minas Gerais, Brasil; 2020.
126. Ferreira DA, Carneiro MAC, Saggin JOJ. Fungos micorrízicos arbusculares em um latossolo vermelho sob manejos e usos no cerrado. *Revista Brasileira de Ciências do Solo*. 2012; 36(1): 51-61.
127. Ferreira MC, et al. Diversity of the endophytic fungi associated with the ancient and narrowly endemic neotropical plant *Vellozia gigantea* from the endangered Brazilian rupestrian grasslands. *Biochemical Systematics and Ecology*. 2017. 71: 163-169.
128. Fisher P, Petrini O, Scott HL. The distribution of some fungal and bacterial endophytes in maize (*Zea mays* L.). *New Phytologist. 2005:* 122 299–305.
129. Fonseca-García C, Coleman-Derr D, et al. The Cacti Microbiome: Interplay between Habitat-Filtering and Host-Specificity. *Frontiers Microbiology*. 2016; 7:150.

130. Fonseca-García C, Coleman-Derr D, Garrido E, Visel A, Tringe SG, Partida-Martínez LP. The Cacti Microbiome: Interaction between Habitat Filtering and Host Specificity. *Frontiers in Microbiology*. 2016; 7: 150.
131. Fontana DC, de Paula S, Torres AG, de Souza VHM, Pascholati SF, Schmidt D, Dourado Neto D. Endophytic Fungi: Biological Control and Induced Resistance to Phytopathogens and Abiotic Stresses. *Pathogens.* 2021; 8;10(5):570.
132. Forbes JD, Knox NC, Ronholm J, Pagotto F, Reimer A. Metagenomics: the next culture-independent game changer. *Frontiers in Microbiology*. 2017; 4(8):1069.
133. Fosso B, Santamaria M, Marzano M, Alonso-Alemany D, Valiente G, Donvito G, et al. BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. *BMC Bioinformatics*. 2015; 16: 203.
134. Fouda A, Eid AM, Elsaied A, et al. A plant growth-promoting endophytic bacterial community that inhabits the leaves of *Pulicaria incisa* (Lam.) DC inherent in arid regions. *Plants* (*Basel*). 2021; 10 (1): 76.
135. Franco AC et al. Leaf functional traits of Neotropical savanna trees in relation to seasonal water deficit. *Trees*. 2005; 19 :326-335.
136. Frey-Klett P, Burlinson P, Deveau A, Barret M, Tarkka M, Sarniguet A. Bacterial-fungal interactions: hyphens between agricultural, clinical, environmental, and food microbiologists. *Microbiology and Molecular Biology Reviews*. 2011; 75 (4): 583-609.
137. Fuchs B, Haselwandter K. Red list plants: colonization by arbuscular mycorrhizal fungi and dark septate endophytes. *Mycorrhiza*. 2004; 14(4): 277-281.
138. Gagic M, Faville MJ, Zhang W, et al. Seed transmission of Epichloë endophytes in *Lolium perenne* is strongly influenced by host genetics. *Frontiers in Plant Sciences*. 2018; 9: 1580.
139. Gakuubi MM, Munusamy M, Liang ZX, Ng SB. Fungal Endophytes: A Promising Frontier for Discovery of Novel Bioactive Compounds. *Journal of Fungi* (Basel). 2021; 22;7(10):786. doi: 10.3390/jof7100786.
140. Gamboa MA, Laureano S, e Bayman P. Measuring endophytic fungal diversity in leaf fragments: size matters?. *Mycopathologia*. 2003; 156: 41 - 45.
141. Gamboa MA, Bayman P. Endophytic fungal communities on leaves of a tropical hardwood tree (*Guarea guidonia: Meliaceae*). *Biotropica.* 2001; 33: 352 - 360.
142. Gardes M, Bruns TD (1993). ITS *primers* with enhanced specificity for basidiomycetes--application to the identification of mycorrhizae and rusts. *Molecular Ecology*. 2(2):113-118.
143. Gashgari R, Gherbawy Y, Ameen F, Alsharari S. Molecular Characterization and Analysis of Antimicrobial Activity of Endophytic Fungi From Medicinal Plants in Saudi Arabia. *Jundishapur Journal Microbiology*. 2016; 9(1): e26157.
144. Geiser DM, Jimenez-Gasco MM, Kang S et al. FUSARIUM-ID v. 1.0: A DNA Sequence Database for Identifying *Fusarium*. *European Journal of Plant Pathology*. 2004; 110: 473 - 479.
145. Genre A, Chabaud M, Balzergue C, Puech-Pages V, et al. Short-chain chitin oligomers from arbuscular mycorrhizal fungi trigger nuclear Ca^{2+} spiking in *Medicago truncatula* roots and their production is enhanced by strigolactone. *New Phytologist. 2013;* 198:179–189.

146. Gerrits van den Ende AHG, de Hoog GS. Variability and molecular diagnostics of the neurotropic species *Cladophialophora bantiana*. *Viga Mycology. 1999;* 43: 151–162.
147. Glaeser SP, Imani J, Alabid I, Guo H, Kumar N, Kämpfer P, et al. *Rhizobium radiobacter* F4 não patogênico desenvolve atividade benéfica para as plantas independente de seu hospedeiro *Piriformospora indica*. *ISME Journal. 2016;* 10: 871–884.
148. Glass NL & Donaldson GC. Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Applied and environmental microbiology. 1995;* 61: 1323–1330.
149. Gołębiewski M, Deja-Sikora E, Cichosz M, Tretyn A, Wróbel B. Pyrosequencing analysis of 16S rDNA of the bacterial community in soils polluted with heavy metals. *Microbial Ecology*. 2014; 67: 635–647.
150. Gomes T, Pereira JA, Benhadi J, Lino-Neto T, Baptista P. Endophytic and Epiphytic Phyllosphere Fungal Communities Are Shaped by Different Environmental Factors in a Mediterranean Ecosystem. *Microbial Ecology*. 2018; 76(3): 668-679.
151. Gonçalves-Alvim, SJ, Collevatti, RG, & Fernandes, GW. Effects of genetic variability and habitat of Qualea parviflora (Vochysiaceae) on herbivory by free-feed and galling insects. *Annals of Botany*. 2004; *94* (2): 259–268.
152. Gong A, Zhou T, Xiao C, et al. Association between the level of dipsacus saponin VI and the diversity of endophytic fungi in roots of *Dipsacus asperoides*. *World of Journal Microbiology Biotechnology*. 2019; 35 (3): 42.
153. Gong A, Zhou T, Xiao C, Jiang W, Zhou Y, Zhang J, Liang Q, Yang C, Zheng W, Zhang C. Association between dipsacus saponin VI level and diversity of endophytic fungi in roots of *Dipsacus asperoides*. *World Journal of Microbiology and Biotechnology*. 2019; 35 (3): 42.
154. Gong B, Yao XH, Zhang YQ, Fang HY, Pang TC, Dong QL. A cultured endophyte community is associated with the plant *Clerodendrum inerme* and antifungal activity. *Genetic Molecular Research*. 2015;14(2):6084-6093.
155. Gough C, Cullimore J. Lipo-chitooligosaccharide signaling in endosymbiotic plant-microbe interactions. *Mol Plant Microbe Interact*. 2011; 24:867–878.
156. Guimarães DO, Borges WS, Vieira NJ, de Oliveira LF, da Silva CH, Lopes NP, Dias LG, Durán-Patrón R, Collado IG, Pupo MT. Diketopiperazines produced by endophytic fungi found in association with two *Asteraceae* species. *Phytochemistry*. 2010; 71(11-12):1423-9.
157. Gul Jan F, Hamayun M, Hussain A, et al. An endophytic isolate of the fungus *Yarrowia lipolytica* produces metabolites that ameliorate the negative impact of salt stress on corn physiology. *BMC Microbiology*. 2019; 19 (1): 3.
158. Guo DJ, Singh RK, Singh P, et al. Complete genome sequence of *Enterobacter roggenkampii* ED5, an endophytic bacterium that promotes the growth of nitrogen-fixing plants with biocontrol and stress tolerance properties, isolated from sugarcane roots. *Frontiers Microbiology*. 2020; 11: 580081.
159. Guo LD, Hyde KD, Liew ECY. Identification of endophytic fungi of *Livistona chinensis* based on morphology and rDNA sequences. *New Phytologist.* 2000; 147: 617–630.

160. Gutiérrez EE, Marinho-Filho J. The mammalian faunas endemic to the Cerrado and the Caatinga. *Zookeys*. 2017; (644):105-157.
161. Guzmán JPS, Nguyen K, Hart SC. Simple methods to remove microbes from leaf surfaces. *Journal Basic Microbiology*. 2020; 60:730–734.
162. Gweon HS, Oliver A, Taylor J, Booth T, Gibbs M, Read DS, et al. PIPITS: an automated pipeline for analyses of fungal internal transcribed spacer sequences from the *Illumina sequencing platform*. *Methods Ecology Evolution*. 2015; 6 (8): 973–80.
163. Hamzah TNT, Lee SY, Hidayat A, Terhem R, Faridah-Hanum I, Mohamed R. Diversity and Characterization of Endophytic Fungi Isolated From the Tropical Mangrove Species, *Rhizophora mucronata*, and Identification of Potential Antagonists Against the Soil-Borne Fungus, *Fusarium solani*. *Frontiers in Microbiology*. 2018; 9: 1707.
164. Hardoim PR, van Overbeek LS, Berg G, Pirttilä AM, Compant S, Campisano A, Döring M, Sessitsch A. The hidden world within plants: ecological and evolutionary considerations for defining functioning of microbial endophytes. *Microbiol Mol Biol ver.* 2015; 79(3): 293-320.
165. Hardoim PR, van Overbeek LS, Berg G, Pirttilä AM, Compant S, Campisano A, Döring M, Sessitsch A. The hidden world in plants: ecological and evolutionary considerations to define the functioning of microbial endophytes. *Microbiology and Molecular Bioliology*. 2015; 79 (3): 293–320.
166. Harrison JG, Griffin EA. The diversity and distribution of endophytes across biomes, plant phylogeny and host tissues: how far have we come and where do we go from here?. *Environmental Microbiology*. 2020; 22(6): 2107-2123.
167. Hassan SE. Plant growth promotion activities for bacterial and fungal endophytes isolated from *Teucrium polium* L medicinal plant. *Journal of Advanced Ressearch*. 2017; 8 (6): 687-695.
168. Hawksworth DL. The fungal dimension of biodiversity: Magnitude, importance and conservation. *Mycology Research.* 1991; 95: 641–655.
169. Hawksworth DL, Lücking R. Fungal diversity revisited: 2.2 to 3.8 million species. In: Heitman J, Howlett BJ, Crous PW, Stukenbrock EH, James TY, Gow NAR (eds) The Fungal Kingdom. ASM Press, Washington, DC. 2018; 79–95.
170. Hawksworth DL, Lücking R. Fungal Diversity Revisited: 2.2 to 3.8 Million Species. *Microbiology Spectrum*. 2017; 5(4): 10.1128.
171. Hebert PD, Cywinska A, Ball SL, deWaard JR. Biological identifications through DNA barcodes. *Proc Biol Sci*. 2003; 7, 270(1512):313-21.
172. Henriques RPB. Influência da história, solo e fogo na distribuição da dinâmica das fitofisionomias no bioma Cerrado. In: SCARIOT, A.; SOUSA-SILVA, J. C.; FELFILI, J. M. (Orgs.) Cerrado: ecologia, biodiversidade e conservação. Brasília: Ministério do Meio Ambiente. 2015; 73-92.
173. Hernandez-Gutierrez A, Chaves ZM, Dornelo-Silva D, Dianese JC. Additions to the cercosporoid fungi from the Brazilian Cerrado: 1. New species on hosts belonging in family Fabaceae, and reallocations of four *Stenella* species into Zasmidium. *Mycobiota*. 2015; 5: 33-64.
174. Herre EA, Bael SAV, Maynard Z, Robbins N, Bischoff J, Arnold AE, Rojas E, Mejía LC, Cordero RA, Woodward C, Kyllo DA. Tropical plants as chimeras: some implications of leaf endophytic fungi for the study of host plant

defence, physiology and genetics. In: DFRP Burslem, MA Pinard, SE Hartley, eds. Biotic interactions in the tropics. Cambridge, UK: Cambridge University Press. 2005; 226-240.

175. Herrera J, Poudel R, Bokati D. Assessment of root-associated fungal communities colonizing two tropical grass species reveals incongruity for fungal communities of native North American grasses. *Fungal Ecology.* 2013; 6: 65–69.
176. Higgins KL, Arnold AE, Miadlikowska J, Sarvate SD, Lutzoni F. Phylogenetic relationships, host affinity, and geographic structure of boreal and arctic endophytes from three major plant lineages. *Molecular Phylogenetics and Evolution*. 2007; 42(2): 543-555.
177. Hoffman MT, Arnold AE. Geographic locality and host identity shape fungal endophyte communities in cupressaceous trees. *Mycology Research*. 2008; 112(3): 331-344.
178. Holdenrieder O. Endophytes and rhizoplane fungi of Norway spruce. In: Morrison DJ, ed. Proceedings of the Seventh International Conference on Root and Butt Rots. Victoria, BC, Canada: Forestry Canada, Pacific Forestry Centre. 1989; pp 531–545.
179. Hong SB, Hye-Sun S, Hyeon-Dong F, Robert JS. Novel Neosartorya species isolated from soil in Korea. *International journal of systematic and evolutionary microbiology*. 2005; 56: 477-86. 10.1099/ijs.0.63980-0.
180. Hongsanan S, Jeewon R, Purahong W, Xie N, Liu JK, Jayawardena RS, Ekanayaka AH, Dissanayake A, Raspé O, Hyde KD, et al. Podemos usar DNA ambiental como holótipos? *Fungal Diversity*. 2018; 92: 1–30.
181. Houbraken J, Kocsubé S, Visagie CM, Yilmaz N, Wang XC, Meijer M, Kraak B, Hubka V, Bensch K, Samson RA, Frisvad JC. Classification of *Aspergillus*, *Penicillium, Talaromyces* and related genera (Eurotiales): An overview of families, genera, subgenera, sections, series and species. *Study in Mycology*. 2020; 27; 95: 5-169.
182. Houbraken J, Spierenburg H, Frisvad JC. *Rasamsonia*, a new genus comprising thermotolerant and thermophilic Talaromyces and Geosmithia species. *Antonie van Leeuwenhoek. 2012;* 101: 403–421.
183. Huang YL, Devan MM, U'Ren JM, Furr SH, Arnold AE. Invasive effects of forest fire on leaf endophytic communities in montane forest trees. *Microbial Ecology*. 2016; 71 (2): 452-468.
184. Hudler GW, Jensen-Tracy S, Banik MT. *Rhytisma americanum* sp. nov.: a previously undescribed species of *Rhytisma* on maple (Acer spp.). *Mycotaxonomy.* 1998; 68: 405–416.
185. Hurtado-McCormick V, Kahlke T., Petrou K., Jeffries T., Ralph PJ, Seymour JR (2019). Regional and Microenvironmental Scale Characterization of the Zostera muelleri Seagrass Microbiome. *Frontiers in Microbiology*. 2019;10: 1011.
186. Huusko K, Ruotsalainen AL, Markkola AM. A shift from arbuscular mycorrhizal to dark septate endophytic colonization in *Deschampsia flexuosa* roots occurs along primary successional gradient. *Mycorrhiza*. 2017; 27(2): 129-138.

187. IBGE, Censo Agropecuário. Brasil, grandes regiões e unidades da federação. Rio de Janeiro: Instituto Brasileiro de Geografia e Estatística. 2006; 777p.
188. Ibrahim M, Kaushik N, Sowemimo A, Chhipa H, Koekemoer T, van de Venter M, Odukoya AO. Antifungal and antiproliferative activities of endophytic fungi isolated from the leaves of *Markhamia tomentosa*. *Pharmaceutical Biology*. 2017; 55 (1): 590-595.
189. Ibrahim M, Oyebanji E, Fowora M, Aiyeolemi A, Orabuchi C, Akinnawo B, Adekunle AA. Extracts of endophytic fungi from leaves of selected Nigerian ethnomedicinal plants exhibited antioxidant activity. *BMC Complementary Medicine Therapies*. 2021; 21 (1): 98.
190. Ikeda A, Matsuoka S, Masuya H, Mori AS, Hirose D, Osono T. Comparison of host diversity, composition and recurrence of xylar endophytes in subtropical, cool temperate and subboreal regions in Japan. *Population Ecology.* 2014; 56: 289–300.
191. Ikram M, Ali N, Jan G, Jan FG, Khan N. Endophytic Fungal Diversity and their Interaction with Plants for Agriculture Sustainability Under Stressful Condition. *Recent Patents on Food Nutrition Agriculture*. 2020; 11(2): 115-123.
192. Imam J, Singh PK, Shukla P. Plant Microbe Interactions in Post Genomic Era: Perspectives and Applications. *Frontiers Microbiology*. 2016; 7: 1488.
193. Inácio J, Pereira P, de Carvalho M, Fonseca Á, Amaral-Collaço MT, Spencer-Martins I. Estimation and diversity of the phylloplane mycobiota in selected plants in a Mediterranean-type ecosystem in Portugal. *Microbial Ecology.* 2002; 44: 344–353.
194. Jacobs S, Zechmann B, Molitor A, et al. Broad-spectrum suppression of innate immunity is required for colonization of Arabidopsis roots by the fungus *Piriformospora indica*. *Plant Physiology*. 2011; 156(2): 726-740.
195. Jalgaonwala R. E., Mohite B. V., Mahajan R. T. A review: natural products from plant associated endophytic fungi. J. *Microbiology and Biotechnology Research.* 2017; 1: 21–32.
196. Januário LC & Vitorino AH. 2013. Resposta metabólica induzida por fungos e bactérias endofíticas em microplantas de *H. marrubioides* Epling in vitro. *Quimica Nova*. 2013; 36(7): 1014-1020.
197. Jayatilake PL, Munasinghe H. Antimicrobial Activity of Cultivable Endophytic and Rhizosphere Fungi Associated with "Mile-a-Minute," *Mikania cordata* (Asteraceae). *Biomed Research International*. 2020: 5292571.
198. Jia M, Chen L., Xin HL, et al. A friendly relationship between endophytic fungi and medicinal plants: a systematic review. *Frontiers Microbiology*. 2016; 7: 906.
199. Jin H, Yan Z, Liu Q, Yang X, Chen J, Qin B. Diversity and dynamics of fungal endophytes in leaves, stems and roots of Stellera chamaejasme L. in northwestern China. *Antonie Van Leeuwenhoek*. 2013; 104(6):949-63.
200. Joly CA, Rodrigues RR, Metzger JP, Haddad CF, Verdade LM, Oliveira MC, Bolzani VS. Ecology. Biodiversity conservation research, training, and policy in São Paulo. *Science*. 2010; 11;328(5984):1358-9.
201. Jordaan A, Taylor JE, Rossenkhan R. Occurrence and possible role of endophytic fungi associated with seed pods of *Colophospermum mopane* (Fabaceae) in Botswana. *South African Journal of Botany.* 2006; 72: 245–255.

202. Jumpponen A, Trappe JM. Dark septate endophytes: a review of fungi colonizing facultative biotrophic roots. *New Phytologist.* 1998; 140: 295 – 310.

203. Junker RR, Keller A. Microhabitat heterogeneity in leaves and flower organs promotes bacterial diversity. *FEMS Microbiology Ecology.* 2015; 91: fiv097.

204. Juybari HZ, Tajick Ghanbary MA, Rahimian H, Karimi K, Arzanlou M. Seasonal, tissue and age influences on frequency and biodiversity of endophytic fungi of *Citrus sinensis* in Iran. *For Path*. 49:e12559.

205. Kamel NM, Abdel-Motaal FF, El-Zayat SA. Endophytic fungi from the medicinal herb Euphorbia geniculata as a potential source for bioactive metabolites. *Archives of Microbiology*. 2020; 202(2): 247-255.

206. Katoch M, Paul A, Singh G, Sridhar SNC. Fungal endophytes associated with *Viola odorata* Linn. as a bioresource for pancreatic lipase inhibitors. *BMC Complementary and Alternative Medicine*. 2017B; 17 (1): 385.

207. Katoch M, Phull S, Vaid S, Singh S. Diversity, Phylogeny, anticancer and antimicrobial potential of fungal endophytes associated with *Monarda citriodora* L. *BMC Microbiology*. 2017a; 17(1):44.

208. Katoch M, Pull S. Endophytic fungi associated with *Monarda citriodora*, an aromatic and medicinal plant and their biocontrol potential. *Pharmaceutical Biology*. 2017c; 55(1): 1528-1535.

209. Kaul S, Gupta S, Ahmed M, Dhar MK. Endophytic fungi of medicinal plants: The treasure hunt for bioactive metabolites. *Phytochemistry Reviews.* 2012; 11: 487–505.

210. Kembel SW, et al. Relationships between bacterial communities of the phylosphere and functional characteristics of plants in a neotropical forest. *Proceedings of the National Academy of Sciences.* 2014; 111: 13715–13720.

211. Khalil AMA, Hassan SE, Alsharif SM, et al. Isolation and characterization of fungal endophytes isolated from the medicinal plant Ephedra pachyclada as plant growth promoters. *Biomolecules*. 2021; 11 (2): 140.

212. Khan AL, Al-Harrasi A, Al-Rawahi A, Al-Farsi Z, Al-Mamari A, Waqas M, Asaf S, Elyassi A, Mabood F, Shin JH, Lee IJ. Endophytic Fungi from Frankincense Tree Improves Host Growth and Produces Extracellular Enzymes and Indole Acetic Acid. *Plos One*. 2016; 11 (6): e0158207.

213. Khan Chowdhury MDE, Jeon J, Ok Rim S, Park YH, Kyu Lee S, Bae H. Composition, diversity and bioactivity of cultivable endophytic bacteria in mountain-grown ginseng in Korea. *Scientific Reports*. 2017; 7 (1): 10098.

214. Kirk P, Cannon P, Minter D, Stalpers J. Ainsworth and Bisby's dictionary of the Fungi, 10ª ed. Wallingford, Reino Unido: CAB International. 2008.

215. Kirk PM, Cannon PF, David JC, Stalpers JA. *Dicionário dos fungos*. Wallingford, Reino Unido: *CABI Publishing*. 2001.

216. Kiss L. Limits of nuclear ribosomal DNA internal transcribed spacer (ITS) sequences as species barcodes for Fungi. *Proceedings of the National Academy of Science USA*. 2012; 109 (27): E1811.

217. Klein HS, Luna FV. Feeding the world: Brazil's transformation into a modern agricultural economy. Cambridge University Press; Cambridge, UK. 2019.

218. Klink CA, Machado RB. Conservation of the Brazilian Cerrado. *Megadiversity.* 2005; 1(1): 147-155.

219. Klink CA, Moreira AG. The Cerrados of Brazil. Press, CU; New York, NY, USA. Past and Current Human Occupation and Land Use. 2002; 69–88.
220. Klink CA, Sato MN, Cordeiro GG, Ramos MIM. The Role of Vegetation in Water and Fire Dynamics in Cerrado Ecosystems: Implications for Management and Conservation. *Plants (Basileia)*. 2020; 9 (12): 1803.
221. Klink CA. Maned Wolf Ecology and Conservation: Multidisciplinary Perspectives. Press Cross; Boca Raton, FL, USA: 2014. Intervention Policy in the Savannas of the Cerrado of Brazil: Land Use Changes and Conservation Effects. 2014; 293–308.
222. Kluting K, Clemmensen K, Jonaitis S, Vasaitis R, Holmström S, Finlay R, Rosling A (2019). Distribution patterns of fungal taxa and inferred functional traits reflect the non-uniform vertical stratification of soil microhabitats in a coastal pine forest. *FEMS Microbiology Ecology*. 2019; 95 (11): fiz149.
223. Knapp DG, Kovács GM. Interspecific metabolic diversity of root-colonizing endophytic fungi revealed by enzyme activity tests. *FEMS Microbiology Ecology*. 2016; 92(12): fiw190.
224. Knapp DG, Németh JB, Barry K, et al. Comparative genomics provides lifestyle insights and reveals the functional heterogeneity of dark-septate endophytic fungi. *Scientific Reports*. 2018; 8 (1): 6321.
225. Knief C. Analysis of plant microbe interactions in the era of next generation sequencing technologies. *Frontiers in Plant Science*. 2014; 5: 216.
226. Koch RA, DJ Lodge, Sourell S, Nakasone K, McCoy AG, Aime MC. Tying loose threads: revised taxonomy and phylogeny of a bird-dispersed neotropical rhizomorph-forming fungus. *Mycological Progress*. 2018; 17: 989–998.
227. Koch RA, Wilson AW, Séné O, Henkel TW, Aime MC. Resolved phylogeny and biogeography of the root pathogen *Armillaria* and its gasteroid relative, Guyanagaster. *BMC Evolution Biology*. 2017; 17(1): 33.
228. Kogel KH, Franken P, Hückelhoven R. Endophyte or parasite--what decides?. *Current Opinion in Plant Biology*. 2006; 9(4): 358-363.
229. Koljalg U., Nilsson RH, Abarenkov K. Towards a unified paradigm for sequence-based identification of fungi. *Molecular Ecology. 2013;* 22: 5271–5277.
230. Kowal J, Arrigoni E, Serra J, Bidartondo M. Prevalence and phenology of fine root endophyte colonization across populations of *Lycopodiella inundata*. *Mycorrhiza.* 2020; 30(5): 577-587.
231. Kumar S, Carlsen T, Mevik BH, Enger P, Blaalid R, Shalchian-Tabrizi K, et al. CLOTU: an online pipeline for processing and clustering of 454 amplicon reads into OTUs followed by taxonomic annotation. *BMC Bioinformatics*. 2011; 12: 182.
232. Kusari S., Lamshöft M., Spiteller M. *Aspergillus fumigatus* Fresenius, an endophytic fungus of *Juniperus communis* L. Horstmann as a new source of the anticancer prodrug deoxypodophyllotoxin. *Journal of Applied Microbiology.* 2009; 107: 1019–1030.
233. Lanfranco L, Fiorilli V, Gutjahr C. Partner communication and role of nutrients in the arbuscular mycorrhizal symbiosis. *New Phytologist*. 2018; 220(4): 1031-1046.

234. Larkin BG, Hunt LS, Ramsey PW. Leaf nutrients shape endophytic fungal communities in white pine (*Pinus monticola*) with implications for white-tailed deer herbivory. *Fungal Ecology.* 2012; 5: 252–260.
235. Latz MAC, Kerrn MH, Sørensen H, et al. Succession of the fungal endophytic microbiome of wheat is dependent on tissue-specific interactions between host genotype and environment. *Science Total Environmental*. 2021; 759: 143804.
236. Lau MK, Arnold AE, Johnson NC. Factors influencing foliar fungal endophyte communities in riparian woody plants. *Fungal Ecology*. 2013; 6: 365–378.
237. Leia DJ, Ducket JG, Francis R, Ligron R, Russell A. Associations of symbiotic fungi in 'lower' land plants. *Philosophical Transactions of the Royal Society London B: Biological Sciences*. 2000; 355 (1398): 815-831.
238. Lenza E & Klink CA. Comportamento fenológico de espécies lenhosas em um cerrado sentido restrito de Brasília, DF. *Revista Brasileira de Botânica.* 2006; 29 (4): 627-638.
239. Li HL, Ma B, Zhang XL, et al. Diversity of culturable endophytic fungi of common reed (*Phragmites australis*) in coastal wetland *Ying, Yong Sheng Tai Xue Bao*. 2016B; 27(7): 2066-2074.
240. Li HY, Wei DQ, Shen M, Zhou ZP. Endophytes and their role in phytoremediation. *Fungal Diversity.* 2012; 54: 11–18.
241. Li JL, Sun X, Chen L, Guo LD. Endophytic fungal community structure of four mangrove species in southern China. *Mycology. 2016A;* 7: 180–190.
242. Li JL, Sun X, Zheng Y, Lü PP, Wang YL, Guo LD. Diversity and community of culturable endophytic fungi from stems and roots of desert halophytes in northwest China. *MycoKeys*. 2020; 62:75-95.
243. Li P, Wu Z, Liu T, Wang Y. Biodiversity, Phylogeny and Antifungal Functions of Endophytic Fungi Associated with *Zanthoxylum bungeanum*. *International Journal of Molecular Sciences*. 2016b; 17 (9): 1541.
244. Li XJ, Zhang Q, Zhang AL, Gao JM. Metabolites from *Aspergillus fumigatus*, an endophytic fungus associated with *Melia azedarach*, and their antifungal, antifeedant, and toxic activities. *Journal Agricultural and Food Chemistry*. 2012; 60(13): 3424-3431.
245. Lindahl BD, Nilsson RH, Tedersoo L et al. Fungal community analysis by high-743 throughput sequencing of amplified markers – a user's guide. *New Phytology*. 2013; 199: 288–299.
246. Lisboa HC, Biasetto CR, de Medeiros JB, Âraújo AR, Silva DH, Teles HL, Trevisan HC. Esterase-producing endophytic fungi: in vitro evaluation of enzymatic activity using a pH indicator. *Brazilian Journal Microbiology*. 2014; 44 (3): 923-6.
247. Liu H, Carvalhais LC, Crawford M, et al. Internal plant values: Diversity, colonization and benefits of endophytic bacteria. *Frontiers Microbiology*. 2017; 8: 25-52.
248. Liu H, Wu M, Liu J, Qu Y, Gao Y, Ren A. Tripartite Interactions Between Endophytic Fungi, Arbuscular Mycorrhizal Fungi, and *Leymus chinensis*. *Microbial Ecology*. 2020; 79(1): 98-109.

249. Liu J, Zhang J, Li D, Xu C, Xiang X. Differential responses of arbuscular mycorrhizal fungal communities to mineral and organic fertilization. *Microbiologyopen*. 2020; 9 (1): e00920.
250. Liu YJ, Whelen S & Hall BD. Phylogenetic relationships among ascomycetes: evidence from an RNA polymerse II subunit. *Molecular Biology and Evolution. 1999;* 16: 1799-1808.
251. Losos J. B. Phylogenetic niche conservatism, phylogenetic signal and the relationship between phylogenetic relatedness and ecological similarity among species. *Ecology Letters 2008;* 11: 995–1003.
252. Lücking R, Aime MC, Robbertse B, et al. Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal DNA barcoding?. *IMA Fungus*. 2020; 11: 14.
253. Lugo MA, Menoyo E, Allione LR, Negritto MA, Henning JA, Anton AM. Arbuscular mycorrhizas and dark septate endophytes associated with grasses from the *Argentine Puna. Mycologia*. 2018; 110(4): 654-665.
254. Lumbsch HT, Huhndorf SM. Myconet Vol 14. Part One. Ascomycota Sketch - 2009. Part Two. Notes on the systematics of Ascomycete. Nos. 4751-5113 . Fieldiana Life and Earth Sciences. 2010; 1-64.
255. Lundberg DS, Lebeis SL, Paredes SH, et al. Defining the core *Arabidopsis thaliana* root microbiome. *Nature*. 2012; 488: 86 - 90.
256. Lyu D, Msimbira LA, Nazari M, Antar M, Pagé A, Shah A, Monjezi N, Zajonc J, Tanney CAS, Backer R, Smith DL. The Coevolution of Plants and Microbes Underpins Sustainable Agriculture. Microorganisms. 2021; 12;9(5):1036.
257. Ma Z, Zhu L, Song T, et al. A paralogous decoy protects *Phytophthora sojae* apoplastic effector PsXEG1 from a host inhibitor. *Science*. 2017; 355(6326): 710-714.
258. Machado RB, Aguiar LMS, Castro AAJF, Nogueira CC & Ramos-Neto MB. Caracterização da fauna e flora do Cerrado. In,Savanas: desafios e estratégias para o equilíbrio entre sociedade, agronegócio e recursos naturais. EMBRAPA ed., Brasília, DF. 2008; p, 284–300
259. Machado RB., et al. Caracterização da fauna e flora do cerrado. In: FALEIRO, F. G.; FARIA NETO, A. L. (Ed.) Savanas: desafios e estratégias para o equilíbrio entre sociedade, agronegócio e recursos naturais. Planaltina, DF: Embrapa Cerrados; Brasília, DF: Embrapa Informação Tecnológico. 2008; p. 285-300.
260. Maharachchikumbura SS, Hyde KD, Jones EG, McKenzie EHC, Bhat JD, Dayarathne MC, et al. Families of sordariomycetes. *Fungal Diversity*. 2016; 79 1–317.
261. Man B, Wang H, Xiang X, Wang R, Yun Y, Gong L. Phylogenetic diversity of culturable fungi in the Heshang Cave, central China. *Frontiers in Microbiology*. 2015; 21(6): 1158.
262. Mandyam K, Jumpponen A. Looking for the elusive function of dark septate endophytic root colonizing fungi*. Mycology.* 2005; 53: 173–189.
263. Mandyam K, Jumpponen A. Seasonal and temporal dynamics of arbuscular mycorrhizal and dark septate endophytic fungi in a tallgrass prairie ecosystem are minimally affected by nitrogen enrichment. *Mycorrhiza.* 2008; 18(3): 145-155.

264. Manganyi MC, Ateba CN. Untapped Potentials of Endophytic Fungi: A Review of Novel Bioactive Compounds with Biological Applications. *Microorganisms*. 2020; 8(12): 1934.
265. Manzotti A, Bergna A, Burow M, et al. Insights into the community structure and lifestyle of tomato fungal root endophytes, combining amplicon sequencing and isolation approaches with phytohormone profiles. *FEMS Microbiology Ecology.* 2020; 96 (5): fiaa052.
266. Maracahipes-Santos L, Lenza E, Santos JO, Mews HA, Oliveira B. Effects of soil and space on the woody species composition and vegetation structure of three Cerrado phytophysiognomies in the Cerrado-Amazon transition. *Brazilian Journal Biology*. 2017; 77(4): 830-839.
267. Martín JA, Witzell J, Blumenstein K, et al. Dutch elm disease resistance reduces the presence of endophytic xylem fungi in elm trees (*Ulmus* spp.). *Plos one*. 2013; 8 (2): e56987.
268. Martin R, Gazis R, Skaltsas D, Chaverri P, Hibbett D. Unexpected diversity of basidiomycete endophytes in sapwood and Hevea leaves. *Mycologia.* 2015; 107: 284–297.
269. Masclaux F, Guého E, de Hoog R. Christen Phylogenetic relationships of human-pathogenic *Cladosporium* (Xylohypha) species inferred from partial LS rRNA sequences. *Journal of Medical and Veterinary Mycology*. 1995; 33, 5: 327–338.
270. Massimo NC, Devan MMN, Arendt KR, et al. Fungal endophytes in aboveground tissues of desert plants: infrequent in culture, but highly diverse and distinct symbionts. *Microbial Ecology.* 2015; 70: 61–76.
271. Materatski P, Varanda C, Carvalho T, et al. Spatial and temporal variation of fungal endophytic richness and diversity associated to the phyllosphere of olive cultivars. *Fungal Biology*. 2019; 123(1): 66-76.
272. Mazzolin LP et al. Antidiarrheal and intestinal antiinflammatory activities of a methanolic extract of *Qualea parviflora* Mart. in experimental models. *Journal of Ethnopharmacology*. 2013; 150: 1016-1023.
273. Mazzolin LP et al. *Qualea parviflora* Mart.: An integrative study to validate the gastroprotective, antidiarrheal, antihemorragic and mutagenic action. *Journal of Ethnopharmacology*. 2010; 127: 508-514.
274. McGuire KL, Fierer N, Bateman C, Treseder KK, Turner BL. Fungal community composition in neotropical rain forests: the influence of tree diversity and precipitation. *Microbial Ecology*. 2012; 63(4): 804-812.
275. Mefteh FB, Daoud A, Chenari Bouket A, et al. Fungal root microbiome of palms with healthy, brittle leaves (*Phoenix dactylifera* L.) reveals a hidden and untapped arsenal of antibacterial and broad-spectrum antifungal secondary metabolites. *Frontiers Microbiology*. 2017; 8: 307.
276. Mendes MAS, et al. Fungos em plantas no Brasil. EMBRAPA. 1998; 555p.
277. Mendonça R, Felfili B, Walter JC, Silva Jr, Rezende A T. Filgueiras & P. Nogueira. 1998. Flora vascular do Cerrado. In: S. Sano & S. Almeida (eds.). Cerrado. Ambiente e flora. pp. 288-556. Empresa Brasileira de Pesquisa Agropecuária – Embrapa - Cerrados, Planaltina, Brasil.

278. Milner ML, Rossetto M, Crisp MD, Weston PH. The impact of multiple biogeographic barriers and hybridization on species-level differentiation. *American Journal of Botany*. 2012; 99 (12): 2045-2057.
279. Miranda JCC & Miranda LN. Micorriza arbuscular. In: VARGAS, M.A. & HUNGRIA, M., eds. Biologia dos solos dos Cerrados. Planaltina, Embrapa-CPAC. 1997. p.69-123.
280. Miranda JCC, Vilela L. & Miranda LN. Dynamics and contribution of arbuscular mycorrhiza in production systems with crop rotation. Brazilian Agricultural Research. 2005; 40:1005-1014.
281. Miranda JCC. Cerrado: Arbuscular mycorrhiza, occurrence and management. Planaltina, Embrapa Cerrados. 2008; 169.
282. Mishra A, Gond SK, Kumar A, Sharma VK, Verma SK, Kharwar RN, Sieber TN. Season and tissue type affect fungal endophyte communities of the Indian medicinal plant *Tinospora cordifolia* more strongly than geographic location. *Microbial Ecology*. 2012; 64(2):388-98.
283. Mitter B, Petric A, Shin MW, Chain PS, Hauberg-Lotte L, Reinhold-Hurek B, et al. Comparative genome analysis of *Burkholderia phytofirmans* PsJN reveals a broad spectrum of endophytic lifestyles based on interaction strategies with host plants. *Frentiers in Plant Science. 2013;* 4: 120.
284. Moreira IC, Carvalho MG, Bastos ABFO, Braz-Filho R. A flavone dimer from *Ouratea hexasperma*. *Phytochemistry*. 1999; 51: 833-838.
285. Moricca S, Ragazzi A. Fungal endophytes in Mediterranean oak forests: a lesson from *Discula quercina*. P*hytopathology*. 2008; 98(4): 380-386.
286. Moura JB. Diversidade e colonização micorrízica em diferentes usos do solo no cerrado. Tese de doutorado, Universidade de Brasília, Brasília, Brasil. 2015.
287. Mourad EF, Sarhan MS, Daanaa HA, et al. Plant Materials are Sustainable Substrates Supporting New Technologies of Plant-Only-Based Culture Media for in vitro Culturing of the Plant Microbiot. *Microbes Environmental*. 2018; 33 (1): 40-49.
288. Mueller B., Mueller C. The political economy of the Brazilian model of agricultural development: Institutions versus sectoral policy. *The Quarterly Review Economics Finance.* 2016; 62: 12–20
289. Muhsin TM, Booth T. Fungi associated with halophytes of a interior salt marsh, Manitoba, Canada. *Canadian Journal of Botany.* 1987; 65: 1137–1151.
290. Myers N, Mittermier RA, Mittermier CG, et al. Biodiversity hotspots for conservation 500 priorities. *Nature*. 2000; 403(24): 853–858.
291. Naranjo-Ortiz MA, Gabaldón T. Fungal evolution: major ecological adaptations and evolutionary transitions. *Biological Reviews the Cambridge Philosophical Society*. 2019; 94(4): 1443-1476.
292. Nimer E, Brandão AMPM. Balanço hídrico e clima da região dos Cerrados. Rio de Janeiro: IBGE, 1989.
293. Nisa H, Kamili AN, Nawchoo IA, Shafi S, Shameem N, Bandh SA. Fungal endophytes as prolific source of phytochemicals and other bioactive natural products: A review. *Microbial Pathogenesis*. 2015; 82: 50-9.

294. Nishad R, Ahmed T, Rahman VJ, Kareem A. Modulation of Plant Defense System in Response to Microbial Interactions. *Frontiers Microbiology*. 2020; 11: 1298.
295. Nóbrega RLB, Guzha AC, Lamparter G, et al. Impacts of land-use and land-cover change on stream hydrochemistry in the Cerrado and Amazon biomes. *Science Total Environmental*. 2018; 635: 259-274.
296. Nóbrega RLB, Guzha AC, Torres GN, et al. Effects of converting native cerrado vegetation into pasture on soil hydrophysical properties, evapotranspiration and river flow in the Amazon agricultural frontier. *Plos one*. 2017; 12 (6): e0179414.
297. Noriler SA, Savi DC, Aluizio R, Palácio-Cortes AM, Possiede YM, Glienke C. Bioprospection and community structure of fungal endophytes found in the Brazilian, Pantanal and Cerrado biomes. *Frontiers Microbiology*. 2018; 9: 1526.
298. Noriler SA, Savi DC, Ponomareva LV et al. Vochysiamides A and B: Two new bioactive carboxamides produced by the new species Diaporthe vochysiae. *Phytotherapy*. 2019; 138: 104273. doi: 10.1016 / j.fitote.2019.104273.
299. Novaes RM, Ribeiro RA, Lemos-Filho JP, Lovato MB. Agreement between phylogeographic and biogeographic patterns in the Brazilian Cerrado: diversification of the endemic tree *Dalbergia miscolobium* (Fabaceae). *Plos one*. 2013; 8 (12): e82198.
300. O'Donnell K, Kistler HC, Cigelnik E and Ploetz RC. Multiple evolutionary origins of the fungus causing Panama disease of banana: Concordant evidence from nuclear and mitochondrial gene genealogies. *Proceedings of the National Academy of Sciences of the United States of America*. 1998; 95: 2044–2049.
301. O'Dell TE, Massicotte HB, Trappe JM. Root colonization of Lupinus latifolius Agardh. and Pinus contorts Dougl. by Phialocephala fortinii Wang & Wilcox. *New Phytologist.* 1993; 124: 93 – 100.
302. O'Donnell K. " *Fusarium* and its new relatives", in *The Fungal Holomorph:* Mitotic, Meiotic and Pleomorphic Speciation *in Fungal Systematics* , eds Reynolds DR, Taylor JW Wallingford: CAB International. 1993; 225–233.
303. Ohm RA, Feau N, Henrissat B, et al. Diverse lifestyles and plant pathogenesis strategies encoded in the genomes of eighteen *Dothideomycetes* fungi. *Plos Pathogens*. 2012; 8 (12): e1003037.
304. Oita S, Ibáñez A, Lutzoni F, et al. Climate and seasonality drive the richness and composition of tropical fungal endophytes at a landscape scale. *Communications Biology*. 2021; 4(1): 313.
305. Oki, Yumi et al. Efeito do fertilizante CO2 no crescimento, polifenóis e endófitos em duas espécies de *Baccharis*. Arquivos Brasileiros de Biologia e Tecnologia. 2020.
306. Oliveira CM, et al. Dihydroisocoumarins produced by *Xylaria* sp and *Penicillium* sp., endophytic fungi associated with *Piper aduncum* and *Alibertia macrophylla*. *Phytochemistry Letters*. 2011; 4 (2): 93-96.
307. Oliveira CM, Regasini LO, Silva GH, Pfenning LH, et al. Dihydroisocoumarins produced by *Xylaria* sp. and *Penicillium* sp., endophytic fungi associated

with *Piper aduncum* and *Alibertia macrophylla*. *Phytochemistry Letters*. 2011; 4(2): 93-96.

308. Oliveira DM, Pereira CB, Mendes G, et al. Two new usnic acid derivatives from the endophytic fungus *Mycosphaerella* sp.. *Naturforsch CJ Bioscience*. 2018; 73 (11-12): 449-455.
309. Oliveira Filho AT, Ratter JA. Plant physiognomies and woody flora of the Cerrado biome In: Oliveira PS, Marquês RJ, editors. The Cerrados of Brazil: ecology and natural history of a neotropical savanna. Nova York: Columbia University Press; 2002. 91-120.
310. Oliveira PE. Fenologia e biologia reprodutiva das espécies de Cerrado. In Cerrado: ambiente e flora. (S. M. Sano & S.P. Almeida, eds.). EMBRAPA - Cerrados, Planaltina. 2008; p.169-188.
311. Oliveira RS, et al. Deep root function in soil water dynamics in cerrado savannas of central Brazil. *Functional Ecology*. 2005; 19(4):574-581.
312. Oliveira-Filho AT & Martins FR. A comparative study of five cerrado areas in southern Mato Grosso, Brazil. *Edinburgh Journal of Botany*. 1991; 48(3):307–332.
313. Oliveira-Filho AT, Shepherd GJGJ, Martins FR, Stubblebine WH & Shephered GJ. Environmental factors affecting physiognomic and floristic variation in an area of cerrado in central Brazil. *Journal of Tropical Ecology*. 1989 5(4):413–431.
314. Oliveira-Filho AT. Estudo florístico e fitossociológico em um cerrado na Chapada dos Guimarães - Mato Grosso - uma análise de gradiente. Universidade Estadual de Campinas. 1984.
315. Olmo-Ruiz MD, Arnold AE. Interannual variation and host affiliations of endophytic fungi associated with ferns at La Selva, Costa Rica. *Mycologia*. 2014; 106(1): 8-21.
316. Oono R, Lefèvre E, Simha A, Lutzoni F. A comparison of the community diversity of foliar fungal endophytes between seedling and adult loblolly pines (Pinus taeda). *Fungal Biology*. 2015; 119(10): 917-928.
317. Ori F, Leonardi M, Faccio A, et al. Synthesis and ultrastructural observation of arbutoid mycorrhizae of black truffles (Tuber melanosporum and T. aestivum). *Mycorrhiza*. 2020; 30(6): 715-723.
318. Osono T. Endophytic and epiphytic phyllosphere fungi of red-wicker dogwood (*Cornus stolonifera*) in British Columbia. *Mycoscience.* 2007; 48: 47–52.
319. Padovan MP, et al. Pioneer native tree species in biodiverse agroforestry systems. Ver. *GeoPantanal*. 2018; 24: 53-68.
320. Pagotto TCS, et al. Bioma cerrado e área estudada. In: PAGOTTO, T. C. S.; SOUZA, P. R. Biodiversidade do complexo Aporé-Sucuriú: subsídios à conservação e ao manejo do cerrado: área prioritária 316-Jauru. Campo Grande: UFMS, 2006. p. 18-30.
321. Pan XX, Yuan MQ, Xiang SY, et al. The symbioses of endophytic fungi shaped the metabolic profiles in grape leaves of different varieties. *Plos One*. 2020; 15(9): e0238734.
322. Panchen ZA, Primack RB, Gallinat AS, et al. Substantial variation in leaf senescence times among 1360 temperate woody plant species: implications

for phenology and ecosystem processes. *Annal Botany*. 2015; 116 (6): 865-873.

323. Pang KL, Guo SY, Chen IA, Burgaud G, et al. Insights into fungal diversity of a shallow-water hydrothermal vent field at Kueishan Island, Taiwan by culture-based and metabarcoding analyses . *Plos One*. 2019; 14 (12): e0226616.
324. Pang Z, Chen J, Wang T, et al. Linking Plant Secondary Metabolites and Plant Microbiomes: A Review. *Frontiers in Plant Science*. 2021; 12: 621276.
325. Park YH, et al. Screening and characterization of endophytic fungi from *Panax ginseng* Meyer for biocontrol activity against ginseng pathogens. *Biol. Ao controle.* 2015; 91: 71–81.
326. Park YH, Kim Y, Mishra RC, Bae H. Endophytes of fungi inhabiting mountain cultivated ginseng (*Panax ginseng* Meyer): Diversity and biocontrol activity against ginseng pathogens. *Scientific Reports*. 2017; 7(1): 16221.
327. Park YH, *et al*. Diversity of fungal endophytes in various tissues of panax ginseng meyer cultivated in Korea. *Journal Ginseng Res*. 2012; 36.
328. Parthasarathy R, Sathiyabama M. Gymnemagenin-producing endophytic fungus isolated from a medicinal plant *Gymnema sylvestre* R.Br. *Appl Biochemistry and Biotechnology*. 2014; 172(6): 3141-3152.
329. Passos MM. THE CLIMATE-VEGETATION RELATIONSHIP IN THE BRAZILIAN SEMI-ARID: bioclimatic approach to the Caatinga/Cerrado contact in the Middle São Francisco valley – Semi-arid region of the Brazilian Northeast. *Rev. Esp. em Rev*. 2020; 22 (1): 42-60.
330. Paszkowski U. Mutualism and parasitism: the yin and yang of plant symbioses. *Current Opinion in Plant Biology*. 2006;9(4): 364-370.
331. Pedrero-Méndez A, Insuasti HC, Neagu T, Illescas M, Rubio MB, Monte E, Hermosa R. Why Is the Correct Selection of *Trichoderma* Strains Important? The Case of Wheat Endophytic Strains of T. harzianum and T. simmonsii. J Fungi (Basel). 2021;17;7(12):1087.
332. Peterson SW. Phylogenetic analysis of *Aspergillus* species using DNA sequences from four *loci*. *Mycologia*. 2008; 100(2): 205-26.
333. Pietro-Souza W, Mello IS, Vendruscullo SJ et al. Endophytic fungal communities of *Polygonum acuminatum* and *Aeschynomene fluminensis* are influenced by soil mercury contamination. *Plos One*. 2017; 12 (7): e0182017.
334. Pietro-Souza W, Mello IS, Vendruscullo SJ et al. Endophytic fungal communities of *Polygonum acuminatum* and *Aeschynomene fluminensis* are influenced by soil contamination with mercury. *Plos One*. 2017; 12 (7): e0182017.
335. Pilon NAL. et al. Phenological patterns of 111 Cerrado species under cultivation conditions. *Hoehnea*. 2015. 42(3): 425-443.
336. Pinski A, Betekhtin A, Hupert-Kocurek K, Mur LAJ, Hasterok R. Defining the Genetic Basis of Plant⁻Endophytic Bacteria Interactions. *International Journal Molecular and Science*. 2019; 20 (8): 1947.
337. Pires TL, Lange D, Del-Claro K. Witches’ brooms increases arthropod-plant interactions in *Ouratea hexasperma* (Baill.) (Ochnaceae). *Acta Oecologica*. 2020; 102: 103508.
338. Põlme S, Bahram M, Jacquemyn H, Kennedy P, Kohout P, Moora M, Oja J, Öpik M, Pecoraro L, Tedersoo L. Host preference and network properties in

biotrophic plant-fungal associations. *New Phytologist.* 2018; 217(3):1230-1239.

339. Porras-Alfaro A, Raghavan S, Garcia M, Sinsabaugh RL, Natvig DO, Lowrey TK. Endophytic fungal symbionts associated with gypsophilic plants. *Botany.* 2014; 92: 295–301.
340. Prieto P, Navarro-Raya C, Valverde-Corredor A, et al. Process of colonization of olive tissues by Verticillium dahliae and its interaction in planta with the biocontrol root endophyte *Pseudomonas fluorescens* PICF7. *Microbiology Biotechnology.* 2009; 2 (4): 499-511.
341. Protasio TP et al. 2014. Canonical correlation analysis of the characteristics of charcoal from *Qualea parviflora* Mart. *Cerne*. 2014;.20: 81-88.
342. Provorov NA. [Plant-microbe symbioses as an evolutionary continuum]. *Zh Obshch Biologii*. 2009;70(1):10-34.
343. Pudasaini S, Wilson J, Ji M, et al. Microbial Diversity of Browning Peninsula, Eastern Antarctica Revealed Using Molecular and Cultivation Methods. *Frontiers Microbiology*. 2017; 8: 591.
344. Pudasaini S, Wilson J, Ji M, et al. Microbial Diversity of Browning Peninsula, Eastern Antarctica Revealed Using Molecular and Cultivation Methods. *Frontiers Microbiology*. 2017; 8: 591.
345. Püschel D, Janoušková M, Hujslová M, Slavíková R, Gryndlerová H, Jansa J. Plant-fungus competition for nitrogen erases mycorrhizal growth benefits of *Andropogon gerardii* under limited nitrogen supply. *Ecology and Evolution*. 2016; 6(13): 4332-4346.
346. Qadri M, Rajput R, Abdin MZ, Vishwakarma RA, Riyaz-Ul-Hassan S. Diversity, molecular phylogeny, and bioactive potential of fungal endophytes associated with the Himalayan blue pine (*Pinus wallichiana*). *Microbiology Ecology*. 2014; 67(4): 877-887.
347. Rai M, Agarkar G. Plant-fungal interactions: What triggers the fungi to switch among lifestyles?. *Critical Reviews Microbiology*. 2016; 42(3): 428-438.
348. Rajala T, Velmala SM, Tuomivirta T, Haapanen M, Müller M, Pennanen T. Endophyte communities vary in the needles of Norway spruce clones. *Fungal Biology*. 2013; 117(3):182-190.
349. Rampelotto PH, de Siqueira Ferreira A, Barboza AD, Roesch LF. Changes in diversity, abundance, and structure of soil bacterial communities in Brazilian Savanna under different land use systems. *Microbial Ecology*. 2013; 66(3): 593-607.
350. Rana KL, Kour D, Kaur T, et al. Endophytic microbes: biodiversity, plant growth-promoting mechanisms and potential applications for agricultural sustainability. *Antonie Van Leeuwenhoek*. 2020; 113(8): 1075-1107.
351. Rashmi M, Kushveer JS, Sarma VV. A worldwide list of endophytic fungi with notes on ecology and diversity. *Mycosphere*. 2019, 10(1): 798–1079.
352. Ratter JA & Dargie TCD. An analysis of the floristic composition of 26 Cerrado ares in 517 Brazil. *Edinburgh Journal of Botany*. 1992; 49(02):235.
353. Ratter JA, Bridgewater S & Ribeiro JF. Analysis of the Floristic Composition of the Brazilian Cerrado Vegetation III: Comparison of the Woody Vegetation of 376 Areas. *Edinburgh Journal of Botany*. 2003; 60(01): 57–109.

354. Ratter JA, Bridgewater S, Atkinson R & Ribeiro JF. Analysis of the floristic composition of the Brazilian cerrado vegetation II: Comparison of the woody vegetation of 98 areas. *Edinburgh Journal of Botany*. 1996; 53(02): 153.
355. Ratter JA, Bridgewater S, Ribeiro JF, et al. Analysis of the floristic composition of the Brazilian cerrado vegetation IV: Presentation of a Revised Data-Base of 367 Areas. (http://cerrado.rbge.org.uk/cerrado/download/download.php).
356. Réblová M, Miller AN, Rossman AY, et al. Recomendações para nomes genéricos com tipificação sexual assexuada em Sordariomycetes (exceto Diaporthales, Hypocreales e Magnaporthales). IMA Fungus. Junho de 2016; 7 (1): 131-53.
357. Redford AJ, Bowers RM, Knight R, Linhart Y, Fierer N. The ecology of the phylosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. *Environmental Microbiology.* 2010; 12: 2885–2893.
358. Reissinger A, Vilich V e Vsikora RA. Detection of fungi in planta: effectiveness of surface sterilization methods. *Mycology*. 2001; 105(5): 563- 566.
359. Richards TA, Leonard G, Wideman JG. What Defines the "Kingdom" Fungi? Microbiol Spectr. 2017; 5(3).
360. Richards TA, Soanes DM, Foster PG, Leonard G, Thornton CR, Talbot NJ. Phylogenomic analysis demonstrates a pattern of rare and ancient horizontal gene transfer between plants and fungi. *Plant Cell*. 2009; 21(7):1897-911.
361. Rimington WR, Pressel S, Duckett JG, Field KJ, Read DJ, Bidartondo MI. Ancient plants with ancestral fungi: liverworts associated with early divergent arbuscular mycorrhizal fungi. *Proc Biol Sei Journal scientific*. 2018; 285 (1888): 20181600.
362. Rodrigues KF. The leaf endophytic fungi of the Amazonian palm *Euterpe oleracea*. *Mycologia*. 1994; 86: 376–385.
363. Rodriguez RL. Fungos endofiticos associados à *Vellozia compacta* Mart. ex Schult. F. (*Velloziaceae*) presente em afloramentos rochosos nos estados de Minas Gerais e Tocantins. Dissertação (Mestrado em Ecologia de Biomas Tropicais) Universidade Federal de Ouro Preto, Ouro Preto, Minas Gerais, Brasil. 2010.
364. Roitman I, Bustamante MMC, Haidar RF, et al. Optimizing savanna forest biomass estimates at different spatial scales in the Brazilian Cerrado: Re-evaluating allometric equations and environmental influences. *Plos One*. 2018; 13 (8): e0196742.
365. Rojas EC, Sapkota R, Jensen B, et al. *Fusarium* head rust modifies endophytic fungal communities during wheat ear infection. *Microbiology Ecology*. 2020; 79 (2): 397-408.
366. Romão-Dumaresq AS, Dourado MN, Fávaro LC, Mendes R, Ferreira A, Araújo WL. Diversity of Cultured Fungi Associated with Conventional and Transgenic Sugar Cane and the Interaction between Endophytic *Trichoderma virens* and the Host Plant. *Plo O*ne. 2016; 11 (7): e0158974.
367. Ruiz Gómez FJ, Navarro-Cerrillo RM, Pérez-de-Luque A, Oβwald W, Vannini A, Morales-Rodríguez C. Assessment of functional and structural changes of soil fungal and oomycete communities in holm oak declined dehesas through metabarcoding analysis . *Scientific Reports.* 2019; 9 (1): 5315.

368. Rutter BD, Innes RW. Extracellular vesicles as key mediators of plant-microbe interactions. *Current Opin Plant Biology. 2018;* 44:16–22.
369. Sagita R, Quax WJ, Haslinger K. Current State and Future Directions of Genetics and Genomics of Endophytic Fungi for Bioprospecting Efforts. *Frontiers Bioengineering and Biotechnology*. 2021; 15(9): 649906.
370. Sagita R, Quax WJ, Haslinger K. Current Status and Future Directions of Endophytic Fungal Genetics and Genomics for Bioprospecting Efforts. *Frontiers in Bioengineering Biotechnology*. 2021; 9: 649906.
371. Sahoo S, Sarangi S, Kerry RG. Bioprospection of Endophytes for Agricultural and Environmental Sustainability. *Microbial Biotechnology*. 2017; 429-458.
372. Saijo Y, Loo EP, Yasuda S. Pattern recognition receptors and signaling in plant-microbe interactions. *Plant Journal. 2018;* 93(4):592-613.
373. Saikkonen K, Wäli P, Helander M, Faeth SH. Evolution of endophyte-plant symbioses. *Trends Plant Sci*ence. 2004; 9(6):275-280.
374. Saldierna Guzmán JP, Nguyen K, Hart SC. Simple methods to remove microbes from leaf surfaces. *Journal of Basic Microbiology*. 2020; 60(8):730-734.
375. Saldierna Guzmán JP, Nguyen K, Hart SC. Simple methods to remove microbes from leaf surfaces. *Journal of Basic Microbiology*. 2020; 60(8):730-734.
376. Samson RA, Visagie CM, Houbraken J, Hong SB, Hubka V, et al. Phylogeny, identification and nomenclature of the genus *Aspergillus*. *Stud Mycol*ogy. 2014; 78:141-73.
377. Sanabria NM, Huang JC, Dubery IA. Auto / não-percepção em plantas na imunidade e defesa inatas. *Self Nonself*. 2010; 1 (1): 40-54.
378. Sandberg DC, Battista LJ, Arnold AE. Fungal endophytes of aquatic macrophytes: diverse host-generalists characterized by tissue preferences and geographic structure. *Microbiology Ecology*. 2014; 67(4):735-747.
379. Sano EE, Rodrigues AA, Martins ES, et al. Cerrado ecoregions: A spatial framework to assess and prioritize Brazilian savanna environmental diversity for conservation. *Journal Environmental Manage*. 2019; 232:818-828.
380. Sano EE, Rosa R, Brito JL, Ferreira LG. Land cover mapping of the tropical savanna region in Brazil. *Environmental Monitoring and Assessment*. 2010;166(1-4):113-124.
381. Santamaria J, Bayman P. Fungal epiphytes and endophytes of coffee leaves (*Coffea arabica*). *Microbiology Ecology*. 2005; 50: 1–8.
382. Santos BTA. Estudo da atividade dos extratos de plantas e fungos endofíticos isolados do cerrado brasileiro em linhagem celular de feocromocitoma. 73 f., il. Dissertação (Mestrado em Ciências Farmacêuticas) Universidade de Brasília, Brasil. 2014.
383. Santos M, Cesanelli I, Diánez F, Sánchez-Montesinos B, Moreno-Gavíra A. Advances in the Role of Dark Septate Endophytes in the Plant Resistance to Abiotic and Biotic Stresses. *Journal of Fungi* (Basel). 2021 Nov 4;7(11):939.
384. Sarmiento G & Monasteri MO. Life forms and phenology. In Ecosystems of the World: tropical savannas (*F. Bouliere*, ed.). *Elsevier*. 1983; 3:79-108.
385. Sarsaiya S, Jain A, Jia Q, Fan X, Shu F, Chen Z, Zhou Q, Shi J, Chen J. Molecular Identification of Endophytic Fungi and Their Pathogenicity

Evaluation Against *Dendrobium nobile* and *Dendrobium officinale*. *International Journal of Molecular Sciences*. 2020; 21 (1): 316.

386. Satish Chander P, Vijeshwar V, Touseef A, Ghulam Nabi Q, Michael S. An endophytic fungus of *Nothapodytes foetida* that produces camptothecin. *Journal of Natural Products.* 2005; 68: 1717–1719.
387. Saucedo-García A, Anaya AL, Espinosa-García FJ, González MC. Diversity and communities of endophytic foliar fungi of different agroecosystems of Coffea arabica L. in two regions of Veracruz, Mexico. *Plos One*. 2014; 9 (6): e98454.
388. Savary R, Dupuis C, Masclaux FG, Mateus ID, Rojas EC, Sanders IR. Genetic variation and evolutionary history of a mycorrhizal fungus regulate the currency of exchange in symbiosis with the food security crop cassava. *ISME Journal*. 2020;14(6):1333-1344.
389. Savi, DC, Noriler, SA, Ponomareva, LV et al. Diidroisocumarinas produzidas por *Diaporthe cf. heveae* LGMF1631 inibindo patógenos de citros. *Foliar Microbiology.* 2020; 65, 381–392.
390. Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, et al. Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied Environmental Microbiology*. 2009; 75 (23): 7537–41.
391. Schoch CL, Robbertse B, et al. Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. *Database (Oxford)*. 2014: bau061.
392. Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Science USA*. 2012; 109 (16): 6241-6.
393. Schoch CL, Sung GH, López-Giráldez F, et al. The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. *Systematic Biology*. 2002 58 (2): 224-39.
394. Schulz B, Boyle C. The endophytic continnum. *Mycological Research*. 2005; 109: 661-686.
395. Schulz B, Wanke U, Draeger S, Aust HJ. Endophytes of herbaceous plants and shrubs: effectiveness of surface sterilization methods. *Mycological Research*. 1993; 97 : 1447–1450.
396. Schwieder M, Leitão PJ, Pinto JRR, et al. Landsat phenological metrics and their relationship with aboveground carbon in the Brazilian Cerrado. *Carbon Balance Manage*. 2018; 13 (1): 7.
397. Scorzetti G, Fell JW, Fonseca A, Statzell-Tallman. Systematics of basidiomycetous yeasts: a comparison of large subunit D1/D2 and internal transcribed spacer rDNA regions. *FEMS Yeast Research*. 2002; 2(4):495-517.
398. Seetharaman P, Gnanasekar S, Chandrasekaran R, et al. Isolation of limonoid compound (Hamisonine) from endophytic fungi *Penicillium oxalicum* LA-1 (KX622790) *of Limonia acidissima* L. for its larvicidal efficacy against LF vector, *Culex quinquefasciatus* (Diptera: Culicidae). *Environmental Science Pollution Research*. 2017; 24(26): 21272-21282.

399. Seifert KA. Progress towards DNA barcoding of fungi. *Molecular Ecology Resour*. 2009; 9(1): 83-9.

400. Selbmann L, Stoppiello GA, Onofri S, Stajich JE, Coleine C. Culture-Dependent and Amplicon Sequencing Approaches Reveal Diversity and Distribution of Black Fungi in Antárctic Cryptoendolithic Communities. *Journal Fungi* (*Basileia*). 2021; 7 (3): 213.

401. Selosse MA, Vohník M, Chauvet E. Outside rivers: some aquatic hyphomycetes are endophytes? *New Phytologist.* 2008; 178: 3 - 7.

402. Serba DD, Yadav RS. Genomic Tools in Pearl Millet Breeding for Drought Tolerance: Status and Prospects. *Frontiers in Plant Science*. 2016; 7:1724.

403. Sessitsch A, Hardoim P, Döring J, Weilharter A, Krause A, Woyke T, et al. Functional characteristics of an endophytic community colonizing rice roots revealed by metagenomic analysis. *Molecular Plant-Microbe Interaction.* 2012; 25: 28–36.

404. Sette DM. The savanna's climates of brasilian west mid land region. *Brazilian Journal of Climatology*. 2015. 1 (1): 29-42.

405. Sharma D, Pramanik A, Agrawal PK. Evaluation of bioactive secondary metabolites from endophytic fungus Pestalotiopsis neglecta BAB-5510 isolated from leaves of *Cupressus torulosa* D.Don. *Biotechnology*. 2016; 6 (2): 210.

406. Sheibani-Tezerji R, Rattei T, Sessitsch A, Trognitz F, Mitter B. The transcriptome profile of the endophyte *Burkholderia phytofirmans* PsJN indicates detection of the plant environment and water stress. *mBio. 2015;* 6: e00621-15.

407. Shen XY, Cheng YL, Cai CJ, Fan L, Gao J, Hou CL. Diversity and antimicrobial activity of cultivable endophytic fungi isolated from moso bamboo seeds. *Plos O*ne. 2014; 9 (4): e95838.

408. Short DP, O'Donnell K, Thrane U, Nielsen KF, Zhang N, Juba JH, Geiser DM. Phylogenetic relationships among members of the *Fusarium solani* species complex in human infections and the descriptions of *F. keratoplasticum* sp. nov. and *F. petroliphilum* stat. nov. *Fungal Genetics Biology*. 2013; 53: 59-70.

409. Shruti S & Verinder W. Influence of different sterilizing methods on isolation endophytic bacteria from *Rauvolfia serpentina*. *The Pharma Innovation Journal*. 2019; 8(1): 38-41.

410. Sieber TN. Fendophytic fungi in forest trees: they are mutualists? *Fungal Biology Reviews*. 2007; 21: 75–89.

411. Silva CMS et al. Physiological and structural traits of the congeneric species *Styrax ferrugineus* and *S. pohlii* occurring in contrasting environments. *Flora*. 2017; 235: 51-58.

412. Silva CRS, Venturieri GA e Figueira A. Descrição de coleções Amazônicas de *Theobroma* L., identificação de espécies e caracterização de híbridos inter-específicos. *Acta Botanica Brasilica*. 2004; 18(2): 333-341.

413. Silva FA, Liotti RG, Boleti APA, et al. Diversity of cultivable fungal endophytes in *Paullinia cupana* (Mart.) Ducke and bioactivity of their secondary metabolites . *Plos One*. 2018; 13 (4): e0195874.

414. Silva GH, et al. Cadinane sesquiterpenoids of *Phomopsis cassiae*, an endophytic fungus associated with *Cassia spectabilis* (Leguminosae). Phytochemistry. 2006; 67(17): 1964-9.

415. Silva GH, et al. Citocalasinas produzidas por *Xylaria* sp., um fungo endofítico de *Piper aduncum* (piperaceae). Quím. Nova. 2010; 33(10): 2038-2041.
416. Silva GPA & Miranda MCC. Quaternário: cienciometria e mapeamento dos estudos palinológicos do bioma cerrado e importância para arqueologia. *GeoSUL*. 2019; 34: 73.
417. Silva JF, Fariñas MR, Felfili JM, Klink CA. Spatial heterogeneity, land use and conservation in the cerrado region of Brazil. *Journal Biogeography.* 2006; 33: 536–548.
418. Silva JMC & Bates JM. Biogeographic patterns and conservation in the Cerrado of South America: a tropical savanna hotspot. *BioScience.* 2002; 52: 225–233.
419. Silva Júnior MC. 100 árvores do Cerrado: guia de campo. Brasília, DF: Rede de Sementes do Cerrado. 2005.
420. Silva LE, et al. 2015. Chemical Investigation of leaves of *Acosmium dasycarpum* (VOGEL) YAKOVLEV. *Ciência e Natura*. 2015; 37: 664-672.
421. Silva TA, et al. *Styrax camporum* and S. *ferrugineus fruits*: norneolignans, antioxidant and cytotoxic activities. *Journal of Applied Pharmaceutical Science*. 2016; 6 (11): 075-080.
422. Silva-Hughes AF, Wedge DE, Cantrell CL, et al. Diversity and antifungal activity of the endophytic fungi associated with the native medicinal cactus *Opuntia humifusa* (Cactaceae) from the United States. *Microbiology Research*. 2015; 175: 67-77.
423. Silveira R, Mello TRB, Sartori MRS, et al. Efeitos sazonais e de longo prazo da adição de nutrientes e calagem no gene nifH em solos de cerrado sob vegetação nativa. *Science*. 2021; 24 (4): 102349.
424. Silverio DV and Lenza E. Phenology of woody species in a typical cerrado in Parque Municipal do Bacaba, Nova Xavantina, Mato Grosso, Brasil. *Biota Neotropical.* 2010; 10(3): 205-216.
425. Singh G, Singh N., Marwaha TS. Crop genotype and a novel symbiotic fungus influence the potential for endophytic root colonization of plant growth-promoting rhizobacteria. *Physiology and Molecular Biology of Plants*. 2009; 15 (1): 87-92.
426. Singh R, Dubey AK. Diversity and Applications of Endophytic Actinobacteria of Plants in Special and Other Ecological Niches. *Frontiers Microbiology*. 2018; 9:1767.
427. Šmilauer P, Košnar J, Kotilínek M, Šmilauerová M. Contrasting effects of host identity, plant community, and local species pool on the composition and colonization levels of arbuscular mycorrhizal fungal community in a temperate grassland. *New Phytologist*. 2020; 225(1): 461-473.
428. Smith ME, Douhan GW, Rizzo DM. Intra-specific and intra-sporocarp ITS variation of ectomycorrhizal fungi as assessed by rDNA sequencing of sporocarps and pooled ectomycorrhizal roots from a Quercus woodland . *Mycorrhiza. 2007;* 18: 15–22.
429. Soonvald L, Loit K, Runno-Paurson E, Astover A, Tedersoo L. Characterization of the effect of crop species and fertilization treatment on root fungal communities. *Scientific Reports*. 2020; 10 (1): 18741.

430. Soterroni AC, Ramos FM, Mosnier A, et al. Expanding the Soy Moratorium to the Brazilian Cerrado. *Scientific Advances*. 2019; 5 (7): eaav7336.
431. Souza CM, Shimbo JZ, Rosa MR, Parente LL, Alencar AA, Rudorff BFT, Hasenack H., Matsumoto M., Ferreira LG, Souza-Filho PWM, et al. Reconstructing three decades of changes in land use and land cover in Brazilian biomes with the land archive and the land machine. Remote Sensing. 2020; 12: 27-35.
432. Souza HA, Collevatti RG, Lima-Ribeiro MS, Lemos-Filho JP, Lovato MB. A large historic refuge explains spatial patterns of genetic diversity in a Neotropical savanna tree species. *Annals of Botsny* . 2017; 119 (2): 239-252.
433. Souza RC, Mendes IC, Reis-Junior FB, et al. Changes in taxonomic and functional microbial diversity with agriculture: how fragile is the Brazilian Cerrado?. *BMC Microbiology*. 2016; 16: 42.
434. Spatafora JW, Owensby CA, Douhan GW, Boehm EW, Schoch CL. Phylogenetic placement of the ectomycorrhizal genus *Cenococcum* in *Gloniaceae* (*Dothideomycetes*). *Mycologia*. 2012;104(3):758-65.
435. Spera SA, Galford GL, Coe MT, Macedo MN, Mustard JF. Land-use change affects water recycling in Brazil's last agricultural frontier. *Global Change Biology*. 2016; 22(10): 3405-3413.
436. Staniek A, Woerdenbag HJ, Kayser O. *Taxomyces andreanae*: a presumed paclitaxel producer demystified?. *Plant Medicinal*. 2009; 75(15): 1561-566.
437. Stielow JB, Lévesque CA, Seifert KA, Meyer W, et al. One fungus, which genes? Development and assessment of universal primers for potential secondary fungal DNA barcodes. *Persoonia*. 2015; 35: 242-63.
438. Stierle A, Strobel G, Stierle D. Taxol and taxane production by *Taxomyces andreanae*, an endophytic fungus of Pacific yew. *Science*. 1993; 260(5105): 214-216.
439. Stone JK, Polishook JD, White JF. Endophytic fungi. In: Mueller G, Bills GF, Foster MS, (eds) Biodiversity of fungi: inventory and monitoring methods. Burlington, MA, USA: 832 *Elsevier*. 2004; 241–270.
440. Strobel G, Daisy B, Castillo U, Harper J. Natural Products from Endophytic Microorganisms. *Journal of Natural Products*. 2004; 67: 257-268.
441. Strobel G., Daisy B. Bioprospecting for microbial endophytes and their natural products. *Microbiology and Molecular Biology Reviews.* 2003; 67: 491–502.
442. Su, Lei & Deng, Hui & Niu, Yong-Chun. *Phialemoniopsis endophytica* sp. nov., a new species of endophytic fungi from *Luffa cylindrica* in Henan, China. *Mycological Progress*. 2016; 15: 1189-5.
443. Sun JQ, Guo LD, Zang W, Ping WX e Chi DF. Diversity and ecological distribution of endophytic fungi associated with medicinal plants. *Sciences in China Series C*. 2008b; 51: 751-759.
444. Sun MG, Wang L, Wang L et al. Fungal sporulation in two-stage cultivation. *Mycosystema.* 2008a; 2008: 28.
445. Sun S, Zeng X, Zhang D, Guo S. Several fungi associated with partial irregular heartwood of *Dalbergia odorifera*. *Scientific Reports*. 2015; 5: 8464.

446. Sun X, Ding Q, Hyde KD, Guo LD. Community structure and endophytic fungal preference of three woody plants in a mixed forest. *Fungal Ecology*. 2012a; 5: 624–632.

447. Sun X, Guo LD & Hyde KD. Community composition of endophytic fungi in *Acer truncatum* and their role in decomposition. *Fungal diversety*. 2011; 47: 85–95.011

448. Sun X, Guo LD. Endophytic fungal diversity: review of traditional and molecular techniques. *Micology*. 2012; 3(1): 65 – 76.

449. Supaphon P, Phongpaichit S, Rukachaisirikul V, Sakayaroj J. Antimicrobial Potential of Endophytic Fungi Derived from Three Seagrass Species: *Cymodocea serrulata, Halophila ovalis* and *Thalassia hemprichii*. *Plos One*. 2013; 8 (8): e72520.

450. Szűcs Z, Plaszkó T, Cziáky Z, Kiss-Szikszai A, Emri T, Bertóti R, Sinka LT, Vasas G, Gonda S. Endophytic fungi from the roots of horseradish (*Armoracia rusticana*) and their interactions with the defensive metabolites of the glucosinolate - myrosinase - isothiocyanate system. *BMC Plant Biology*. 2018; 18 (1): 85.

451. Tan RX, Zou WX. Endophytes: a rich source of functional metabolites. *Natural Product Reports*. 2001;18(4):448-459.

452. Tang D, Wang G, Zhou JM. Receptor Kinases in Plant-Pathogen Interactions: More Than Pattern Recognition. *Plant Cell*. 2017; 29(4): 618-637.

453. Tang Z, Wang Y, Yang J, Xiao Y, Cai Y, Wan Y, Chen H, Yao H, Shan Z, Li C, Wang G. Isolation and identification of flavonoid-producing endophytic fungi from medicinal plant *Conyza blinii* H.Lév that exhibit higher antioxidant and antibacterial activities. *Peer Journal*. 2020; 8: e8978.

454. Taylor DL, Walters WA, Lennon NJ, Bochicchio J, Krohn A, Caporaso JG, Pennanen T. Accurate Estimation of Fungal Diversity and Abundance through Improved Lineage-Specific Primers Optimized for Illumina Amplicon Sequencing. *Appl Environ Microbiol*. 2016; 21;82(24): 7217-7226.

455. Taylor JE, Hyde KD e Jones EBG. Endophytic Fungi Associated with the Temperate Palm, *Trachycarpus fortunei*, within and Outside Its Natural Geographic Range. *New Fitologist*. 1999; 142: 335 - 346.

456. Tazik, Zahra & Rahnama, Kamran & Iranshahi, Mehrdad & White, James & Soltanloo, Hassan. A new species of *Pithoascus* and first report of this genus as endophyte associated with *Ferula ovina*. *Mycoscience*. 2020; 61 (3).

457. Teimoori-Boghsani Y, Ganjeali A, Cernava T, Müller H, Asili J, Berg G, Endophytic Fungi of Native *Salvia abrotanoides* Plants Reveal High Taxonomic Diversity and Unique Profiles of Secondary Metabolites. *Frontiers in Microbiology*. 2020; 17(10):3013.

458. Teles HL et al. Benzopyrans from *Curvularia* sp., an endophytic fungus associated with *Ocotea corymbosa* (Lauraceae). *Phytochemistry.* 2005; 66 (19): 2363-2367.

459. Teles HL, et al. Aromatic compounds produced by *Periconia atropurpurea*, an endophytic fungus associated with *Xylopia aromatica*. *Phytochemistry.* 2006; 67 (24): 2686-2690.

460. Thi MLT, Thi HHA, Thi BLT, Thi BVT, Van QD, Hoang CH. Isolation of endophytic fungi and screening of Huperzine A–producing fungus from *Huperzia serrata* in Vietnam. *Scientific Reports*. 2019; 9 (1): 16152.

461. Thiem D, Gołebiewski M, Hulisz P, Piernik A, Hrynkiewicz K. How does salinity shape the bacterial and fungal microbiomes of Alnus glutinosa roots?. *Frontiers Microbiology*. 2018; 9: 651.

462. Tian W, Hou CC, Ren ZJ, Wang C, Zhao FG, Dahlbeck D, Hu SP,et al. A calmodulin-gated calcium channel links pathogen patterns to plant immunity. Nature. 2019; 572:131.

463. Toghueo RMK. Bioprospecting endophytic fungi from *Fusarium* genus as sources of bioactive metabolites. *Mycology*. 2019; 31;11(1): 1-21.

464. Toghueo RMK, Boyom FF. Endophytic species of *Penicillium* and their agricultural, biotechnological and pharmaceutical applications. *Biotechnology*. 2020; 10 (3): 107.

465. Tonial F, Beatriz HLNS Maia, Andrea M. Sobottka, Daiani C. Savi, Vânia A. Vicente, Renata R. Gomes, Chirlei Glienke. Biological activity of extracts of Diaporthe terebinthifolii against Phyllosticta citricarpa. *FEMS Microbiology Letters*. 2017; 364(5): fnx026,

466. Torres FL. Isolamento, caracterização e potencial biotecnológico de fungos endofíticos associados à plantas do cerrado. Dissertação (Mestrado em Biotecnologia) da Universidade Federal de São Carlos, São Carlos, São Paulo, Brasil. 2014.

467. Trevisan TC, Silva EA, Dall'Oglio EL, Silva LE, Velozo ES, Vieira PC, Sousa PT. New quinolizidine and diaza-adamantane alkaloids from *Acosmium dasycarpum* (Vog.) Yakovlev—Fabaceae. *Tetrahedron Letters*. 2008 49 (44): 6289-6292.

468. Turbat A, Rakk D, Vigneshwari A, et al. Characterization of Plant Growth-Promoting Activities of Endophytic Fungi Isolated from Sophora flavescens. *Microorganisms*. 2020; 8 (5): 683.

469. Tyburska-Woś J, Nowak K, Kieliszewska-Rokicka B. Influence of leaf damage by the horse chestnut leafminer (*Cameraria ohridella* Deschka & Dimić) on mycorrhiza of *Aesculus hippocastanum* L. *Mycorrhiza*. 2019; 29(1):61-67.

470. Unterseher M., Schnittler M. Species richness analysis and ITS rDNA phylogeny revealed the majority of cultivable leaf endophytes of beech (*Fagus sylvatica). Fungal Ecology*. 2010; 3: 366–378.

471. U'Ren JM, Lutzoni F, Miadlikowska J, Laetsch AD, Arnold AE. Host and geographic structure of endophytic and endolichenic fungi at a continental scale. *American Journal Botanic*. 2012; 99(5): 898-914.

472. Uzma F, Mohan CD, Hashem A, et al. Endophytic Fungi-Alternative Sources of Cytotoxic Compounds: A Review. *Frontiers Pharmacology*. 2018; 9: 309.

473. Vale HMM et al. Yeasts in native fruits of the Cerrado: occurrence, diversity and enzymatic potential. *Neotropical Biota*. 2021; 21, 4: e20201184.

474. Van Geel M, Jacquemyn H, Plue J, et al. Abiotic rather than biotic filtering shapes the arbuscular mycorrhizal fungal communities of European seminatural grasslands. *New Phytologist*. 2018; 220(4): 1262-1272.

475. Vandana UK, Rajkumari J, Singha LP, et al. The Endophytic Microbiome as a Hotspot of Synergistic Interactions, with Prospects of Plant Growth Promotion. *Biology (Basel)*. 2021; 10(2): 101.

476. Vandenkoornhuyse P, Quaiser A, Duhamel M, Van AL, Dufresne A. The importance of the plant holobiont microbiome. *New Phytologist*. 2015; 206 (4): 1196–1206.

477. Vasconcelos VV et al. Characterization of Cerrado and Atlantic Forest phyto-environments through stone lineage and paleosols study. *Geography, Teaching & Research*. 2011; 14 (3): 06-14.

478. Vasundhara M, Kumar A, Reddy MS. Molecular approaches to tracking bioactive compounds from endophytic fungi. *Frontiers in Microbiology*. 2016; 7: 1774.

479. Veldman, J.W., Mattingly, W.B. & Brudvig, L. Understory plant communities and the functional distinction between savana trees, forest trees, and pines. *Ecology*. 2013; 94: 424-434.

480. Veloso HP, Oliveira-Filho LD, Vaz AM, Lima MP, Marquete R, Brazao JE. Manual técnico da vegetação brasileira. Rio de Janeiro: IBGE; 1992.

481. Verma SK, Gond SK, et at. Exploring Endophytic Communities of Plants: Methods for Assessing Diversity, Effects on Host Development and Potential. *Biotechnological Applications*. 2019; doi: 10.1007/978-3-030-10504-4_4.

482. Verma SK, Gond, SK, Mishra, A. et al. Impact of environmental variables on isolation, diversity and antibacterial activity of endophytic fungal communities of Madhuca indica Gmel. in different places in India. *Ann Microbiol* 2014; 64, 721–734.

483. Verma VC, Gond SK, Kumar A, Kharwar RN, Strobel GA. Endophytic mycoflora of the leaf, bark and stem of Azadirachta indica A Juss. from Varanasi India. *Microbial Ecology*. 2007; 54:882 119-125.

484. Viana LT, Bustamante MMC, Molina M, Pinto AS, Kisselle K, Zepp R, Burke RA. Comunidades microbianas em solos de Cerrado sob vegetação nativa submetida a fogo controlado e sob pastagem. *Pesquisa Agropecuária Brasileira.* 2011; 46 (12): 1665–72.

485. Vidal A, Parada R, Mendoza L, Cotoras M. Endophytic fungi isolated from plants growing in the central Andean pre-cordillera of Chile with antifungal activity against *Botrytis cinerea*. *Journal Fungi (Basileia)*. 2020; 6 (3): 149.

486. Vieira Junior GT, de Moura JB, de Souza RF, et al. Seasonal Variation in the Mycorrhizal Community of Different Cerrado Phytophysiologies. *Frontiers Microbiology*. 2020; 11: 576764.

487. Vieira ML, Hughes AF, Gil VB, et al. Diversity and antimicrobial activities of the fungal endophyte community associated with the traditional Brazilian medicinal plant *Solanum cernuum* Vell. (Solanaceae). *Canadian Journal Microbiology*. 2012; 58(1): 54-66.

488. Vieira ML, Johann S, Hughes FM, Rosa CA, Rosa LH. The diversity and antimicrobial activity of endophytic fungi associated with medicinal plant *Baccharis trimera* (Asteraceae) from the Brazilian savannah. *Canadian Journal Microbiology*. 2014; 60(12): 847-856.

489. Vilgalys R & Sun BL. Assessment of species distributions in *Pleurotus* based on trapping or airborne basidiospores. *Mycology*. 1990; 86, 270-274.

490. Vilgalys R, & Sun B L. Ancient and recent patterns of geographic speciation in the oyster mushroom *Pleurotus* revealed by phylogenetic analysis of ribosomal DNA sequences. *Proceedings of the National Academy of Sciences of the United States of America*. 1994; 91(10): 4599–4603.

491. Vincent JB, Weiblen GD, May G. Host associations and beta diversity of fungal endophyte communities in New Guinea rainforest trees. *Molecular Ecology*. 2016; 25(3): 825-841.

492. Vorholt JA. Microbial life in the phylosphere. *Nature reviews Microbiology*. 2012; 10 (12): 828–40.
493. Vu D, Groenewald M, de Vries M. Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. *Studies in Mycology*. 2019; 92: 135-154.
494. Vu D, Groenewald M, Szöke S, Cardinali G, Eberhardt U, Stielow B, de Vries M, Verkleij GJ, Crous PW, Boekhout T, Robert V (2016). DNA barcoding analysis of more than 9 000 yeast isolates contributes to quantitative thresholds for yeast species and genera delimitation. *Studies in Mycology*. 85: 91-105.
495. Waheeda K & Shyam KV (2017). Formulation of Novel Surface Sterilization Method and Culture Media for the Isolation of Endophytic Actinomycetes from Medicinal Plants and its Antibacterial Activity. *Journal of Plant Pathology & Microbiology*. 8:2.
496. Wang L, Ren L, Li C, et al. Efeitos da diversidade de fungos endofíticos em diferentes espécies de coníferas na colonização de Sirex noctilio (Hymenoptera: Siricidae). *Scientific Reports*. 2019; 9 (1): 5077.
497. Wang L, Ren L, Li C, Gao C, Liu X, Wang M, Luo Y (2019). Effects of endophytic fungi diversity in different coniferous species on the colonization of *Sirex noctilio* (Hymenoptera: Siricidae).*Scientific Reports*. 9 (1): 5077.
498. Wang Y e Guo LD (2007). A comparative study of endophytic fungi in needles, bark, and xylem of *Pinus tabulaeformis*. *Canadian Journal of Botany*. 85: 911 - 917.
499. Wantzen, K.M., et al. Soil carbon stocks in stream-valley-ecosystems in the Brazilian Cerrado agroscape. *Agriculture, Ecosystems and Environment.* 2012; (151): 70-79.
500. Warming E. Lagoa Santa: contribuição para a geographia phytobiologica. Belo Horizonte: Imprensa Oficial do Estado de Minas Gerais, 1908.
501. Wawra S, Fesel P, Widmer H, et al. FGB1 and WSC3 are in planta-induced β-glucan-binding fungal lectins with different functions. *New Phytologist*. 2019; 222(3): 1493-1506.
502. Wawra S, Fesel P, Widmer H, et al. A lectina FGB1 de ligação a β-glucana específica para fungos altera a composição da parede celular e suprime a imunidade desencadeada por glucana nas plantas. *Nature Communications*. 2016; 7: 13188.
503. Wearn JA, Sutton BC, Morley NJ, Gange AC. Species and organ specificity of fungal endophytes in grassland herbaceous plants. *Journal of Ecology*. 2012; 100: 1085–1092.
504. Webber JA. natural control of Dutch elm disease. *Nature*. 1981; 292: 449-451.
505. Wei J, Chen F, Liu Y, Abudoukerimu A, Zheng Q, Zhang X, Sun Y, Yimiti D. Comparative Metabolomics Revealed the Potential Antitumor Characteristics of Four Endophytic Fungi of Brassica rapa L. *ACS Omega*. 2020; 5 (11): 5939-5950.
506. Weitemier K, Straub SC, Fishbein M, Liston A. Intragenomic polymorphisms among high-copy loci: a genus-wide study of nuclear ribosomal DNA in Asclepias (Apocynaceae). *PeerJournal*. 2015; 3: e718.

507. Wemheuer B, Thomas T, Wemheuer F. Endophytic fungal communities of three agriculturally important grass species differ in their response to management regimes. *Microorganisms*. 2019; 7 (2): 37.
508. Wemheuer F, Berkelmann D, Wemheuer B, Daniel R, Vidal S, Bisseleua Daghela HB. Agroforestry management systems boost the composition, diversity and function of endophytic communities of fungi and bacteria in Theobroma Cacao leaves. microorganisms. 2020; 8 (3): 405.
509. Wen YC, Li HY, Lin ZA, et al. Long-term fertilization alters soil properties and fungal community composition in fluvo-aquic soil of the North China Plain. *Scientific Reports*. 2020; 10(1): 7198.
510. Wereszczuk A, Leblois R, Zalewski A. Genetic diversity and structure related to expansion history and habitat isolation: stone marten populating rural-urban habitats. *BMC Ecology*. 2017; 17(1):46.
511. White JR, Maddox C, White O, Angiuoli SV, Fricke WF. CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. *Microbiome*. 2013; 1 (1): 6.
512. White TJ, Bruns TD, Lee SB, Taylor JW. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. Em Innis MA, Gelfand DH, Sninsky JJ, White TJ (ed), protocolos de PCR: um guia para métodos e aplicações Academic Press, New York, NY. 1990; p 315-322.
513. Wijayawardene NN, Bahram M, Sánchez-Castro I, Dai DQ, Ariyawansa KGSU, Jayalal U, Suwannarach N, Tedersoo L (2021). Current Insight into Culture-Dependent and Culture-Independent Methods in Discovering Ascomycetous Taxa. *Journal Fungi* (Basel). 2021; 28;7(9):703. doi: 10.3390/jof7090703.
514. Willis KJ, editor. 2018 State of the World Fungi Report. Kew: *Royal Botanic Gardens*. 2018.
515. Wolińska A, Kuźniar A, Zielenkiewicz U, et al. Metagenomic Analysis of Some Potential Nitrogen-Fixing Bacteria in Arable Soils at Different Formation Processes. *Microbiology Ecology*. 2017; 73(1):162-176.
516. Wu B, Hussain M, Zhang W, Stadler M, Liu X, Xiang M. Current insights into fungal species diversity and perspective on naming the environmental DNA sequences of fungi. *Micology*. 2019; 10 (3): 127-140.
517. Wu CH, Derevnina L, Kamoun S. Receptor networks underpin plant immunity. *Science*. 2018; 22; 360 (6395):1300-1301.
518. Xiang X, Gibbons SM, He JS, et al. Rapid response of arbuscular mycorrhizal fungal communities to short-term fertilization in an alpine grassland on the Qinghai-Tibet Plateau. *PeerJ*. 2016;4: e2226.
519. Xiao J, Zhang Q, Gao YQ, Tang JJ, Zhang AL, Gao JM. Secondary metabolites from the endophytic *Botryosphaeria dothidea* of *Melia azedarach* and their antifungal, antibacterial, antioxidant, and cytotoxic activities. *Journal of Agricultural and Food Chemistry*. 2014; 62(16): 3584-3590.
520. Xie ML, Wei TZ, Fu YP, Li D, Qi LL, Xing PJ, Cheng GH, Ji RQ, Li Y. Three new species of Cortinarius subgenus *Telamonia* (*Cortinariaceae, Agaricales*) from China. *MycoKeys*. 2020 69:91-109.

521. Xing XK, Chen J, Xu MJ, Lin WH, Guo SX. Endophytic fungi associated with Sonneratia mangrove plants (Sonneratiaceae) on the southern coast of China. *Forest Pathology*. 2011; 41: 334–340.
522. Xu J (2016). Fungal DNA barcoding. *Genome.* 59 913–932.
523. Xu R, Adam L, Chapados J, Soliman A, Daayf F, Tambong JT. MinION Nanopore-based detection of *Clavibacter nebraskensis*, the corn Goss's wilt pathogen, and bacteriomic profiling of necrotic lesions of naturally-infected leaf samples. Plos One. 2021; 16(1): e0245333.
524. Yadav A. N. Biodiversity and biotechnological applications of host-specific endophytic fungi for sustainable agriculture and allied sectors. *Acta Scientific.* 2018; 1: 44.
525. Yan L, Zhao HB, Zhao XX, Xu XG, Di YC, Jiang CM, Shi JL, Shao DY, Huang QS, Yang H, Jin ML. Production of bioproducts by endophytic fungi: chemical ecology, biotechnological applications, bottlenecks and solutions. *Applied Microbiology and Biotechnology*. 2018; 102 (15): 6279–6298.
526. Yang F, Zhang J, Zhang H, et al. Bacterial Blight Induced Shifts in Endophytic Microbiome of Rice Leaves and the Enrichment of Specific Bacterial Strains With Pathogen Antagonism. *Frontiers in Plant Science*. 2020; 11: 963.
527. Yang G, Li P, Meng L, Xv K, Dong F, Qiu Y, He L, Lin L. Diversity and communities of cultivable endophytic fungi of different tree peonies (geoherbs and non-geoherbs) and their biosynthetic potential analysis. *Brazilian Journal Microbiology*. 2018; 49 1: 47-58.
528. Yang RX, Zhang SW, Xue D, Xuan JH, Zhang YB, Peng BB. Diversity of cultivable endophytes isolated from *Paeonia ostii* and the genetic basis for its bioactivity. *Polish Journal Microbiology*. 2018; 67 (4): 441-454.
529. Yao H, Sun X, He C, Maitra P, Li XC, Guo LD. Phyllosphere epiphytic and endophytic fungal community and network structures differ in a tropical mangrove ecosystem. *Microbiome*. 2019; 9;7(1):57.
530. Yao YQ, Lan F, Qiao YM, Wei JG, Huang RS, Li LB. Endophytic fungi harbored in the root of *Sophora tonkinensis* Gapnep: Diversity and biocontrol potential against phytopathogens. *Microbiology open*. 2017; 6 (3): e00437.
531. Yu J, Wu Y, He Z, Li M, Zhu K, Gao B. Diversity and antifungal activity of endophytic fungi associated with Camelia oleifera. Mycobiology. 2018; 46 (2): 85-91.
532. Yu X, Feng BM, He P, Shan LB. From Chaos to Harmony: Responses and signaling upon microbial pattern recognition. In: Leach J.E., Lindow S.E., editors. Annu Rev Phytopathol. 2017; 55pp. 109–137.
533. Zalles V, Hansen MC, Potapov PV, et al. Near doubling of Brazil's intensive row crop area since 2000. *Proceedings of the National Academy of Science*. 2019; 116(2): 428-435.
534. Zambriano SMV. Taxonomia de fungos associados a plantas do Cerrado do Distrito Federal e Mato Grosso. Dissertação de Mestrado, Universidade de Brasília, Distrito Federal, Brasil, 2016.
535. Zhang H, Wei TP, Li LZ, Luo MY, Jia WY, Zeng Y, Jiang YL, Tao GC. Multigene Phylogeny, Diversity and Antimicrobial Potential of Endophytic Sordariomycetes From Rosa roxburghii . Front Microbiol. 29 de novembro de 2021; 12: 755919.

536. Zhang L, Yan J, Fu Z, et al. FoEG1, a glycoside hydrolase family 12 protein secreted from Fusarium oxysporum, triggers cell death and modulates plant immunity. *Molecular Plant Pathology*. 2021; 22 (5): 522-538.

537. Zhang N, Castlebury LA, Miller AN, et al. An overview of the systematics of the Sordariomycetes based on a four-gene phylogeny. *Mycologia*. 2006 ;98(6):1076-87. doi: 10.3852/mycologia.98.6.1076.

538. Zhang T, Yao YF. Endophytic fungal communities associated with vascular plants in the high arctic zone are highly diverse and host plant specific. *Plos O*ne. 2015; 10 (6): e0130051.

539. Zhao K, Penttinen P, Guan T, et al. The diversity and anti-microbial activity of endophytic actinomycetes isolated from medicinal plants in *Panxi plateau*, China. Current Microbiol. 2011; 62(1): 182-190.

540. Zheng R, Li S, Zhang X, Zhao C. Biological Activities of Some New Secondary Metabolites Isolated from Endophytic Fungi: A Review Study. *International Journal MoleculaR Science*. 2021; 22(2): 959.

541. Zheng Y, Gong X. Niche differentiation rather than biogeography shapes the diversity and composition of microbiome of *Cycas panzhihuaensis*. *Microbiome*. 2019; 7(1):152.

542. Zhou S, Qiao L, Jayawardena RS, Hyde KD, Ma X, Wen T, Kang J. Two new endophytic *Colletotrichum* species from *Nothapodytes pittosporoides* in China. *MycoKeys.* 2019; 49: 1-14.

CHAPTER 2: DIVERSITY, STRUCTURE AND SPECIES-SHARING NETWORK OF THE ENDOPHYTIC MYCOBIOME OF SIX WOODY SPECIES FROM THE BRAZILIAN NEOTROPICAL SAVANNA

Abstract: Elucidating the complex relationship between plants and endophytic fungi is very important to understanding the maintenance of biodiversity, equity, stability, and ecosystem functioning. However, knowledge of the diversity of endophytic fungi species related to native Cerrado species is poorly documented and remains largely unknown. Due to knowledge gaps, this study aimed to describe the diversity of leaf endophytic fungi related to the species *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperma*, and *Styrax ferrugineus*, and how the host identity factor is related to the taxonomic structure of this community. For this, the culture-dependent methods were used in together with metabarcoding. The results show that each host is individually colonized by a pool of endophytic fungi species, evidencing the diversity of species that occur in this niche. In both hosts the phylum *Ascomycota* and the classes *Sordariomycetes* and *Dothideomycetes* were dominant. In total, 114 taxa of the six host species were recovered, which were later classified into more than 20 genera and 50 species. More than half of the isolates belong to the genus *Diaporthe* and were distributed in more than 20 species. Other genera and species were found, but in lower abundance. The *metabarcoding* also showed the occurrence of other fungal phyla not yet reported in the endophytic mycobiome of Cerrado plant species, such as *Monoblepharomycota, Rozelomycota and Zoopagomycota*. The communities differed not only in terms of the presence and absence of fungal species, but also in terms of the abundance of shared species. These findings, in addition to reinforcing the importance of the Brazilian Cerrado as a reservoir of microbial species, demonstrate how the community of endophytic fungi is complex and its taxonomic structure is influenced by the identity of the host.

Key-words: *Metabarcoding*; Tropical savannah; Mycobiota; *Ascomycota*; *Sordariomycetes; Diaporthe*; ITS.

1. INTRODUCTION

Fungi constitute the second largest group of organisms (Purvis and Hector, 2000) and are responsible for a series of important ecological roles, among which fungi with an endophytic lifestyle stand out, capable of conferring a series of benefits to their hosts (see Chapter 1). Unlike saprophytic species, which colonize the soil, endophytic fungi reside in plant tissues and can grow within the root, trunk, and leaves without causing apparent disease (Stone et al., 2004). These microorganisms evolved along with their host plants, establishing ecological relationships, so that, in some cases, these microorganisms depend on their host to complete part or all of their life cycle (Clay et al., 2002; Yao et al., 2002; Yao et al., 2002; Yao et al., 2002; Yao et al. al., 2019).

As a result of the coevolution process, endophytic fungi can present a varying degree of specialization depending on the range of hosts they can colonize (Su et al., 2011; Vieira et al., 2012; Sun et al., 2012; Li et al., 2012; 2016a; Li et al., 2016a; Li et al. al., 2016b; Yao et al., 2019; Yao et al., 2019; Li et al., 2020). The degree of specificity that endophytic fungi show in colonizing certain hosts has already been demonstrated in plant species from the most varied terrestrial ecosystems (Higgins et al., 2007; Martín et al., 2013; Sandberg et al., 2014; Gomes et al., 2018; Yao et al., 2019). Therefore, the endophytic fungal community is predefined by a set of factors, which include the degree of specialization of the fungus in colonizing one or more hosts and the host identity factor (genotype and phenotype) that acts as an environmental filter.

In Cerrado plant species, the effect of host identity on the taxonomic structuring of the endophytic fungal community has already been reported using Cultivation-dependent approaches (Noriler et al., 2018). Cultivation-dependent methods have been used to study endophytic fungi over the years (Sun et al., 2012; Gautam et al., 2022). These methods have numerous inaccuracies that make it difficult to know the real diversity, such as the presence of non-culturable taxa; variations in the growth rates of the isolates that make their separation and recovery difficult; and chances of contamination with saprophytic fungi from the environment (Sun et al., 2012; Chi et al., 2019; Gautam et al., 2022). In contrast, *Metabarcoding* (independent of cultivation) has proven to be a powerful tool for inferring ecological data and evaluating the community of endophytic fungi (Chi et al., 2019; Yao et al., 2019; Durán et al., 2021; Gautam et al., 2022).

Based on the above, this chapter aims to a) characterize the leaf endophytic mycobiome of six Cerrado woody species, namely, *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperma*, and *Styrax ferrugineus*, b) using cultivation methods and culture-independent, and c) evaluate the effect of host identity on the richness and abundance of endophytic fungal species among the mycobiome of these host.

2. SPECIFIC OBJECTIVES

- To characterize the leaf endophytic mycobiota of the host species Caryocar brasiliense, *Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperma*, and *Styrax ferrugineus*;
- Survey the easily cultivable leaf endophytic mycobiota in these species;
- Observe if there are differences in the pool of cultivable species between the hosts;
- Observe if there is a sharing of cultivable species between the hosts;
- Carry out cultivation-independent approaches to real diversity assessment;
- To evaluate the effect of host identity on species richness and equity in the endophytic fungal community among these hosts;
- To report the similarities and dissimilarities, at different taxonomic levels, of the community of endophytic fungi associated with these six host species.

3. MATERIALS AND METHODS

3.1. Description of the study area

The area where the study was carried out is located in the Ecological Reserve of the Brazilian Institute of Geography and Statistics (RECOR / IBGE) (Figure 21), which is 35 km south of the center of Brasília, DF, km 0 of BR – 251, Brazil (15° 55' S, 47° 51' W), at an average altitude of 1,100 m and occupies 1,350 ha. According to the Köppen classification, the climate is tropical (Aw), with average annual precipitation between 1.100 and 1.600 mm and with two well-defined seasons: the dry season, which occurs from May to September; and the rainy season from October to April. The region's soil is characterized as Red

Latosol (dystrophic, deep and well-drained, and with clay minerals of the 1:1 type, with a predominance of iron and aluminum oxides). The vegetation of the study area is characterized as *Cerrado stricto sensu*, a vegetation physiognomic formation that characterizes the Cerrados of the Central region of Brazil (Eiten, 1972). The plots where the leaves of Cerrado native plants were collected are part of the project "Study of the Effects of Global Changes that Determine the Structure and Functioning of Cerrado Ecosystems" (IAIPRONEX), which was implemented at RECOR in 1998.

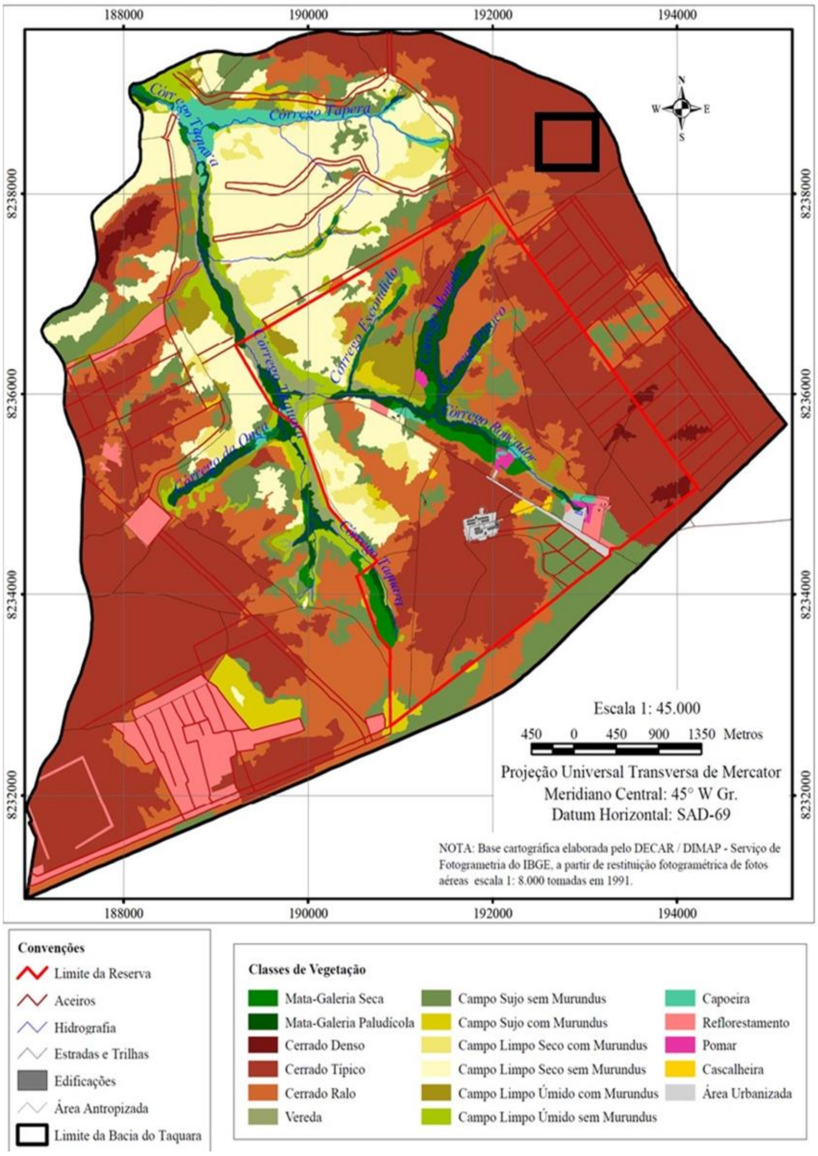


Figure 21. Vegetation map of the IBGE Ecological Reserve (RECOR-IBGE). The black square in the upper right region of the figure represents the location of the Cerrado fertilization project. Source: Costa et al., 2019.

3.2. *Sampling and Collection*

Six plant species present in the control plots were selected, being the species *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperna,* and *Styrax ferrugineus* (Figure 22). In total, three individuals per species were sampled considering height, stem circumference, and nutritional characteristics of the leaves (Supplementary table 1). For the analysis of the endophytic fungal community, ten healthy leaves without apparent disease symptoms were collected per individual, totaling 30 leaves per species. The collected samples were stored in sterile plastic bags, placed in thermal boxes with controlled temperature, and transported to the laboratory where they were washed using neutral soap and running tap water to remove main epiphytes (Silva et al., 2018). After washing, the leaves were submitted to the superficial disinfection process.

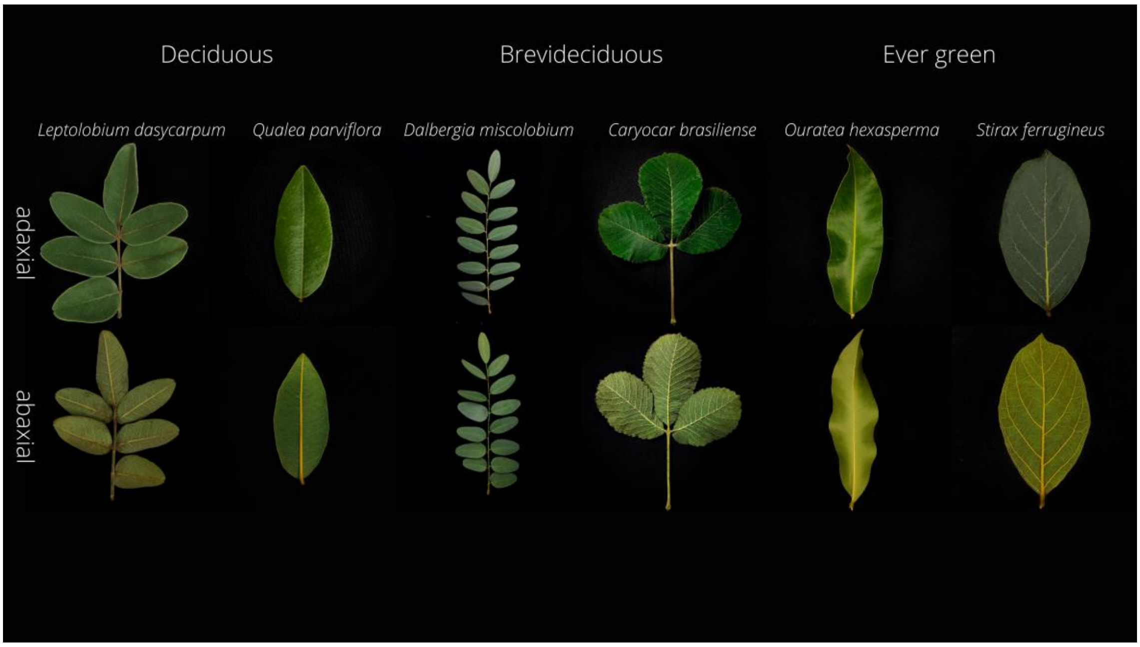


Figure 22. Morphology of the leaves of the plant species sampled.

3.3. *Surface disinfection and sample processing*

For the surface disinfection process, the samples were submerged for two minutes in glass Erlenmeyer flasks containing alcohol (70%), followed by immersion in sodium hypochlorite (4%) for five minutes and, finally, five successive washes with previously autoclaved distilled water (Araújo et al., 2001).

The water from the last rinse was collected in a sterile 15 mL Falcon tube and seeded in duplicate on Potato Dextrose Agar (PDA) in order to ensure the effectiveness of surface disinfection.

After surface disinfection, the samples were dried in a flow chamber, then processed to be subjected to dependent and independent cultivation techniques (Figure 23). For this, the protocol by Khan et al. (2017) and Dhayanithy et al. (2019) with some adaptations: the ten leaves per sampled individual were overlapped and then, with the aid of eyelet pliers, they were perforated 15 times, generating approximately 150 leaf fragments with a diameter of five millimeters. After that, eight leaf fragments for each individual sampled (24 fragments per species) were placed in Petri dishes containing PDA (four fragments per plate) supplemented with streptomycin 250 mg L $^{-1}$ and chloramphenicol 100 mg L $^{-1}$ (Khan et al., 2017), and incubated in BOD (*Biological Oxygen Demand*) at 25 °C in the dark for up to five days. The other fragments were placed in sterile 50 mL falcon tubes and stored in a freezer at -20ºC to later be subjected to eDNA extraction (*environmental DNA*) to carry out the independent culture methodology (*Metabarcoding*).

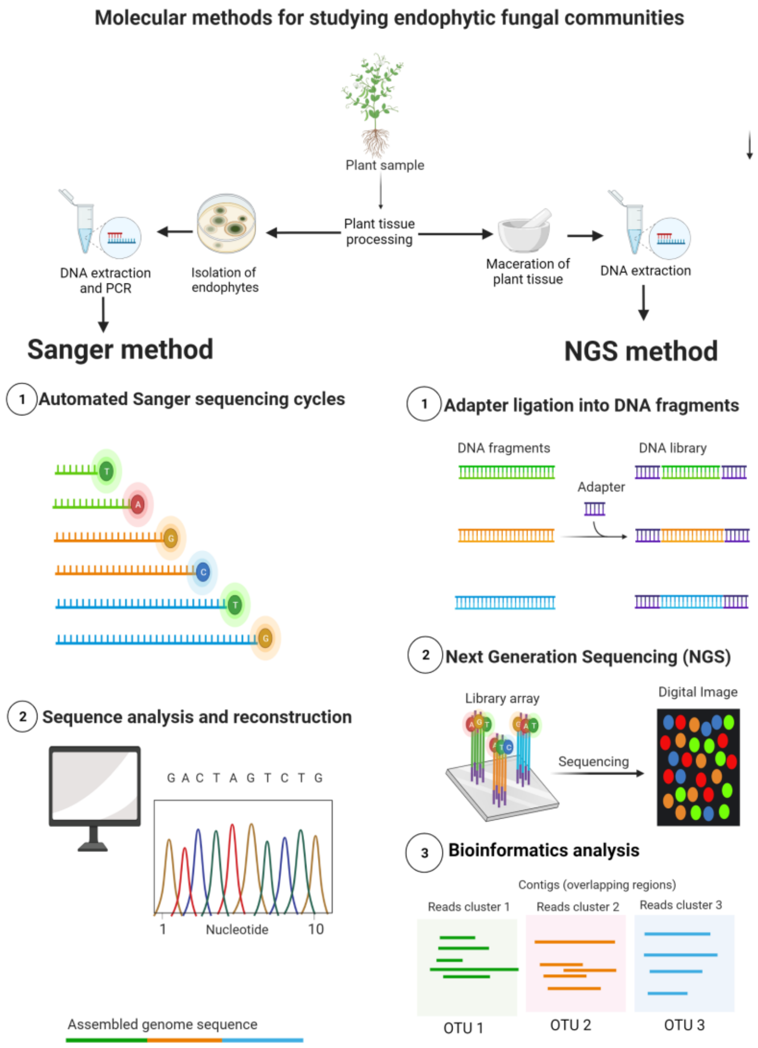


Figure 23. Overview of the methodology used to study the taxonomic composition of the endophytic fungal community in the present study.

3.4. Cultivation, purification and deposit of isolated fungal taxon

For the isolation of cultivable taxa, as mycelial growth was observed from the edge of the plant tissue arranged in the PDA, they were reisolated by collecting a mycelial fragment with sterile needles from the edge of the colony in evidence and inoculated into a new plate containing PDA for further purification of the isolate by the hyphal tip. For hyphal tip purification, the fungi were inoculated in Water Agar (WA) at 25 ºC for three days. After the incubation period, with the aid of a magnifying glass (Leican M205C®), for microscopic visualization of the edges of the colony in AW, and a flamed insulin needle, small fragments of the culture medium containing an individual hypha were collected (Figure 24), inoculated in PDA medium (two plates per isolate) and incubated at 25 ºC for later deposit in the Mycological Collection of the University of Brasília (CCUB) and DNA extraction. The fungal colonies, already pure, were stored in cryotubes according to the CCUB deposit specifications, using two methods of preserving the fungi, the Castellani method (Castellani, 1967) and glycerol (10%) (Parks & Graham et al., 1992).

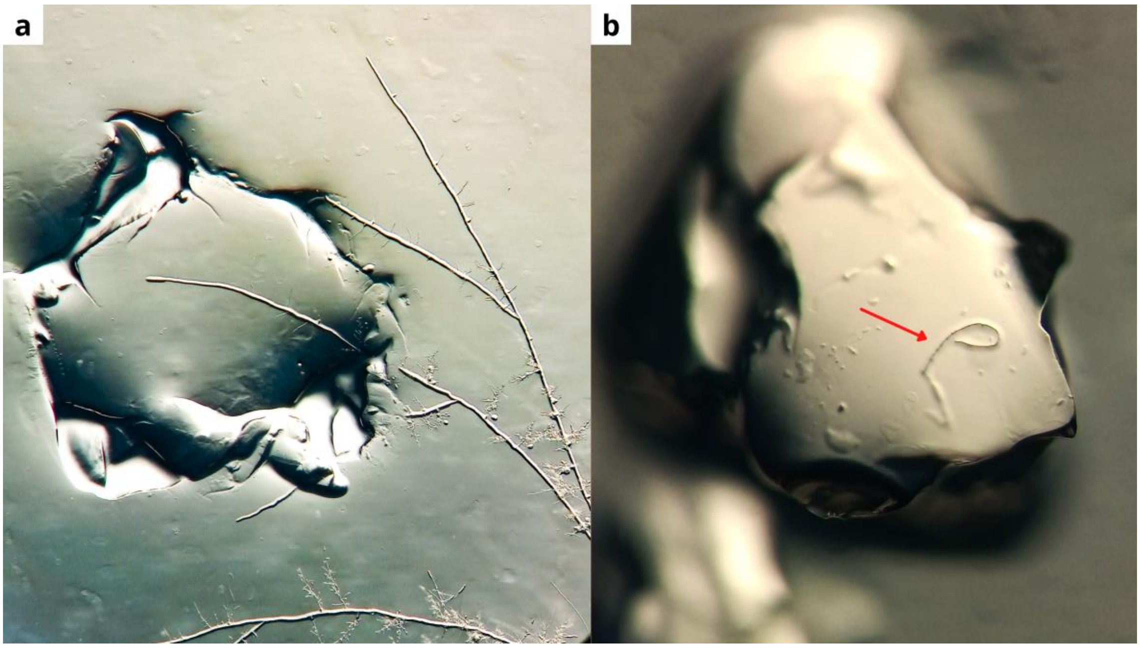


Figure 24. Exemplification of the method used for hyphal tip purification. In a) it is demonstrated how the environment around the hypha is fragmented to obtain a hypha isolated from the other hyphae constituting the mycelium; while in b) the fragment of the WA medium containing a fungal hypha (indicated by the red arrow) already inoculated in PDA is shown.

3.5. *DNA extraction and molecular identification of isolates*

Genomic DNA (gDNA) was extracted from pure cultures using the Wizard® Genomic DNA Purification Kit. For this, approximately 400 mg of mycelium were scraped from the surface of the PDA plate and transferred to 2 mL Eppendorf tubes containing 700 µl of *Nuclear Lysis Solution*, and 40 µl of TE (Tris-EDTA pH 8.0), 400 mg of polyvinylpyrrolidone 40 and four beads. Negative control was included containing all components except mycelium. The tubes were placed in the macerator at 4,350 rpm for the 90s, followed by incubation in a dry bath at 65 °C and 500 rpm. After incubation, 200 µl of Protein Precipitation

Solution were added to each tube, followed by vigorous vortexing for 30 seconds to homogenize the samples. The mixture was centrifuged at 14,000 rpm for ten minutes in a non-refrigerated microcentrifuge and 700 µl of the supernatant was recovered and transferred to new 1.5 ml Eppendorf tubes containing 700 µl of ice-cold propanol. The tubes were placed in a -20°C freezer for at least one hour and then centrifuged at 14,000 rpm for DNA precipitation. The supernatant was discarded and the pellet present in the tube was washed twice with 700 µl of 70% ethanol and dried under ambient conditions. Finally, the pellet was rehydrated with 100 µl TE (Tris-EDTA pH). The success of the extraction and the quality of the gDNA were evaluated by electrophoresis at 80 V for 30 minutes on a 1% (w/v) agarose gel stained with GelredTM, and visualized under ultraviolet light.

The 18S-ITS1-5.8S-ITS2 region was amplified using the primer pair V9G (Forward 5'TTA CGT CCC TGC CCT TTG TA'3) (from Hoog et al., 1998) and LR5 (Reverse 5' TCC TGA GGG AAA CTT CG'3) (Vilgalys et al., 1990). Amplification was performed in a 15 µL volume containing 1X 10X PCR Buffer (200 mM Tris-HCL, 500 mM KLC), 0.2 mM deoxyribonucleotide pool, 1 mM MgCl2, 0.2 mM each primer, 1.0 U Taq DNA Polymerase (Invitrogen DNA Polymerases - Invitrogen PCR Enzymes), 0.2 mM gDNA and Ultrapure Deionized Water for Injection to the pre-set final volume. The amplification program was as follows: five minutes of initial denaturation at 95°C, followed by 35th cycles of 30 seconds of denaturation at 95°C, 45 seconds of annealing at 55°C, one-minute extension at 72°C; and a final extension of five minutes at 72ºC. A negative control (no gDNA) was included in the amplification process to validate the amplification. After amplification, 2 µL of PCR products stained with GelredTM were subjected to electrophoresis at 90 V for 40 minutes using a 1% (w/v) agarose gel and visualized under ultraviolet light. The presence of fragments >800 bp was determined by 1kb marker biomarkers.

PCR products were purified using ExoSAP-IT™ PCR Product Cleanup Reagent (Thermo Fisher Scientific) and sent for sequencing at Macrogen (South Korea) using the same primer pair used for amplification. The generated sequences were treated for noise removal using the *DNA Baser assembler software*. Taxonomic assignments for each sequence (isolated) were made by comparing it with other sequences deposited in the GenBank of the National Center for Biotechnology Information (NCBI), using the *Basic Local Alignment*

Search Tool (BLAST) (Altschul et al., 1990), to obtain the percentage of identity between them.

3.6. DNA Metabarcoding Analysis

3.6.1. DNA extraction from plant tissue

For the extraction and purification of eDNA from plant tissue, different protocols were used together (Guo et al., 2000; Romão-Dumaresq et al., 2016; Chi et al. 2019) with numerous adaptations. Initially, the samples were vigorously macerated in liquid nitrogen using a mortar and pestle, previously autoclaved and cooled to avoid oxidation of the plant material, until a slightly off-white powder was formed. Approximately 400 mg of the macerate was transferred to 2 mL Eppendorf tubes containing 700 µL of CTAB extraction buffer (7%-10% CTAB, 100 mM Tris-HCl, 20 mM EDTA pH 8.0, 1.4 M NaCl), 400 mg of polyvinylpyrrolidone 40 and 2-5 µL of β-Mercaptoethanol, this step was carried out in a cooling rack for 2 mL Eppendorf tubes. Two negative controls were included, one containing all the components mentioned above, except the macerate, to validate the sterility of the buffer solution; and another containing all the aforementioned components, except the macerate, and Milli-Q water collected from a mortar and pestle to validate its sterility.

The tubes containing the mixture were incubated in a dry bath at 65 °C for 30 minutes, being vigorously vortexed every five minutes. After incubation, 700 µl of chloroform: isoamyl alcohol (24:1) were added to each tube and mixed for ten minutes by gentle inversion in a cooling rack. The mixture was centrifuged at 14.000 rpm for ten minutes in a non-refrigerated microcentrifuge and the water phase was transferred to new 1.5 mL Eppendorf tubes containing 55 µl of CTAB (7%). Again, 700 µl of chloroform: isoamyl alcohol (24:1) were added to each tube, shaken by gentle inversion in the cooler for ten minutes, followed by centrifugation under the same previous conditions, this last step was repeated until no interphase between the aqueous and organic phases.

Approximately 700 µl of the aqueous phase was recovered and transferred to new 1.5 ml eppendorfs tubes containing 700 µl of ice-cold propanol and 30 µl of 5M KOAc, being shaken by gentle inversion in a cooler rack for five minutes and taken to a freezer -20 ºC for a period of at least two hour. Subsequently, the tubes were centrifuged at 14.000 rpm for DNA precipitation. The supernatant was discarded and the pellet present in the tube was subsequently washed, once with 700 µl of PA ethanol (99.8%), five times with 700 µl of 70% ethanol and dried at room temperature. Finally, the pellet was rehydrated in 100 µl TE (Tris-EDTA pH). The success of eDNA extraction and quality was evaluated by electrophoresis at 80 V for 30 minutes on a 1% (w/v) agarose gel stained with GelredTM, and visualized under ultraviolet light.

3.6.2. Building the libraries and sequencing

The extracted and purified eDNA was sent to Novogene (Beijing, China) for library assembly, targeting the ITS1 region using the primer pair ITS1-1F-F (5'CTTGGTCATTTAGAGGAAGTAA'3) and ITS1-1F-R (5'GCTGCGTTCTTCATCGATGC'3) used to study endophytic fungal communities from eDNA extracted from plant tissue; and sequenced using the Miseq 25,000 platform (Illumina, San Diego, California, USA).

Raw sequences were filtered with a phred value of ≥Q29 (an accuracy of ≥99.87%). Raw reads were paired into single reads and adapters were removed using the QIIME script “split_library.py” (Caporaso et al., 2010). Sequence clustering was performed using uclust v1.2.22q (Edgar, 2010) in QIIME 1.9.0 (Caporaso et al., 2010). Reads were processed with UCHIME (Edgar et al., 2011) to remove chimeric sequences. Taxonomic assignments were performed using an open reference OTU collection approach against the UNITE database in QIIME 1.9.0 (Caporaso et al., 2010), with a 97% similarity threshold. Taxonomic assignment of OTUs was performed at a confidence bound of 0.97 against the UNITE ITS1 database with the UNITE 7.2 reference OTU database ("UNITE+INSD" dataset) using the assignTaxonomy method (Kõljalg et al., 2013).

3.7. Data analysis

Bioinformatics analyzes to obtain the relative abundance of the isolates were performed in the R version 4.1.0 software using the packages “ddplyr”, “ggplot2”, “tiddyverse” and “readxls”. For this, the taxa and respective hosts were grouped in separate columns, one for each information. The lines indicated the host and the isolate present in it.

The construction of the species sharing network was performed using Cytoscape v 3.9.1 software. The network was assembled using the "Taxonomicnetwork" package. For this, the information was organized in columns: one for the host, another for the taxon and a third referring to the number of isolates per host species. The layout has been adjusted according to the best way to expose important network information.

All bioinformatics analyzes for *metabacoding* were performed in QIIME2. The alpha metrics and beta diversity were calculated using the q2-diversity plugin (Purcell et al., 2019). The alpha diversity of the leaf endophytic fungal assemblage was examined using the Kruskal-Wallis (KW) test comparing all groups, followed by pairwise comparison using the Kruskal-Wall test (pairwise) (Yao et al., 2019). Principal coordinate analysis (PCoA) was used to visualize differences in endophytic fungal community composition based on Bray curtis dissimilarity, Jaccard distance, Weighted unifrac, and Unweighted unifrac with 999 permutations (Clarke et al., 2006). Permutational multivariate analysis of variance (PERMANOVA) was applied to test for possible variations in the endophytic fungal community between host species (Oksanen et al., 2007). Differential species abundance analyzes were evaluated using the QIIME2 ANCOM45 plugin, consecutively testing each taxonomic level to detect the significant changes in endophytic fungal community abundance among the different host species (Purcell et al., 2019). The relative abundance at each taxonomic level was calculated by ANCOM from the table with the taxonomic attributions of each sequence.

3.8. Analysis of the nutritional composition of leaves

The analysis of the foliar nutritional composition of each species was carried out at the Laboratory of Soil, Plant Tissue and Fertilizer Analysis of the Federal University of Viçosa (UFV). For this, ten leaves were collected per individual, totaling 30 leaves per species. The leaves were dried in an oven and passed through a process of perchloric nitric digestion and evaluation of phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg) and sulfur (S), followed by quantification by reaction colorimetric. The evaluation of nitrogen (N) and aluminum (Al) contents was performed by means of sulfuric digestion and quantification by the Kjeldahl method.

4. RESULTS

4.1. Analysis of the nutritional composition of leaves

Leaf nutrient content, leaf area and specific leaf area (SLA) varied among the six host species (Supplementary table 1). The ranking produced by Principal Component Analysis (PCA) shows the main dissimilarities between the six species (Figure 25). *Caryocar brasiliense* was correlated with high leaf area (cm^2) and leaf dry weight and lower leaf nitrogen concentrations when compared to the other species. *Dalbergia miscolobium* showed the opposite profile to that of *C. brasiliense*, with lower leaf dry weight, lower leaf area (cm^2) and higher concentrations of leaf nitrogen and higher SLA. *Leptolobium dasycarpum* and *Qualea parviflora* were correlated with lower leaf sulfur, nitrogen, magnesium and potassium contents and higher leaf aluminum concentrations. *Ouratea hexasperma and Styrax ferrugineus* were correlated with higher magnesium concentrations, higher leaf area (cm^2), lower SLA and nitrogen contents.

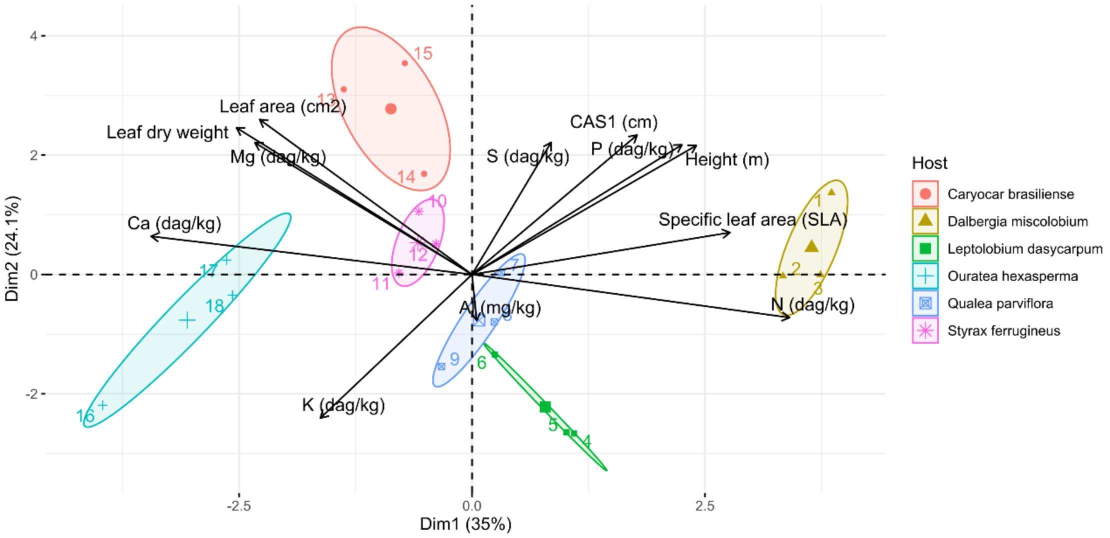


Figure 25. Ordenation produced by Principal Component Analysis (PCA) for variables of leaf nutrient concentration, specific leaf area (SLA) cm²/g and dry mass of leaves of the six host plant species. The X-axis shows PC1 and the y shows PC2. The ellipses show the grouping of biological replicas by host specie. AFE: Specific foliar area; Al: Aluminium; Ca: Calcium; CAS1: Stem circumference; K: Potassium; Mg: Magnesium; P: phosphorus; S: sulfur.

4.2. Molecular identification of isolates

In total, 114 endophytic fungi were selected for molecular identification based on the 18S-ITS1-5.8S-ITS2 region of the rDNA, with ten isolates from *Q. parviflora*, 11 isolates from *C. brasiliense*, 16 from *O. hexasperma*, 19 from *L. dasycarpum*, 29 from *D. miscolobium* and 29 from *S. ferrugineus*. The isolates were classified into 49 different species (Table 10), however, this number may be even higher if we consider that many isolates were classified only at the genus level.

Table 10. Identification of endophytic leaf fungi from six Cerrado woody species using the *basic local alignment search tool* (BLAST) in GenBank.

Host	Isolate code	Taxon	Match	Identity percentage (%)	Query cover (%)
Caryocar brasiliense (Brevideciduous)	CB1629_2	*Diaporthe* sp.	NR_111849.1	95%	88%
	CB1629_22	*Diaporthe schini*	NR_111861.1	99%	100%
	CB1629_25	*Diaporthe* sp.	MG828894.1	91%	73%
	CB1629_3	*Diaporthe* sp.	NR_145303.1	94%	95%
	CB1629_31	*Didymella keratinophila*	NR_158275.1	99%	100%
	CB995_15	*Diaporthe rosae*	MG828894.1	99%	100%
	CB995_2	*Diaporthe* sp.	EU552122.1	95%	100%
	CB995_22	*Diaporthe* sp.	MH171064.1	96%	99%
	CB995_3	*Diaporthe* sp.	NR_137105.1	92%	100%
	CB995_6	*Diaporthe actinidiae*	KC145886.1	99%	100%
	CB995_7	*Diaporthe masirevicii*	NR_147534.1	98%	100%
Dalbergia miscolobium (Brevideciduous)	DM1044_2	*Colletotrichum spicati*	OL842171.1	99%	96%
	DM1044_23	*Didymella chlamydospora*	MK836111.1	98%	100%
	DM1044_3	*Diaporthe* sp.	MH855768.1	95%	100%
	DM1044_6	*Alternaria indefessa*	MH861641.1	99%	100%
	DM1044_16	*Diaporthe masirevicii*	KJ197276.1	98%	100%
	DM1044_8	*Didymella keratinophila*	NR_158275.1	99%	100%
	DM1044_19	*Diaporthe* sp.	EU552122.1	93%	100%
	DM1044_9	*Diaporthe raonikayaporum*	NR_111860.1	99%	100%
	DM11044_5	*Didymella keratinophila*	NR_158275.1	99%	100%
	DM18_1	*Epicoccum sorghicola*	OK442368.1	98%	100%
	DM18_12	*Diaporthe* sp.	MH864501.1	93%	100%
	DM18_2	*Epicoccum sorghicola*	OK442368.1	98%	100%
	DM18_8	*Diaporthe* sp.	MN152927.1	93%	99%
	DM2226_10	*Diaporthe* sp.	MH855768.1	95%	100%

	DM2226_1	*Diaporthe parapterocarpi*	NR_168152.1	99%	100%
	DM2226_11	*Ascochyta phacae*	MH857437.1	98%	99%
	DM2226_16	*Diaporthe velutina*	NR_152470.1	97%	100%
	DM2226_13	*Colletotrichum* sp.	MK541032.1	92%	100%
	DM2226_14	*Seiridium marginatum*	KT949914.1	98%	99%
	DM2226_15	*Colletotrichum chrysophilum*	NR_160821.1	99%	100%
	DM2226_19	*Colletotrichum philoxeroidis*	OL842188.1	97%	96%
	DM2226_22	*Stenocarpella* sp.	NR_173403.1	93%	100%
	DM2226_29	*Diaporthe* sp.	NR_168240.1	94%	92%
	DM2226_3	*Ascochyta rabiei*	EU167600.1	99%	99%
	DM2226_4	*Diaporthe* sp.	EU552122.1	90%	100%
	DM2226_17	*Ascochyta phacae*	MH857437.1	98%	99%
	DM2226_5	*Colletotrichum brevisporum*	KC790943.1	98%	95%
	DM2226_6	*Epicoccum sorghicola*	OK442368.1	99%	100%
	DM18_6	*Didymella keratinophila*	NR_158275.1	99%	100%
Leptolobium dsycarpum (Deciduous)	LD2293_12	*Diaporthe stewartii*	MH855768.1	99%	100%
	LD2293_13	*Diaporthe stewartii*	MH855768.1	96%	100%
	LD2293_23	*Diaporthe cynaroidis*	EU552122.1	96%	100%
	LD2293_3	*Diaporthe terebinthifolii*	NR_111862.1	99%	99%
	LD2293_4	*Diaporthe* sp.	NR_147596.1	93%	100%
	LD2293_7	*Microdiplodia* sp.	DQ885897.1	96%	100%
	LD2299_1	*Diaporthe macadamiae*	NR_168240.1	98%	98%
	LD2299_2	*Diaporthe terebinthifolii*	NR_111862.1	99%	100%
	LD2299_3	*Diaporthe ocoteae*	NR_147596.1	98%	100%
	LD2299_35	*Diaporthe macadamiae*	NR_168240.1	98%	100%
	LD2299_4	*Diaporthe* sp.	NR_111849.1	90%	99%
	LD2299_5	*Diaporthe rosiphthora*	MT311197.1	99%	100%
	LD2299_6	*Diaporthe* sp.	MH171064.1	96%	100%
	LD2304_1	*Diaporthe* sp.	NR_168240.1	95%	96%
	LD2304_2	*Diaporthe foeniculina*	NR_145303.1	97%	100%
	LD2304_30	*Neopestalotiopsis dendrobii*	MK993572.1	99%	100%
	LD2304_34	*Diaporthe macintoshii*	NR_147539.1	98%	99%

	LD2304_35	*Diaporthe macintoshii*	NR_147539.1	98%	100%
	LD2304_50	*Diaporthe inconspicua*	NR_111849.1	99%	99%
Ouratea hexasperma (Evergreen)	OH1078_22	*Kalmusia erioi*	MN473058.1	99%	100%
	OH1078_12	*Phyllosticta catimbauensis*	NR_156631.1	99%	88%
	OH1078_2	*Diaporthe novem*	MH864503.1	98%	100%
	OH1078_3	*Diaporthe* sp.	NR_120138.1	93%	97%
	OH1078_31	*Kalmusia erioi*	MN473058.1	97%	97%
	OH1078_24	*Dendrothyrium* sp.	JX496097.1	93%	98%
	OH2206_31	*Phyllosticta fallopiae*	AB454307.1	100%	99%
	OH2208_3	*Stilbospora* sp.	KF570166.1	88%	100%
	OH2208_4	*Phyllosticta capitalensis*	OL957169.1	100%	100%
	OH2262_2	*Diaporthe maytenicola*	NR_137826.1	97%	100%
	OH2262_30	*Diaporthe* sp.	EU552122.1	92%	100%
	OH2262_31	*Epicoccum sorghicola*	OK442368.1	98%	100%
	OH2262_4	*Coniochaeta* sp.	NR_173009.1	90%	99%
	OH2262_40	*Diaporthe* sp.	NR_147596.1	93%	100%
	OH2262_5	*Diaporthe* sp.	NR_158416.1	93%	100%
	OH2262_6	*Diaporthe* sp.	MH855768.1	95%	100%
Qualea parviflora (Deciduous)	QP1131_11	*Pestalotiopsis protearum*	JN712498.1	99%	100%
	QP1646_1	*Diaporthe macintoshii*	NR_147539.1	98%	100%
	QP1646_11	*Neopestalotiopsis dendrobii*	MK993572.1	99%	100%
	QP1646_13	*Diaporthe* sp.	NR_147539.1	96%	100%
	QP1646_3	*Diaporthe inconspicua*	NR_111849.1	99%	100%
	QP1646_4	*Diaporthe inconspicua*	NR_111849.1	99%	100%
	QP65_0	*Kalmusia erioi*	MN473058.1	97%	97%
	QP65_30	*Cytospora viridistroma*	MN172408.1	99%	100%
	QP65_4	*Cytospora viridistroma*	MN172408.1	99%	100%
	QP971_2	*Clathrosporium* sp.	NR_153908.1	88%	86%
	SF134_13	*Cytospora viridistroma*	MN172408.1	99%	100%
	SF134_14	*Diaporthe* sp.	NR_111857.1	93%	100%
	SF134_2	*Diaporthe macintoshii*	NR_147539.1	98%	100%

Styrax ferrugineus (Evergreen)	SF134_22	*Diaporthe macintoshii*	NR_147539.1	98%	100%
	SF134_25	*Diaporthe foeniculina*	NR_145303.1	97%	100%
	SF134_3	*Hymenopleella* sp.	KT949901.1	90%	100%
	SF134_3_1	*Diaporthe* sp.	NR_137825.1	96%	100%
	SF134_4	*Diaporthe ilicicola*	MH171064.1	98%	99%
	SF134_6	*Monochaetia* sp.	LC146750.1	95%	90%
	SF134_7	*Monochaetia* sp.	LC146750.1	95%	90%
	SF1697_10	*Diaporthe novem*	MH864503.1	99%	100%
	SF1697_16	*Diaporthe* sp.	EU552122.1	90%	100%
	SF1697_17	*Diaporthe stewartii*	MH855768.1	98%	100%
	SF1697_3	*Lasiodiplodia parva*	MH861166.1	99%	100%
	SF1697_6	*Cytospora* sp.	MK912135.1	98%	100%
	SF1697_7	*Melanconis* sp.	MN784964.1	90%	100%
	SF1697_8	*Diaporthe* sp.	MH855768.1	95%	100%
	SF1697_0	*Diaporthe terebinthifolii*	NR_111862.1	99%	100%
	SF1697_15	*Diaporthe* sp.	MH855768.1	96%	100%
	SF1756_12	*Diaporthe baccae*	NR_152458.1	97%	100%
	SF1756_13	*Diaporthe ilicicola*	MH171064.1	97%	92%
	SF1756_18	*Diaporthe* sp.	NR_172435.1	96%	100%
	SF1756_2	*Diaporthe* sp.	MH171064.1	95%	89%
	SF1756_3	*Diaporthe ilicicola*	MH171064.1	97%	99%
	SF1756_4	*Diaporthe* sp.	MH171064.1	95%	100%
	SF1756_5	*Diaporthe* sp.	NR_137126.1	96%	100%
	SF1756_6	*Diaporthe ilicicola*	MH171064.1	97%	99%
	SF1756_8	*Diaporthe* sp.	NR_111849.1	95%	90%
	SF1756_9	*Diaporthe terebinthifolii*	NR_111862.1	99%	100%

Taxons with an identity percentage below 97% were classified only at the genus level.

All endophytic fungi recovered from both host plant species belong to the phylum *Ascomycota* (100%) and are divided into three classes, the dominant being *Sordariomycetes* (78%), followed by *Dothideomycetes* (21.2%) and *Leotiomycetes* (0. 8%), seven orders and 14 families, with the *Diaporthaceae* family being the dominant one (63%) (Figure 26), and 22 genus.

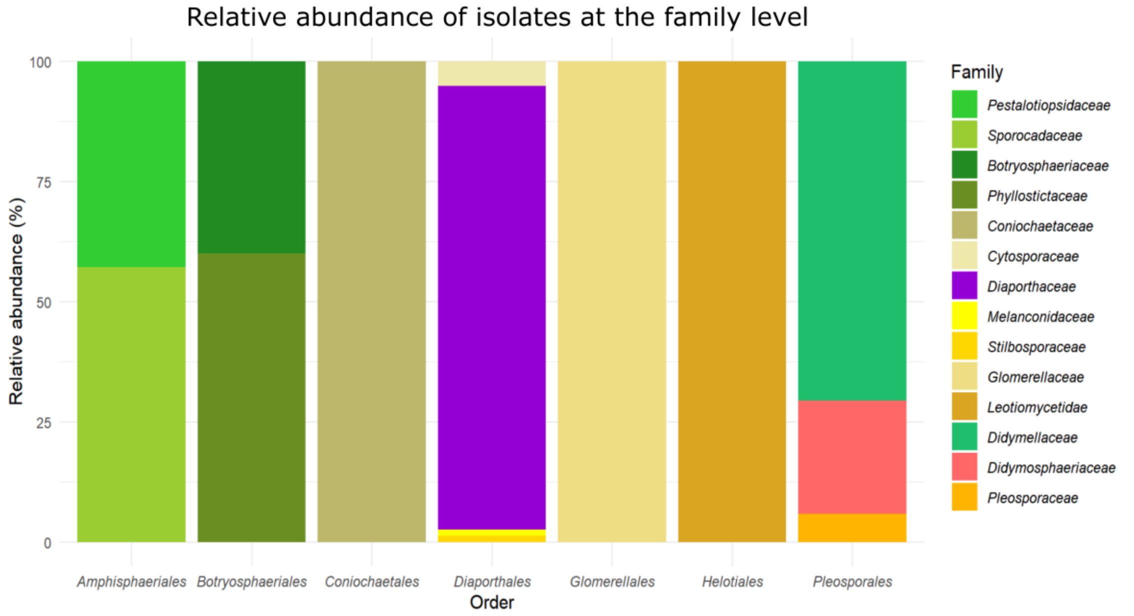


Figure 26. Taxonomic distribution of isolates at the Family level.

The host with the highest number of endophytic fungal species was *D. miscolobium* with 18 species, followed by *S. ferrugineus* with 14 species, *L. dasycarpum* with 12 species, *O. hexasperma* with 11 species, and *Q. parviflora* with eight species (Figure 27). The host with the lowest number of fungal endophyte species was *C. brasiliense*, with only five species. However, it should be considered that more than 50% of the isolates in *C. brasiliense* were classified only at the genus level.

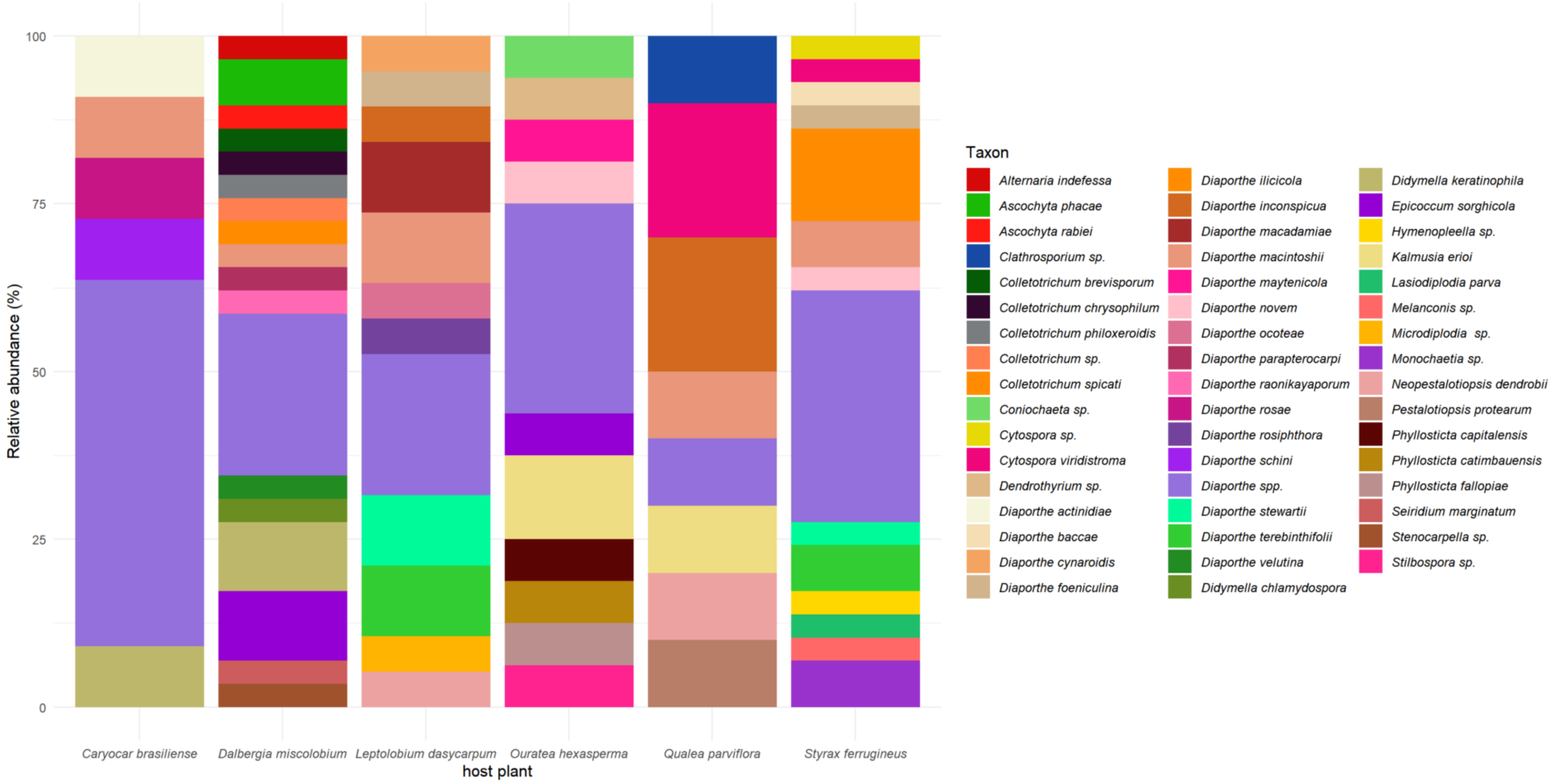


Figure 27. Species-level relative abundance of the endophytic fungal community of six host species. On the X axis the host plant species is shown; on the Y axis the percentage of relative abundance of each fungal species is shown.

The most abundant and ubiquitous endophytic fungus genus in all host plants analyzed here was *Diaporthe* (Figure 28), with 71 taxa (62% of the total isolates), which were distributed in more than 20 species. In the host *L. dasycarpum*, 89.5% of the endophytic fungi isolated belong to the genus *Diaporthe*; while in *C. brasiliense*, this number is 91%. In the other host species, *Diaporthe* spp. correspond to > 15% of the total number of isolated and identified taxa.

Figure 28. Isolates of endophytic fungi belonging to the genus *Diaporthe*. Cultures of *Diaporthe* spp. endophytes grown in PDA at 27ºC, without lighting, for 15 days. The columns show the host plant of the respective isolates. The codes CB1629-2, CB995-3, DM18-8, DM2226-10, DM2226-29, LD2299-4, OH2262-30, OH2262-40, OH2262-6, QP1646-13 and SF1697-16 correspond to *Diaporthe* species unidentified. CB1629-22: *Diaporthe schin;* LD2293-13: *Diaporthe stewartii;* LD2299-35: *Diaporthe macadamiae;* QP1646-1: *Diaporthe macintoshii*; QP1646-4: *Diaporthe inconspícua;* SF134-25*: Diaporthe foeniculina;* SF1756-3: *Diaporthe ilicicola.*

In addition to the genus *Diaporthe*, another 21 genera of endophytic fungi were also found in the different hosts, but in lower abundance. The genera *Didymella* and *Colletotrichum* were the second most abundant, both corresponding to 4.3% of the total isolates. The other genera found corresponded to less than < 2.5%. The most diverse host species in the genera of endophytic fungi were *D. miscolobium, O. hexasperma*, and *S. ferrugineus* (Figure 29).

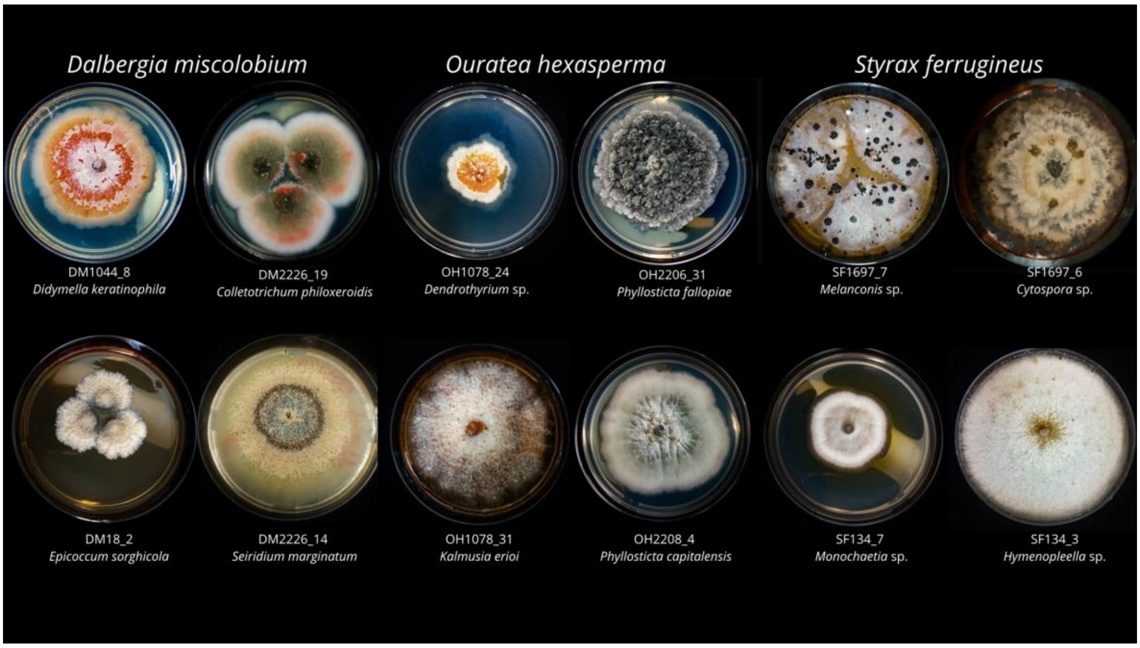


Figure 29. Endophytic fungi isolated from host plants *Dalbergia miscolobium, Ouratea hexasperma,* and *Styrax ferrugineus*. Cultures of endophytic fungi grown in PDA at 27ºC, without lighting, for 15 days.

Although *Diaporthe* was the most abundant genus among the cultivable taxa isolated from the six host species, not all identified species of this genus were found in more than one host (Figure 30). The species *D. actinidiae, D. schini*, and *D. rosae* were exclusive to the host *C. brasiliense*; *D. cynaroidis*, *D. macadamiae* and *D. rosiphthora* were exclusive to the host *L. dasycarpum*; *D. parapterocarpi* and *D. raonikayaporum* were exclusive to the host *D. miscolobium*; *D. baccae* and *D. ilicicola* were exclusive to the host *S. ferrugineus* and *D. maytenicola* to the host O*. hexasperma*. The only *Diaporthe* species shared between more than three of the host plants was *D. macintoshii*, which was found in five of the six hosts, except in *O. hexasperma*. Other species of fungal endophytes were shared between the hosts, namely *Cytospora viridistroma*, *Epicoccum sorghicola, Didymella keratinophila*, and *Kalmusia erioi*. However, most isolates were found in only one host.

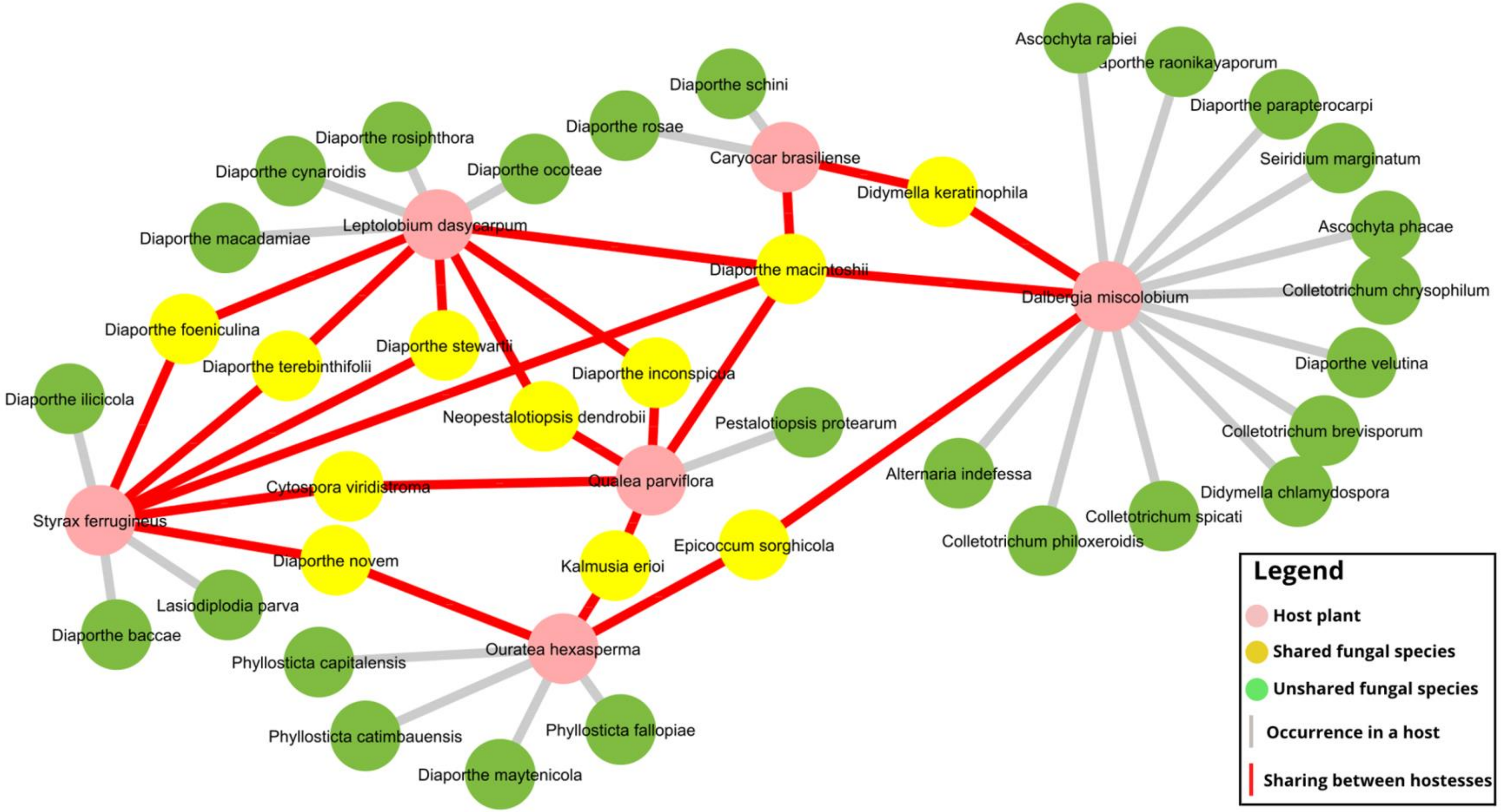


Figure 30. Architecture of the distribution network of endophytic fungi among the six species of host plants. Pink nodes represent host plants; the green nodes represent the fungal taxa not shared between the host plants; those in yellow show the shared fungal species. Gray edges indicate the occurrence of the taxon within a host; while those in red show species sharing. We did not consider taxa classified only by genus level.

The alpha diversity metrics showed no statistical difference regarding the diversity of endophytic fungal species between hosts (p>0.05). The Shannon Wiener diversity index (H'), a parameter that measures the diversity of species in a given niche, showed that the isolated fungi of *D. miscolobium* (H' 3.92) were more diverse than the other groups (Figure 31a). Second, the highest diversity values were observed in *L. dasycarpum* (H'3.40), followed by *S. ferrugineus* (H' 3.03), *O. hexasperma* (H' 2.83), *Q. parviflora* (H'2.72) and finally *C. brasiliense* (H' 2.26). The index that estimates the species richness of 1st Order Jackknife showed that the number of species of cultivable endophytic fungi in *D. miscolobium* can reach approximately 19 species, and this value was partially achieved if we consider the isolates identified at the level of the genus as potential unreported species (Figure 31b). The 1st Order Jackknife Requiza Estimator also showed that the diversity of endophytic fungi species in *Q. parviflora* can reach 10 species, in *S. ferrugineus* it can reach 22 species, it in *C. brasiliense* it can reach 12 and in *L. dasycarpum* can reach 22 species. It should be considered that the value of the species identified in these hosts was partially reached, except for *S. ferrugineus* and *L. dasycarpum*, since less than 60% of the estimated richness was observed.

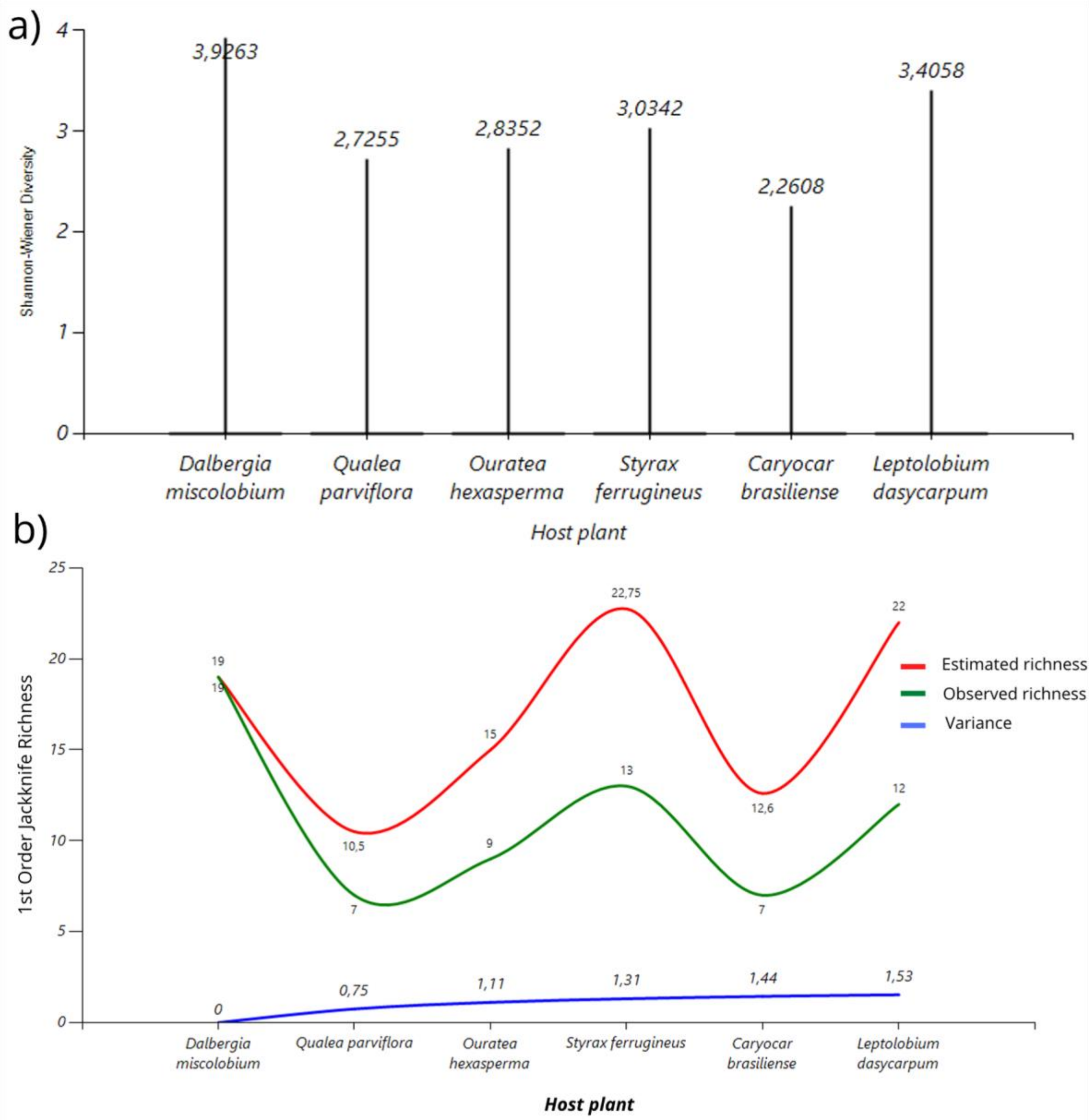


Figure 31. Metrics of alpha diversity and richness estimation of the cultivable endophytic fungal community in six Cerrado plant species. In a) the Shannon Wiener diversity index is shown. In b) the estimate of 1st Order Jackknife species richness is shown.

4.3. Metabarcoding and metadata quality

All samples sent for metabarcoding for both experiments underwent quality control (Figure 32). However, five eDNA samples were lost during transport, two belonging to the host *Dalbergia miscolobium*, two belonging to *Caryocar brasiliense* from the nutrient addition experiment (liming), and one from the phosphate group for *Ouratea hexasperma*.

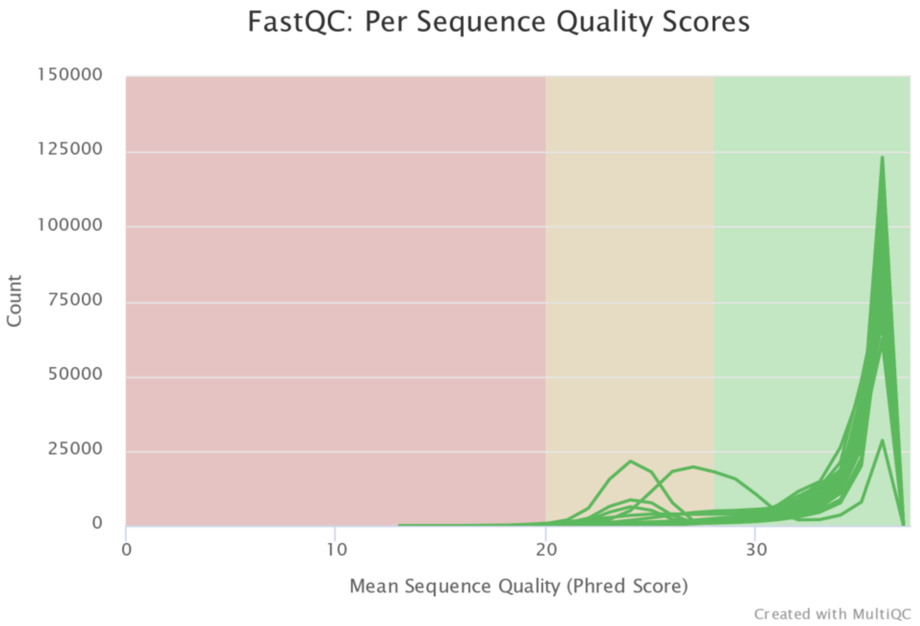


Figure 32. Quality of amplicons generated by metabarcoding for all samples from both experiments.

4.4. Taxonomic attributions

The quantitative data from the metabarcoding allowed the characterization of the enormous diversity of taxa constituting the endophytic mycobiota of the six woody species studied here. In total, 3.822 OTUs were grouped based on the sequences read, which were later classified into 468 OTUs at the genus level based on high genetic similarity (threshold of 97%). The other sequences were classified in higher taxonomic levels (family, order, class, phylum and kingdom fungi) (supplemental table 2). An overview of the taxonomic distribution of OTUs is shown in Figure 33.

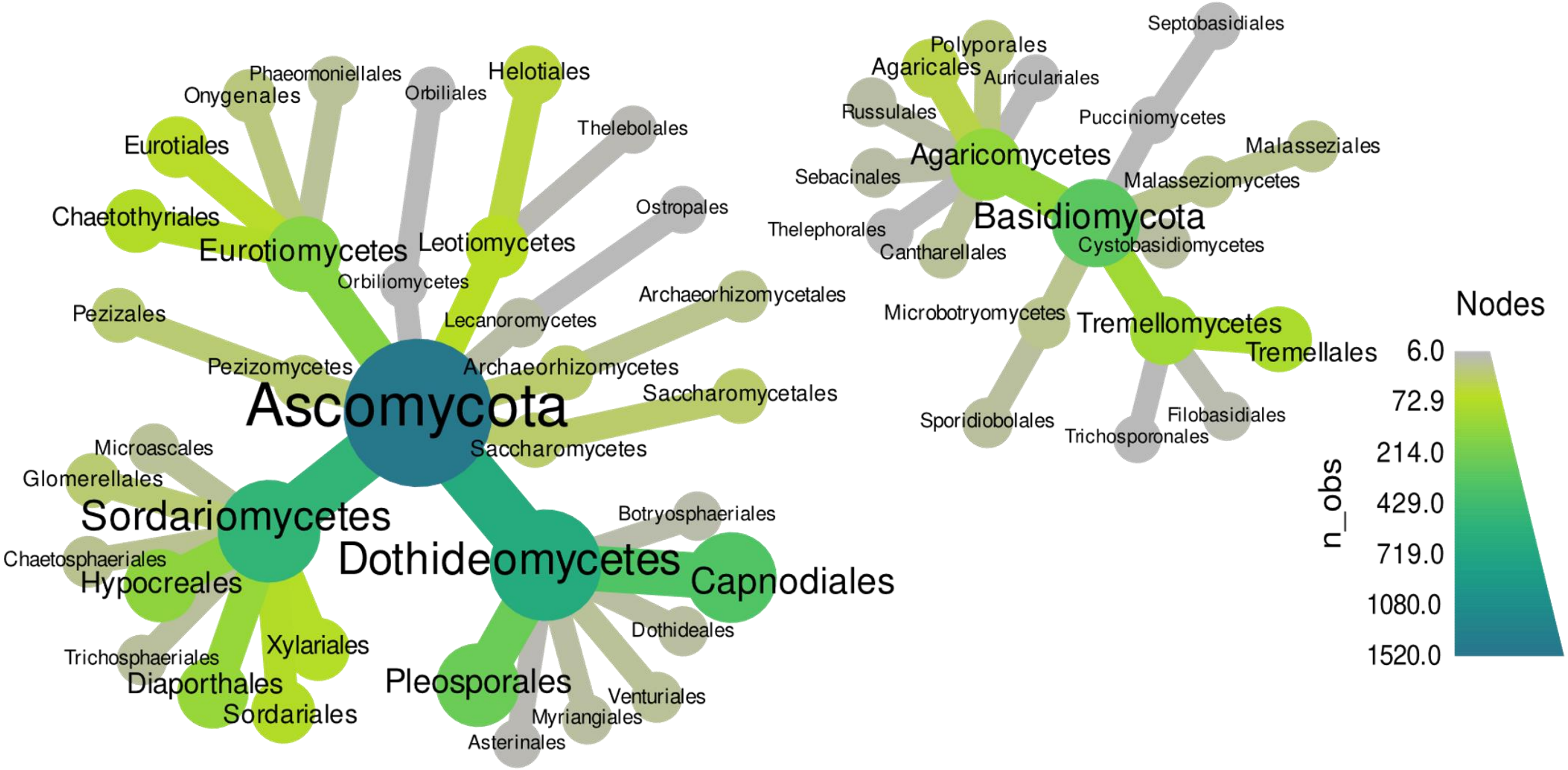


Figure 33. Heat tree showing the distribution of operational taxonomic units (OTUs) of leaf endophytic fungi related to six plant species. Each node represents a taxonomic group, and the borders determine where it fits into the overall taxonomic hierarchy. Node diameter is proportional to the number of reads for each OTUs; while the color represents the percentage of OTUs assigned based on the closest reference similarity (>90% sequence identity).

4.5. Relative abundance

The relative abundance of the endophytic fungal community at the phylum level revealed that *Ascomycota* was the most abundant in the hosts *S. ferrugineus* (97%-99%), *D. miscolobium* (91%), *L. dasycarpum* (65-95%), *Q. parviflora* (90%), and *O. hexasperma* (71%-85%). For *C. brasiliense* the abundance of *Ascomycota* varied among the hosts from 27% to 68% among the three individuals sampled. It is important to note that more than 60% of the taxonomic attributions made of the endophytic fungi community in two samples of *Q. parviflora* and two samples of *C. brasiliense* were classified only at the Fungi Kingdom level (Figure 34). The host *O. hexasperma* presented the highest values for abundance of *Basidiomycota* (3%-22%). In the other hosts, *Basidiomycota* represented <2% of the relative abundance. Other phylum, such as *Olpidiomycota, Glomeromycota,* and *Rozellomycota*, were reported in the host *C. brasiliense*, but in lower abundance (<1%).

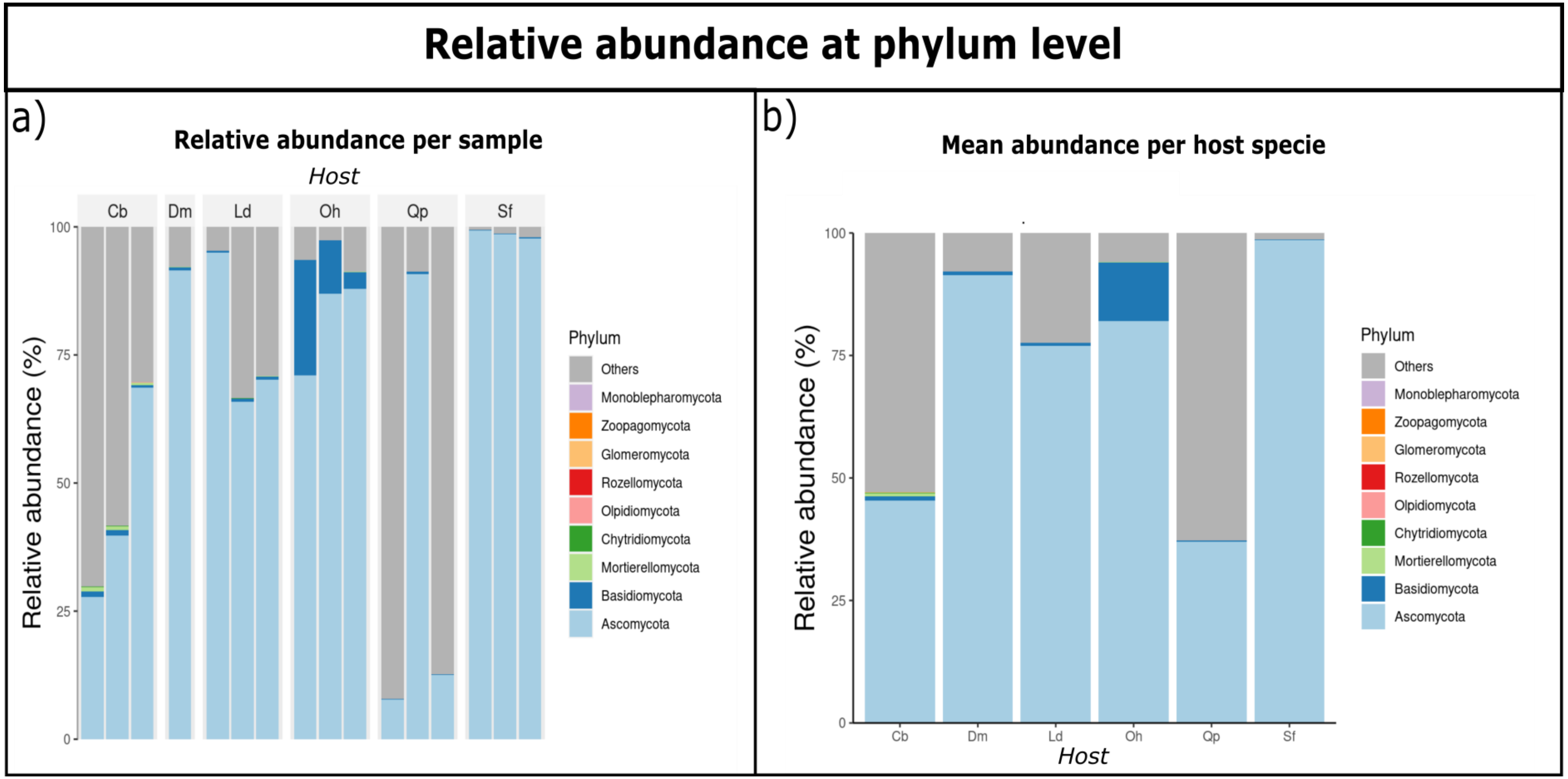


Figure 34. Phylum-level relative abundance of the leaf endophytic fungal community associated with six Cerrado woody species. In a) the relative abundance by sampling effort per host is shown; while in b) the average relative abundance by host species. Sequences classified only at kingdom level were grouped into “Others”. Cb: *Caryocar brasiliense*; Dm: *Dalbergia miscolobium*; Ld: *Leptolobium dasyrcarpum*; Oh: *Ouratea hexasperma*; Qp: *Qualea parviflora*; and Sf: *Styrax ferrugineus*.

The class *Sordariomycetes* was the most abundant in both hosts, followed by *Dothideomycetes*. At the taxonomic level of order, the distribution of taxa varied greatly between hosts (Figure 35). In *S. ferrugineus* the order *Asterinales* was the most abundant (mean 73%), followed by *Hypocreales* (mean 9.6%) and *Capnodiales* (8.3%). For Q. *parviflora* and *C. brasiliense*, *Capnodiales* were the most abundant in both hosts, with mean abundances of 31% and 24%, respectively. In O*. hexasperma, Pleosporales* (mean 39%), *Diaporthales* (mean 12%), and *Tremelales* (mean 9.7%) were the most abundant orders. Similar to *O. hexasperma, Pleosporales* (44%) and *Diaporthales* were the most abundant orders in *D. miscolobium*. In the host *L. dasycarpum* were *Capnodiales* (mean 37%) and *Diaporthales* (mean 27%).

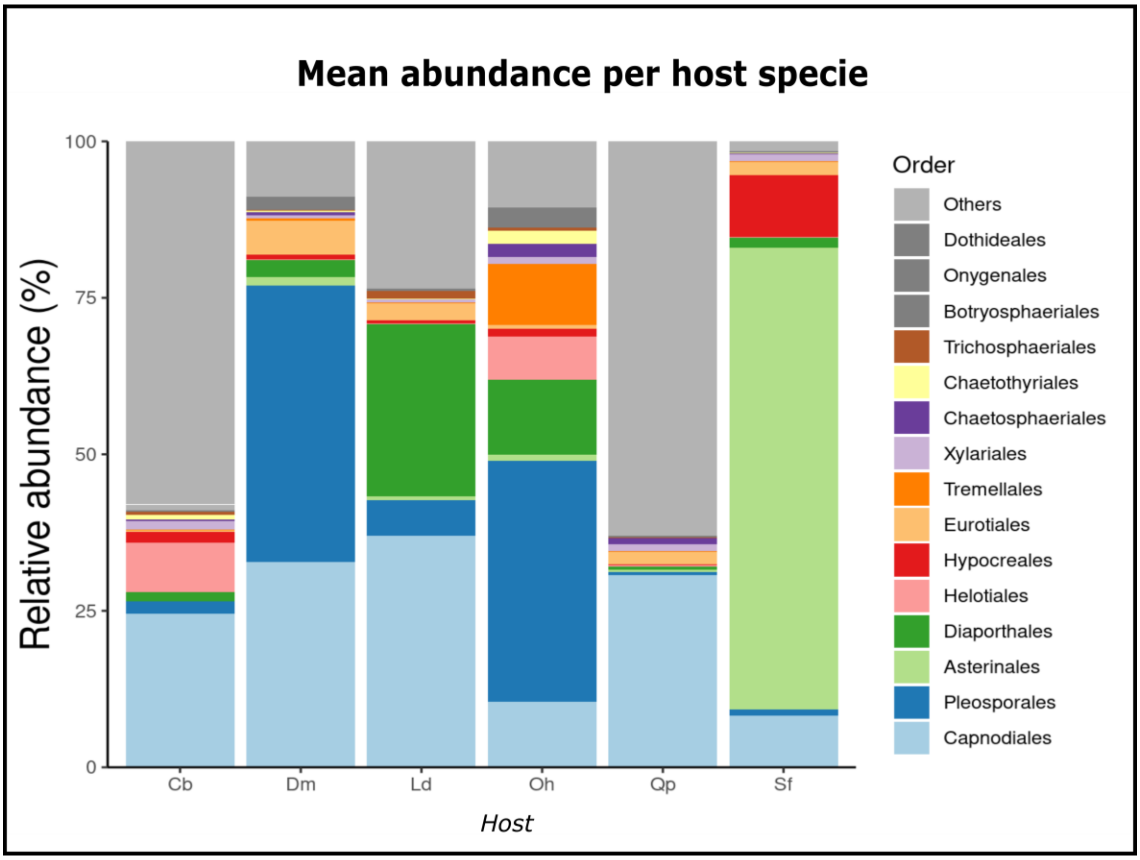


Figura 35. Order-level relative abundance of the leaf endophytic fungal community associated with six Cerrado woody species. The relative abundance by host species is sampled. Sequences classified only at kingdom level were grouped into "Others". Cb: *Caryocar brasiliense*; Dm: *Dalbergia miscolobium*; Ld*: Leptolobium dasyrcarpum*; Oh: *Ouratea hexasperma*; Qp: *Qualea parviflora*; and Sf: *Styrax ferrugineus*.

The data suggest the presence of more than 100 fungal families as constituents of the foliar endophytic fungal community in all hosts. In order to improve data visualization, taxonomic families with an abundance < 1% were grouped into “Others” (Figure 36b). In total, 40 families of endophytic fungi showed significantly different abundances among the six plant hosts analyzed (Figure 36a). *Parmulariaceae* was the most abundant family in *S. ferrugineus*, while *Mycospharellaceae* was the most abundant in *Q. parvilhora* and *C. brasiliense*. For *L. dasyrcarpum* it was *Diaporthaceae*, for *O. hexasperma* it was *Didymosphaeriaceae* and, finally, for the host *D. miscolobium*, it was the *Didymellaceae* family.

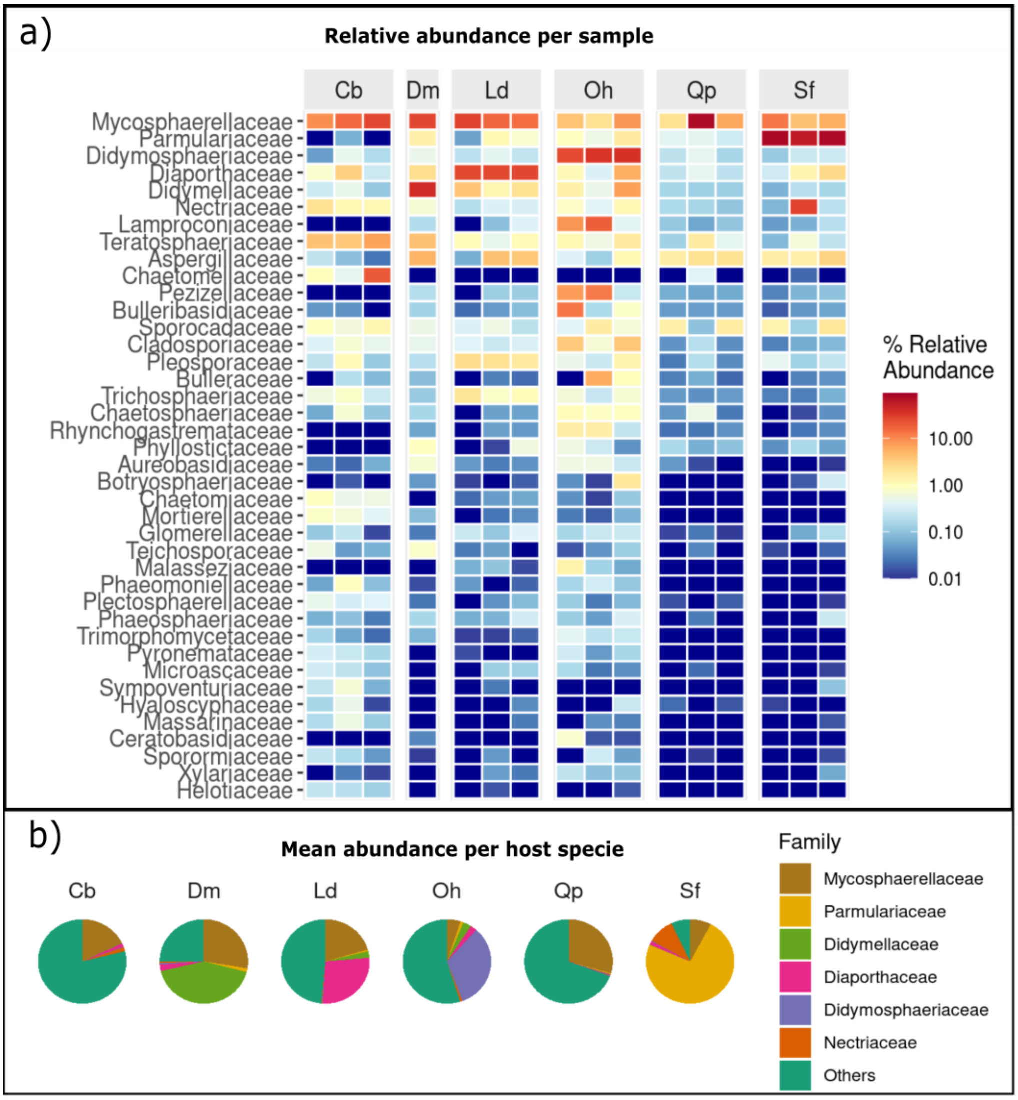


Figure 36. Data on the taxonomic composition of the endophytic fungal community at the taxonomic family level. a) Heatmap of fungal families with significant differences (p<0.05) among the six host species. Relative abundance data were z-score normalized by line. Darker red indicates greater abundance,

while white indicates absence. In b) the mean of the most abundant fungal families in each host species is shown (three individuals sampled per species). The families with less than 2% abundance and sequences classified only at kingdom level were grouped under “Others”. Cb: *Caryocar brasiliense*; Dm: *Dalbergia miscolobium*; Ld*: Leptolobium dasyrcarpum*; Oh: *Ouratea hexasperma*; Qp: *Qualea parviflora*; and Sf: *Styrax ferrugineus*.

A total of 487 genera of endophytic fungi were identified, which are heterogeneously distributed among the different species of host plants (complementary table 1). The 40 genera that showed significantly different values (p < 0.05) among the six host species are shown in Figure 37a. The most abundant genus in *S. ferrugineus* was *Purmularia*, in *C. brasiliense* it was *Paramycosphaerella*, in *Q. parviflora* it was *Madagascaromyces* and in *O. hexasperma* it was *Kalmusia* (Figure 37b). In *D. miscolobium* the most abundant genera were *Didymella* and *Paramycospharella* while in *L. dasyrcarpum* they were *Diaporthe* and *Paeamycospharella*.

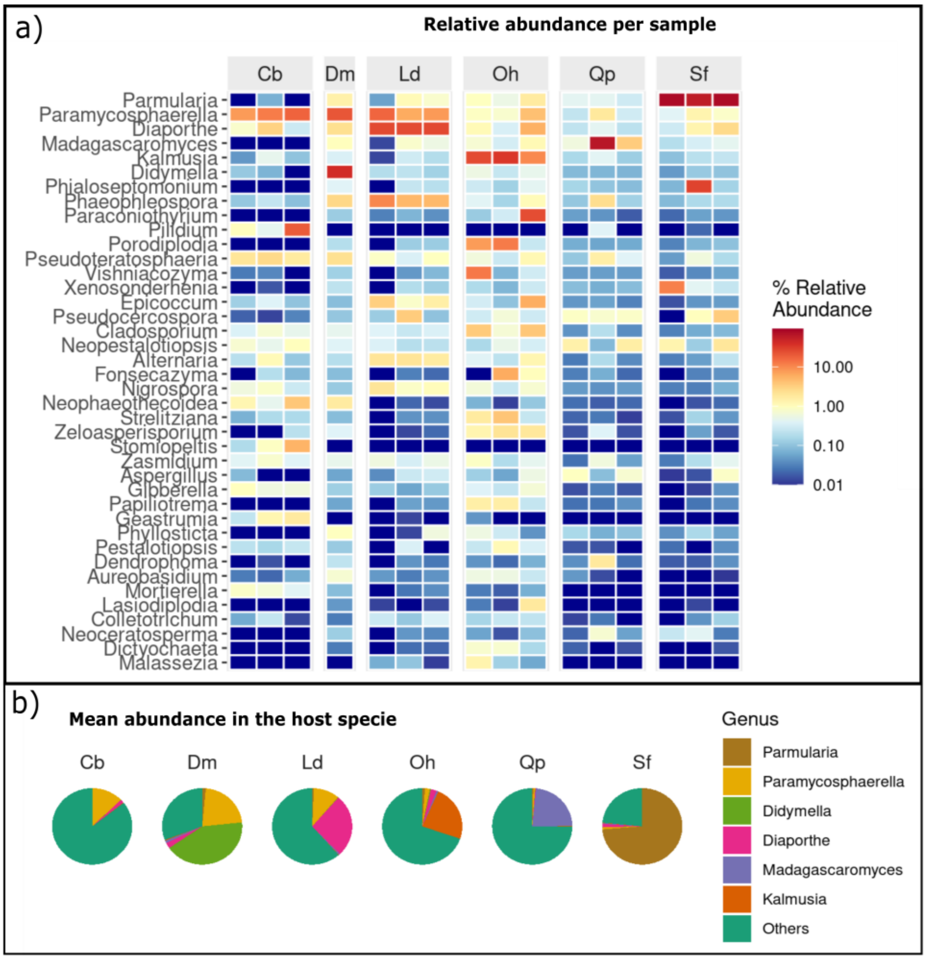


Figure 37. Data on the taxonomic composition of the endophytic fungal community at the taxonomic genus level. a) Heatmap of fungal genus with

significant differences ($p<0.05$) among the six host species. Relative abundance data were z-score normalized by line. Darker red indicates greater abundance, while white indicates absence. In b) the mean of the most abundant fungal genus in each host species is shown (three individuals sampled per species). The genus with less than 2% abundance and sequences classified only at kingdom level were grouped under “Others”. Cb: *Caryocar brasiliense*; Dm: *Dalbergia miscolobium*; Ld*: Leptolobium dasyrcarpum*; Oh: *Ouratea hexasperma*; Qp: *Qualea parviflora*; and Sf: *Styrax ferrugineus*.

4.6. Alpha and Beta diversity

The influence of the host species identity factor on the richness and evenness of endophytic fungi was evaluated by different alpha divers ity indices. Pielou's evenness, Faith's Phylogenetic Diversity and Shannon's Entropy indicate that the greatest species richness of endophytic fungi are present in the species *Caryocar brasiliense* and *Ouratea hexasperma*, while *Qualea parviflora* and *Styrax ferrugineus* presented the lowest values for all indices when compared with the other four species sampled.

Significant statistical differences ($p < 0.03$) were observed in all diversity indices used here when the host species were compared with each Other (Figure 38). The Kruskal-Wallis Pairwise test showed in which groups these differences were found. Pielou evenness, an index that measures the distribution of individuals between species, and Faith's phylogenetic diversity, an index that measures the diversity of species in a given niche based on the number of species present and the phylogenetic difference between them, showed significant differences ($p < 0.05$) in the diversity of endophytic leaf fungi existing in the host *C. brasiliense*, which differed from the hosts *L. dasycarpum, O. hexasperma, Q. parviflora and S. ferrugineus* ($p= 0.05$); *L. dasycarpum* differed from the species *O. hexasperma*, *Q. parviflora* and *S. ferrugineus* ($p=0.05$); while *O. hexasperma*, *Q. parviflora* and *S. ferrugineus* also differed from each other ($p=0.05$). Shannon entropy showed statistical differences between these same species, with the exception of *O. hexasmerpa* when compared to *S. ferrugineus*; and *C. brasiliense* when compared to *L. dasycarpum* and *O. hexasperma* ($p> 0.05$).

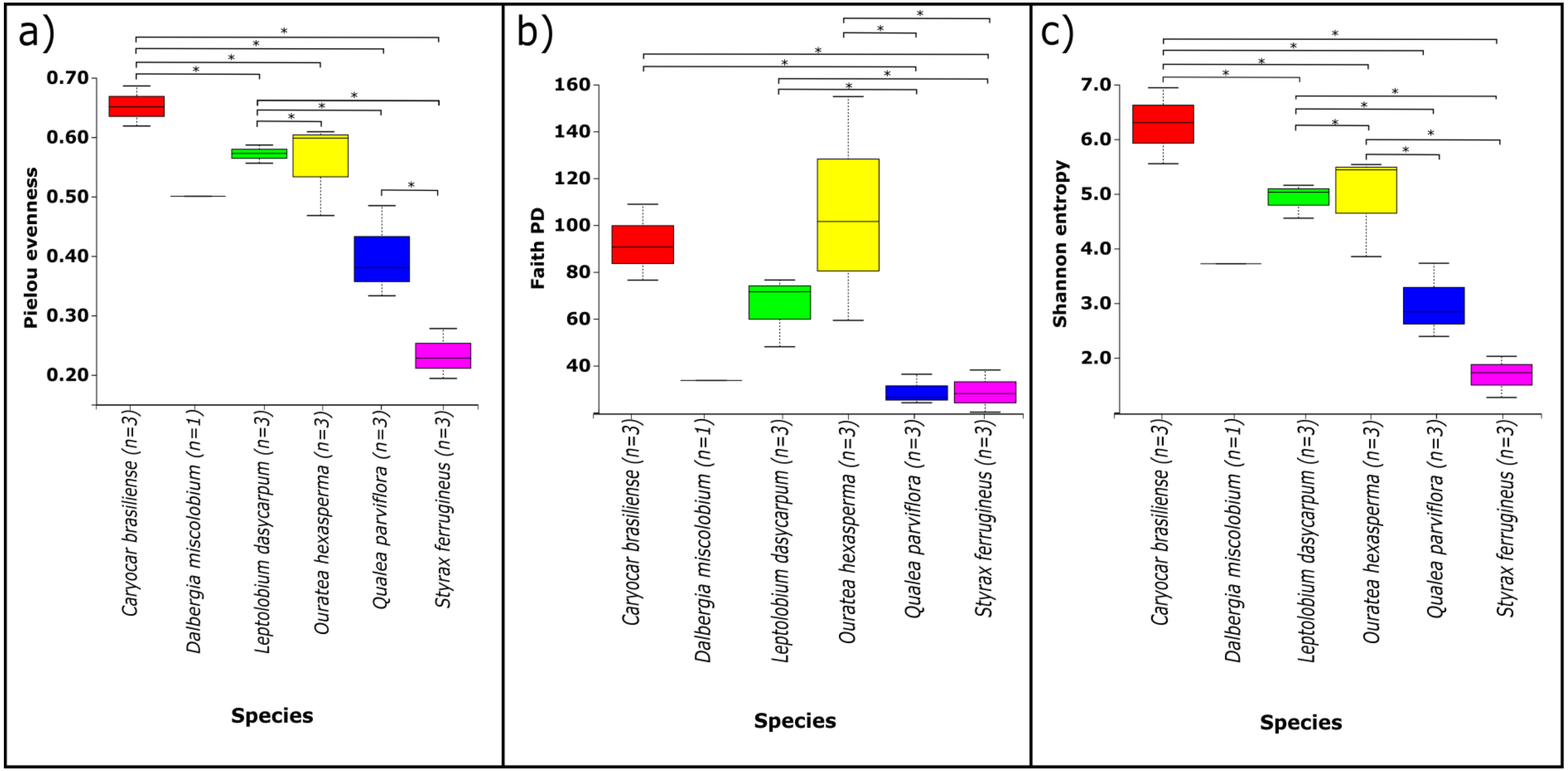


Figure 38. Alpha diversity indices. a) Pielou evenness, b) Faith's phylogenetic diversity and c) Shannon's entropy of the leaf endophytic mycobiota of the hosts *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperna* and *Styrax ferrugineus*. The "*" shows where statistically significant differences were found between the community of endophytic fungi among the different host species (p<0.05 pairwise comparison Kruskal-Wall pairwise test). The boxplots represent the inter-hip range (IQR) between the first and third quartiles (25th and 75th percentiles, respectively). The tails represent the lowest and highest values found, and the middle horizontal line inside the box represents the mean.

The low values of Pielou evenness in the hosts *S. ferrugineus* and *Q. parviflora* are strong indications that there is low evenness in the distribution of species of endophytic fungi that occur in this host, suggesting that a certain taxonomic group is dominant in relation to the other existing ones. On the other hand, the values close to 1.0 of equitability for the other host plants are strongly suggestive that the distribution of individuals (*amplicons*) among the species of endophytic fungi is more equitable. The high value of the PD index for the endophytic fungal community in *O. hexasperma* shows that the fungal species in this host are not phylogenetically close, suggesting that the *pool* of fungal species that colonizes it endophytically presents different evolutionary lines. The PD value in the other species shows that the mycobiota in them is composed of phylogenetically close fungi. The Shannon entropy value shows which communities of endophytic fungi are richest in species, the most diverse being C. *brasiliense, O. hexasperma*, and L. *dasycarpum;* and the least diverse being *S. ferrugineus, Q. parviflora*, and *D. miscolobium*.

The principal coordinate analysis (PCoA), derived from the Bray curtis distance, shows a uniform distribution pattern between the biological replicas of the same host species (Figure 39a). However, when the endophytic mycobiota of the different species of host plants is compared with each other, significant differences are not observed ($p > 0.05$) (Figure 39b). However, it should be considered that although there are no significant differences, it does not mean that the communities of endophytic fungi are homogeneous in terms of taxonomic composition. The endophytic mycobiota of the hosts *Q. parviflora, O. hexasperma* and *C. brasiliense* present greater dissimilarity in relation to the community of *S. ferrugineus* and *L. dasycarpum*.

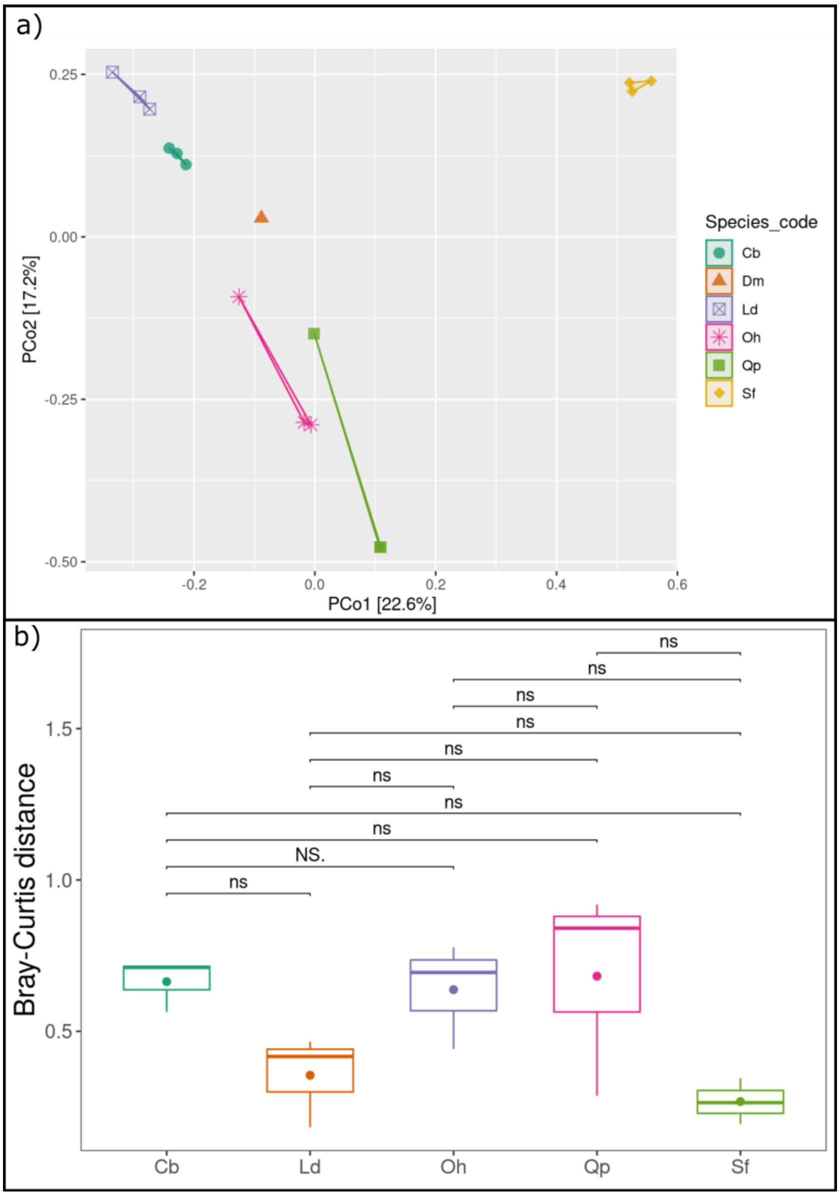


Figure 39. Beta diversity of the endophytic fungal community in six Cerrado woody species. In a) Principal coordinates Analysis (PCoA) derived from Bray Curtis distances between samples of the six host species (p= 0.0001 by PERMANOVA). The colored dots represent the different species of host plants. In b) the Bray Curtis distance between the community of the six hostesses is shown. D. miscolobium was not considered. The boxplots represent the inter-hip range (IQR) between the first and third quartiles (25th and 75th percentiles, respectively). The tails represent the lowest and highest values found, and the middle horizontal line inside the box represents the mean. Cb: *Caryocar brasiliense*; Dm: *Dalbergia miscolobium*; Ld: *Leptolobium dasyrcarpum*; Oh: *Ouratea hexasperma*; Qp: *Qualea parviflora*; and Sf: *Styrax ferrugineus*.

4.7. Differential abundance

Differential abundance analyzes were performed to identify which fungal groups are responsible for the differences between the communities of the different host species. The Ancom test showed considerable statistical differences in the percentage of abundance at six taxonomic levels (Phylum, subphylum, class, order, family, and genus) in the foliar endophytic fungal community among the six plant species analyzed. The abundance of the phylum *Mortierellomycota* (W= 7) and *Chytridiomycota* (W= 7) was significantly higher in the host *C. brasiliense* compared to the other plant species analyzed (Figure 40); the phylum *Basidiomycota* (W= 5) presented the highest percentage of abundance in the host *Ouratea hexasperma*, followed by *Caryocar brasiliense* and *Leptolobium darsycarpum*. The subphylum *Ustilaginomycetes* (W= 32) and the classes *Malasseziomycetes* (W= 30), and *Pezizomycetes* (W= 31) were also more abundant in *O. hexasperma*.

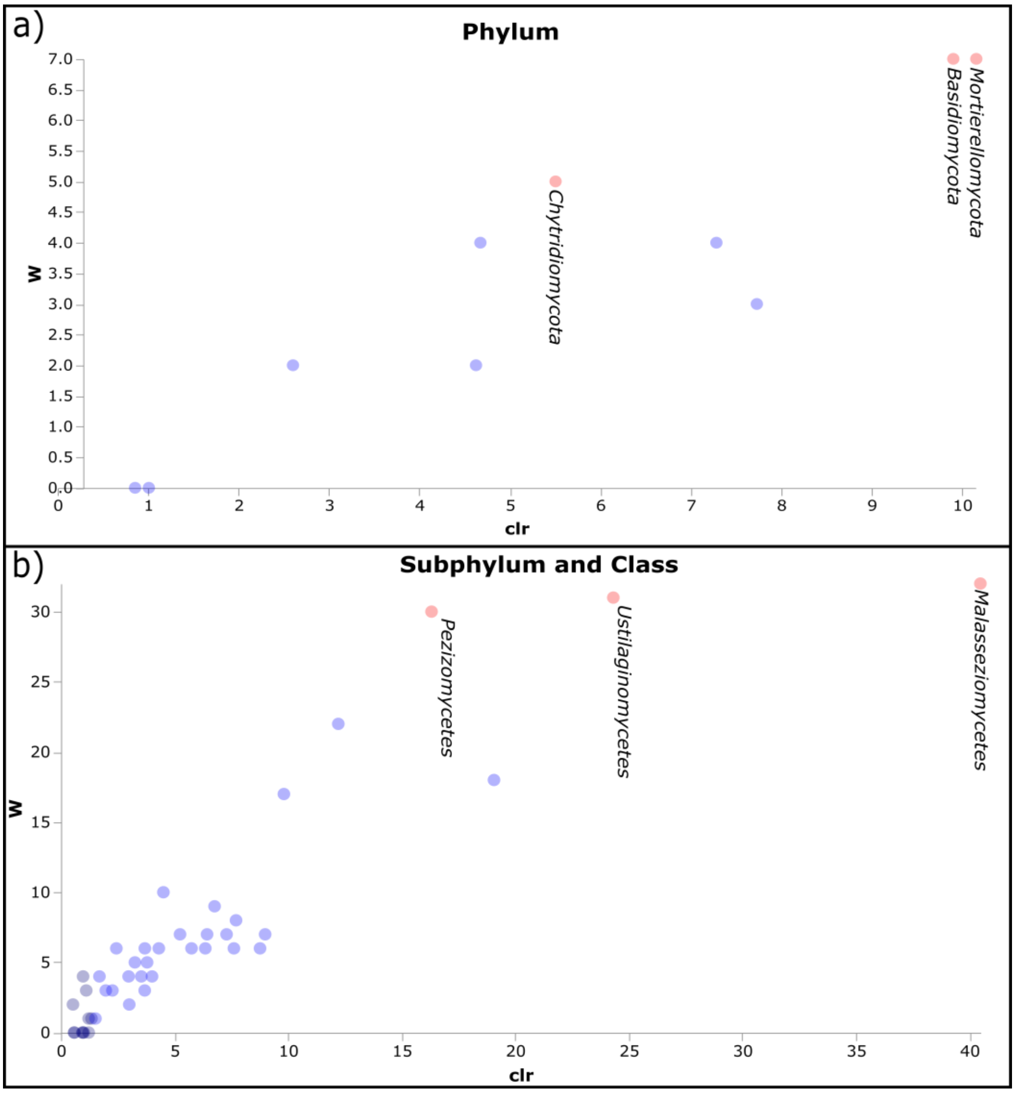


Figure 40. Vulcanoplot of differential endophytic fungal community abundance among the six hosts. ANCOM generated volcanic plots showing

differentially abundant features among the hosts *Caryocar brasiliense, Dalbergia miscolobium, Leptolobium dasycarpum, Qualea parviflora, Ouratea hexasperna* and *Styrax ferrugineus*. The W is the ANCOM test statistic and demonstrates the number of times the null hypothesis is rejected by the analysis. The higher the value of W, the greater the probability that a characteristic differs statistically. The clr shows the change in size between the groups compared by the test. The statistically expressive characteristics found among the host species were labeled at the level of a) phylum and b) subphylum/class.

Considering a more general taxonomic classification, the order *Asterinales* (W= 103) and family *Parmulariaceae* (W= 234) were substantially more abundant in *Styrax ferrugineus* compared to the other host plant species. For genus level, *Mastigosporella* (W= 416) was more abundant in *Q. parviflora*, while *Pseudombrophila* (W=268) and *Tausonia* (W= 317) were more abundant in *Caryocar brasiliense*. These findings suggest that the identity of the host plants tested here influenced the structuring of the endophytic fungal community related to them.

Using the *Metastats* method (White et al., 2009), a test used based on counting data obtained through sequencing to detect differentially abundant characteristics between different sample groups, treatments, host species etc., which are generally not shown in the tests commonly used to assess differential abundance, showed that other taxonomic groups at the genus level may be contributing significantly to the differences between endophytic fungal communities among host plant species (Figure 41).

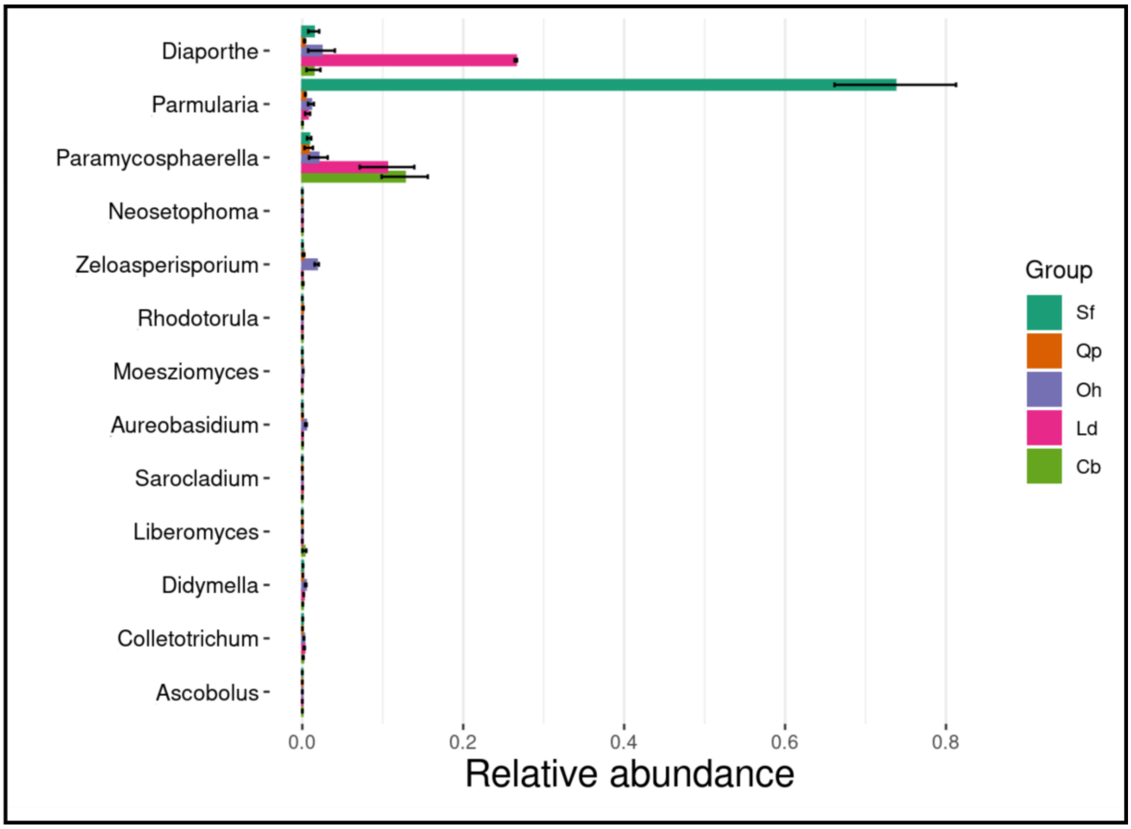


Figure 41. Taxon (genus-level) differentially abundant among the different host species shown by the *Metastat*. On the Y-axis, the main differentially abundant genera are shown; the X-axis shows the relative abundance of each, respectively. The host plant *Dalbergia miscolobium* was not considered, since *Metastat* requires at least two biological replicas for each group. Cb: *Caryocar brasiliense*; Ld*: Leptolobium dasyrcarpum*; Oh: *Ouratea hexasperma*; Qp: *Qualea parviflora*; and Sf: *Styrax ferrugineus*.

5. DISCUSSION

5.1. Cultivation dependent methods

Our findings show that the community of cultivable endophytic fungi related to plant species from the Brazilian Cerrado, a dry tropical savanna, is diverse in genera and species, corroborating the results of other studies (Carvalho et al., 2012; Noriler et al., 2018) and further reinforcing the importance of this biome as a reservoir of microbial species. Furthermore, to the best of our knowledge, this is the first report of the community of endophytic foliar fungi associated with the hosts *L. dasycarpum* and *Q. parviflora*, and also one of the first to gather information on the diversity of cultivable endophytic fungi related to six plant species, host species, since most studies are focused on characterizing the endophytic mycobiome of one to two host species (Carvalho et al., 2012; Ferreira et al., 2017; Noriler et al., 2018).

All endophytic fungal isolates recovered from the six plant species analyzed here belong to the phylum *Ascomycota*, which was expected, since the majority of cultivable endophytic fungi are ascomycetes (Li et al., 2016; Du et al., 2020; An et al., 2020). Studies show that although ascomycetes comprise the dominant group of the cultivable endophytic fungi community, the phylum *Basidiomycota* occurs in a smaller proportion (Li et al., 2016; Du et al., 2020; An et al., 2020). However, in our study, none of the isolates were classified as basidiomycetes and this may be related to the sampling effort employed (24 segments of leaf tissue per host species), since, as *Ascomycota* is the dominant group, a greater effort sampling would be necessary to sample rare and low-abundance species (de la Sancha et al., 2019; Botella et al., 2020), in this case, the basidiomycetes. The findings regarding species estimation reinforce this explanation, as they demonstrate that for the endophytic fungal community of five of the six hosts, species diversity was partially demonstrated.

Other explanations for the absence of fungal isolates belonging to *Basidiomycota i*nvolve the conditions of isolation and cultivation. In our study, we chose to use the PDA culture medium, as it is a medium rich in simple sugars considered generalist and traditionally used for the isolation of endophytic fungi (Du et al., 2020; Fontana et al., 2021). The sudden transition concerning the number of resources present between the leaf and the culture medium may end up favoring the isolation of ascomycetes fungi, since, although this group has a smaller genome (Shen et al., 2020) than the basidiomycetes (Mujic et al., 2017), Ascomycetes present rapid evolutionary rates, are metabolically versatile and can excel in adaptive and transitive capacities when compared to basidiomycetes (Wang et al., 2017; Wijayawardene et al., 2021). Thus, we can theorize that under the conditions tested, ascomycetes regulate their metabolism more efficiently than basidiomycetes, so that they use available resources quickly and become dominant. Other facts that may explain the absence of basidiomycetes fungi among the isolates may be linked to relationships of antagonism and inhibition, since the ability to produce metabolites with antimicrobial activity in culture medium is well known in ascomycetes fungi (Mapook et al., 2020).

The dominant class was *Sordariomycetes*, followed by *Dothideomycetes*, which is commonly reported in studies involving endophytic fungi (Li et al., 2016; Yang et al., 2018; Du et al., 2020; Na et al., 2020; Sarsaiya et al., 2020; Silva et al., 2022). In addition, these classes are the most diverse in species in Ascomycota (Hernández-Restrepo et al., 2017; Dube et al., 2018; Zhang et al., 2021) and have important fungal groups considered to be generalists that are known to establish symbiotic relationships with plants (Wang et al., 2020; Ortega et al., 2021).

In total, 22 genera and 50 species were identified, which is close to the results found by Noriler et al. (2018). The genus *Diaporthe* was dominant in the endophytic fungal community for the six species analyzed here, with more than twenty species recovered. This particular finding is in agreement with the information discussed in Chapter 1, where our survey of the diversity of endophytic fungi in Cerrado species showed that most of the species found belong to this genus (Figure 17). In addition, there are numerous reports of *Diaporthe* species as endophytes of woody species that occur in the most diverse terrestrial ecosystems (Dissanayake et al., 2020; Yang et al., 2021; Dong et al., 2021; Sun et al., 2021; Huang et al., 2021; Xu et al., 2021). Recent studies show that this genus of fungus is a paraphyletic group, with numerous species that evolved independently and are obligatorily endophytic fungi associated with woody species (Gao et al., 2017).

Other genera found here, such as *Alternaria, Phyllosticta, Epicoccum, Colletotrichum, Fusarium, Stenocarpella*, and *Lasiodiplodia*, have already been reported as endophytic fungi that occur in Cerrado species (Carvalho et al., 2012; Ferreira et al., 2017; Noriler et al., 2018) and in plant species from numerous other ecosystems (Li et al., 2016; Yang et al., 2018; Du et al., 2020; Na et al., 2020; Sarsaiya et al., 2020; Silva et al., 2020; ., 2022). However, as far as we know, the genera *Ascochyta, Clathrosporium, Dendrothyrium, Hymenopleella, Kalmusia, Melanconis, Monochaetia, Seiridium*, and *Stilbospora* are the first reported as endophytic fungi related to native Cerrado plant species. Among these genera, *Clathrosporium* and *Hymenopleella* are genera of fungi not yet described as endophytic. This information shows that the diversity of endophytic fungi in Cerrado species is high and harbors different taxonomic groups not yet reported as endophytic fungi.

Identification at lower taxonomic levels is critical for a better understanding of the taxonomic structure of the endophytic fungal community (Singh et al., 2017). Although there are intrinsic limitations to delimiting species using only the ITS region (Yahr et al., 2016; Amend et al., 2019; Lücking et al., 2020), for the in our case, this region allowed all the isolates to be classified at the genus level and part of them to reach the species delimitation. This ambiguity forced us to work with two data matrices, one at the genus level and the other at the species level, in the last case disregarding those taxa classified at the genus level. Despite the bivalence, this was enough to observe differences in the taxonomic structure of the community in terms of diversity/occurrence of genera and/or species in the different host plants. Thus, the ITS region, although it did not provide species resolution for all taxa, served the purpose of showing similarities or dissimilarities in the pool of cultivable endophytic fungi of the host species analyzed here. Furthermore, as discussed by Lücking et al. (2020) although the ITS region is not sufficient to delimit species, it provides sufficient taxonomic resolution for choosing the next molecular markers to be used.

The effect of the “environmental filter” that the taxonomic identity of the host plant exerts on the richness and abundance of fungal species that colonized it is already well known (Yao et al., 2019; Li et al., 2021; Zuo et al., 2021; AlSharari et al., 2022; Zhong et al., 2022) and was also observed in the present study. Most genera and isolated species were found in only one host plant species, suggesting host specificity. This becomes clear when observing the species sharing network between host species and it is noted that only a fraction of species occurs in more than two hosts. This may be related to numerous factors, such as phytochemistry and the micro and macronutrient content present in the leaf tissue of the plant, which acts by selecting the fungal species that will colonize it (Arnold et al., 2003; Noriler et al., 2019). It should also be considered that plant colonization by the endophytic fungus depends on genetic and molecular mechanisms present in both groups (Douanla-Meli et al. 2013; Carvalho et al. al., 2016). Therefore, these findings may be indicative that the endophytic fungal communities of the analyzed species are determined by the host identity factor.

5.2. Metabarcoding

Culture-independent tools such as *Metabarcoding* have been used to study fungal communities in numerous ecological niches (Rojas et al., 2020; Duan et al., 2021; Marczylo et al., 2021; Yang et al., 2022), which recently includes analyzes of the endophytic mycobiome of plant species in the most diverse terrestrial ecosystems (Chi et al., 2019; Yao et al., 2019; Durán et al., 2021). However, this is one of the first studies to use *Metabarcoding* to characterize the foliar endophytic fungal community of Cerrado plant species, especially *D. miscolobium, C. brasiliense, L. dasyrcarpum, O. hexasperma, Q. parviflora* and *S. ferrugineus*. In this way, our data provide previously unreported information about the richness, abundance and structure of the endophytic mycobiome of these species.

The *metabarcoding* result showed 562 OTUs that were distributed among the six host species, and of the total of OTUs, only 83.27% (468 OTUs) reached the taxonomic level of the genus. Studies using this tool to characterize the endophytic mycobiome of plant species from tropical and desert climates have shown that these communities are diverse and under-sampled by the traditional methods used to study the diversity of endophytic fungi (Chi et al., 2019; Yao et al., 2019; Durán et al., 2021). However, a high number of OTUs similar to those found here were only observed in the community of endophytic fungi associated with *Olea europaea*, in microbial communities associated with soil (Sato et al., 2015; Duan et al., 2021; Marczylo et al., 2021), and in community of forest epiphytic fungi (Materatski et al., 2018; Gomes et al., 2018; Castro et al., 2022). Therefore, our data demonstrate that the foliar endophytic fungal community that occurs in Cerrado plant species is highly species-diverse and underestimated by cultivation-dependent methodologies.

About 16.73% of OTUs were identified only at higher taxonomic levels such as class, phylum, and kingdom. These OTUs represent more than 50% of the fungal amplicons in the host *C. brasiliense* and more than 70% of the fungal amplicons in *Q. parviflora*. This particular finding raises some key questions about what we know in terms of the diversity of fungi that occur in the Cerrado, as these OTU may represent taxonomic groups that are not yet known. Methodological limitations should also be considered, since these OTUs may belong to already known taxonomic groups, but do not have sequences deposited in databases, which makes comparison impossible (Lücking et al., 2020; Gautam et al., 2022). In any case, the use of tools such as *metabarcoding* has brought up an important discussion on understanding the diversity of fungi that occur in all ecological niches (Vargas-Gastélum et al., 2020; Gautam et al., 2022).

The phylum *Ascomycota* was dominant in the community of endophytic fungi of all six species of host plants, corresponding to more than 80% of the OTUs classified at taxonomic levels below Kingdom Fungi; while *Basidiomycota* was found in a smaller proportion. This finding was expected since the community of endophytic fungi is predominantly composed of ascomycetes fungi (Chi et al., 2019; Yao et al., 2019; Castro et al., 2020; Durán et al., 2021). The highlight is the fact that the metabarcoding showed that the community of endophytic fungi of the host species analyzed here had other phyla besides *Ascomycota* and *Basidiomycota*, namely *Monoblepharomycota, Mortierellomycota, Olpidiomycota, Glomeromycota, Chytridiomycota, Rozellomycota*, and *Zoopagomycota*. These fungal phyla were recently proposed (Tedersoo et al., 2018) and, to the best of our knowledge, this is the first report of them as members of the foliar mycobiome of plant species native to the Cerrado.

Except for *Glomeromycota*, a well-studied phylum of plant symbiotic fungi (Lee et al., 2018), the knowledge we have about *Monoblepharomycota, Mortierellomycota, Olpidiomycota, Glomeromycota, Chytridiomycota, Rozellomycota* and *Zoopagomycota* concerning lifestyle and evolution is still quite limited, being built over the last four years through multigene and phylogenetic phylogeny approaches (Tedersoo et al., 2018; Wijayawardene et al., 2018; James et al., 2020). Our findings may help to resolve important questions about the variety of ecological niches in which these taxonomic groups occur.

The class *Sordariomycetes* followed by *Dothideomycetes* were the two dominant classes in the endophytic mycobiome of the six host species. Other studies using a methodology similar to that used here (Chi et al., 2019; Yao et al., 2019; Castro et al., 2020; Durán et al., 2021), as well as cultivation-dependent methodologies (Noriler et al., 2018), bring the same result. This may be related to the fact that these classes are the most diverse in *Ascomycota* and are known to have orders and fungal families that establish ecological relationships with plants (Li et al., 2016; Hernández-Restrepo et al., 2017; Dube et al., 2018; Yang et al., 2018; Du et al., 2020; Na et al., 2020; Sarsaiya et al., 2020; Wang et al., 2020; Ortega et al., 2021; Zhang et al., 2021; Silva et al., 2022).

Although the phyla and dominant classes of the endophytic fungal community were the same for both hosts, starting from the order level our study shows that the endophytic fungal community of the six host species harbors a unique mycobiome, with occurrence, richness, and dominance of families, genera, and species of endophytic fungi specific to each host. The *Parmulariaceae* family and the *Parmularia* genus were dominant in *S. ferrugineus*. The association of these groups of fungi with this host plant is already known and extensively studied (Guatimosim et al., 2015; Guatimosim et al., 2016; de Souza, 2017). In *D. miscolobium* the dominant family and genus were *Didymellaceae* and *Dydimella*. In this host in question, this fungal genus, in its asexual form (*Phoma*), has already been studied (Braz et al., 2000). In the other hosts, numerous genera were dominant, belonging to the families *Mycospharellaceae, Diaporthaceae*, and *Didymosphaeriaceae*. These fungal families are known to have numerous species that establish symbiotic or parasitic relationships with woody plant species (Videira et al., 2017; Samarakoon et al., 2020; Huang et al., 2021; Xu et al., 2021).

Alpha diversity metrics show that the endophytic mycobiome of all hosts is similarly rich (Shannon and PD) and has an organization in terms of equity and dominance of specific fungal species for each host (Pielou evenness). Our data suggest that the endophytic mycobiome of native Cerrado species is more species-diverse than the endophytic mycobiome of mangrove plant species (Yao et al., 2019), desert (AlSharari et al., 2022) and grasses from temperate regions (Durán et al., 2021). Furthermore, the alpha diversity of fungi observed here is higher than that observed in other ecological niches, which include soil (Gschwend et al., 2021), phyllosphere (Li et al., 2022), and aquatic environments (Pang et al., 2019).

The communities of endophytic fungi among the hosts, although equally diverse, show dissimilarities in terms of diversity and abundance of taxa, as shown by PCoA and by the Ancom and metastatic test. These differences are suggestive of the host factor as an environmental filter, which acts in the selection of taxa that will compose the endophytic mycobiome, as already reported in studies involving communities of endophytic fungi (Chi et al., 2019; Yao et al., 2019). This fact can be reinforced by the metastatic result (White et al., 2009), since this method shows the taxa that are significantly influenced by a certain characteristic, in this case, the host identity.

5.3. Dependent and independent cultivation-methods

Due to sample differences, it is not possible to compare the data obtained from the cultivation-dependent and *metabarcoding* methods. However, we have important considerations to make about both methodologies.

The ITS region is a primary DNA barcode used for fungal identification (White et al., 1990). This was our region of choice for dependent cultivation methods and *metabarcoding*, and it met our primary goal, which was to report diversity, similarities, or dissimilarities in the endophytic fungal community. However, for molecular identification of the isolates, the pair of primers used (Vilgalys et al., 1990; Hoog et al., 1998) allows the amplification of fragments > 1000pb (ITS1-5.8S-ITS2) which helps in the resolution of some taxonomic inconsistencies when compared to smaller fragments (Ebach et al., 2011). As discussed, the size of the fragment can facilitate the taxonomic delimitation of certain groups, but it must be considered that the inclusion of conserved regions, such as the 18S and or 5.8S regions, can result in the formation of chimeric sequences, making sequencing impossible (Haas et al., 2011).

For *metabarcoding*, the generated fragments presented sizes of 300-400 bp, which may be enough to delimit some genera, but it is important to note that short fragments can generate erroneous identifications or taxonomic delimitations at higher levels of family, order, class etc. (Lücking et al., 2020; Durán et al., 2021). For example, the isolate identified as *Codinaea* sp., based on the ITS1-5.8S-ITS2 region, was identified only as *Chaetosphaeriaceae* using metabarcoding. This may be one of the facts that could explain the high number of OTUs identified at a higher level than the family in our study. On the other hand, metabarcoding makes it possible to cover greater diversity, which cannot be achieved using traditional cultivation methods or which would require substantial sampling effort (Lücking et al., 2020; Durán et al., 2021; Wijayawardene et al., 2021). Furthermore, this approach shows taxonomic groups that are not possible to be cultivated (Shapiro et al., 2021).

The cultivation-dependent methods showed that *Diaporthe* spp. was present in all host species and this was also shown by metabarcoding. However, metabarcoding showed that *Diaporthe* spp. was present in all hosts, but was not the dominant genus of the mycobiome for most of them. For example, *Parmularia* spp. was dominant in *S. ferrugineus*, but none of the isolates from this host belonged to this genus. In this way, metabarcoding proved to be more efficient.

In the context of observing dissimilarities, both methods met this objective. However, it was more complete using *metabarcoding*. In contrast, isolation and cultivation-dependent methods provide isolates, which represent a precious genetic resource, which can be used for bioprospecting (Noriler et al., 2018). In conclusion, our work demonstrates that the analysis of the diversity of endophytic fungi is more complete using culture-dependent and culture-independent approaches.

6. CONCLUSION

The endophytic mycobiome of the plant species analyzed here is diverse and differs between hosts in terms of occurrence, equity, and dominance of fungal species. In addition, the composition of the community of endophytic fungi is affected by the identity of the host plant, as some endophytic fungi show preferences for a certain species of the host plant.

Both methodologies used allowed the observation of dissimilarity trends between the leaf endophytic mycobiome of the host species. However, comparatively, metabarcoding produced more consistent results, showing the richness and diversity of taxa not observed in the cultivation-dependent methods.

Despite the promising results produced by metabarcoding, the combination of this with the cultivation-dependent methodology is the best option, since the first method measures ecological data and the second provides a genetic pool in terms of an isolate.

Finally, the current study provides important data for future studies of the endophytic fungal community, both in terms of the choice of methodologies employed, as well as in the elaboration of experimental designs.

BIBLIOGRAPHIC REFERENCES

1. Alibrandi P, Schnell S, Perotto S, Cardinale M. Diversity and structure of endophytic bacterial communities associated with three terrestrial orchid species, as revealed by 16S rRNA Gene Metabarcoding. *Frontiers Microbiology*. 2020; 11: 604964.
2. Al-Maliki S, Al-Masoudi M. Interactions between Mycorrhizal Fungi, Tea Wastes, and Algal Biomass Affecting the Microbial Community, Soil Structure, and Alleviating of Salinity Stress in Corn Yield (*Zeamays* L.). *Plants (Basel)*. 2018; 7(3):63.
3. Almendras K, García J, Carú M, Orlando J. Nitrogen-Fixing Bacteria Associated with *Peltigera* Cyanolichens and *Cladonia* Chlorolichens. *Molecules*. 2018; 23(12):3077.
4. AlSharari SS, Galal FH, Seufi AM. Composition and Diversity of the Culturable Endophytic Community of Six Stress-Tolerant Dessert Plants Grown in Stressful Soil in a Hot Dry Desert Region. *J Fungi* (Basel). 2022; 28; 8(3):241. doi: 10.3390/jof8030241.
5. Alteio LV, Schulz F, Seshadri R, et al. Complementary Metagenomics Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. *mSystems*. 2020; 5 (2): e00768-19.
6. Amend A, Burgaud G, Cunliffe M et al. Fungi in the Marine Environment: Open Questions and Unsolved Problems. *mBio*. 2019; 5;10(2):e01189-18. doi: 10.1128/mBio.01189-18.
7. An C, Ma S, Shi X, Xue W, Liu C, Ding H. Diversity and Antimicrobial Activity of Endophytic Fungi Isolated from *Chloranthus japonicus* Sieb in Qinling Mountains, China. *Int J Mol Sci*. 2020; 19;21(17):5958. doi: 10.3390/ijms21175958.
8. Anguita-Maeso M, Olivares-García C, Haro C, Imperial J, Navas-Cortés JA, Landa BB. Culture-dependent and culture-independent characterization of olive xylem microbiota: effect of sap extraction methods. *Frontiers in Plant Science*. 2020; 10: 1708.
9. Araujo JF, de Castro AP, Costa MM, et al. Characterization of soil bacterial assemblies in Brazilian savanna-like vegetation reveals acidobacteria dominance. *Microbial Ecology*. 2012; 64(3): 760-770.
10. Arnold AE, Herre EA. Canopy cover and leaf age affect colonization by tropical fungal endophytes: Ecological pattern and process in *Theobroma cacao* (Malvaceae). *Mycologia*. 2003; 95(3): 388-398.
11. Arnold AE, Lutzoni FL. *Ecology Diversity and host range of foliar fungal endophytes: are tropical leaf biodiversity hotspots¿. Ecology.* 2007; 88: 541–549.
12. Arnold AE, Mejía L, Kyllo D, Rojas D, Maynard Z, Herre AE. Fungal endophytes limit pathogen damage in a tropical tree. *Proceedings of the National Academy of Sciences USA.* 2003; 100: 15649–15654.
13. Arnold AE, Miadlikowska J, Higgins KL, Sarvate SD, Gugger P, Way A, Hofstetter V, Kauff F, Lutzoni F. A phylogenetic estimation of trophic transition networks for ascomycete fungi: are lichens cradles of symbiotrophic fungi diversification?. *Systematic Biology.* 2009; 58: 283–297.

14. Arnold AE, Herre EA. Canopy cover and leaf age affect colonization by tropical endophytic fungi: ecological pattern and process in *Theobroma cacao* (Malvaceae). *Mycologia.* 2003; 95: 388 - 398.
15. Ateba JET, Toghueo RMK, Awantu AF, et al. Antiplasmodial Properties and Cytotoxicity of Endophytic Fungi from *Symphonia globulifera* (Clusiaceae). *Journal Fungi (Basel)*. 2018; 4(2):70.
16. Bálint M, Bartha L, O'Hara RB, Olson MS, Otte J, Pfenninger M, et al. Relocation, high latitude warming, and host genetic identity shape the foliar fungal microbiome of poplars. *Molecular Ecology.* 2015; 24: 235–248.
17. Batalha MA & Martins FR. The vascular flora of the cerrado in Emas National Park 427 (Central Brazil): a savanna flora summarized. *Brazilian Archives of Biology and Technology*. 2007; 50(2):269–277.
18. Bengtsson-Palme J, Ryberg M, Hartmann M, Branco S et al. Enhanced software detection and extraction of ITS1 and ITS2 from ribosomal ITS sequences from fungi and other eukaryotes for analysis of environmental sequencing data. *Methods Ecology*. 2013; 4: 919.
19. Bezerra JD, Nascimento CC, Barbosa Rdo N, et al. Endophytic fungi from medicinal plant *Bauhinia forficata*: Diversity and biotechnological potential. *Brazilian of Journal Microbiology*. 2015; 46(1): 49-57.
20. Bezerra JD, Santos MG, Svedese VM, et al. Richness of endophytic fungi isolated from *Opuntia ficus-indica* Mill. (Cactaceae) and preliminary screening for enzyme production. *World of Journal Microbiology Biotechnology*. 2012; 28(5):1989-1995.
21. Botella C, Joly A, Monestiez P, Bonnet P, Munoz F. Bias in presence-only niche models related to sampling effort and species niches: Lessons for background point selection. *Plos One*. 2020; 20;15(5):e0232078. doi: 10.1371/journal.pone.0232078.
22. Brannstrom C., et al. Land change in the Brazilian Savanna (Cerrado), 1986-2002: Comparative analysis and implications for land-use policy. *Land Use Policy*. 2008; 25: 579-595.
23. Bridgewater SMG, and Stirton CH. “A Morphological and Biogeographic Study of the *Acosmium Dasycarpum* Complex (Leguminosae: *Papilionoideae, Sophoreae*).” *Kew Bulletin*. 1997; 52(2): 471–475.
24. Bukovská P, Rozmoš M, Kotianová M, et al. Arbuscular Mycorrhiza Mediates Efficient Recycling From Soil to Plants of Nitrogen Bound in Chitin. *Frontiers Microbiology*. 2021; 12: 574060.
25. Caporaso et al. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK. QIIME allows analysis of high-throughput community sequencing data. *Nature Methods.* 2010; 7:335–336.
26. Carvalho APF, Bustamante MMC, kozovits AR and Asner GP. Variações sazonais nas concentrações de pigmentos e nutrientes em folhas de espécies de cerrado com diferentes estratégias fenológicas. *Revista Brasileira de Botânica.* 2007; 30, (1): 19-27.
27. Carvalho CR, Gonçalves VN, Pereira CB, Johann S, Galliza IV, Rosa CA, et al. The diversity, antimicrobial and anticancer activity of endophytic fungi associated with the medicinal plant *Stryphnodendron adstringens* (Mart.) Coville (Fabaceae) from the Brazilian savannah. *Symbiosis. 2012;* 57, 95–107. 10.1007/s13199-012-0182-2

28. Castellani A. A maintenance and cultivation of the comon pathogenic fungi of man in sterile distilled water: further researches. Journal of Tropical Medicine & Hygiene. 1967; 7:181-184.
29. Castro J, Costa D, Tavares RM, Baptista P, Lino-Neto T. Olive Fungal Epiphytic Communities Are Affected by Their Maturation Stage. *Microorganisms*. 2022; 5;10(2):376. doi: 10.3390/microorganisms10020376.
30. Chi WC, Chen W, He CC, et al. A highly diverse fungal community associated with the leaves of the mangrove plant Acanthus ilicifolius var. xiamenensis revealed by isolation and metabocoding analyzes. *PeerJ* . 2019; 7: e7293.
31. Chi WC, Chen W, He CC, Guo SY, Cha HJ, Tsang LM, Ho TW, Pang KL. A highly diverse fungal community associated with leaves of the mangrove plant *Acanthus ilicifolius* var. *xiamenensis* revealed by isolation and metabarcoding analyses. *PeerJ*. 2019; 9; 7:e7293. doi: 10.7717/peerj.7293.
32. Ciccolini V, Ercoli L, Davison J, Vasar M, Öpik M, Pellegrino E. Land-use intensity and host plant simultaneously shape the composition of arbuscular mycorrhizal fungal communities in a Mediterranean drained peatland. *FEMS Microbial Ecology*. 2016; 92(12):fiw186.
33. Clarke KR, Somerfield PJ, Chapman MG. On resemblance measures for ecological studies, including taxonomic dissimilarities and a zero-adjusted Bray–Curtis coefficient for denuded assemblages. J. Exp. Mar. Biol. Ecol. 2006;330:55–80.
34. Coelho LGF, Moreira GAM, Bomfim CA, & Vale HMM. Structure of yeast communities in fruits of different native plant species from the Brazilian Cerrado. *Journal of Neotropical Biology*, 2020; *17*(1): 35–46.
35. Cordeiro MAS, et al. Colonização e densidade de esporos de fungos micorrízicos em dois solos do Cerrado sob diferentes sistemas de manejo. *Pesquisa Agropecuária Tropical*. 2005; 35 (3): 147-153.
36. Costa AM. Efeito da adição de nutrientes em longo prazo nas interações acima e abaixo do solo de espécies lenhosas do Cerrado. Dissertação (Mestrado) Universidade de Brasília, Distrito Federal, Brasil. 2019.
37. Costa D, Fernandes T, Martins F, Pereira JA, Tavares RM, Santos PM, Baptista P, Lino-Neto T. Illuminating Olea europaea L. endophyte fungal community. *Microbiol Res*. 2021; 245:126693. doi: 10.1016/j.micres.2020.126693.
38. Cottenie K. Integrating environmental and spatial processes in the dynamics of ecological communities. *Ecology Letters. 2005;* 8: 1175–1182.
39. Coutinho BG, Licastro D, Mendonça-Previato L, Cámara M, Venturi V. Plant-influenced gene expression in the rice endophyte *Burkholderia kururiensis* M130*. 2015;* 28 10–21.
40. Davis EC, Shaw AJ. Biogeographic and phylogenetic patterns in liver-associated endophyte diversity. *American Journal of Botany.* 2008; 95: 914–924.
41. de Hoog GS, Gerrits van den Ende AH. Molecular diagnostics of clinical strains of filamentous Basidiomycetes. *Mycoses*. 1998; 41(5-6):183-9.
42. de la Sancha NU, Boyle SA. Predictive sampling effort and species-area relationship models for estimating richness in fragmented landscapes. *Plos One*. 2019; 31;14(12):e0226529. doi: 10.1371/journal.pone.0226529.

43. Del Carmen H Rodríguez M, Evans HC, de Abreu LM, et al. New species and records of *Trichoderma* isolated as mycoparasites and endophytes from cultivated and wild coffee in Africa. *Sci Rep*. 2021;11(1):5671.
44. Dhayanithy G, Subban K, Chelliah J. Diversity and biological activities of endophytic fungi associated with *Catharanthus roseus*. *BMC Microbiology*. 2019; 19 (1): 22.
45. Dissanayake AJ, Chen YY, Liu JJ. Unravelling *Diaporthe* Species Associated with Woody Hosts from Karst Formations (Guizhou) in China. *J Fungi* (Basel). 2020; 27;6(4):251. doi: 10.3390/jof6040251.
46. Dong Z, Manawasinghe IS, Huang Y, Shu Y, Phillips AJL, Dissanayake AJ, Hyde KD, Xiang M, Luo M. Endophytic *Diaporthe* Associated With *Citrus grandis* cv. Tomentosa in China. *Front in Microbiol*. 2021. 9; 11: 609387. doi: 10.3389/fmicb.2020.609387.
47. Dos Santos IR, Abdel-Azeem AM, Mohesien MT et al. Insights into the Bioprospection of Endophytic Fungi of the Medicinal Plant *Palicourea rigida* Kunth (Rubiaceae): Detailed Biological Activities. J Fungi (Basileia). 2021;7(9):689. doi: 10.3390/jof7090689.
48. Du W, Yao Z, Li J, Sun C, Xia J, Wang B, Shi D, Ren L. Diversity and antimicrobial activity of endophytic fungi isolated from Securinega suffruticosa in the Yellow River Delta. *Plos One*. 2020; 10;15(3):e0229589. doi: 10.1371/journal.pone.0229589.
49. Duan M, Bau T. Grassland fairy rings of Leucocalocybe mongolica represent the center of a rich soil microbial community. *Braz J Microbiol*. 2021; 52(3):1357-1369. doi: 10.1007/s42770-021-00478-3.
50. Dube G, Kadoo N, Prashant R. Exploring the biological roles of Dothideomycetes ABC proteins: Leads from their phylogenetic relationships with functionally-characterized Ascomycetes homologs. PLoS One. 2018; 2;13(8):e0197447. doi: 10.1371/journal.pone.0197447.
51. Durán M, San Emeterio L, Canals RM. Comparison of Culturing and Metabarcoding Methods to Describe the Fungal Endophytic Assemblage of *Brachypodium rupestre* Growing in a Range of Anthropized Disturbance Regimes. *Biology* (Basel). 2021; 29;10(12):1246. doi: 10.3390/biology10121246.
52. Ebach MC, Valdecasas AG, Wheeler Q.D. Impediments to taxonomy and users of taxonomy: Accessibility and impact evaluation. *Cladistics.* 2011;27:550–557. doi: 10.1111/j.1096-0031.2011.00348.x.
53. El-Sayed ASA, El-Sayed MT, Rady A, et al. Exploiting the Biosynthetic Potency of Taxol from Fungal Endophytes of Conifers Plants; Genome Mining and Metabolic Manipulation. *Molecules*. 2020; 25(13):3000.
54. Espírito-Santo MM, Leite ME, Silva JO, et al. Understanding patterns of land-cover change in the Brazilian Cerrado from 2000 to 2015. *Proceedings of the Royal Society B: Biological Sciences*. 2016; 371(1703): 20150435.
55. Fahey M., Rossetto M., Wilson PD, Ho SYW. Habitat preference differentiates Holocene dynamics, but not barrier effects on two sympatric and congeneric trees (*Tristaniopsis*, Myrtaceae). Heredity *(Edinb)*. 2019; 123 (4): 532-548.

56. Fang K, Miao YF, Chen L, et al. Tissue-Specific and Geographic Variation in Endophytic Fungi of Ageratin adenophora and Fungal Associations with the Environment. *Frontiers Microbiology*. 2019; 10: 2919.
57. Ferreira CA. Estudo fitoquímico e ensaios da atividade antioxidante dos extratos de *Acosmium dasycarpum* (vogel) yakovlev (fabaceae) e croton antisyphiliticus mart. (euphorbiaceae). Dissertação de mestrado, Universidade Federal dos Vales do Jequitinhonha e Mucuri, Minas Gerais, Brasil; 2020.
58. Ferreira MC, et al. Diversity of the endophytic fungi associated with the ancient and narrowly endemic neotropical plant *Vellozia gigantea* from the endangered Brazilian rupestrian grasslands. *Biochemical Systematics and Ecology*. 2017. 71: 163-169.
59. Fisher P., Petrini O., Scott HL. The distribution of some fungal and bacterial endophytes in maize (*Zea mays* L.). *New Phytol.* 2005; 122 299–305.
60. Fontana DC, de Paula S, Torres AG, de Souza VHM, Pascholati SF, Schmidt D, Dourado Neto D. Endophytic Fungi: Biological Control and Induced Resistance to Phytopathogens and Abiotic Stresses. Pathogens. 2021; 8;10(5):570. doi: 10.3390/pathogens10050570.
61. Franco AC et al. Leaf functional traits of Neotropical savanna trees in relation to seasonal water deficit. *Trees*. 2005; 19 :326-335.
62. Frey-Klett P, Burlinson P, Deveau A, Barret M, Tarkka M, Sarniguet A. Bacterial-fungal interactions: hyphens between agricultural, clinical, environmental, and food microbiologists. *Microbiology and Molecular Biology Reviews*. 2011; 75 (4): 583-609.
63. Fusconi A. Regulation of root morphogenesis in arbuscular mycorrhizae: what role do fungal exudates, phosphate, sugars and hormones play in lateral root formation?. *Annals of Botany*. 2014;113(1):19-33.
64. Gamboa MA, Bayman P. Comunidades de fungos endofíticos em folhas de uma árvore de madeira tropical (*Guarea guidonia*: Meliaceae). *Biotropica.* 2001; 33: 352 - 360.
65. Gamboa MA, Laureano S, Bayman P. Measuring the diversity of endophytic fungi in leaf fragments: size. matter?. *Mycopathologia.* 2003; 156: 41 - 45.
66. Gao Y, Liu F, Duan W, Crous PW, Cai L. *Diaporthe* is paraphyletic. IMA Fungus. 2017 Jun;8(1):153-187. doi: 10.5598/imafungus.2017.08.01.11.
67. Gardes M, Bruns TD. ITS primers with enhanced specificity for basidiomycetes—application to the identification of mycor-rhizae and rusts. *Molecular Ecology*. 1993; 2(2):113–118.
68. Gashgari R, Gherbawy Y, Ameen F, Alsharari S. Molecular Characterization and Analysis of Antimicrobial Activity of Endophytic Fungi From Medicinal Plants in Saudi Arabia. *Jundishapur Journal Microbiology*. 2016; 9(1): e26157.
69. Gautam AK, Verma RK, Avasthi S, Sushma, Bohra Y, Devadatha B, Niranjan M, Suwannarach N. Current Insight into Traditional and Modern Methods in Fungal Diversity Estimates. *J Fungi* (Basel). 2022 Feb 24;8(3):226. doi: 10.3390/jof8030226.
70. Gazis R, Chaverri P. Diversity of endophytic fungi on leaves and stems of wild rubber trees (*Hevea brasiliensis*) in Peru. *Fungal Ecology.* 2009; 3 : 240–254.

71. Gołębiewski M, Deja-Sikora E, Cichosz M, Tretyn A, Wróbel B. Pyrosequencing analysis of 16S rDNA of the bacterial community in soils polluted with heavy metals. *Microbial Ecology*. 2014; 67: 635–647.
72. Gomes T, Pereira JA, Benhadi J, Lino-Neto T, Baptista P. Endophytic and Epiphytic Phyllosphere Fungal Communities Are Shaped by Different Environmental Factors in a Mediterranean Ecosystem. *Microb Ecol.* 2018; 76(3):668-679. doi: 10.1007/s00248-018-1161-9.
73. Gong B, Yao XH, Zhang YQ, Fang HY, Pang TC, Dong QL. A cultured endophyte community is associated with the plant *Clerodendrum inerme* and antifungal activity. *Genetics Molecular Research*. 2015;14(2):6084-6093.
74. Gschwend F, Hartmann M, Mayerhofer J, Hug AS, Enkerli J, Gubler A, Meuli RG, Frey B, Widmer F. Site and land-use associations of soil bacteria and fungi define core and indicative taxa. *FEMS Microbiol Ecol*. 2022; 7 97(12):fiab165. doi: 10.1093/femsec/fiab165.
75. Guatimosim E, Firmino AB, et al. Towards a phylogenetic reappraisal of *Parmulariaceae and Asterinaceae* (*Dothideomycetes*). Persoonia. 2016; 35: 230-41. 10.3767/003158515X688046.
76. Guo LD, Hyde KD, Liew ECY. Identification of endophytic fungi from *Livistona chinensis* based on morphology and rDNA sequences. New Phytologist. 2000. 147: 617–630. 10.1046/j.1469-8137.2000.00716.x
77. Gutiérrez EE, Marinho-Filho J. 2017.The mammalian faunas endemic to the Cerrado and the Caatinga. *Zookeys*. 644: 105-157.
78. Haas BJ, Gevers D, Earl AM, Feldgarden M, Ward DV, et al. Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. *Genome Res*. 2011; 21: 494–504.
79. Harrison JG, Griffin EA. The diversity and distribution of endophytes across biomes, plant phylogeny and host tissues: how far have we come and where do we go from here?. *Environmental Microbiology*. 2020; 22(6): 2107-2123.
80. Hawksworth DL. The fungal dimension of biodiversity: Magnitude, importance and conservation. *Mycological Research.* 1991; 95: 641–655.
81. Henriques RPB. Influência da história, solo e fogo na distribuição da dinâmica das fitofisionomias no bioma Cerrado. In: SCARIOT, A.; SOUSA-SILVA, J. C.; FELFILI, J. M. (Orgs.) Cerrado: ecologia, biodiversidade e conservação. Brasília: Ministério do Meio Ambiente; p. 2015; 73-92.
82. Hernandez-Gutierrez A., Chaves ZM., Dornelo-Silva D., Dianese JC. Additions to the cercosporoid fungi from the Brazilian Cerrado: 1. New species on hosts belonging in family Fabaceae, and reallocations of four Stenella species into Zasmidium. *Mycobiota*. 2015; 5: 33-64.
83. Hernández-Restrepo M, Gené J, Castañeda-Ruiz RF, Mena-Portales J, Crous PW, Guarro J. Phylogeny of saprobic microfungi from Southern Europe. *Stud Mycol*. 2017; 86:53-97. doi: 10.1016/j.simyco.2017.05.002.
84. Hoffman MT, Arnold AE. Geographic locality and host identity shape fungal endophyte communities in cupressaceous trees. *Mycological Research*. 2008; 112(3):331-344.

85. Huang S, Xia J, Zhang X, Sun W. Morphological and phylogenetic analyses reveal three new species of *Diaporthe* from Yunnan, China. *MycoKeys*. 2021; 19; 78:49-77. doi: 10.3897/mycokeys.78.60878.
86. IBGE, Censo Agropecuário. Brasil, grandes regiões e unidades da federação. Rio de Janeiro: Instituto Brasileiro de Geografia e Estatística. 2006; 777p.
87. James TY, Stajich JE, Hittinger CT, Rokas A. Toward a Fully Resolved Fungal Tree of Life. Annu. Rev. *Microbiol*. 2020;7 4:291–313. doi: 10.1146/annurev-micro-022020-051835.
88. Jin H, Yan Z, Liu Q, Yang X, Chen J, Qin B. Diversity and dynamics of fungal endophytes in leaves, stems and roots of *Stellera chamaejasme* L. in northwestern China. *Antonie Van Leeuwenhoek*. 2013; 104(6):949-63.
89. Junker RR, Keller A. Microhabitat heterogeneity in leaves and flower organs promotes bacterial diversity. *FEMS Microbiology Ecology.* 2015; 91: fiv097.
90. Katoch M, Pull S. Endophytic fungi associated with *Monarda citriodora*, an aromatic and medicinal plant and their biocontrol potential. *Pharmaceutical Biology*. 2017b;55(1):1528-1535.
91. Kaul S., Gupta S., Ahmed M., Dhar MK. Endophytics of medicinal plants: The treasure hunt for bioactive metabolites. *Phytochemistry Reviews.* 2012; 11: 487–505.
92. Kembel SW, et al. Relationships between bacterial communities of the phylosphere and functional characteristics of plants in a neotropical forest. *Proceedings of the National Academy of Science.* 2014; 111: 13715–13720
93. Khan AL, Al-Harrasi A., Al-Rawahi A., et al. Frankincense tree endophytic fungi enhance host growth and produce extracellular enzymes and indole acetic acid. *Plos One*. 2016; 11 (6): e0158207.
94. Klein HS, Luna FV. 2019. Feeding the world: Brazil's transformation into a modern agricultural economy. Cambridge University Press; Cambridge, UK: 2019.
95. Klink CA, et al. "The Role of Vegetation in the Dynamics of Water and Fire in Cerrado Ecosystems: Implications for Management and Conservation". *Plants. 2020*; 9 (12): 1803.
96. Klink CA, Moreira AG. 2002. *Os Cerrados do Brasil.* Imprensa, CU; New York, NY, USA: 2002. Passado e Atual Ocupação Humana e Uso da Terra. 2002: 69–88.
97. Klink CA. *Ecologia e Conservação do Lobo-guará: Perspectivas Multidisciplinares.* Pressione Cross; Boca Raton, FL, USA: 2014. Política de Intervenção nas Savanas do Cerrado do Brasil: *Mudanças no Uso da Terra e Efeitos na Conservação*. 2014: 293–308.
98. Klink CA., Machado RB. The conservation of the Brazilian Cerrado. Megadiversity. 2005; 1(1): 147-155.
99. Knief C. Analysis of plant microbe interactions in the era of next generation sequencing technologies. *Frontiers in Plant Science*. 2014; 5:216.
100. Kumaresan V, Suryanarayanan TS. Endophyte assemblages in young, mature and senescent leaves of *Rhizophora apiculata*: evidence for the role of endophytes in mangrove leaf litter degradation. *Fungal Diversity.* 2002; 9: 81–91.

101. Kusari S., Lamshöft M., Spiteller M. *Aspergillus fumigatus* Fresenius, an endophytic fungus of Juniperus communis L. Horstmann as a new source of the anticancer prodrug deoxypodophyllotoxin. *Journal of Applied Microbiology.* 2009; 107: 1019–1030.
102. Lee SJ, Kong M, Harrison P, Hijri M. Conserved Proteins of the RNA Interference System in the Arbuscular Mycorrhizal Fungus Rhizoglomus irregulare Provide New Insight into the Evolutionary History of *Glomeromycota*. *Genome Biol Evol*. 2018; 1;10(1):328-343. doi: 10.1093/gbe/evy002.
103. Lehnert H, Serfling A, Friedt W, Ordon F. Genome-Wide Association Studies Reveal Genomic Regions Associated With the Response of Wheat (*Triticum aestivum* L.) to Mycorrhizae Under Drought Stress Conditions. *Frontiers and Plant Science*. 2018; 9:1728.
104. Li JL, Sun X, Chen L, Guo LD. Endophytic fungal community structure of four mangrove species in southern China. Mycology. 2016; 7 (4): 180-190.
105. Li JL, Sun X, Zheng Y, Lü PP, Wang YL, Guo LD. Diversity and community of culturable endophytic fungi from stems and roots of desert halophytes in northwest China. *MycoKeys*. 2020; 3;62:75-95. doi: 10.3897/mycokeys.62.38923.
106. Li P, Wu Z, Liu T, Wang Y. Biodiversity, Phylogeny, and Antifungal Functions of Endophytic Fungi Associated with Zanthoxylum bungeanum. *Int J Mol Sci*. 2016; 13;17(9):1541. doi: 10.3390/ijms17091541.
107. Li PD, Zhu ZR, Zhang Y, Xu J, Wang H, Wang Z, Li H. The phyllosphere microbiome shifts toward combating melanose pathogen. *Microbiome*. 2022; 2; 10(1):56. doi: 10.1186/s40168-022-01234-x.
108. Li XJ, Zhang Q, Zhang AL, Gao JM. Metabolites from *Aspergillus fumigatus*, an endophytic fungus associated with Melia azedarach, and their antifungal, antifeedant, and toxic activities. *Journal of Agricultural and Food Chemistry*. 2012;60(13):3424-3431.
109. Liu H, Carvalhais LC, Crawford M, et al. Internal plant values: Diversity, colonization and benefits of endophytic bacteria. *Frontiers Microbiol*ogy. 2017; 8: 25-52.
110. Losos J. B. Phylogenetic niche conservatism, phylogenetic signal and the relationship between phylogenetic relatedness and ecological similarity among species. *Ecology Letters. 2008;* 11: 995–1003.
111. Lücking R, Aime MC, Robbertse B et al. Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal DNA barcoding? *IMA Fungus*. 2020; 10;11:14. doi: 10.1186/s43008-020-00033-z.
112. Machado RB., et al. Caracterização da fauna e flora do Cerrado. In: FALEIRO, F. G.; FARIA NETO, A. L. (Ed.) Savanas: desafios e estratégias para o equilíbrio entre sociedade, agronegócio e recursos naturais. Planaltina, DF: Embrapa Cerrados; Brasília, DF: *Embrapa Informação Tecnológico*. 2008; 1: 285-300.
113. Manganyi MC, Ateba CN. Untapped Potentials of Endophytic Fungi: A Review of Novel Bioactive Compounds with Biological Applications. *Microorganisms*. 2020; 8(12):1934.
114. Mapook A, Macabeo APG, Thongbai B, Hyde KD, Stadler M. Polyketide-Derived Secondary Metabolites from a Dothideomycetes Fungus,

Pseudopalawania siamensisgen. et sp. nov., (Muyocopronales) with Antimicrobial and Cytotoxic Activities. *Biomolecules*. 2020; 8;10(4):569. doi: 10.3390/biom10040569.

115. Marczylo EL, Macchiarulo S, Gant TW. Metabarcoding of Soil Fungi from Different Urban Greenspaces Around Bournemouth in the UK. *Ecohealth*. 2021; 18(3):315-330. doi: 10.1007/s10393-021-01523-1. 2021; 5. Erratum in: Ecohealth. 2021; 5

116. Martin & Rygiewicz. Martin KJ, Rygiewicz PT. Fungal-specific PCR primers developed for analysis of the ITS region of environmental DNA extracts. *BMC Microbiology.* 2005; 5:28.
117. Martin R, Gazis R, Skaltsas D, Chaverri P, Hibbett D. Unexpected diversity of basidiomycete endophytes in sapwood and Hevea leaves. *Mycologia.* 2015; 107: 284–297

118. Materatski P, Varanda C, Carvalho T, Dias AB, Campos MD, Rei F, Félix MDR. Spatial and temporal variation of fungal endophytic richness and diversity associated to the phyllosphere of olive cultivars. *Fungal Biol*. 2019; 123(1):66-76. doi: 10.1016/j.funbio.2018.11.004.

119. Materatski P, Varanda C, Carvalho T, et al. Spatial and temporal variation of fungal endophytic richness and diversity associated to the phyllosphere of olive cultivars. *Fungal Biology*. 2019;123(1): 66-76.
120. Mena E, Garaycochea S, Stewart S, Montesano M, Ponce De León I. Comparative genomics of plant pathogenic Diaporthe species and transcriptomics of Diaporthe caulivora during host infection reveal insights into pathogenic strategies of the genus. *BMC Genomics*. 2022; 3;23(1):175. doi: 10.1186/s12864-022-08413-y.
121. Millar NS, Bennett AE. Stressed out symbiotes: hypotheses for the influence of abiotic stress on arbuscular mycorrhizal fungi. *Oecologia*. 2016;182(3):625-641.
122. Milner ML, Rossetto M, Crisp MD, Weston PH. The impact of multiple biogeographic barriers and hybridization on species-level differentiation. *American Journal of Botany*. 2012; 99 (12):2045-2057.
123. Mishra A, Gond SK, Kumar A, Sharma VK, Verma SK, Kharwar RN, Sieber TN. Season and tissue type affect fungal endophyte communities of the Indian medicinal plant Tinospora cordifolia more strongly than geographic location. *Microbial Ecology*. 2012; 64(2):388-98.
124. Mujic AB, Kuo A, Tritt A, Lipzen A, Chen C, Johnson J, Sharma A, Barry K, Grigoriev IV, Spatafora JW. Comparative Genomics of the Ectomycorrhizal Sister Species Rhizopogon vinicolor and Rhizopogon vesiculosus (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type B Locus. G3 (Bethesda). 2017; 7;7(6):1775-1789. doi: 10.1534/g3.117.039396.
125. Myers N, Mittermier RA, Mittermier CG, et al. Biodiversity hotspots for conservation 500 priorities. *Nature*. 2000; 403(24):853–858.
126. Nicoletti R, Di Vaio C, Cirillo C. Endophytic Fungi of Olive Tree. *Microorganisms*. 2020; 8(9):1321.
127. Noriler SA, Savi DC, Aluizio R, Palácio-Cortes AM, Possiede YM, Glienke C. Bioprospection and structure of fungal endophyte communities

found in the Brazilian, Pantanal and Cerrado biomes. *Frontiers Microbiology*.L. 2018; 9: 1526.

128. Noriler SA, Savi DC, Aluizio R, Palácio-Cortes AM, Possiede YM, Glienke C. Bioprospecting and Structure of Fungal Endophyte Communities Found in the Brazilian Biomes, Pantanal, and Cerrado. *Front Microbiol*. 2018; 24;9:1526. doi: 10.3389/fmicb.2018.01526.
129. Oksanen J, Kindt R, Legendre P, O'Hara B. Vegan: Community Ecology Package. 2007. p. 4. R package Version 2.4.
130. Ori F, Leonardi M, Faccio A, et al. Synthesis and ultrastructural observation of arbutoid mycorrhizae of black truffles (Tuber melanosporum and T. aestivum). *Mycorrhiza*. 2020; 30(6):715-723.
131. Ortega HE, Torres-Mendoza D, Caballero E Z, Cubilla-Rios L. Structurally Uncommon Secondary Metabolites Derived from Endophytic Fungi. J Fungi (Basel). 2021 Jul 17;7(7):570. doi: 10.3390/jof7070570.
132. Padovan MP, et al. Pioneer native tree species in biodiverse agroforestry systems. *GeoPantanal*. 2018; 24: 53-68.
133. Pan XX, Yuan MQ, Xiang SY, et al. The symbioses of endophytic fungi shaped the metabolic profiles in grape leaves of different varieties. *Plos one*. 2020; 15(9):e0238734.
134. Pang KL, Guo SY, Chen IA, Burgaud G, Luo ZH, Dahms HU, Hwang JS, Lin YL, Huang JS, Ho TW, Tsang LM, Chiang MW, Cha HJ. Insights into fungal diversity of a shallow-water hydrothermal vent field at Kueishan Island, Taiwan by culture-based and metabarcoding analyses. *Plos One*. 2019; 30;14(12):e0226616. doi: 10.1371/journal.pone.0226616.
135. Park YH, et al. Screening and characterization of endophytic fungi from *Panax ginseng* Meyer for biocontrol activity against ginseng pathogens. *Biology.* 2015; 91: 71–81.
136. Park YH, Kim Y, Mishra RC, Bae H. Endophytes of fungi inhabiting mountain cultivated ginseng (*Panax ginseng* Meyer): Diversity and biocontrol activity against ginseng pathogens. *Science Reports*. 2017; 7 (1): 16221.
137. Park YH, *et al*. Diversity of fungal endophytes in various tissues of Panax ginseng meyer cultivated in Korea. Journal of *Ginseng Research*. 2012; 36.
138. Parks, JE & Graham, JK. Effects of cryopreservation procedures on sperm membranes. Theriogenology, Stoneham. 1992; 38; 2: 209-222.
139. Parthasarathy R, Sathiyabama M. Gymnemagenin-producing endophytic fungus isolated from a medicinal plant *Gymnema sylvestre* R.Br. *Applied Biochemistry Biotechnology*. 2014;172(6):3141-3152.
140. Pinski A, Betekhtin A, Hupert-Kocurek K, Mur LAJ, Hasterok R. 2019. Defining the Genetic Basis of Plant⁻Endophytic Bacteria Interactions. *International Journal of Molecular Science*. 2019; 20 (8): 1947.
141. Prieto P, Navarro-Raya C, Valverde-Corredor A, Amyotte SG, Dobinson KF, Mercado-Blanco J. Process of colonization of olive tissues by *Verticillium dahliae* and its interaction in planta with the biocontrol root endophyte *Pseudomonas fluorescens* PICF7. *Microbial Biotechnology*. 2009; 2 (4): 499-511.
142. Purcell SA et al. Human gut microbiome changes during a 10 week Randomised Control Trial for micronutrient supplementation in children

with attention deficit hyperactivity disorder. Scientific Reports. 2019; 9. 10.1038/s41598-019-46146-3.

143. Purvis A, Hector A. Getting the measure of biodiversity. *Nature*. 2000; 405: 212–219.
144. Qadri M, Rajput R, Abdin MZ, Vishwakarma RA, Riyaz-Ul-Hassan S. Diversity, molecular phylogeny, and bioactive potential of fungal endophytes associated with the Himalayan blue pine (*Pinus wallichiana*). *Microbial Ecology*. 2014; 67(4): 877-887.
145. Rampelotto PH, de Siqueira Ferreira A, Barboza AD, Roesch LF. Changes in diversity, abundance, and structure of soil bacterial communities in Brazilian Savanna under different land use systems. *Microbial Ecology*. 2013;66(3): 593-607.
146. Rashmi M, Kushveer JS, Sarma VV. A worldwide list of endophytic fungi with notes on ecology and diversity. *Mycosphere*. 2019; 10: 798–1079.
147. Ratter JA & Dargie TCD. An analysis of the floristic composition of 26 Cerrado ares in 517 Brazil. *Edinburgh Journal of Botany*. 1992; 49(02):235.
148. Ratter JA, Bridgewater S, Atkinson R & Ribeiro JF. Analysis of the floristic composition of the Brazilian cerrado vegetation II: Comparison of the woody vegetation of 98 areas. *Edinburgh Journal of Botany*. 1996; 53 (02):153.
149. Ratter JA, Bridgewater S, Ribeiro JF, et al. Analysis of the floristic composition of the Brazilian cerrado vegetation IV: Presentation of a Revised Data-Base of 367 Areas. (http://cerrado.rbge.org.uk/cerrado/download/download.php).
150. Redford AJ, Bowers RM, Knight R, Linhart Y, Fierer N. The ecology of the phylosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. *Environment. Microbiology.* 2010; 12: 2885–2893.
151. Ricks KD, Koide RT. Biotic filtering of endophytic fungal communities in Bromus tectorum. *Oecologia*. 2019; 189(4): 993-1003.
152. Ricks KD, Koide RT. The role of inoculum dispersal and plant species identity in the formation of leaf endophytic fungal communities. *Plos one*. 2019; 14 (7): e0219832.
153. Rodriguez RJ, Redman RS, Henson JM. The role of fungal symbioses in plant adaptation to high-stress environments. Mitigation and adaptation strategies for global changes. 2004; 9: 261–272.
154. Rojas EC, Sapkota R, Jensen B, Jørgensen HJL, Henriksson T, Jørgensen LN, Nicolaisen M, Collinge DB. Fusarium Head Blight Modifies Fungal Endophytic Communities During Infection of Wheat Spikes. *Microb Ecol*. 2020; 79(2):397-408. doi: 10.1007/s00248-019-01426-3.
155. Romão-Dumaresq AS, Dourado MN, Fávaro LC, Mendes R, Ferreira A, Araújo WL. Diversity of Cultured Fungi Associated with Conventional and Transgenic Sugar Cane and the Interaction between Endophytic Trichoderma virens and the Host Plant. *Plos One*. 2016; 11 (7): e0158974.
156. Sadeghi F, Samsampour D, Seyahooei MA, Bagheri A, Soltani J. Diversity and Spatiotemporal Distribution of Fungal Endophytes Associated with Citrus reticulata cv. Siyahoo. *Current Microbiology*. 2019; 76(3): 279-289.

157. Sagita R, Quax WJ, Haslinger K. Current State and Future Directions of Genetics and Genomics of Endophytic Fungi for Bioprospecting Efforts. *Frontiers Bioengineering and Biotechnology*. 2021; 9: 649906.
158. Sahoo S, Sarangi S, Kerry RG. Bioprospection of Endophytes for Agricultural and Environmental Sustainability. *Microbial Biotechnology*. 2017; 429-458.
159. Samarakoon BC, Phookamsak R, Wanasinghe DN, Chomnunti P, Hyde KD, McKenzie EHC, Promputtha I, Xu JC, Li YJ. Taxonomy and phylogenetic appraisal of *Spegazzinia musae* sp. nov. and *S. deightonii* (Didymosphaeriaceae, Pleosporales) on Musaceae from Thailand. *MycoKeys*. 2020 Jul 21; 70:19-37. doi: 10.3897/mycokeys.70.52043.
160. Sano EE, Rodrigues AA, Martins ES, et al. Cerrado ecoregions: A spatial framework to assess and prioritize Brazilian savanna environmental diversity for conservation. *J Environ Manage*. 2019; 232:818-828.
161. Sano EE, Rosa R, Brito JL, Ferreira LG. Land cover mapping of the tropical savanna region in Brazil. *Environmental Monitoring Assessment*. 2010; 166(1-4):113-124.
162. Sarmiento G & Monasteri MO. Life forms and phenology. In Ecosystems of the World: tropical savannas (F. Bouliere, ed.). *Elsevier*. 1983; 3:79-108.
163. Sarsaiya S, Jain A, Jia Q, Fan X, Shu F, Chen Z, Zhou Q, Shi J, Chen J. Molecular Identification of Endophytic Fungi and Their Pathogenicity Evaluation Against *Dendrobium nobile* and *Dendrobium officinale*. *Int J Mol Sci*. 2020; 2;21(1):316. doi: 10.3390/ijms21010316.
164. Satish Chander P, Vijeshwar V, et al. An endophytic fungus of Nothapodytes foetida that produces camptothecin. *Journal of Natural Products.* 2005; 68: 1717–1719.
165. Saucedo-García A, Anaya AL, Espinosa-García FJ, González MC. Diversity and communities of endophytic foliar fungi of different agroecosystems of Coffea arabica L. in two regions of Veracruz, Mexico. *Plos One*. 2014; 9 (6): e98454.
166. Schwieder M, Leitão PJ, Pinto JRR, et al. Landsat phenological metrics and their relationship with aboveground carbon in the Brazilian Cerrado. Carbon Balance Management. 2018; 13 (1): 7.
167. Seetharaman P, Gnanasekar S, Chandrasekaran R, et al. Isolation of limonoid compound (Hamisonine) from endophytic fungi *Penicillium oxalicum* LA-1 (KX622790) *of Limonia acidissima* L. for its larvicidal efficacy against LF vector, *Culex quinquefasciatus* (Diptera: Culicidae). *Environment Science Pollution Research*. 2017; 24(26): 21272-21282.
168. Sessitsch A, Hardoim P, Döring J, Weilharter A, et al. Functional characteristics of an endophytic community colonizing rice roots revealed by metagenomic analysis. *Mololecular Plant-Microbe Interactions.* 2012; 25: 28–36.
169. Sette DM. The savanna's climates of brasilian west mid land region. *Revista Brasileira de Climatologia*. 2015. 1 (1): 29-42.
170. Sheibani-Tezerji R, Rattei T, Sessitsch A, Trognitz F and Mitter BO. Transcriptome profile of the endophyte Burkholderia phytofirmans PsJN indicates detection of plant environment and water stress. *mBio.* 2015; 6: e00621-15.

171. Shen XX, Steenwyk JL, LaBella AL, Opulente DA, Zhou X, Kominek J, Li Y, Groenewald M, Hittinger CT, Rokas A. Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. Sci Adv. 2020 Nov 4;6(45):eabd0079. doi: 10.1126/sciadv.abd0079.
172. Silva CMS et al. Physiological and structural traits of the congeneric species *Styrax ferrugineus* and *S. pohlii* occurring in contrasting environments. *Flora*. 2017; 235: 51-58.
173. Silva FA, Liotti RG, Boleti APA, et al. Diversity of cultivable fungal endophytes in *Paullinia cupana* (Mart.) Ducke and bioactivity of their secondary metabolites. *Plos one*. 2018; 13(4):e0195874.
174. Silva GPA & Miranda MCC. Quaternary: scientometrics and mapping of palynological studies of the cerrado biome and importance for archeology. *GeoSUL*. 2019; 34: 73.
175. Silva JF, Fariñas MR, Felfili JM, Klink CA. Spatial heterogeneity, land use and conservation in the cerrado region of Brazil. *Journal Biogeography.* 2006; 33: 536–548.
176. Silva Júnior MC. 100 árvores do Cerrado: guia de campo. Brasília, DF: Rede de Sementes do Cerrado. 2005.
177. Silva LE, et al. 2015. Chemical Investigation of leaves of *Acosmium dasycarpum* (VOGEL) YAKOVLEV. *Science and Nature.* 2015; 37: 664-672.
178. Silva TA, et al. *Styrax camporum* and S. *ferrugineus fruits*: norneolignans, antioxidant and cytotoxic activities. *Journal of Applied Pharmaceutical Science*. 2016. 6 (11): 075-080.
179. Silva, P. S. et al. Filtrates from cultures of endophytic fungi isolated from leaves of Copaifera oblongifolia (Fabaceae) affect germination and seedling development differently. *Brazilian Journal of Biology* [online]. 2023; 83 , e242070.
180. Silva-Hughes AF, Wedge DE, Cantrell CL, et al. Diversity and antifungal activity of the endophytic fungi associated with the native medicinal cactus *Opuntia humifusa* (Cactaceae) from the United States. *Microbiological Resseach*. 2015; 175: 67-77.
181. Silverio DV & Lenza E. 2010. Phenology of woody species in a typical cerrado at Parque Municipal do Bacaba, Nova Xavantina, Mato Grosso, Brazil. *Biota Neotropical.* 2010; 10, n.3: 205-216.
182. Singh DK, Sharma VK, Kumar J, Mishra A, Verma SK, Sieber TN, Kharwar RN. Diversity of endophytic mycobiota of tropical tree Tectona grandis Linn.f.: Spatiotemporal and tissue type effects. *Sci Rep*. 2017; 16;7(1):3745. doi: 10.1038/s41598-017-03933-0.
183. Singh G, Singh N., Marwaha TS. Crop genotype and a novel symbiotic fungus influence the potential for endophytic root colonization of plant growth-promoting rhizobacteria. *Physiology and Molecular Biology of Plants*. 2009; 15 (1): 87-92.
184. Singh P, Singh RK, Guo DJ, et al. Whole-genome analysis of the sugarcane root-associated endophyte *Pseudomonas aeruginosa* B18-A plant growth-promoting bacterium with antagonistic potential against *Sporisorium scitamineum*. *Frontiers Microbiology*. 2021; 12: 628376.
185. Singh R, Dubey AK. Diversity and Applications of Endophytic Actinobacteria of Plants in Special and Other Ecological Niches. *Frontiers Microbiology*. 2018; 9:1767.

186. Šmilauer P, Košnar J, Kotilínek M, Šmilauerová M. Contrasting effects of host identity, plant community, and local species pool on the composition and colonization levels of arbuscular mycorrhizal fungal community in a temperate grassland. *New Phytologist*. 2020; 225(1):461-473.
187. Souza HA, Collevatti RG, Lima-Ribeiro MS, Lemos-Filho JP, Lovato MB. A large historic refuge explains spatial patterns of genetic diversity in a Neotropical savanna tree species. *Annals of Botany*. 2017; 119 (2): 239-252.
188. Souza RC, Mendes IC, Reis-Junior FB, et al. Changes in taxonomic and functional microbial diversity with agriculture: how fragile is the Brazilian Cerrado?. *BMC Microbiology.* 2016; 16: 42.
189. Stone JK, Polishook JD, White JRJ. Endophytic fungi. In: Mueller G, Bills GF, Foster MS, eds. Fungal biodiversity: inventory and monitoring methods. Burlington, MA, EUA: *Elsevier*. 2004 241 - 270.
190. Strobel G & Daisy B. Bioprospecting for microbial endophytes and their natural products. *Microbiol Mol Biol Rev.* 2003; 67: 491–502.
191. Sun W, Huang S, Xia J, Zhang X, Li Z. Morphological and molecular identification of *Diaporthe* species in south-western China, with description of eight new species. *MycoKeys*. 2021; 14;77:65-95. doi: 10.3897/mycokeys.77.59852.
192. Sun X, Guo LD. Endophytic fungal diversity: Review of traditional and molecular techniques. *Mycology.* 2012; 3:65–76.
193. Sun X, Guo LD. Diversity of endophytic fungi: review of traditional and molecular techniques. Mycology*.* 2012; 3: 65–76.
194. Tedersoo L, Sánchez-Ramírez S, Kõljalg U, Bahram M, Döring M, Schigel D, May T, Ryberg M, Abarenkov K. High-level classification of the Fungi and a tool for evolutionary ecological analyses. *Fungal Divers*. 2018; 90:135–159.
195. Thiem D, Gołebiewski M, Hulisz P, Piernik A, Hrynkiewicz K. 2018. How salinity shapes the bacterial and fungal microbiomes of *Alnus glutinosa* roots? *Frontiers Microbiology*. 2018; 9: 651.
196. Toju et al. Toju H, Tanabe AS, Yamamoto S, Sato H. High-coverage ITS primers for the DNA-based identification of ascomycetes and basidiomycetes in environmental samples. *PLoS ONE.* 2012; 7(7): e40863.
197. Trevisan TC, Silva EA, Dall'Oglio EL, Silva LE, Velozo ES, Vieira PC, Sousa PT. New quinolizidine and diaza-adamantane alkaloids from *Acosmium dasycarpum* (Vog.) Yakovlev—Fabaceae. *Tetrahedron Letters*. 2008; 49 (44): 6289-6292.
198. Tyburska-Woś J, Nowak K, Kieliszewska-Rokicka B. Influence of leaf damage by the horse chestnut leafminer (*Cameraria ohridella* Deschka & Dimić) on mycorrhiza of *Aesculus hippocastanum* L. *Mycorrhiza*. 2019; 29(1):61-67.
199. U'Ren JM, Dalling JW, Gallery RE, Maddison DR, Davis EC, Gibson CM, Arnold AE. Diversity and evolutionary origins of fungi associated with seeds of a neotropical pioneer tree: a case study for the analysis of environmental samples of fungi. Mycological Research*.* 2009; 113: 432–449.
200. Vályi K, Rillig MC, Hempel S. Land-use intensity and host plant identity interactively shape communities of arbuscular mycorrhizal fungi in roots of grassland plants. *New Phytologist*. 2015; 205(4):1577-1586.

201. Van Geel M, Jacquemyn H, Plue J, et al. Abiotic rather than biotic filtering shapes the arbuscular mycorrhizal fungal communities of European semi-natural grasslands. *New Phytologist*. 2018; 220(4): 1262-1272.

202. Vargas-Gastélum L, Riquelme M. The Mycobiota of the Deep Sea: What Omics Can Offer. *Life* (Basel). 2020; 19; 10(11):292. doi: 10.3390/life10110292.

203. Vasconcelos VV et al. Caracterização de fito-ambientes de Cerrado e Mata Atlântica por meio de estudo de linhagem de pedra e paleossolos. *Ver. Geo., Ens & Pes*. 2011; 14 (3): 06-14.

204. Videira SIR, Groenewald JZ, Nakashima C, Braun U, Barreto RW, de Wit PJGM, Crous PW. *Mycosphaerellaceae* - Chaos or clarity? *Stud Mycol*. 2017; 87:257-421. doi: 10.1016/j.simyco.2017.09.003.

205. Vieira ML, Hughes AF, Gil VB, et al. Diversity and antimicrobial activities of the fungal endophyte community associated with the traditional Brazilian medicinal plant *Solanum cernuum* Vell. (Solanaceae). *Canadian Journal of Microbiology*. 2012; 58(1): 54-66.

206. Vieira ML, Johann S, Hughes FM, Rosa CA, Rosa LH. The diversity and antimicrobial activity of endophytic fungi associated with medicinal plant *Baccharis trimera* (Asteraceae) from the Brazilian savannah. *Canadian Journal of Microbiology*. 2014; 60(12): 847-856.

207. Vilgalys R., Hester M. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology.* 1990; 172:4238–4246.

208. Vorholt JA. Microbial life in the phylosphere. *Nature reviews Microbiology*. 2012; 10 (12): 828–40.

209. Wang GK, Yang JS, Huang YF, et al. Culture Separation, Identification and Unique Ability of Antipathogenic Fungi from Endophytic Fungi from Gucheng *Salvia Miltiorrhiza. In Vivo*. 2021; 35 (1): 325-332.

210. Wang H, Guo S, Huang M et al. Ascomycota has a faster evolutionary rate and greater species diversity than Basidiomycota. *Sci. China* Life Sci. 53, 1163-1169 (2010). https://doi.org/10.1007/s11427-010-4063-8

211. Wang L, Ren L, Li C, Gao C, Liu X, Wang M, Luo Y. Effects of endophytic fungi diversity in different coniferous species on the colonization of Sirex noctilio (Hymenoptera: Siricidae). *Sci Rep*. 2019; 25;9(1):5077. doi: 10.1038/s41598-019-41419-3.

212. Wang YL, Gao C, Chen L, Ji NN, Wu BW, Lü PP, Li XC, Qian X, Maitra P, Babalola BJ, Zheng Y, Guo LD. Community Assembly of Endophytic Fungi in Ectomycorrhizae of Betulaceae Plants at a Regional Scale. *Front Microbiol*. 2020; 21;10:3105. doi: 10.3389/fmicb.2019.03105.

213. Wantzen, K.M., et al. Soil carbon stocks in stream-valley-ecosystems in the Brazilian Cerrado agroscape. *Agriculture, Ecosystems and Environment.* 2012; (151): 70-79.

214. Wereszczuk A, Leblois R, Zalewski A. Genetic diversity and structure related to expansion history and habitat isolation: stone marten populating rural-urban habitats. *BMC Ecology*. 2017; 17(1):46.

215. White JR, Nagarajan N, Pop M (2009) Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. PLoS Comput Biol 5(4): e1000352. https://doi.org/10.1371/journal.pcbi.1000352.

216. White JR, Nagarajan N, Pop M. Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. *Plos Computacional Biology*. 2009; 5(4): e1000352. https://doi.org/10.1371/journal.pcbi.1000352.
217. White TJ, Burns T, Lee S, Taylor J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. Fungal Diversity In: Innis M, Gelfand D, Sninsky J, White T (eds) PCR protocols: a guide to methods and applications. Academic Press, Cam-bridge.1990; pp 315–322.
218. Wijayawardene NN, Bahram M, Sánchez-Castro I, Dai DQ, Ariyawansa KGSU, Jayalal U, Suwannarach N, Tedersoo L. Current Insight into Culture-Dependent and Culture-Independent Methods in Discovering Ascomycetous Taxa. *J Fungi* (Basel). 2021; 28;7(9):703. doi: 10.3390/jof7090703.
219. Wijayawardene NN, Pawłowska J, Letcher PM, Kirk PM, Humber RA, Schüßler A, Wrzosek M, Muszewska A, Okrasińska A, Istel Ł, et al. Notes for genera: Basal clades of fungi (including *Aphelidiomycota, Basidiobolomycota, Blastocladiomycota, Calcarisporiellomycota, Caulochytriomycota, Chytridiomycota, Entomophthoromycota, Glomeromycota, Kickxellomycota, Monoblepharomycota, Mortierellomycota, Mucoromycota, Neocallimastigomycota, Olpidiomycota, Rozellomycota and Zoopagomycota). Fungal Divers*. 2018;92:43–129.
220. Xia T, Wang Y, He Y, et al. An invasive plant experiences greater benefits of root morphology from enhancing nutrient competition associated with arbuscular mycorrhizae in karst soil than a native plant. *PLoS One*. 2020;15(6):e0234410.
221. Xiao J, Zhang Q, Gao YQ, Tang JJ, Zhang AL, Gao JM. Secondary metabolites from the endophytic *Botryosphaeria dothidea* of *Melia azedarach* and their antifungal, antibacterial, antioxidant, and cytotoxic activities. *Journal of Agricultural and Food Chemistry*. 2014; 62(16):3584-3590.
222. Xu TC, Lu YH, Wang JF, Song ZQ, Hou YG, Liu SS, Liu CS, Wu SH. Bioactive Secondary Metabolites of the Genus *Diaporthe* and Anamorph *Phomopsis* from Terrestrial and Marine Habitats and Endophytes: 2010-2019. *Microorganisms*. 2021; 21;9(2):217. doi: 10.3390/microorganisms9020217.
223. Yahr R, Schoch CL, Dentinger BT. Scaling up discovery of hidden diversity in fungi: impacts of barcoding approaches. Philos Trans R Soc *Lond B Biol Sci*. 2016; 5;371(1702):20150336. doi: 10.1098/rstb.2015.0336.
224. Yang F, Zhang J, Zhang H, et al. Bacterial Blight Induced Shifts in Endophytic Microbiome of Rice Leaves and the Enrichment of Specific Bacterial Strains With Pathogen Antagonism. *Frontiers in Plant Science*. 2020; 11:963.
225. Yang G, Li P, Meng L, et al. Diversity and communities of cultivable endophytic fungi of different tree peonies (geoherbs and non-geoherbs), and their analysis of biosynthetic potential. *Brazilian Journal Microbiology*. 2018a; 49: 47-58.
226. Yang JH, Oh SY, Kim W, Hur JS. Endolichenic Fungal Community Analysis by Pure Culture Isolation and Metabarcoding: A Case Study of

Parmotrema tinctorum. *Mycobiology*. 2022; 24;50(1):55-65. doi: 10.1080/12298093.2022.2040112.

227. Yang Q, Jiang N, Tian CM. New species and records of *Diaporthe* from Jiangxi Province, China. *MycoKeys*. 2021 14; 77: 41-64. doi: 10.3897/mycokeys.77.59999.
228. Yao H, Sun X, He C, Maitra P, Li XC, Guo LD. Phyllosphere epiphytic and endophytic fungal community and network structures differ in a tropical mangrove ecosystem. *Microbiome*. 2019; 9;7(1):57. doi: 10.1186/s40168-019-0671-0.
229. Yao H, Sun X, He C, Maitra P, Li XC, Guo LD. Phyllosphere epiphytic and endophytic fungal community and network structures differ in a tropical mangrove ecosystem. *Microbiome*. 2019; 7 (1): 57.
230. Zambriano SMV. Taxonomia de fungos associados a plantas do Cerrado do Distrito Federal e Mato Grosso. Dissertação (Mestrado), Universidade de Brasília, Distrito Federal, Brasil, 2016.
231. Zhang H, Wei TP, Li LZ, Luo MY, Jia WY, Zeng Y, Jiang YL, Tao GC. Multigene Phylogeny, Diversity and Antimicrobial Potential of Endophytic Sordariomycetes From *Rosa roxburghii*. *Front Microbiol*. 2021; 29;12:755919. doi: 10.3389/fmicb.2021.755919.
232. Zhang T & Yao YF. Comunidades de fungos endofíticos associadas a plantas vasculares na zona alta do Ártico são altamente diversificadas e específicas de plantas hospedeiras. *Plos One*. 2015; 10 (6): e0130051.
233. Zheng Y, Gong X. Niche differentiation rather than biogeography shapes the diversity and composition of microbiome of *Cycas panzhihuaensis. Microbiome*. 2019;7(1):152.
234. Zhong F, Fan X, Ji W, Hai Z, Hu N, Li X, Liu G, Yu C, Chen Y, Lian B, Wei H, Zhang J. Soil Fungal Community Composition and Diversity of Culturable Endophytic Fungi from Plant Roots in the Reclaimed Area of the Eastern Coast of China. *J Fungi (Basel*). 2022; 27;8(2):124. doi: 10.3390/jof8020124.
235. Zuo Y, Li X, Yang J, Liu J, Zhao L, He X. Fungal Endophytic Community and Diversity Associated with Desert Shrubs Driven by Plant Identity and Organ Differentiation in Extremely Arid Desert Ecosystem. *J Fungi (Basel)*. 2021; 20;7 (7):578. doi: 10.3390/jof7070578.
236. Shapiro T, Chekanov K, Alexandrova A, Dolnikova G, Ivanova E, Lobakova E. Revealing of Non-Cultivable Bacteria Associated with the Mycelium of Fungi in the Kerosene-Degrading Community Isolated from the Contaminated Jet Fuel. *J Fungi* (Basel). 2021; 11;7(1):43. doi: 10.3390/jof7010043.
237. Sato H, Tanabe AS, Toju H. Contrasting diversity and host association of ectomycorrhizal basidiomycetes versus root-associated ascomycetes in a dipterocarp rainforest. *Plos One*. 2015 Apr 17;10(4):e0125550. doi: 10.1371/journal.pone.0125550.

CHAPTER 3: *THE TYPE OF LEAF PHENOLOGY HAS AN EFFECT ON THE DIVERSITY OF THE ENDOPHYTIC MYCOBIOME IN A NEOTROPICAL SAVANNA ECOSYSTEM*

Abstract: Leaf tissue comprises a unique microhabitat and its characteristics, such as photoassimilates, macro, and micronutrients, and leaf senescence, act as an ecological filter, selecting the pool of microorganisms that colonize it. In our study, we evaluated the effect of leaf phenology on the endophytic fungal community using cultive-dependent and metabarcoding approaches. For this, we grouped different plant species according to their leaf phenology, with the species *Dalbergia miscolobium* and *Caryocar brasiliense* for the brevideciduous group, *Qualea parviflora* and *Leptolobium dasycarpum* for the deciduous group, and *Styrax ferrugineus* and *Ouratea hexasperma* for the evergreen group. Our results, obtained in both methodologies, show that *Ascomycota* is the dominant phylum in all groups and the brevideciduous species present a greater diversity of endophytic fungal species when compared to the deciduous and evergreen group. 114 isolates were recovered from the three groups, 45 from brevideciduous, 40 from evergreen, and 29 from deciduous. These isolates were distributed in 22 genera. The evergreen group showed greater diversity in taxonomic levels of family, order, and genus for the cultivable taxa, but less species diversity than the brevideciduous and deciduous. *Diaporthe* spp. were found in all phenologies, but in greater abundance in the deciduous group. *Diaporthe terebinthifolii, D. macintoshii, Kalmusia erioi*, and *Cytospora* viridistroma were common to the evergreen and deciduous group. The metabarcoding showed that *Basidiomycota* occurs in greater proportion in the evergreen group (15%) when compared to the other phenologies, where this group corresponds to less than 5% of the OTUs. The phyla *Monoblepharomycota, Rozelomycota*, and *Zoopagomycota* were exclusive to the brevideciduous. The foliar endophytic fungal community was more diverse in the brevideciduous group (6.4 H'). The highest Pielou evenness was observed in the brevideciduous group (6.4J), while the lowest value was observed in the evergreen group (3.6J). The abundance of the genus *Paramycosphaerella* was significantly influenced by the type of phenology, being more abundant in the group of brevideciduous and deciduous. In conclusion, our results suggest that the taxonomic structure of the endophytic mycobiome is influenced by the type of phenology in terms of diversity and dominance of certain taxa.

Key-words: *metabarcoding*; *Ascomycota*; Savanna; Illumina MiSeq sequencing; Brevideciduous; Deciduous; Ever green;

1. INTRODUTION

The different leaf characteristics present in vascular plant species are the result of thousands of years of evolution (Kenrick & Crane, 1997; Jill et al., 2017; Harrison et al., 2018; Vasco et al., 2020; Tomescu et al., 2020; Tomescu et al., 2017; Del Pazo et al., 2020; Pepe et al., 2022). These variations have made leaf tissue a unique, complex and highly dynamic microenvironment (Whipps et al., 2008; Yao et al., 2019; Into et al., 2020; Xi et al., 2021), characterized by drastic variations in nutrient availability, exposure to ultraviolet light, extreme conditions of variation in relative humidity, and temperature (Beattie & Lindow, 1999). However, the leaves comprise a microhabitat densely colonized by different species of microorganisms (Santana et al., 2018; Terhonen et al., 2019). Among the numerous groups of microorganisms that colonize the leaves, we can mention the endophytic fungi (Yao et al., 2019; Terhonen et al., 2019). Endophytic fungi are microorganisms that reside in plant tissues asymptomatically (Terhonen et al., 2019).

From an ecological and ecosystem-level point of view, different types of leaf phenology play crucial roles in the maintenance, structuring, and functionality of forests around the world (Franklin et al., 2015; Kharouba et al., 2018). However, considering the leaf tissue as a dynamic ecological unit, rich in species and which presents numerous variations in the availability of resources and environmental characteristics (abiotic and biotic factors), there is no knowledge about the effects that the different types of leaf phenology exert on the taxonomic composition of the endophytic fungal community.

Studies on the effect of different types of plant phenology and how they interact with the microphytobiome demonstrate that this is one of the key factors for structuring the microbial community at levels of occurrence and abundance of plant-associated microbial species (Ding & Melcher, 2016; Were et al., 2020; Igwe et al., 2021). On the other hand, it is also known that the community of microorganisms associated with plants also exert effects on the phenology of plants, either inducing the flowering period (Lu et al., 2018) or prolonging/decreasing the life of leaves in deciduous or evergreen species (Were et al., 2021). Taken together, these findings suggest that plant phenology exerts an ecological filter effect, modulating the diversity and abundance of species in the leaf microbiome, while the microorganisms of this community play important ecological roles for their host at the local (leaf) and systemic levels (host plant).

Leaf phenology is one of the factors responsible for structuring the community of microorganisms present in the leaf microbiome and, in short, the fact that there is no data relating the effect of leaf phenology on the diversity of endophytic fungi that occur in native plant species of the Cerrado, this chapter aims to: a) evaluate the effect of leaf phenology on the taxonomic composition of the endophytic fungal community; b) to compare whether plant species from different families, but with similar leaf phenology, present some degree of similarity in the composition of the endophytic fungi community related to them; c) compare plant species of the same family, but with different phenology, and observe if there is any degree of difference in the composition of the endophytic fungi community related to them; and finally, to compare different plant species with different phenologies and to observe the similarities and differences in the composition of the endophytic fungal community.

2. SPECIFIC OBJECTIVES

- Evaluate the community of endophytic fungi in different groups that occur in brevideciduous, deciduous and evergreen species;
- analyzes the community of endophytic fungi in different phenologies using culture-dependent and metabarcoding approaches;
- Infer metrics of alpha and beta diversity of the community of endophytic fungi associated with different types of phenology;
- Compare the community of endophytic fungi between the different phenology groups and observe if there is taxon sharing;

3. MATERIALS AND METHODS

3.1. Description of the study area

The area where the study was carried out is described in ***Chapter 2***.

3.2. Selection of plant species and sampling

Six plant species present in the control plots were selected, being the species *Caryocar brasiliense* and *Dalbergia miscolobium* for the brevideciduous; *Leptolobium dasycarpum* and *Qualea parviflora* for deciduous; and *Ouratea hexasperna* and *Styrax ferrugineus* for evergreens (Figure 42). In total, three individuals were sampled for each species, and ten leaves without disease symptoms were collected per individual, totaling 30 leaves per species and 60 per phenology type.

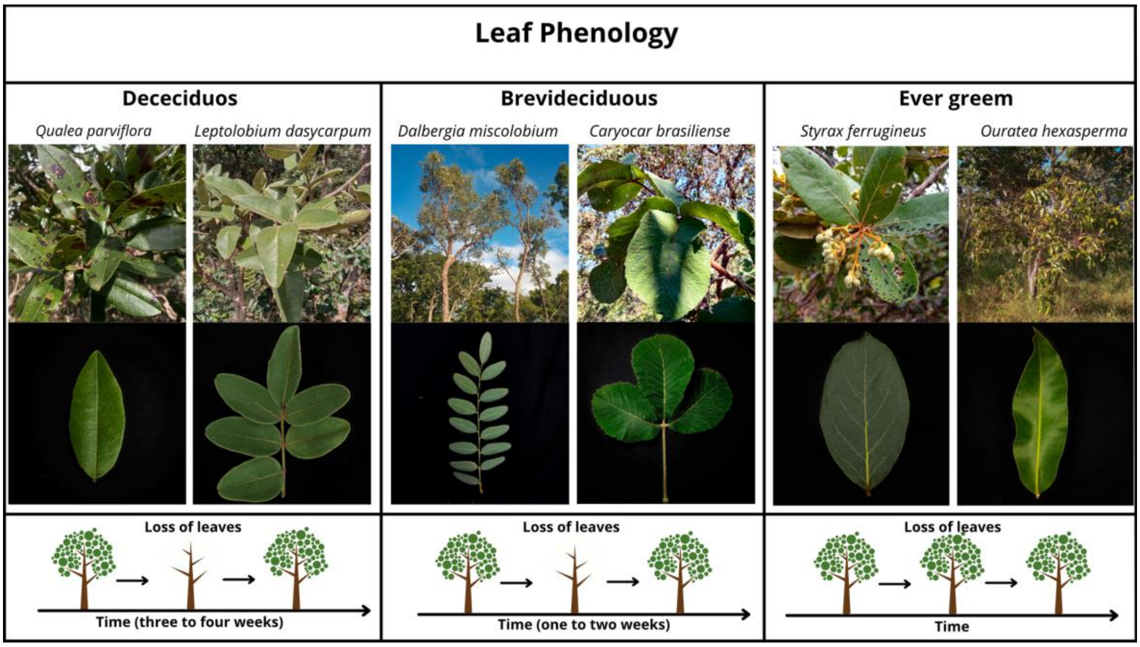


Figure 42. Types of leaf phenology for the plant species sampled.

3.3. Isolation and molecular identification of isolates

The isolation, cultivation conditions, purification, DNA extraction and molecular identification of the isolates are described in ***Chapter 2.***

3.4. Metabarcoding analysis

The eDNA extraction methods, primers used, sequencing conditions are described in ***Chapter 2***.

3.5. Data analysis

The analysis of sequencing quality, data processing, alpha and beta diversity metrics and differential abundance are described in ***Chapter 2***.

3.6. Analysis of the nutritional composition of leaves

The analysis of the nutritional composition of leaves are described in ***Chapter 2***.

4. RESULTS

4.1. Analysis of the nutritional composition of leaves

Leaf nutrient content, leaf area and specific leaf area (SLA) varied among different types of leaf phenology (Supplementary table 1). The ordering produced by Principal Component Analysis (PCA) shows the main differences between the phenologies (Figure 43). The deciduous species were related to higher levels of phosphorus, sulfur and leaf nitrogen, and specific leaf area (SLA) and lower levels of aluminum, magnesium, lower dry mass and leaf area (cm^2). The deciduous species were related to higher levels of aluminum and foliar potassium. Perennial species were correlated with higher leaf area (cm^2), higher leaf weight, leaf calcium and magnesium concentration.

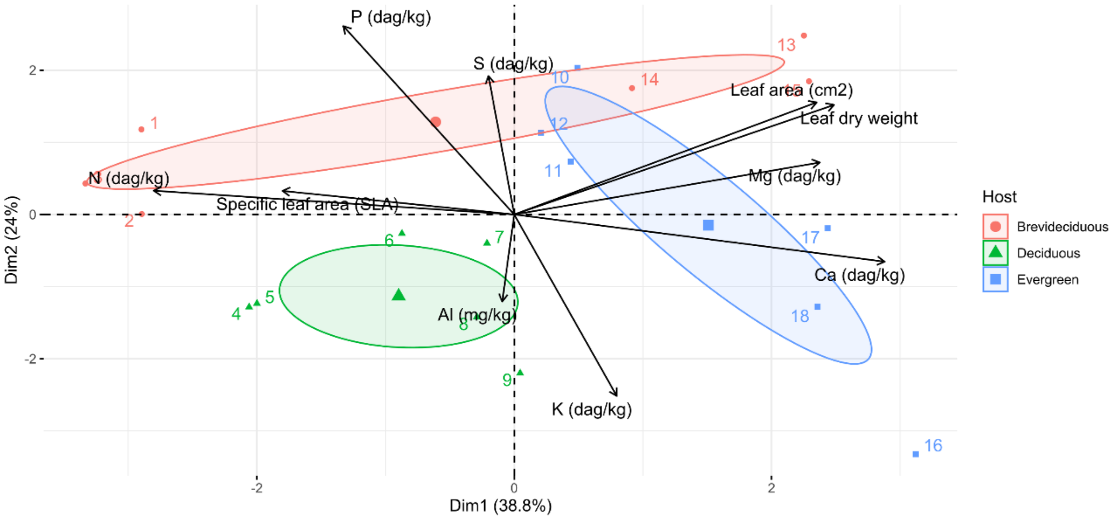


Figure 43. Ordenation produced by Principal Component Analysis (PCA) for variables of concentration of leaf nutrients, specific leaf area (SLA) cm²/g, dry mass of leaves among the three types of leaf phenology analyzed. The X-axis shows PC1 and the y shows PC2. The ellipses show the grouping of biological replicas by treatment. AFE: Specific foliar area; Al: Aluminium; Ca:

Calcium; CAS1: Stem circumference; K: Potassium; Mg: Magnesium; P: phosphorus; S: sulfur.

4.2. Distribution of isolates among the different groups of leaf phenology

When the host species were grouped by phenology, the evergreen group had the highest number of isolated endophytic fungi, with 45 isolates, while the brevideciduous group was in second place, with 40 isolates, and finally the deciduous group, with 29 isolates (Table 10). The phylum *Ascomycota* was dominant in the community of endophytic fungi in both types of leaf phenology and the distribution at taxonomic level of class showed equity in the dominance of Sordariomycetes and *Dothideomycetes* for the three types of phenology evaluated. Differences were noted from the taxonomic level of the family. The most abundant family in all types of phenology was *Diaphortaceae*, with a dominance of 72% in deciduous, 62% in evergreen and 55% in brevideciduous. *Didymellaceae* (27.5%) was the second most dominant family in the brevideciduous species; *Cytosporaceae* (6.6%) was the second most dominant in deciduous species; while in the evergreen species the different families found showed equity in dominance (Figure 44).

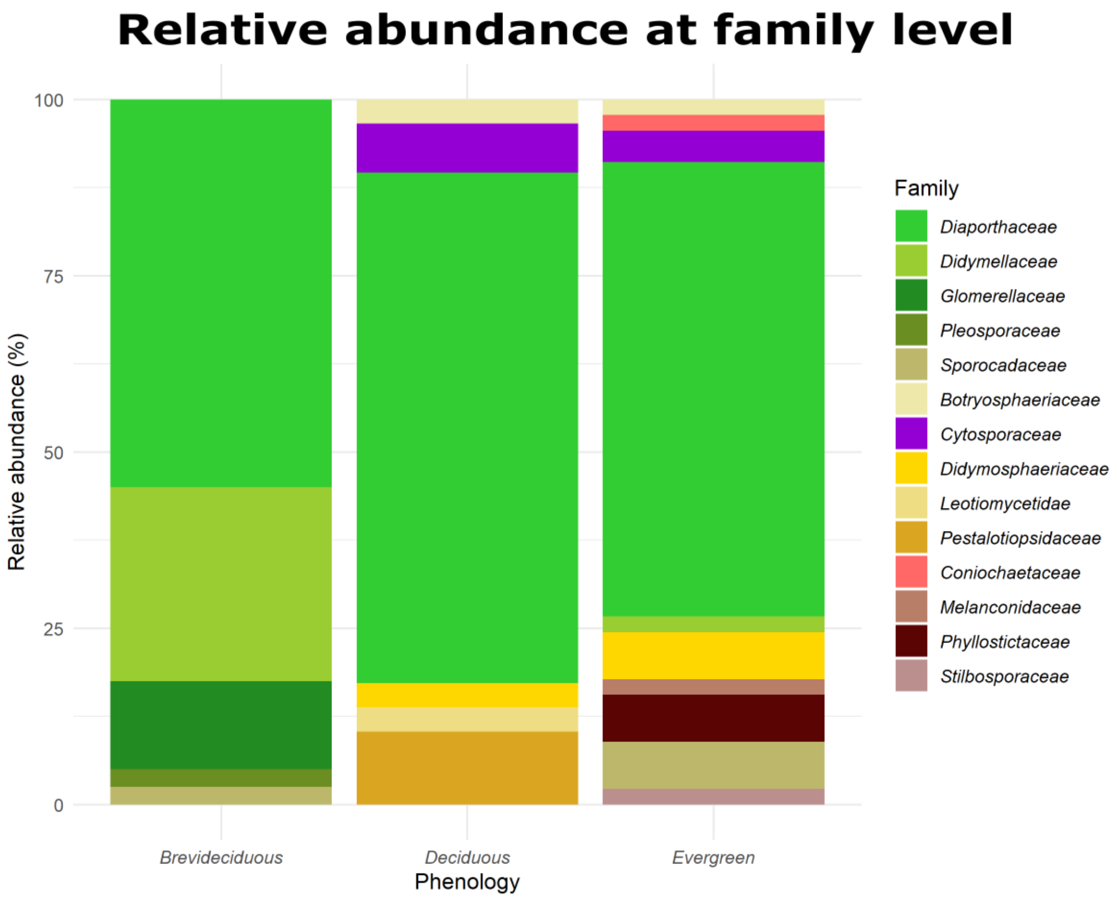


Figure 44. Relative abundance at the taxonomic family level of the endophytic fungal community in groups of host species with different types of phenologies. The distribution of fungal families was based on the grouping of taxa isolated from host species with the same type of phenology, being the species *Dalbergia miscolobium* and *Caryocar brasiliense* for the group of Brevideciduous; *Leptolobium dasycarpum* and *Qualea parviflora* for deciduous; and *Ouratea hexasperma* and *Styrax ferrugineus* for evergreens.

Diaporthe was dominant in the community of leaf endophytic fungi in both types of phenology, with a relative abundance of 72% in the deciduous group, 64% in the evergreen group, and 52% in the of brevideciduous. The other genera found corresponded to the dominance of less than 7%, except for the genus *Colletotrichum* in the brevideciduous group, which presented an abundance of 12.5% (Figure 45).

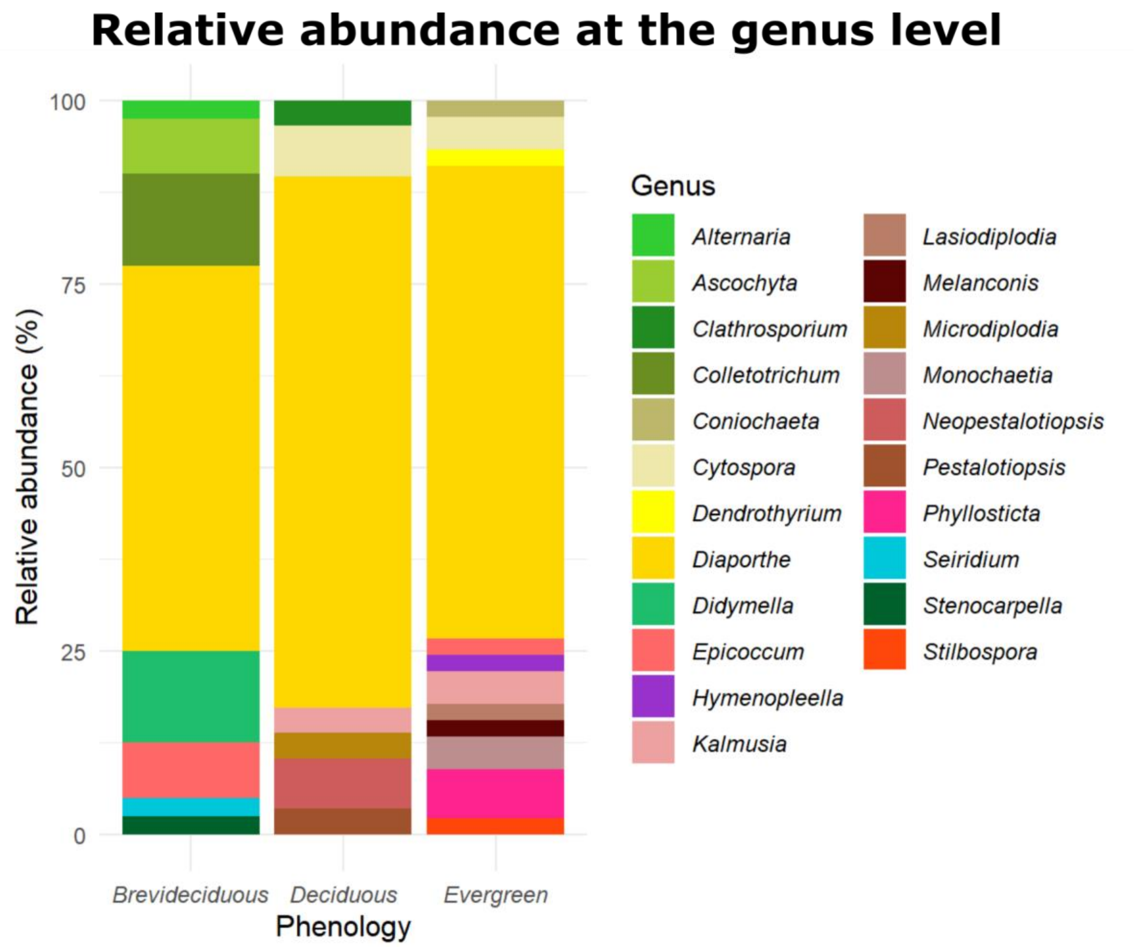


Figure 45. Relative abundance at the taxonomic level of the genus of the endophytic fungal community in groups of host species with different types of phenologies. The distribution of fungal genera was based on the grouping of taxa isolated from host species with the same type of phenology, being the species *Dalbergia miscolobium* and *Caryocar brasiliense* for the group of brevideciduous; *Leptolobium dasycarpum* and *Qualea parviflora* for *deciduous*; and *Ouratea hexasperma* and *Styrax ferrugineus* for evergreens.

The different groups of leaf phenology presented a heterogeneous and diverse mosaic of endophytic fungi species (Figure 46), with different species occurring in each group respectively. With a total of 22 species, the evergreen group presented a larger *pool* in the number of species than the other groups. The group of brevideciduous species was in second place, with a total of 20 species, while the group of deciduous species presented the lowest species diversity, with a total of 15 isolated species.

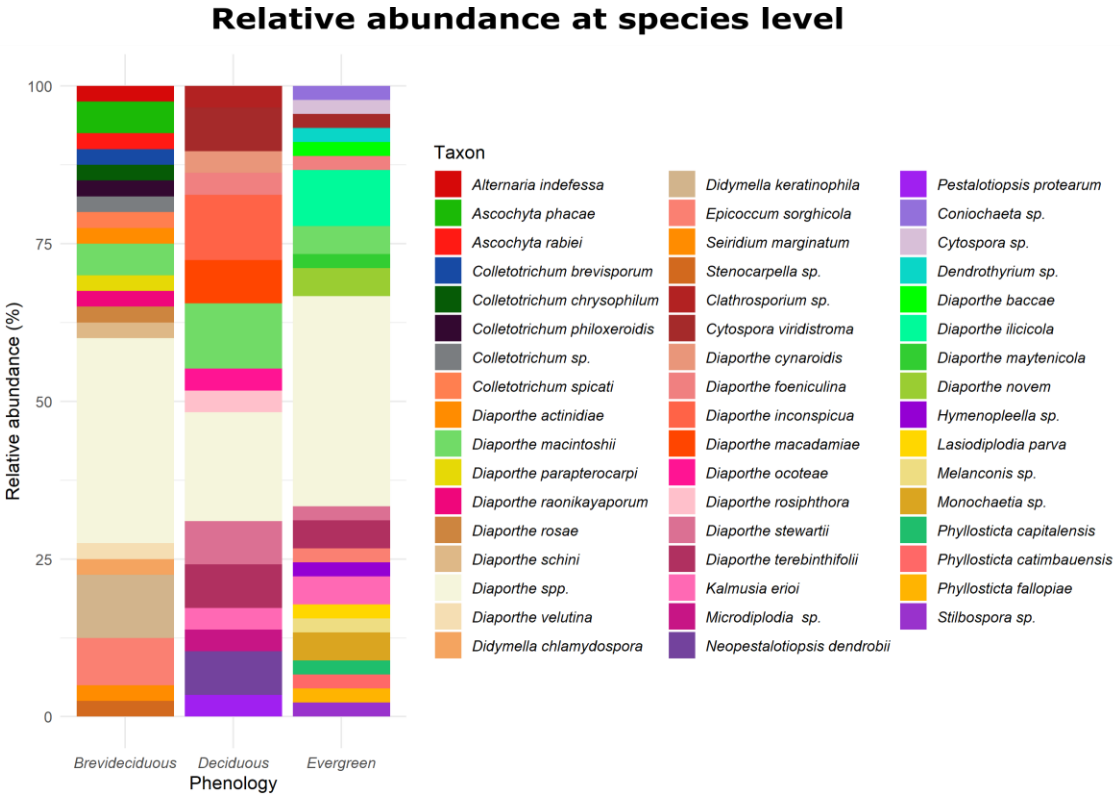


Figure 46. Relative abundance at the taxonomic level of the species of the endophytic fungal community in groups of host species with different types of phenologies. The distribution of fungal species was based on the grouping of taxa isolated from host species with the same type of phenology, being the species *Dalbergia miscolobium* and *Caryocar brasiliense* for the group of brevideciduous; *Leptolobium dasycarpum* and *Qualea parviflora* for *deciduous*; and *Ouratea hexasperma* and *Styrax ferrugineus* for evergreens.

Of the 22 genera of endophytic fungi identified among the different phenology groups, only four were found in more than one type of phenology, and the only one present in the three phenology groups was the genus *Diaporthe* (Figure 47). Six genera were found exclusively in the brevideciduous species, four in the deciduous, and eight in the evergreen species. The genus *Epicoccum* was found in the group of evergreens and deciduous, while the genera *Kalmusia* and *Cytospora* were common among evergreens and deciduous. In addition to the genus *Diaporthe*, the deciduous did not share other genera of endophytic fungi with the brevideciduous species.

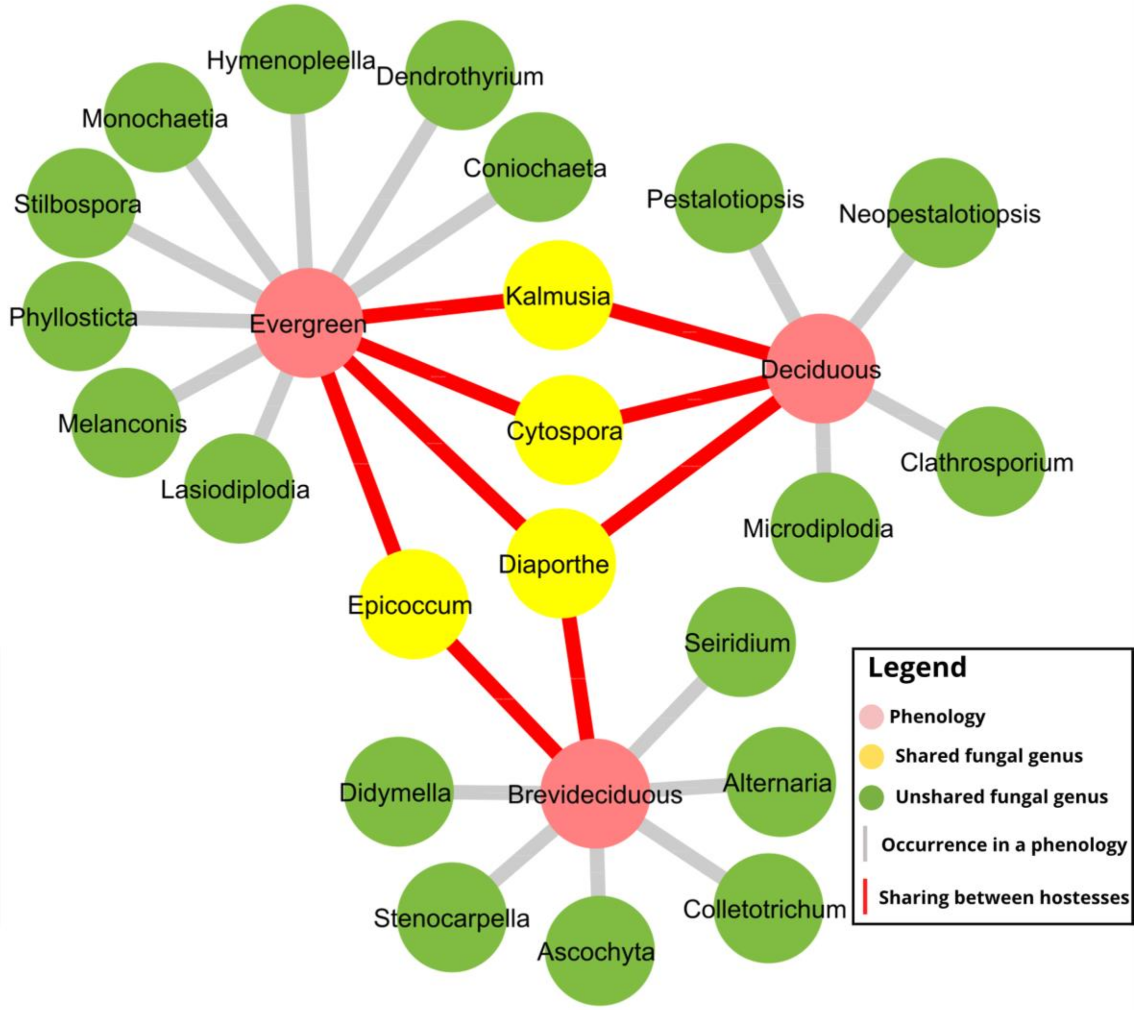


Figura 47. Architecture of the distribution network of endophytic fungi among leaf phenology groups. Pink nodes represent the phenology types of the host plant species; the green nodes represent the fungal genera not shared between the types of phenology; those in yellow show the shared fungal genera. Gray edges indicate the occurrence of the taxon within a type of a given phenology; while those in red show genera sharing.

Most of the endophytic fungi species found were exclusive to each phenology group (Figure 48). Of the 15 isolates identified at species level in the evergreen group, only four species were shared with the deciduous group, namely *Diaporthe terebinthifolii, D. macintoshii, Kalmusia erioi* and *Cytospora viridistroma*. The other isolates in both groups were exclusive, with 11 species exclusive to the evergreen group and eight species exclusive to the deciduous group. All identified species of endophytic fungi isolated from the brevideciduous group were exclusive to this group.

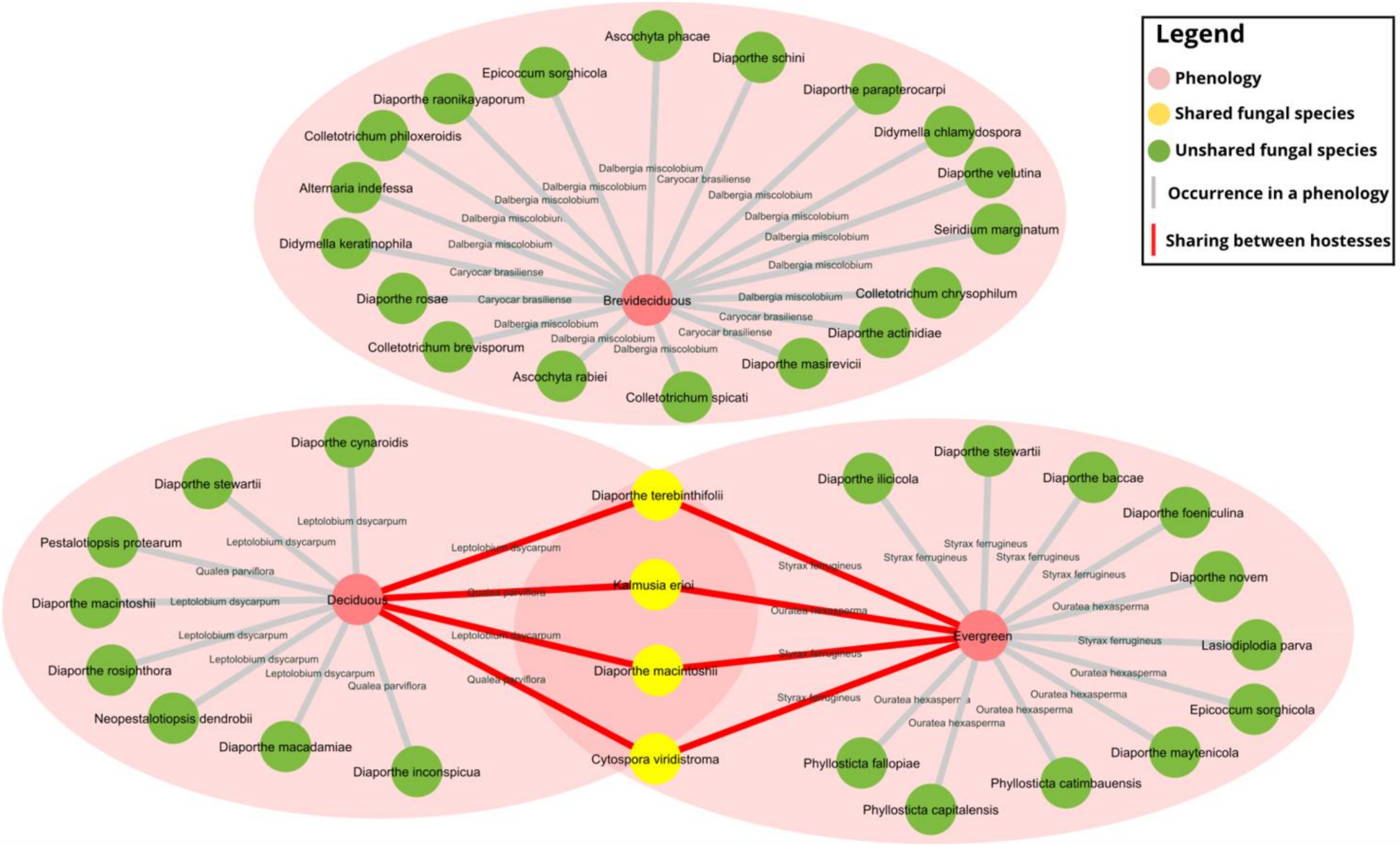


Figure 48. Architecture of the distribution network of endophytic fungi among leaf phenology groups. Pink nodes represent the phenology types of the host plant species; the green nodes represent the fungal taxa not shared among the host plants; those in yellow show the shared fungal species. Gray edges indicate the occurrence of the taxon within a host and phenology type; while those in red show species sharing. The ellipses in pink are the clusters according to the type of phenology. Taxons classified only by genus level were not consider.

The diversity of fungal species in the different groups of leaf phenology, no statistical differences were found (p> 0.05). However, the pool of fungi isolated from the brevideciduous species was richer in species (H' 3.8) than the deciduous (H'3.7) and evergreen (H' 3.5) species (Figure 49a). The 1st Order Jackknife Index, which estimates the species richness in a given niche, showed that the number of species in the brevideciduous group the cultivable endophytic fungal community can reach 19 species, in the deciduous it can reach 24 species and in the always -greens can reach 33 species (Figure 49b). Our sampled effort reached 100% of the estimated richness for the group of deciduous species. However, only 66.6% of the estimated endophytic fungal species diversity was observed in the deciduous group, while for the evergreen this value was 60%.

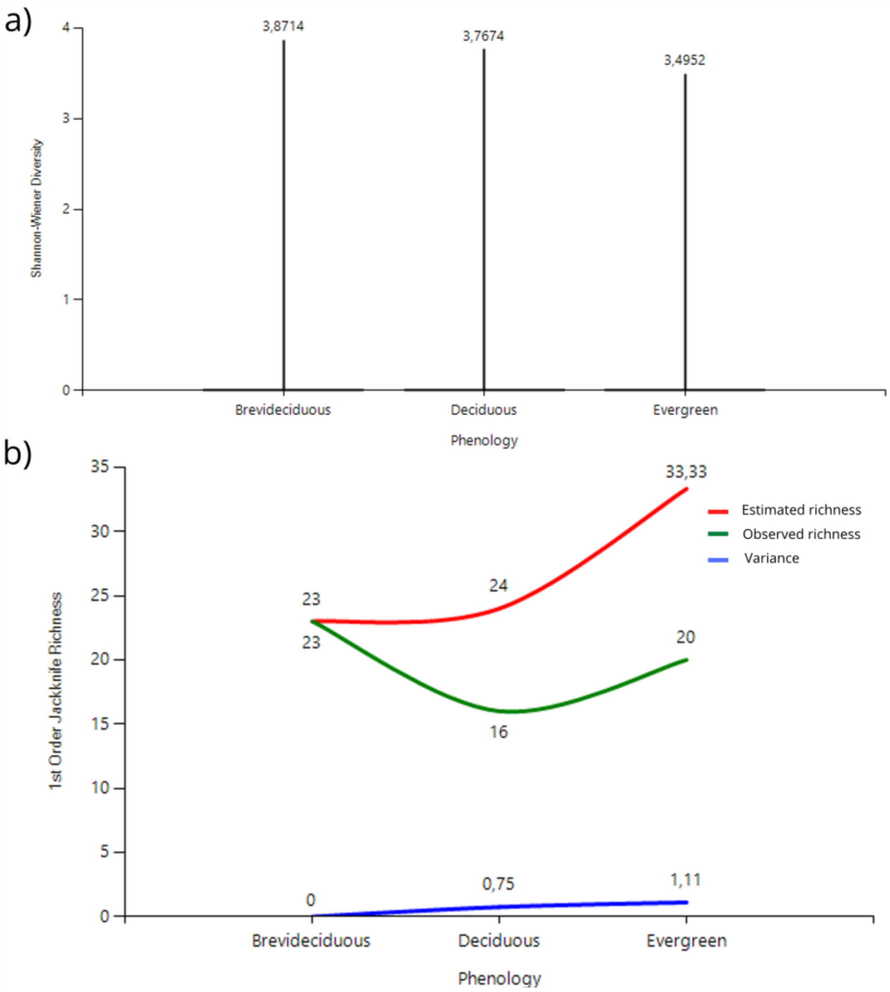


Figura 49. Metrics of alpha diversity and richness estimation of the endophytic fungal community in three types of leaf phenology. In a) the Shannon Wiener diversity index is shown. In b) the estimate of 1st Order Jackknife species richness is shown.

4.3. Metabarcoding

4.4. Relative abundance

The phylum *Ascomycota* was the most abundant phylum in the endophytic fungal community in both types of leaf phenology (six host species), reaching an average abundance value of approximately 95% for evergreen species and 55% for deciduous species and brevideciduous (Figure 50). It should be considered that approximately 45% of the total endophytic fungal amplicons in the deciduous and brevideciduous phenology species received taxonomic attributions only at kingdom level, leaving a huge gap on the composition of the endophytic fungal community at taxonomic levels of phylum, class, order, family etc. The phylum *Basidiomycota* presented an mean abundance of 5% for the evergreen species while for the deciduous and brevideciduous its abundance was <1%. In contrast, the brevideciduous and deciduous species presented the occurrence of a greater number of phylum.

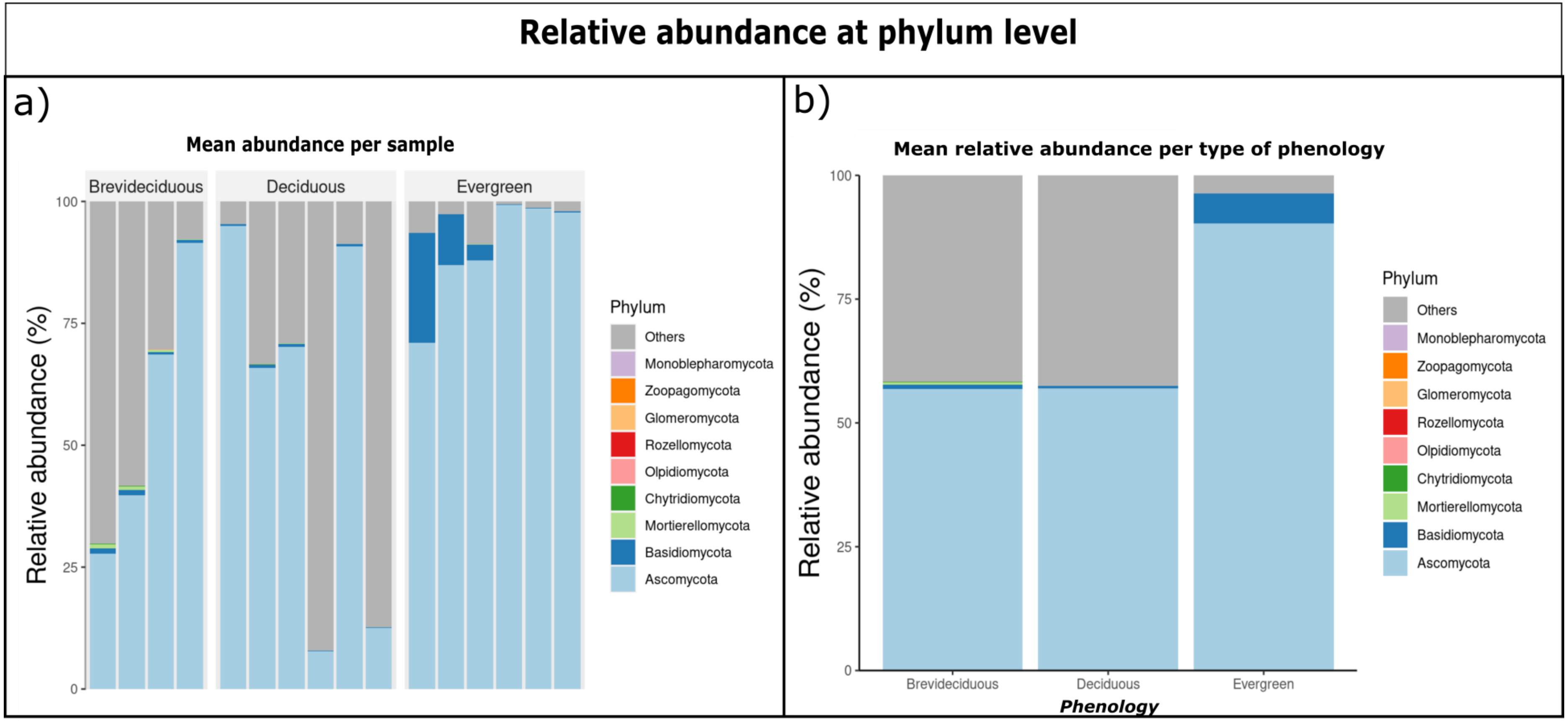


Figure 50. Phylum-level relative abundance of the endophytic fungal community associated with different types of leaf phenology. In a) the relative abundance by sampling effort by type of phenology is presented; while in b) the mean relative abundance by phenology type. Sequences classified only in kingdom level have been grouped under "Other". Brevideciduous (*Caryocar brasiliense* and *Dalbergia miscolobium*), deciduous (*Leptolobium dasycarpum* and *Qualea parviflora*) and evergreen (*Ouratea hexaperma* and *Styrax ferrugineus*).

On a mean, the most abundant class of endophytic fungi in the evergreen species was *Dothideomycetes* while in the deciduous and brevideciduous host species it was the class *Sordarimycetes* followed by *Leotiomycetes* (Figure 51). Regarding the taxonomic classification at the order level, the average for the evergreen hosts was *Asterinales*, followed by *Pleosporales, Capnodiales, Diaporthales*, and *Hypocreales.* For deciduous and brevideciduous species, the most abundant order of endophytic fungi was *Capnodiales*. The second most abundant order for deciduous was *Pleosporales* while for brevideciduous it was *Diaporthales*.

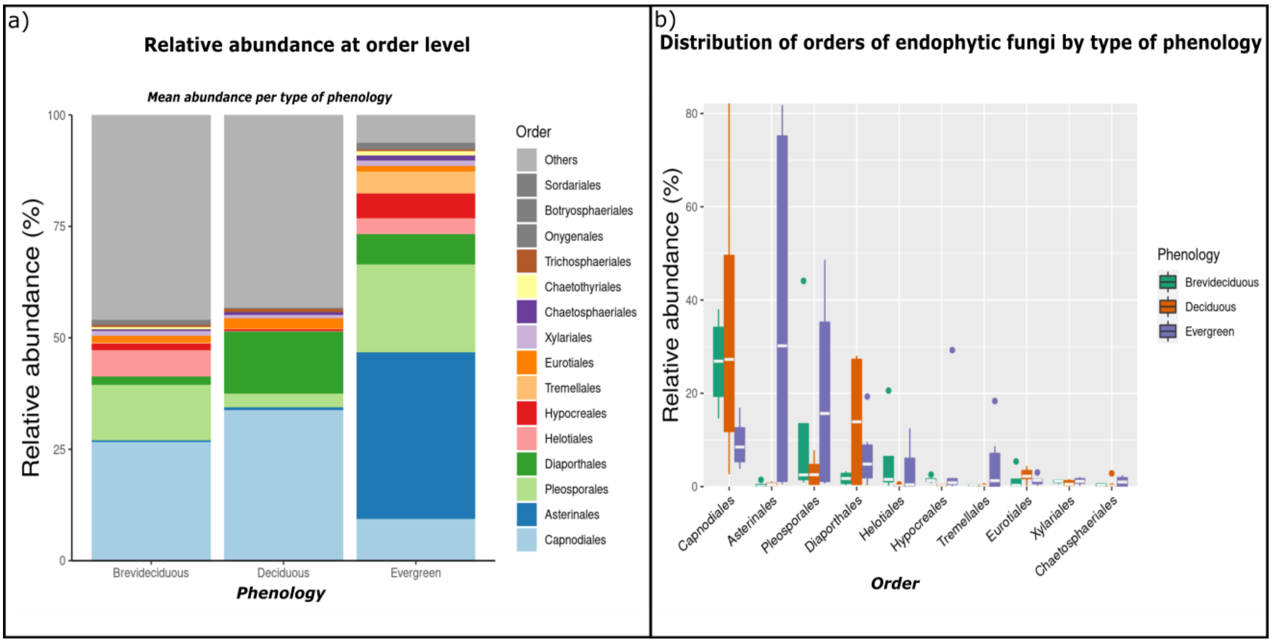


Figura 51. Order-level relative abundance of the leaf endophytic fungal community associated with six Cerrado woody species. The relative abundance by type of leaf phenology, being sampled two plant species by type of phenology. Sequences classified only at kingdom level were grouped into “Others”. Brevideciduous (*Caryocar brasiliense* and *Dalbergia miscolobium*), deciduous (*Leptolobium dasycarpum* and *Qualea parviflora*) and evergreen (*Ouratea hexaperma* and *Styrax ferrugineus*).

The 40 most abundant families of endophytic fungi are shown in Figure 52a. The *Parmulariaceae* and *Didymosphaeriaceae* families showed the highest mean relative abundance among the evergreen phenology host species (Figure 52b). For deciduous and brevideciduous, the *Mycospharellaceae* family was the most abundant.

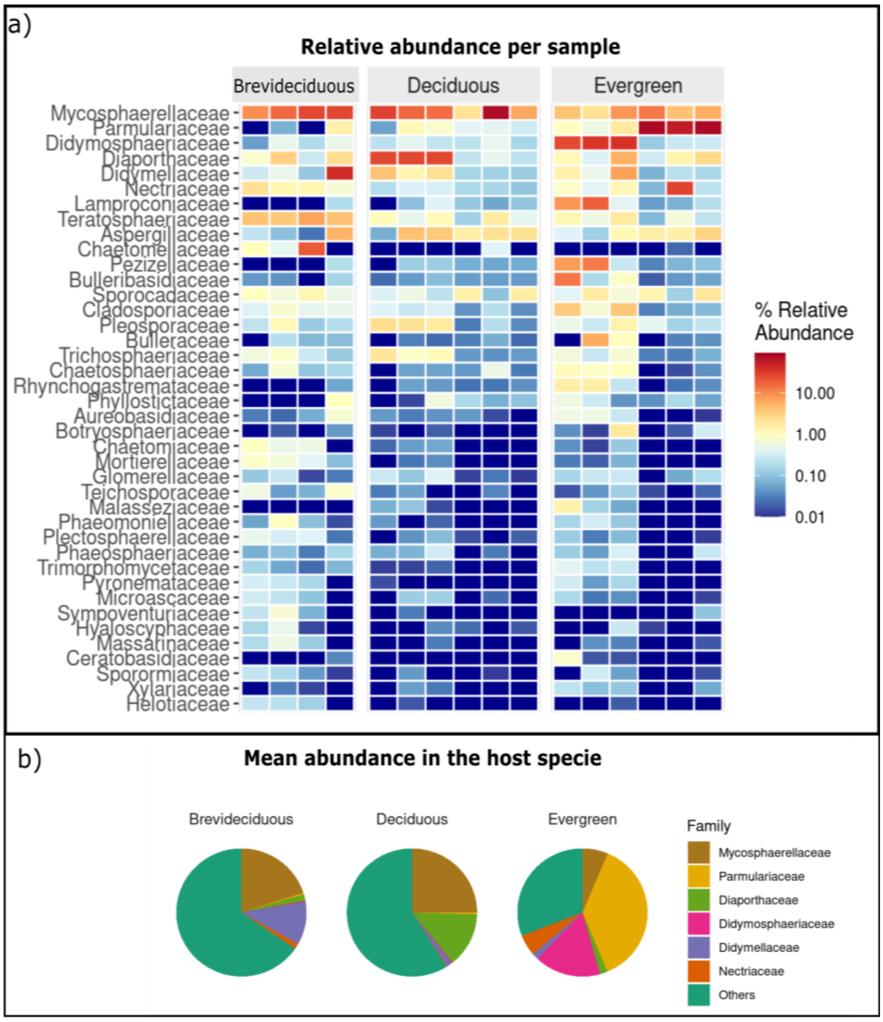


Figure 52. Data on the taxonomic composition of the endophytic fungal community at the taxonomic family level. a) Heatmap of fungal families with significant differences ($p<0.05$) between the three types of leaf phenology analyzed. Relative abundance data were z-score normalized per line. Darker red indicates greater abundance, while white indicates absence. In b) the average of the most abundant fungal families in each type of phenology is presented. The families with less than 2% abundance and sequences classified only at kingdom level were grouped under "Others". Brevideciduous (*Caryocar brasiliense* and *Dalbergia miscolobium*), deciduous (*Leptolobium dasycarpum* and *Qualea parviflora*) and evergreen (*Ouratea hexaperma* and *Styrax ferrugineus*).

In total, 40 genus of fungi showed significantly different abundance values between the three types of phenology studied (Figure 53a). On mean the most abundant genus of fungi present in the endophytic mycobiota of the evergreen species were *Parmularia* and *Kalmusia* (Figure 53b). In deciduous phenology species, the most abundant genus were *Diaporthe, Madagascaromyces* and *Paramycosphaerella*. For the brevideciduous were *Didymella* and *Paramycosphaerella*.

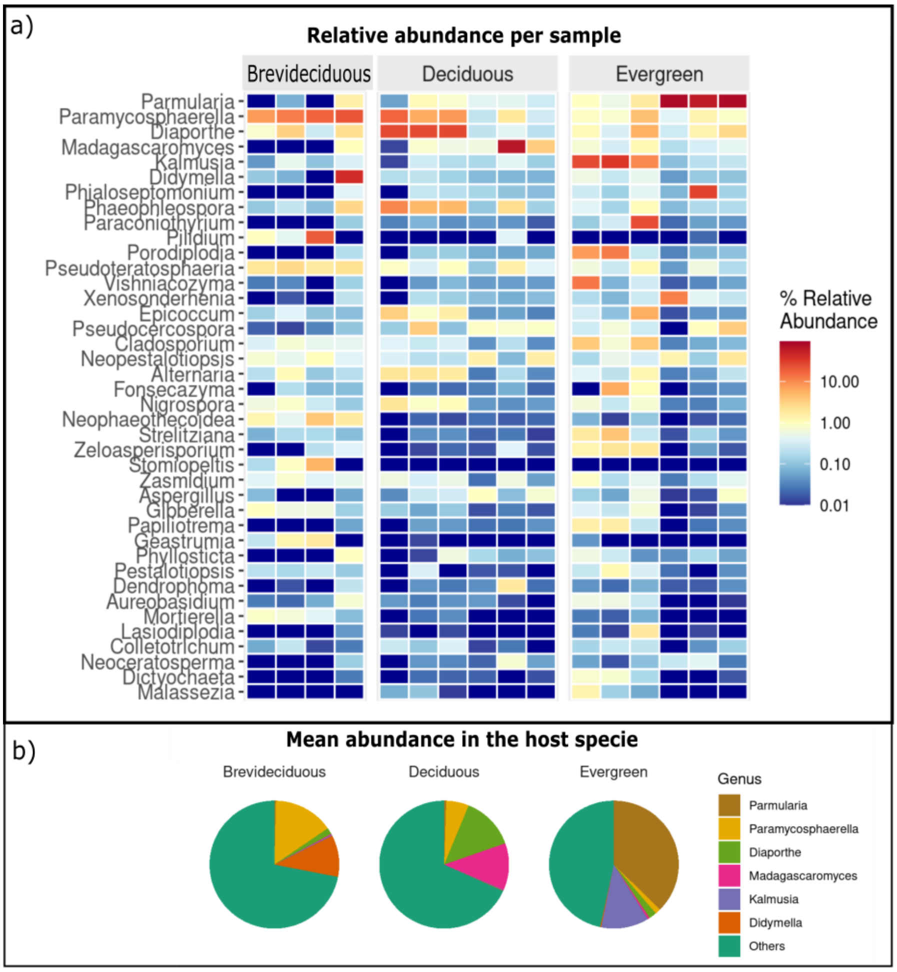


Figure 53. Data on the taxonomic composition of the endophytic fungal community at the taxonomic genus level. a) Heatmap of fungal genus with significant differences (p<0.05) between the three types of leaf phenology analyzed. Relative abundance data were z-score normalized per line. Darker red indicates greater abundance, while white indicates absence. In b) the average of the most abundant fungal genus in each type of phenology is presented. The genus with less than 2% abundance and sequences classified only at kingdom level were grouped under "Others". Brevideciduous (*Caryocar brasiliense* and *Dalbergia miscolobium*), deciduous (*Leptolobium dasycarpum* and *Qualea parviflora*) and evergreen (*Ouratea hexaperma* and *Styrax ferrugineus*).

4.5. *Alpha and Beta diversity*

The alpha diversity indices show that there are no important differences in the species diversity of the endophytic mycobiota between the types of leaf phenology (Figure 54). However, although there are no important differences in the alpha diversity index of the endophytic mycobiota between the different types of leaf phenology, the endophytic mycobiota of the group of brevideciduous species showed greater equitability and species richness when compared to the others (Figure 54a, b and c). As for PD diversity, considering the phylogenetic distance of the OTU's constituting the endophytic mycobiota, the deciduous species presented the lowest values, while the evergreens the highest values. Regarding dissimilarity between the endophytic fungi communities present in each type of phenology, although the analysis of main coordates (PCoA) from the Brary curtis metric suggests that there is dissimilarity between communities, these differences are not significant (p> 0.05) (Figure 54 d and e).

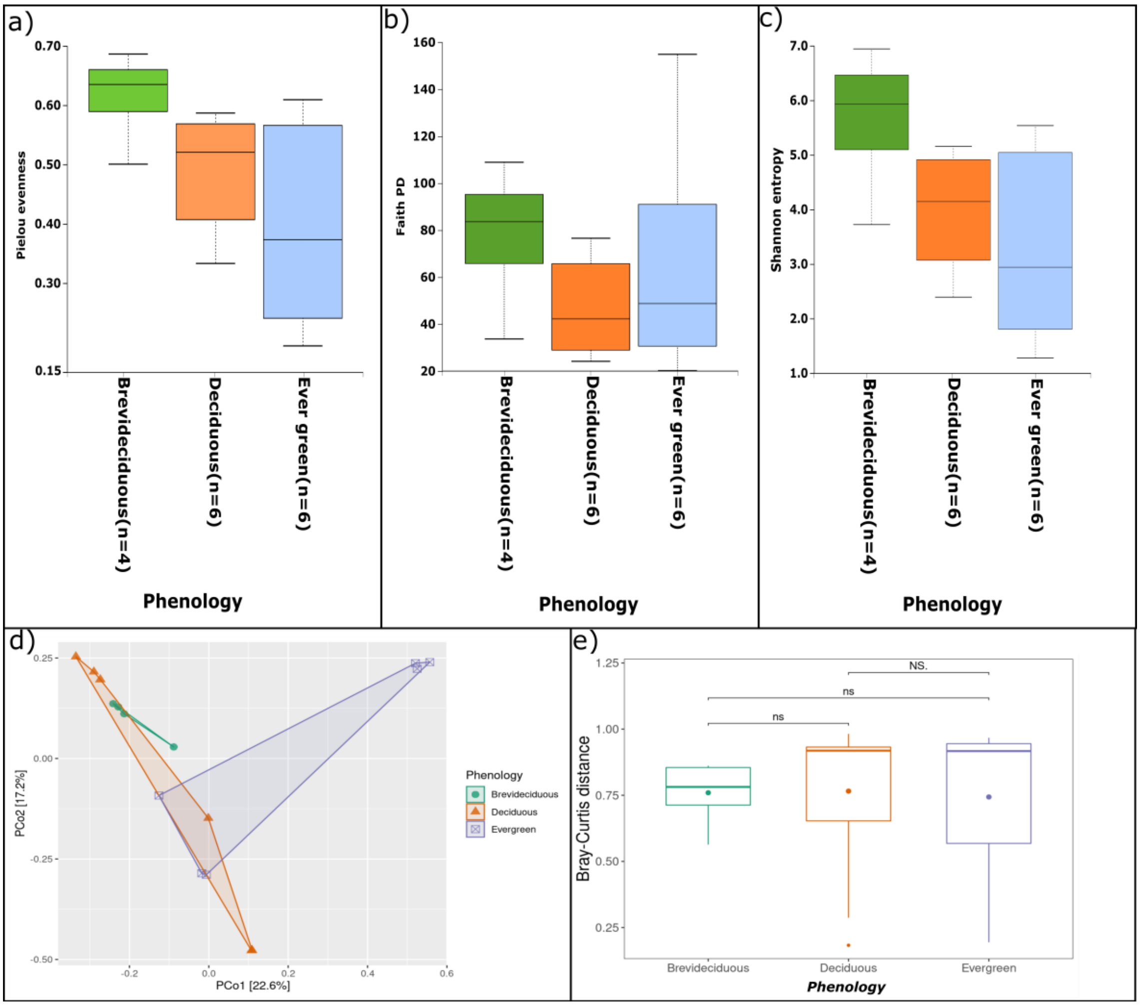


Figure 54. Alpha and Beta Diversity Indexes for the community of endophytic fungi in different types of leafy phenological groups. Alpha diversity metrics a) Pielou evenness, b) Phylogenetic diversity of Faith and c) Shannon entropy of the endophytic fungi community between the Brevideciduous (*Caryocar brasiliense* and *Dalbergia miscolobium*), deciduous (*Leptolobium dasycarpum* and *Qualea parviflora*) and evergreen (*Ouratea hexaperma* and *Styrax ferrugineus*). Beta Diversity Metric: d) Principal coordinates Analysis (PCOA) derivatives of distance from Bray curtis comparing the different phenology groups (p = 0.001 per PERMANOVA); in e) is shown the distance of Bray Curtis among the community of endophytic fungi among the three groups of phenology. No significant statistical difference between the different phenologies for alpha or beta diversity values (p> 0.05) were found. Boxplots represent the interquadil interval (IQR) between the first and third quartis (Percentis 25 and 75,

respectively). Tails represent the lower and highest values found; and the horizontal medium line within the box represents the median.

4.6. *Differential abundance*

Although significant differences have not been observed among the community of endophytic fungi among the three phenology groups analyzed here, this does not mean that there are no differences between communities. The metastast statistical test has shown that the abundance of the genus *Paramycospherella* differs significantly between the three types of phenologies, with greater abundance in the deciduous species and less abundance in the evergreen (Figure 55).

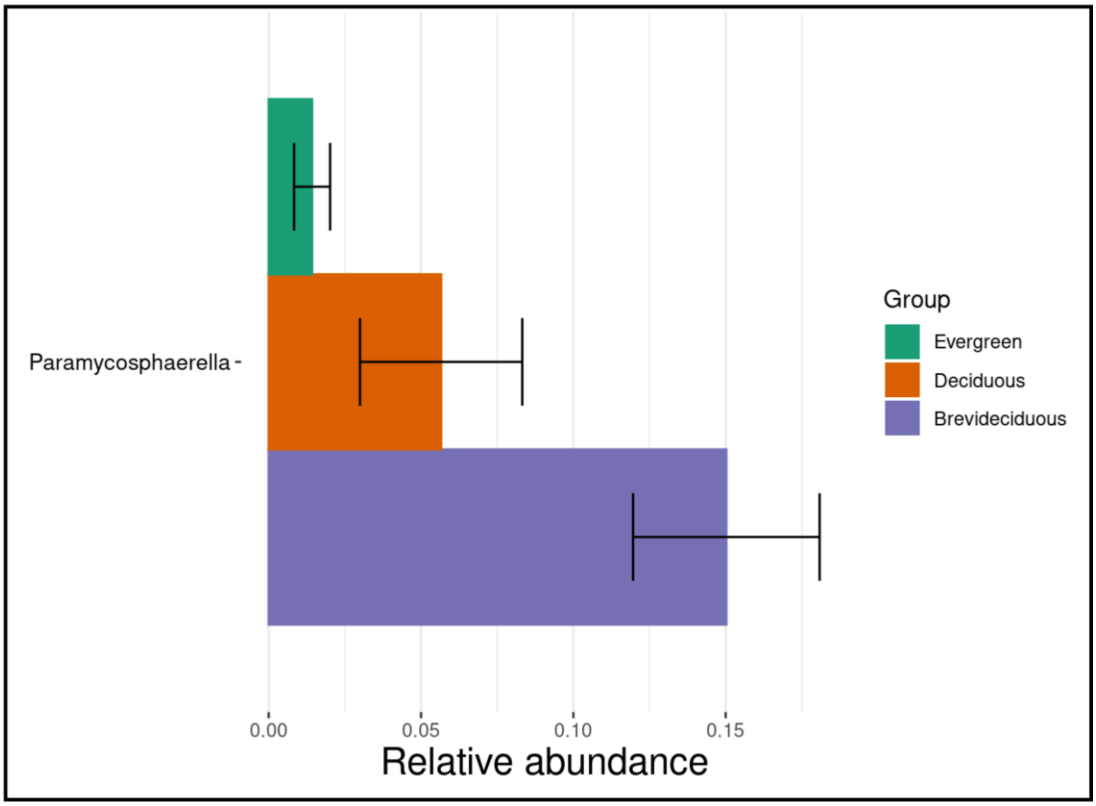


Figure 55. Taxon (genus-level) differentially abundant among the different groups of phenology, shown by the metastat. In the Y axis, the main differentially abundant genre is shown; The x axis shows the relative abundance. Brevideciduous (*Caryocar brasiliense* and *Dalbergia miscolobium*), deciduous (*Leptolobium dasycarpum* and *Qualea parviflora*) and evergreen (*Ouratea hexaperma* and *Styrax ferrugineus*).

5. DISCUSSION

The different types of phenology are dynamic both in terms of space and time as well as in terms of the number of microorganism resources. The leaves of evergreen species have superior durability when compared to the leaves of deciduous and brevideciduous species (Kikuzawa et al., 2013) and therefore we theorized that they could accumulate a greater diversity of endophytic fungi. Deciduous species have a shorter half-life and are exchanged annually, so we theorize that the diversity in this group would be lower compared to the others.

5.1. Cultivation dependent methods

The number of isolates varied among the different types of phenology. Brevideciduous species had the highest number of isolates, with 45, followed by evergreens with 40, and deciduous with 29. Different frequencies of isolation are suggestive of variations in colonization rates (Hata and Futai, 1995). In this context, variations in the number of isolates recovered from different hosts are well known (Pietro-Souza et al., 2017; Du et al., 2020). In our study, this trend was also observed and helps to shed light on one of our hypotheses. Our first hypothesis was that the evergreen group would be densely populated with the other groups. However, the variations in the frequency of isolates between the different phenologies suggest that the group of brevideciduous species has a higher colonization rate than the other groups. The lowest values of frequency of isolates were reported in deciduous species, which supports our hypothesis for this group.

The phylum *Ascomycota* was dominant among the three phenology types, which was to be expected since most cultivable endophytic fungi are ascomycetes (Pietro-Souza et al., 2017; Du et al., 2020; An et al., 2020; An et al., 2022; Cui et al., 2022). Differences were observed from the taxonomic level of the family between the phenologies. Although *Diaporthaceae* was dominant in all phenologies, the evergreen species harbored a greater number of families and genera than the other two groups. The smallest number of families and genera was observed in Brevideciduou. Results similar to those found here have already been reported in communities of endophytic fungi, where it was observed that a high number of isolates does not equate to a similar taxonomic diversity (Noriler et al., 2018; Chand et al., 2020). Thus, our data corroborate their findings and support that a greater number of isolates does not always reflect a greater diversity of families and high genera.

Diaporthe (*Diaporthales, Diaporthaceae*) was dominant in all phenologies. This genus is well known for establishing numerous ecological relationships with woody species (Yang et al., 2018; Tanapichatsakul et al., 2019) and is often reported as endophytic (Tibpromma et al., 2018; Silva et al., 2018; Santos et al., 2020; Dong et al., 2021). Its ubiquity among phenologies can be attributed to the fact that this genus is metabolically versatile and has evolved to use a wide range of strategies to colonize the plant microbiome (Santos et al., 2017; Ariyawansa et al., 2021; Książkiewicz et al., 2021; Mena et al., 2022). Genomic insights together with phylogenetic and comparative genomics approaches show that *Diaporthe* spp. has sophisticated mechanisms to penetrate the interior of the plant tissue, circumvent the host plant's defense system, and establish colonization (Santos et al., 2017; Ariyawansa et al., 2021; Książkiewicz et al., 2021; Mena et al., 2022).

Comparing the occurrence of genera, evergreen species showed greater diversity than deciduous and brevideciduous. However, the greatest diversity of species was observed in isolates from the brevideciduous and deciduous groups. Deciduous and brevideciduous species invest more resources in photosynthetic tissues and have greater carbon assimilation than evergreens (Givnish, 2002; van Ommen Kloeke et al., 2012; Ouédraogo et al., 2016), which makes leaf tissue these a habitat with greater availability of resource sources, which, in turn, can support a more diverse fungal community (Liu et al., 2021; Mancuso et al., 2021). In the space-time context, the community of endophytic fungi of the evergreen group is not seasonally renewed like the community of other phenologies, providing a greater interaction between fungi and plants, which can result in a community with few species, but highly specialized and able to colonize the niche in question (Ruiz-Mirazo et al., 2017). This theory can be supported by the fact that species with a high degree of specialization tend to occupy more space in ecological niches, which reduces the space for other less specialized species to occur, resulting in a less diverse Community (Rabosky DL & Hurlbert, 2015; Schluter et al., 2017; Mandi et al., 2020)

A high sampling effort is critical for sampling rare species or representatively sampling communities with low equity values (Messina et al., 2015; Maxwell et al., 2018). In the context of our study, the 1st order Jackknife diversity estimate suggests that there is greater diversity in endophytic fungi in evergreens since new species are found in each sampling compared to previous samplings. Such findings indicate that the sampling effort was not sufficient to cover the diversity of cultivable endophytic fungi in the evergreen group.

5.2. Metabarcoding

Metabarcoding has been used as a tool for evaluating different microbial communities, to reporting the diversity, occurrence, and sharing of species among them (Liotti et al., 2019; Alibrandi et al., 2020). Here we use this same tool to describe the diversity of leaf endophytic fungi that occur in different types of leaf phenology of native Cerrado species, being one of the first works with this objective. Therefore, our data bring unprecedented information.

The phylum *Ascomycota* was dominant, which is often reported in communities of endophytic fungi (Pietro-Souza et al., 2017; Du et al., 2020; An et al., 2020; An et al., 2022; Cui et al., 2022; Cui et al., 2022). The brevideciduous and deciduous species presented the occurrence of the phyla *Monoblepharomycota, Mortierellomycota, Olpidiomycota, Glomeromycota, Chytridiomycota, Rozellomycota*, and *Zoopagomycota*. This greater diversity of phyla may be related to the availability of photoassimilates present in the leaf tissue of brevideciduous and deciduous species (Givnish, 2002; van Ommen Kloeke et al., 2012; Ouédraogo et al., 2016), which, in turn, represent a resource-rich niche for microorganisms, enabling greater diversity to occur (Zheng et al., 2019).

Another explanation for the high number of phyla present in these two phenology groups may be the low degree of specialization of the fungal community related to them. Because deciduous and brevideciduous leaves have a seasonal lifespan, fungus and plant interact for a shorter period, which does not allow the evolution of a highly specialized symbiotrophic relationship (Alam et al., 2021; Chaudhry et al., 2021; Fukumori et al., 2022), resulting in a more generalist community composed of numerous species (Rabosky et al., 2015). This fact has already been discussed when comparing communities of endophytic fungi related to plant species that occur in Brazilian biomes (Noriler et al., 2018).

The phylum *Basidiomycota* showed greater abundance in the evergreen group concerning the deciduous and brevideciduous groups. Evergreen species have a higher content of complex polysaccharides in their tissues compared to deciduous and brevideciduous species (Soh et al., 2019; Kotowska et al., 2020; Shao et al., 2022), and basidiomycetes fungi have an enzymatic arsenal capable of degrading these carbohydrates (Grass et al., 2011; Metreveli et al., 2021). Thus, we can theorize that the composition of the evergreen leaf tissue plays a biological filter role on the endophytic mycobiota, allowing the occurrence of basidiomycetes in greater abundance in this group than in the other phenologies.

The evergreen species showed greater order diversity, with *Asterinales*, *Pleosporales*, and *Capnodiales* dominating. *Capnodiales* were dominant in deciduous and brevideciduous. *Pleosporales* and *Capnodiales* are the second most diverse orders in *Dothideomycetes* and include fungal taxa with different lifestyles (Abdollahzadeh et al., 2020), many of which are often reported as endophytic fungi (Pietro-Souza et al., 2017; Du et al., 2020; An et al., 2020; An et al., 2022; Cui et al., 2022). *Capnodiales*, in particular, comprise a taxonomic group that derives from an ectophytic ancestor of plants (Abdollahzadeh et al., 2020). These differences in order dominance between phenologies can be explained by the interaction between fungus and phenology type, which involves host specificity, resource availability, together with environmental factors (Peng et al., 2021).

At taxonomic levels of family and genus, differences in occurrence and abundance were observed between the phenology groups. The brevideciduous and deciduous groups presented higher values in alpha diversity indices than the evergreen group, with higher values of richness and equity. This fact can be explained by the 'Ecological Controls' (EC) and 'Diversity Begets Diversity' (DBD) theories (Mandi et al. 2020). EC predicts a negative relationship, where increased diversity or migration of new species is constrained as a niche is filled (Rabosky DL & Hurlbert, 2015; Schluter et al., 2017; Mandi et al., 2020). As evergreen leaves have a longer life span, the fungal taxa that first colonize their leaf tissue become dominant, preventing colonization by other groups. The equity value found in this group supports this hypothesis.

DBD can explain the greater diversity of species in the deciduous and brevideciduous phenologies. This theory predicts that existing diversity in a niche promotes the accumulation of more diversity through the construction of numerous ecological interactions (Whittaker et al., 1972; Calcagno et al., 2017). If we consider that deciduous and brevideciduous have greater sources of photoassimilates (Givnish, 2002; van Ommen Kloeke et al., 2012; Ouédraogo et al., 2016) and less specialized communities, they soon provide conditions to sustain a more diverse community which in turn stimulates more diversity through the construction of microbe-microbe interactions within the ecological niche in question (Emerson BC & Kolm 2005; Bailey et al., 2013).

The dissimilarities shown by PCoA show the greater similarity of the deciduous leaf endophytic mycobiome with the brevideciduous ones, and a greater distance between these groups and the evergreen mycobiome. This particular finding supports everything discussed above. Thus, our data nullify our main hypothesis that the evergreen species would harbor a more diverse mycobiome in relation to the other phenologies analyzed.

5.3. Cultivation dependent methods and Metabarcoding

Communities of endophytic fungi have been studied mainly using cultivation-dependent approaches (Pietro-Souza et al., 2017; Du et al., 2020), which does not allow a representation of the real diversity of fungi due to numerous factors (Chi et al., 2019). On the other extreme, culture-independent approaches have been an excellent alternative to better study communities of microorganisms, as they allow a better characterization of the microbiome (Liotti et al., 2019; Alibrandi et al., 2020). In recent years, the combination of these methodologies has been used to study endophytic fungal communities (Chi et al., 2019; Yao et al., 2019; Castro et al., 2020; Durán et al., 2021) and has been shown to be a potent combination to study microorganisms in their natural niches (Liotti et al., 2019; Alibrandi et al., 2020).

In our study, we used cultive-dependent and *metabarcoding* approaches to describe the endophytic fungal community in different groups of leaf phenologies. Both methods met the proposed objective and, in most cases, showed similarities between the generated data. Both the *metabarcoding* and the cultive-dependent method showed differences in taxonomic levels below order; and the endophytic fungal community was more diverse in the brevideciduous species and less diverse in the evergreen group etc.

6. CONCLUSION

The occurrence, diversity, and equity of the leaf endophytic fungal community appear to be influenced by the type of leaf phenology. Our data show that evergreen species have a lower diversity of species and dominant fungal taxa in their leaf mycobiome, which may be the result of a higher degree of specialization of these taxa. In contrast, the community of leaf endophytic fungi in the brevideciduous and deciduous species is more diverse in species and appears to be composed of more generalist fungi.

Dissimilarities between the leaf mycobiome of the different phenology groups were observed in both cultive-dependent and *metabarcoding* approaches. However, metabarcoding provided more information in terms of species diversity, while differences in dissimilarity were overestimated in cultive-dependent approaches. The use of both techniques allowed a more complete view of the similarities and differences.

In conclusion, our data raise important questions to be further studied about the factors that limit or drive species diversity in the endophytic mycobiome of Cerrado woody species; and on the evolution of specialization of the relationship established between endophytic fungus and host, and how this influences the taxonomic structure of the endophytic mycobiome.

BIBLIOGRAPHIC REFERENCES

1. Abdollahzadeh J, Groenewald JZ, Coetzee MPA, Wingfield MJ, Crous PW. Evolution of lifestyles in *Capnodiales*. *Stud Mycol*. 2020; 5; 95:381-414. doi: 10.1016/j.simyco.2020.02.004.
2. Alam B, Lǐ J, Gě Q, Khan MA, Gōng J, Mehmood S, Yuán Y, Gǒng W. Endophytic Fungi: From Symbiosis to Secondary Metabolite Communications or Vice Versa? *Front Plant Sci*. 2021; 17; 12:791033. doi: 10.3389/fpls.2021.791033.
3. Alibrandi P, Schnell S, Perotto S, Cardinale M. Diversity and Structure of the Endophytic Bacterial Communities Associated With Three Terrestrial Orchid Species as Revealed by 16S rRNA Gene Metabarcoding. *Front Microbiol*. 2020; 15; 11:604964. doi: 10.3389/fmicb.2020.604964.
4. An C, Ma S, Shi X, Liu C, Ding H, Xue W. Diversity and Ginsenoside Biotransformation Potential of Cultivable Endophytic Fungi Associated With *Panax bipinnatifidus* var. *bipinnatifidus* in Qinling Mountains, China. *Front Pharmacol*. 2022; 4;13:762862. doi: 10.3389/fphar.2022.762862.
5. Ariyawansa HA, Tsai I, Wang JY, Withee P, Tanjira M, Lin SR, Suwannarach N, Kumla J, Elgorban AM, Cheewangkoon R. Molecular Phylogenetic Diversity and Biological Characterization of *Diaporthe* Species Associated with Leaf Spots of *Camellia sinensis* in Taiwan. *Plants* (Basel). 2021; 14; 10(7):1434. doi: 10.3390/plants10071434.
6. Bai K, He C, Wan X, Jiang D. Leaf economics of evergreen and deciduous tree species along an elevational gradient in a subtropical mountain. *AoB Plants*. 2015 Jun 8;7:plv064. doi: 10.1093/aobpla/plv064.
7. Bailey SF, Dettman JR, Rainey PB, Kassen R. Competition both drives and impedes diversification in a model adaptive radiation. *Proc Biol Sci*. 2013 Sep 7;280(1766):20131253. doi: 10.1098/rspb.2013.1253. Erratum in: *Proc Biol Sci*. 2016; 27; 283(1829). pii: 20160763. doi: 10.1098/rspb.2016.0763.
8. Bao L, Cai W, Zhang X, Liu J, Chen H, Wei Y, Jia X, Bai Z. Distinct Microbial Community of Phyllosphere Associated with Five Tropical Plants on Yongxing Island, South China Sea. *Microorganisms*. 2019; 4;7(11):525. doi: 10.3390/microorganisms7110525. Erratum in: Microorganisms. 2020; 15;8(4).
9. Barotto AJ, Fernandez ME, Gyenge J, Meyra A, Martinez-Meier A, Monteoliva S. First insights into the functional role of vasicentric tracheids and parenchyma in eucalyptus species with solitary vessels: do they contribute to xylem efficiency or safety? Goldstein G, editor. *Tree Physiol*. 2016; 36: 1485–1497. 10.1093/treephys/tpw072.
10. Barranca VJ, Kovačič G, Zhou D, Cai D. Improved Compressive Sensing of Natural Scenes Using Localized Random Sampling. *Sci Rep*. 2016; 24;6:31976. doi: 10.1038/srep31976.
11. Batalha MA et al. Variações fenológicas das espécies do cerrado em Emas - Pirassununga, SP. *Acta Botanica Brasilica.* 1997; 11 (1): 61-78.
12. Beattie GA, Lindow SE. Bacterial colonization of leaves: a spectrum of strategies. *Phytopathology*. 1999; 89(5):353-9. doi: 10.1094/PHYTO.1999.89.5.353.

13. Calcagno V, Jarne P, Loreau M, Mouquet N, David P. Diversity spurs diversification in ecological communities. *Nature Communications.* 2017;8:15810. doi: 10.1038/ncomms15810.
14. Chacon AI, Baer A, Wheeler JK, Pittermann J. Two coastal Pacific evergreens, Arbutus menziesii, Pursh. and Quercus agrifolia, Née show little water stress during California's exceptional drought. *Plos One*. 2020 Apr 2;15(4):e0230868. doi: 10.1371/journal.pone.0230868.
15. Chand K, Shah S, Sharma J, Paudel MR, Pant B. Isolation, characterization, and plant growth-promoting activities of endophytic fungi from a wild orchid *Vanda cristata*. *Plant Signal Behav*. 2020; 3;15(5):1744294. doi: 10.1080/15592324.2020.1744294.
16. Chaudhry V, Runge P, Sengupta P, Doehlemann G, Parker JE, Kemen E. Shaping the leaf microbiota: plant-microbe-microbe interactions. *J Exp Bot*. 2021; 20;72(1):36-56. doi: 10.1093/jxb/eraa417.
17. Cui XX, Wang L, Fang HY, Zheng YG, Su CY. The cultivable endophytic fungal community of *Scutellaria baicalensis*: diversity and relevance to flavonoid production by the host. *Plant Signal Behav*. 2022; 31;17(1):2068834. doi: 10.1080/15592324.2022.2068834.
18. Del Pozo A, Méndez-Espinoza AM, Romero-Bravo S, Garriga M, Estrada F, Alcaíno M, Camargo-Rodriguez AV, Corke FMK, Doonan JH, Lobos GA. Genotypic variations in leaf and whole-plant water use efficiencies are closely related in bread wheat genotypes under well-watered and water-limited conditions during grain filling. *Sci Rep*. 2020; 16;10(1):460. doi: 10.1038/s41598-019-57116-0.
19. Ding T, Melcher U (2016) Influences of Plant Species, Season and Location on Leaf Endophytic Bacterial Communities of Non-Cultivated Plants. *Plos One*; 11(3): e0150895. https://doi.org/10.1371/journal.pone.0150895.
20. Dong Z, Manawasinghe IS, Huang Y, Shu Y, Phillips AJL, Dissanayake AJ, Hyde KD, Xiang M, Luo M. Endophytic *Diaporthe* Associated With *Citrus grandis* cv. Tomentosa in China. *Front Microbiol*. 2021. 9; 11:609387. doi: 10.3389/fmicb.2020.609387.
21. Du W, Yao Z, Li J, Sun C, Xia J, Wang B, Shi D, Ren L. Diversity and antimicrobial activity of endophytic fungi isolated from Securinega suffruticosa in the Yellow River Delta. *Plos One*. 2020; 10;15(3):e0229589. doi: 10.1371/journal.pone.0229589.
22. Emerson BC & Kolm N. Species diversity can drive speciation. *Nature* 434, 1015–1017 (2005).
23. Feldman TS, O'Brien HE & Arnold AE. Moths that Vector a Plant Pathogen also Transport Endophytic Fungi and Mycoparasitic Antagonists. *Microb Ecol*. 2008, 56, 742–750. https://doi.org/10.1007/s00248-008-9393-8.
24. Franklin S, Comer P, Evens J, Ezcurra, Faber-Langendoen D, Franklin J, Spurrier C.. How a national vegetation classification can help ecological research and management. *Frontiers in Ecology and the Environment*. 2015; 13, 185–186.
25. Fukumori K, Oguchi K, Ikeda H, Shinohara T, Tanahashi M, Moriyama M, Koga R, Fukatsu T. Evolutionary Dynamics of Host Organs for Microbial Symbiosis in Tortoise Leaf Beetles (*Coleoptera: Chrysomelidae: Cassidinae*). *mBio*. 2022; 25;13(1):e0369121. doi: 10.1128/mbio.03691-21.

26. Givnish TJ. Adaptive significance of evergreen vs. deciduous leaves: solving the triple paradox. *Silva Fenn*. 2002; 36:703–743.
27. Grass J, Pabst M, Kolarich D, Pöltl G, Léonard R, Brecker L, Altmann F. Discovery and structural characterization of fucosylated oligomannosidic N-glycans in mushrooms. *J Biol Chem*. 2011; 25;286(8):5977-84. doi: 10.1074/jbc.M110.191304.
28. Guarnaccia V, Groenewald JZ, Woodhall J, Armengol J, Cinelli T, Eichmeier A, Ezra D, Fontaine F, Gramaje D, Gutierrez-Aguirregabiria A, Kaliterna J, Kiss L, Larignon P, Luque J, Mugnai L, Naor V, Raposo R, Sándor E, Váczy KZ, Crous PW. *Diaporthe* diversity and pathogenicity revealed from a broad survey of grapevine diseases in Europe. *Persoonia*. 2018; 40:135-153. doi: 10.3767/persoonia.2018.40.06.
29. Harrison CJ, Morris JL. The origin and early evolution of vascular plant shoots and leaves. *Philos Trans R Soc Lond B Biol Sci*. 2018; 5;373(1739):20160496. doi: 10.1098/rstb.2016.0496.
30. Hata F and Futai K. Endophytic fungi associated with healthy pine needles and needles infested by pine needle gall midge *Thecodiplosis japonensis*. Can J Bot. 1995; 73: 384–390.
31. Igwe NA, Quasem B, Liu N, Vannette RL. Plant phenology influences rhizosphere microbial community and is accelerated by serpentine microorganisms in Plantago erecta, *FEMS Microbiology Ecology*. 2021. 97; 7: fiab085. https://doi.org/10.1093/femsec/fiab085.
32. Into P, Pontes A, Sampaio JP, Limtong S. Yeast Diversity Associated with the Phylloplane of Corn Plants Cultivated in Thailand. *Microorganisms*. 2020 Jan 7;8(1):80. doi: 10.3390/microorganisms8010080.
33. Jia M, Chen L, Xin HL, Zheng CJ, Rahman K, Han T, et al. A friendly relationship between endophytic fungi and medicinal plants: a systematic review. *Front Microbiol*. 2016. June 9 7: 906 10.3389/fmicb.2016.00906.
34. Jill Harrison C. Development and genetics in the evolution of land plant body plans. *Philos Trans R Soc Lond B Biol Sci*. 2017; 5;372(1713):20150490. doi: 10.1098/rstb.2015.0490.
35. Karatassiou M, Karaiskou P, Verykouki E, Rhizopoulou S. Hydraulic Response of Deciduous and Evergreen Broadleaved Shrubs, Grown on Olympus Mountain in Greece, to Vapour Pressure Deficit. *Plants* (Basel). 2022 Apr 8;11(8):1013. doi: 10.3390/plants11081013.
36. Karatassiou M, Karaiskou P, Verykouki E, Rhizopoulou S. Hydraulic Response of Deciduous and Evergreen Broadleaved Shrubs, Grown on Olympus Mountain in Greece, to Vapour Pressure Deficit. *Plants* (Basel). 2022; 8 ; 11(8):1013. doi: 10.3390/plants11081013.
37. Kenrick P, Crane PR. The origin and early evolution of plants on land. *Nature.* 1997, 389, 33–39. (10.1038/37918).

38. Kharouba HM, Ehrlen J, Gelman A, Bolmgren K, Allen JM, Travers SE, & Wolkovich EM. Global shifts in the phenological synchrony of species interactions over recent decades. *Proceedings of the National Academy of Sciences of the United States of America*. 2018; 115, 5211–5216. 10.1073/pnas.1714511115.
39. Kikuzawa K, Onoda Y, Wright IJ & Reich PB. Mechanisms underlying global temperature-related patterns in leaf longevity. *Global Ecology and Biogeography*. 2013; 22, 982–993.
40. Kotowska MM, Wright IJ, Westoby M. *Parenchyma* Abundance in Wood of Evergreen Trees Varies Independently of Nutrients. *Front Plant Sci*. 2020; 19;11:86. doi: 10.3389/fpls.2020.00086.
41. Książkiewicz M, Rychel-Bielska S, Plewiński P, Nuc M, Irzykowski W, Jędryczka M, Krajewski P. The Resistance of Narrow-Leafed Lupin to *Diaporthe toxica* Is Based on the Rapid Activation of Defense Response Genes. *Int J Mol Sci*. 2021; 8; 22(2):574. doi: 10.3390/ijms22020574.
42. Leveau JH. A brief from the leaf: latest research to inform our understanding of the phyllosphere microbiome. *Curr Opin Microbiol*. 2019; 49:41-49. doi: 10.1016/j.mib.2019.10.002.
43. Li YM, Shaffer JP, Hall B, Ko H. Soil-borne fungi influence seed germination and mortality, with implications for coexistence of desert winter annual plants. *Plos One*. 2019; 31;14(10):e0224417. doi: 10.1371/journal.pone.0224417.
44. Liotti RG, da Silva RC, Pinheiro DG, da Silva JM, da Silva GF, de Mendonça EAF, Soares MA. Characterization and comprehensive analysis of the ecological interaction networks of bacterial communities in *Paullinia cupana* var. sorbilis by 16S rRNA gene metabarcoding. *World J Microbiol Biotechnol*. 2019; 14; 35(12):182. doi: 10.1007/s11274-019-2758-y.
45. Liu Y, Qi W, He D, Xiang Y, Liu J, Huang H, Chen M, Tao J. Soil resource availability is much more important than soil resource heterogeneity in determining the species diversity and abundance of karst plant communities. *Ecol Evol*. 2021; 28; 11(23):16680-16692. doi: 10.1002/ece3.8285.
46. Lu T, Ke M, Lavoie M. et al. Rhizosphere microorganisms can influence the timing of plant flowering. *Microbiome*. 2018; 231. https://doi.org/10.1186/s40168-018-0615-0.
47. Madi N, Vos M, Murall CL, Legendre P, Shapiro BJ. Does diversity beget diversity in microbiomes? *Elife*. 2020; 20;9:e58999. doi: 10.7554/eLife.58999.
48. Mancuso CP, Lee H, Abreu CI, Gore J, Khalil AS. Environmental fluctuations reshape an unexpected diversity-disturbance relationship in a microbial community. *Elife*. 2021; 3; 10:e67175. doi: 10.7554/eLife.67175.
49. Maxwell SJ, Hopley PJ, Upchurch P, Soligo C. Sporadic sampling, not climatic forcing, drives observed early hominin diversity. *Proc Natl Acad Sci U S A*. 2018; 8; 115(19):4891-4896. doi: 10.1073/pnas.1721538115.
50. Mena E, Garaycochea S, Stewart S, Montesano M, Ponce De León I. Comparative genomics of plant pathogenic *Diaporthe* species and transcriptomics of Diaporthe caulivora during host infection reveal insights into pathogenic strategies of the genus. *BMC Genomics*. 2022; 3; 23(1):175. doi: 10.1186/s12864-022-08413-y.

51. Mena E, Stewart S, Montesano M, Ponce de León I. Soybean Stem Canker Caused by *Diaporthe caulivora*; Pathogen Diversity, Colonization Process, and Plant Defense Activation. Front Plant Sci. 2020; 23; 10:1733. doi: 10.3389/fpls.2019.01733.
52. Messina G, Cazzolla Gatti R, Droutsa A, Barchitta M, Pezzino E, Agodi A, Lombardo BM. A sampling optimization analysis of soil-bugs diversity (*Crustacea, Isopoda, Oniscidea*). *Ecol Evol*. 2015; 17;6(1):191-201. doi: 10.1002/ece3.1765.
53. Metreveli E, Khardziani T, Elisashvili V. The Carbon Source Controls the Secretion and Yield of Polysaccharide-Hydrolyzing Enzymes of *Basidiomycetes*. Biomolecules. 2021; 10;11(9):1341. doi: 10.3390/biom11091341.
54. Müller C & Riederer M. Plant surface properties in chemical ecology. *J Chem Ecol*. 2005; (11):2621-51. doi: 10.1007/s10886-005-7617-7.
55. Nimer E, Brandão AMPM. Balanço hídrico e clima da região dos Cerrados. Rio de Janeiro: IBGE, 1989.
56. Oliveira PE. Fenologia e biologia reprodutiva das espécies de Cerrado. In Cerrado: ambiente e flora. (S. M. Sano & S.P. Almeida, eds.). EMBRAPA - Cerrados, Planaltina. 2008; p.169-188.
57. Ouédraogo DY, Fayolle A, Gourlet-Fleury S, Mortier F, Freycon V, Fauvet N, Favier C. The determinants of tropical forest deciduousness: Disentangling the effects of rainfall and geology in central Africa. *Journal of Ecology*. 2016; 104, 924–935.
58. Ouédraogo D-Y, Fayolle A, Gourlet-Fleury S, Mortier F, Freycon V, Fauvet N, Favier C. The determinants of tropical forest deciduousness: Disentangling the effects of rainfall and geology in central Africa. *Journal of Ecology*. 2016; 104, 924–935.
59. Peng X, Xie J, Li W, Xie H, Cai Y, Ding X. Comparison of wild rice (Oryza longistaminata) tissues identifies rhizome-specific bacterial and archaeal endophytic microbiomes communities and network structures. Plos One. 2021; 8;16(2):e0246687. doi: 10.1371/journal.pone.0246687.
60. Pepe M, Crescente MF, Varone L. Effect of Water Stress on Physiological and Morphological Leaf Traits: A Comparison among the Three Widely-Spread Invasive Alien Species Ailanthus altissima, Phytolacca americana, and Robinia pseudoacacia. *Plants* (Basel). 2022; 28;11(7):899. doi: 10.3390/plants11070899.
61. Pietro-Souza W, Mello IS, Vendruscullo SJ, Silva GFD, Cunha CND, White JF, Soares MA. Endophytic fungal communities of Polygonum acuminatum and Aeschynomene fluminensis are influenced by soil mercury contamination. *Plos One*. 2017; 25; 12(7):e0182017. doi: 10.1371/journal.pone.0182017.
62. Poorter H, Jagodzinski AM, Ruiz-Peinado R, Kuyah S, Luo Y, Oleksyn J, Usoltsev VA, Buckley TN, Reich PB, Sack L. How does biomass distribution change with size and differ among species? An analysis for 1200 plant species from five continents. *New Phytol*. 2015 Nov;208(3):736-49. doi: 10.1111/nph.13571.
63. Rabosky DL, Hurlbert AH. Species richness at continental scales is dominated by ecological limits. *The American Naturalist.* 2015; 185: 572–583. doi: 10.1086/680850.

64. Reich PB, Walters MB, Ellsworth DS. Leaf life-span in relation to leaf, plant, and stand characteristics among diverse ecosystems. *Ecol Monogr*. 1992; 62:365–392.
65. Ruiz-Mirazo K, Briones C, de la Escosura A. Chemical roots of biological evolution: the origins of life as a process of development of autonomous functional systems. Open Biol. 2017 Apr;7(4):170050. doi: 10.1098/rsob.170050.
66. Santana JO, Gramacho KP, de Souza Eduvirgens Ferreira KT, Rezende RP, Mangabeira PAO, Dias RPM, Couto FM, Pirovani CP. Witches' broom resistant genotype CCN51 shows greater diversity of symbiont bacteria in its phylloplane than susceptible genotype catongo. *BMC Microbiol*. 2018 Nov 23;18(1):194. doi: 10.1186/s12866-018-1339-9.
67. Santos C, Santos da Silva BN, Amorim Ferreira E Ferreira AFT, Santos C, Lima N, Silva Bentes JLD. Fungal Endophytic Community Associated with Guarana (*Paullinia cupana* Var. Sorbilis): Diversity Driver by Genotypes in the Centre of Origin. *J Fungi (Basel).* 2020; 31; 6(3):123. doi: 10.3390/jof6030123.
68. Santos L, Alves A, Alves R. Evaluating multi-locus phylogenies for species boundaries determination in the genus *Diaporthe*. *PeerJ*. 2017; 28; 5:e3120. doi: 10.7717/peerj.3120.
69. Schluter D, Pennell MW. Speciation gradients and the distribution of biodiversity. *Nature.* 2017;546:48–55. doi: 10.1038/nature22897.
70. Shao L, Xu T, Wang X, Zhang R, Wang X, Ren Z, Zhang J, Xia Y, Li D. Integrative Comparative Assessment of Cold Acclimation in Evergreen and Deciduous Iris Species. *Antioxidants* (Basel). 2022; 16;11(5):977. doi: 10.3390/antiox11050977.
71. Shen XY, Cheng YL, Cai CJ, Fan L, Gao J, Hou CL. Diversity and antimicrobial activity of culturable endophytic fungi isolated from moso bamboo seeds. *Plos One*. 2014; 23; 9(4):e95838. doi: 10.1371/journal.pone.0095838.
72. Silva FA, Liotti RG, Boleti APA, Reis ÉM, Passos MBS, Dos Santos EL, Sampaio OM, Januário AH, Branco CLB, Silva GFD, Mendonça EAF, Soares MA. Diversity of cultivable fungal endophytes in Paullinia cupana (Mart.) Ducke and bioactivity of their secondary metabolites. *Plos One*. 2018; 12; 13(4):e0195874. doi: 10.1371/journal.pone.0195874.
73. Soares AP, Guillin EA, Borges LL, Silva AC, Almeida ÁM, Grijalba PE, Gottlieb AM, Bluhm BH, Oliveira LO. More *Cercospora* Species Infect Soybeans across the Americas than Meets the Eye. Plos One. 2015 7;10(8):e0133495. doi: 10.1371/journal.pone.0133495.
74. Soh WK, Yiotis C, Murray M, Parnell A, Wright IJ, Spicer RA, Lawson T, Caballero R, McElwain JC. Rising CO_2 drives divergence in water use efficiency of evergreen and deciduous plants. *Sci Adv*. 2019; 11;5(12):eaax7906. doi: 10.1126/sciadv.aax7906.
75. Tanapichatsakul C, Khruengsai S, Monggoot S, Pripdeevech P. Production of eugenol from fungal endophytes *Neopestalotiopsis* sp. and *Diaporthe* sp. isolated from *Cinnamomum loureiroi* leaves. *PeerJ.* 2019; 12; 7:e6427. doi: 10.7717/peerj.6427.
76. Terhonen E, Blumenstein K, Kovalchuk A, Asiegbu FO. Forest tree microbiomes and associated fungal endophytes: Functional roles and impact on forest health. *Forests*. 2019;10:32. doi: 10.3390/f10010042.

77. Tibpromma S, Hyde KD, Bhat JD, Mortimer PE, Xu J, Promputtha I, Doilom M, Yang JB, Tang AMC, Karunarathna SC. Identification of endophytic fungi from leaves of Pandanaceae based on their morphotypes and DNA sequence data from southern Thailand. *MycoKeys*. 2018; 28;(33):25-67. doi: 10.3897/mycokeys.33.23670.
78. Tomescu AMF, Rothwell GW. Fossils and plant evolution: structural fingerprints and modularity in the evo-devo paradigm. *Evodevo*. 2022; 2;13(1):8. doi: 10.1186/s13227-022-00192-7.
79. van Ommen Kloeke AEE, Douma JC, Ordoñez JC, Reich PB, van Bodegom PM. Global quantification of contrasting leaf life span strategies for deciduous and evergreen species in response to environmental conditions. *Global Ecol Biogeogr*. 2012; 21:224–235.
80. Vasco A, Ambrose BA. Simple and Divided Leaves in Ferns: Exploring the Genetic Basis for Leaf Morphology Differences in the Genus Elaphoglossum (Dryopteridaceae). *Int J Mol Sci*. 2020; 22;21(15):5180. doi: 10.3390/ijms21155180.
81. Wang YL, Gao C, Chne L, Ji NN et al. Community Assembly of Endophytic Fungi in Ectomycorrhizae of *Betulaceae* Plants at a Regional Scale. *Front Microbiol*. 2020, 10. 10.3389/fmicb.2019.03105.
82. Ware IM, Van Nuland ME, Yang ZK, Schadt CW, Schweitzer JA, Bailey JK. Climate-driven divergence in plant-microbiome interactions generates range-wide variation in bud break phenology. *Commun Biol*. 2021; 16;4(1):748. doi: 10.1038/s42003-021-02244-5.
83. Whipps JM, Hand P, Pink D, Bending GD. Phyllosphere microbiology with special reference to diversity and plant genotype. *J Appl Microbiol*. 2008;105:1744–1755. doi: 10.1111/j.1365-2672.2008.03906.x.
84. Whittaker RH. Evolution and measurement of species diversity. *Taxon.* 1972;21:213–251. doi: 10.2307/1218190.
85. Wyka TP, Karolewski P, Żytkowiak R, Chmielarz P, Oleksyn J. Whole-plant allocation to storage and defense in juveniles of related evergreen and deciduous shrub species. *Tree Physiol*. 2016; 36(5): 536-47. doi: 10.1093/treephys/tpv108.
86. Xia Q, Rufty T, & Shi W. Predominant Microbial Colonizers in the Root Endosphere and Rhizosphere of Turfgrass Systems: *Pseudomonas veronii*, *Janthinobacterium lividum*, and *Pseudogymnoascus* spp. *Frontiers in microbiology*. 2021; *12*, 643904. https://doi.org/10.3389/fmicb.2021.643904.
87. Yan K, Pei Z, Meng L, Zheng Y, Wang L, Feng R, Li Q, Liu Y, Zhao X, Wei Q, El-Sappah AH, Abbas M. Determination of Community Structure and Diversity of Seed-Vectored Endophytic Fungi in *Alpinia zerumbet*. Front Microbiol. 2022; 28; 13:814864. doi: 10.3389/fmicb.2022.814864.
88. Yang Q, Fan XL, Guarnaccia V, Tian CM. High diversity of *Diaporthe* species associated with dieback diseases in China, with twelve new species described. *MycoKeys*. 2018; 17; (39):97-149. doi: 10.3897/mycokeys.39.26914.
89. Yao H, Sun X, He C, Maitra P, Li XC, Guo LD. Phyllosphere epiphytic and endophytic fungal community and network structures differ in a tropical mangrove ecosystem. *Microbiome*. 2019; 9;7(1):57. doi: 10.1186/s40168-019-0671-0.

90. Zheng Q, Hu Y, Zhang S, Noll L, Böckle T, Dietrich M, Herbold CW, Eichorst SA, Woebken D, Richter A, Wanek W. Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity. *Soil Biol Biochem*. 2019; 136:107521. doi: 10.1016/j.soilbio.2019.107521.

CHAPTER 4: DIFFERENT RESPONSES OF THE LEAF ENDOPHYTIC MYCOBIOME OF TWO PLANT SPECIES OF A NEOTROPICAL SAVANNA ECOSYSTEM TO LONG-TERM MINERAL FERTILIZATION

Abstract: The anthropization of natural ecosystems can cause negative or positive effects on the diversity of plant symbiotic fungal species. In our study, we evaluated the effect of long-term mineral fertilization with nitrogen (N), phosphate (P), nitrogen+phosphate (NP), and liming (Ca) on the leaf endophytic mycobiome of the species *Caryocar brasiliense* and *Ouratea hexasperma* native to the neotropical savanna. Brazilian. For this, we use cultive-dependent approaches and *metabarcoding*. Both methodologies showed that *Ascomycota* was the dominant phylum and that the diversity of fungal species in the *O. hexasperma* community was negatively influenced in all treatments; while the diversity of the *C. brasiliense* community was positively influenced in the treatments with Ca, P, and NP. In total, 196 fungal taxa were isolated from both hosts, 117 from the host *C. brasiliense* and 79 from *O. hexasperma*. *Diaporthe* was the dominant genus among both hosts and in all treatments. The genera *Alternaria, Curvularia, Phaeodiaporthe, Ascochyta, Ramulariopsis, Didymella, Pestalotiopsis*, and *Cytospora* were found in *C. brasiliense*; while *Coniochaeta, Dendrothyrium, Epicoccum, Kalmusia, Stilbospora,* and *Lasiodilodia* were found in *O. hexasperma*. In total, 2898 Operational Taxonomic Units (OTUs) were obtained from the pooled readings of *C. brasiliense* and 2917 OTUs of the host *O. hexasperma*. The number of fungal genera shown by *metabarcoding* was higher than that observed in cultive-dependent methods. Although no significant community differences were observed between treatments for alpha diversity, the beta diversity indices show dissimilarities in the taxonomic composition of the leaf endophytic mycobiome between treatments for the two host species. In conclusion, our results suggest that the positive or negative correlation of species diversity of leaf endophytic fungi associated with native plants of the Brazilian Neotropical savanna depends on the type of fertilizer added to the soil together with the identity of the host plant.

Keywords: *Metabarcoding*; Nitrogen; Phosphate; Liming; Fungi; Anthropization.

1. INTRODUCTION

The taxonomic structure, diversity, equity, occurrence, and co-occurrence of species in microbial communities are shaped by numerous anthropic variables (Li et al., 2017; Zheng et al., 2019). Anthropization caused by the addition of nutrients to the soil, for example, can have positive effects on microbial communities, which include increased microbial diversity, or negative effects, which include loss of diversity (Khan et al., 2017; Pietro-Souza et al., 2017; Parmar et al., 2018; El-Shafey et al., 2021; Wang et al., 2022).

In plant-associated microbial communities, these effects are widely reported (Chiu et al., 2019; Liu et al., 2020; Lou et al., 2020; Wang et al., 2022). For example, at low doses, the application of nitrogen to the soil induces an increase in the diversity of fungi present in the root endosphere, but at high doses, this macronutrient alters the phytochemistry of the host plant, so that key molecules that mediate the plant and fungus interaction symbiont are not produced and colonization does not occur (Wang et al., 2022).

The effects of mineral fertilization on the plant symbiotic fungal community are mainly studied in mycorrhizal fungi (Chiu et al., 2019; Liu et al., 2020; Lou et al., 2020). Thus, the knowledge we have about the impact of this variable on the community of fungi that occur in aerial parts of plants, especially foliar endophytic fungi, remains unknown.

Leaf endophytic fungi comprise a group of hyperdiverse microorganisms that reside within the plant tissue of numerous plant species without causing disease symptoms (Yao et al., 2019). The establishment of plant tissue colonization by these microorganisms largely depends on the phylogenetic identity of the host plant together with environmental factors (phenotype), since environmental variables can alter the plant's phytochemistry to induce or inhibit their association with endophytic fungi (Khan et al., 2017; Pietro-Souza et al., 2017; Parmar et al., 2018; El-Shafey et al., 2021).

Considering that the taxonomic structure of plant symbiotic microbial communities is influenced by the addition of mineral nutrients to the soil (Chiu et al., 2019; Liu et al., 2020; Lou et al., 2020; Wang et al., 2022;) and in short, the lack of studies on the effect of this anthropic variable on microbial communities associated with aerial parts of plants, our work aims to evaluate the effect of long-term soil mineral fertilization on the leaf endophytic mycobiome of two woody species from Brazilian neotropical savanna, using culture-dependent methods and *metabarcoding*.

2. SPECIFIC OBJECTIVES

- Carry out analyzes from environmental DNA aiming at the identification of endophytic fungal species of two native Cerrado hosts in different fertilization systems;
- To estimate the diversity of fungal species in host plants in different fertilization systems;
- Carry out molecular analyzes of cultivable endophytic fungi;
- Compare the results generated by dependent and independent cultivation techniques.

3. MATERIALS AND METHODS

3.1. Experimental design

The design of the nutrient addition experiment was completely randomized, where experimental plots were fertilized with calcium, phosphorus, nitrogen, and the combination of nitrogen and phosphorus (Figure 56). The treatments were replicated four times in 225 m^2 plots separated by a minimum distance of ten meters. The treatments were divided into control without fertilization (control); addition of $(NH_4)2SO_4$ (+N); addition of $Ca\ (H_2PO_4)^2 + CaSO_4.2H_2O$ – 20% single superphosphate (+P); and addition of ammonium sulfate and 20% simple superphosphate, which were applied to the soil by broadcast, on the litter, in equal amounts in sub-plots of 5x5 m, at the beginning and end of the rainy season.

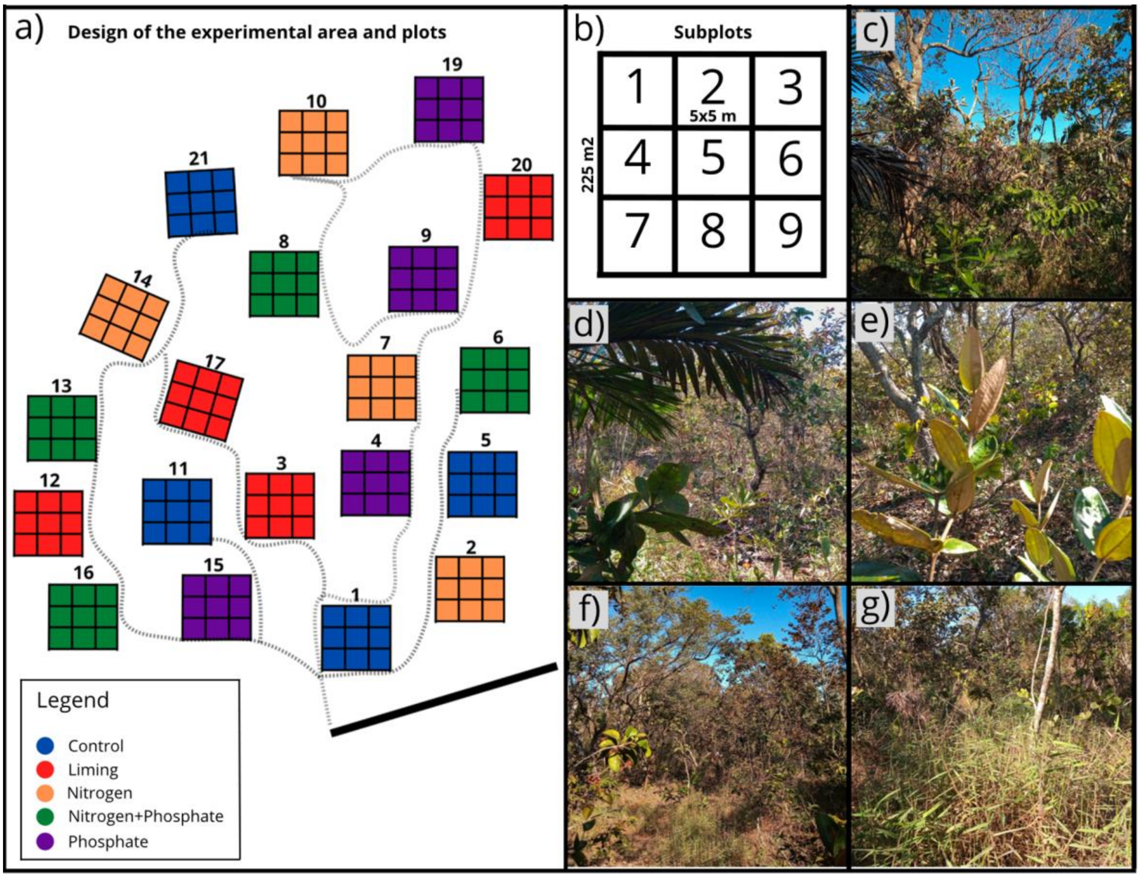


Figure 56. Description of the experiment area "Study of the Effects of Global Changes that Determine the Structure and Functioning of Cerrado Ecosystems", located in the IBGE Ecological Reserve (RECOR-IBGE). a) Plot distribution map with addition of nutrients and control (without addition of nutrients); b) plot division scheme into sub-plots; c) control (Part 1); d) Phosphate treatment (Portion 15); e) treatment with Nitrogen (Part 2); f) treatment with Nitrogen+Phosphate (Portion 16); g) Liming.

Annually, between 1998 and 2006, 100 kg of N, 100 kg of P, and 100 kg of N + 100 kg of P per hectare were added in two seasons (at the beginning and end of the rainy season) to reduce the loss of nutrients by the system, while the liming process (Ca treatment) was carried out by adding 60% dolomitic limestone (CaO+MgO) + 40% agricultural gypsum ($CaSO_4.2H_2O$) (4 t.ha. year -1) once a year at the beginning of the rainy season. Two accidental fires occurred in the area, the first in 1994, before the start of the project, and the second in 2005, seven years after the project was implemented. The last fertilizer applications in the area were made between 2017 and 2018 after the plots were reinstalled.

3.2. Selection of plant hosts

As the distribution of woody species in the Cerrado occurs in a heterogeneous way, for the selection of plant species to have the leaf endophytic mycobiota compared between the different fertilization treatments, the following factors were considered: i) the selected species must be present in at least three control plots (without the addition of nutrients) and three plots with the addition of nutrients for each of the treatments; ii) individuals of the same selected species should have height and stem circumference close to each other. The only species that met these requirements were *Caryocar brasiliense* and *Ouratea hexasperma* (Figure 57), and therefore were the species sampled.

Figure 57. Plant species sampled to study the long-term effects of soil nutrient addition on leaf endophytic mycobiota. a) *Caryocar brasiliense*; b) *Ouratea hexasperma*.

3.3. ***Collection and surface disinfection***

Collection, sampling effort per host and treatment, surface disinfection are similar to that described in ***Chapter 2***.

3.4. *Isolations and molecular identification of isolates*

The process of recovering the isolates, purification, maintenance, cultivation conditions and methods of identifying the isolates are the same as those reported in ***Chapter 2***.

3.5. *Analysis of the nutritional composition of leaves*

The analysis of the nutritional composition of leaves are described in ***Chapter 2***.

3.6. *Analysis of soil composition between treatments of addition of mineral fertilizers*

For analysis of soil characteristics between treatments, five soil samples (0-10 cm depth) were collected per treatment, outside the area of influence of the tree canopy. The samples were stored in plastic bags, packed in thermal boxes and transported to the Ecology department of the Institute of Biological Sciences of the University of Brasília (UnB), where they were dried in an oven. After drying, the samples were sent to the Federal University of Viçosa (UFV), where analyzes were performed to determine the gravimetric content and density.

3.7. *Metabarcoding analysis*

For the identification of fungal endophytes from eDNA, the same methodology described in ***Chapter 2*** will be used.

3.8. *Data analysis*

Biostatistics tests for sequence treatment, OTU clustering, alpha and beta diversity metrics, relative and differential abundance are the same as those reported in ***Chapter 2***.

4. RESULTS

4.1. *Molecular identification of isolates*

In total, 196 endophytic fungi were isolated from the two host species in the different treatments of addition of nutrients to the soil and in the control group

(Table 11). In the host species *C. brasiliense*, 117 fungal taxa were recovered, 11 from the control group, 25 from liming, 32 from nitrogen, 22 from the nitrogen+phosphate treatment, and 28 from the phosphate treatment. While in *O. hexasperma*, 79 endophytic fungi were recovered, being 16 taxa from the control group, 13 from liming, ten from nitrogen, 16 from the nitrogen+phosphate treatment, and 23 from the phosphate treatment.

Table 11. Identification of endophytic foliar fungi of two Cerrado woody species under different conditions of soil nutrient addition

Host	Trateatment	Isolate code	Taxon	Match	Identity percentage (%)	Query cover (%)
Caryocar brasiliense	Control	CB1629_25	*Diaporthe* sp.	MG828894.1	91%	73%
	Control	CB995_3	*Diaporthe* sp.	NR_137105.1	92%	100%
	Control	CB1629_3	*Diaporthe* sp.	NR_145303.1	94%	95%
	Control	CB1629_2	*Diaporthe* sp.	NR_111849.1	95%	88%
	Control	CB995_2	*Diaporthe* sp.	EU552122.1	95%	100%
	Control	CB995_22	*Diaporthe* sp.	MH171064.1	96%	99%
	Control	CB995_7	*Diaporthe masirevicii*	NR_147534.1	98%	100%
	Control	CB1629_22	*Diaporthe schini*	NR_111861.1	99%	100%
	Control	CB1629_31	*Didymella keratinophila*	NR_158275.1	99%	100%
	Control	CB995_15	*Diaporthe rosae*	MG828894.1	99%	100%
	Control	CB995_6	*Diaporthe actinidiae*	KC145886.1	99%	100%
Ouratea hexasperma	Control	OH2208_3	*Stilbospora* sp.	KF570166.1	88%	100%
	Control	OH2262_4	*Coniochaeta* sp.	NR_173009.1	90%	99%
	Control	OH2262_30	*Diaporthe* sp.	EU552122.1	92%	100%
	Control	OH1078_3	*Colletotrichum* sp.	NR_120138.1	93%	97%
	Control	OH1078_24	*Dendrothyrium* sp.	JX496097.1	93%	98%
	Control	OH2262_40	*Diaporthe* sp.	NR_147596.1	93%	100%
	Control	OH2262_5	*Diaporthe* sp.	NR_158416.1	93%	100%
	Control	OH2262_6	*Diaporthe* sp.	MH855768.1	95%	100%
	Control	OH1078_31	*Kalmusia erioi*	MN473058.1	97%	97%
	Control	OH2262_2	*Diaporthe maytenicola*	NR_137826.1	97%	100%
	Control	OH1078_2	*Diaporthe novem*	MH864503.1	98%	100%
	Control	OH2262_30	*Epicoccum sorghicola*	OK442368.1	98%	100%
	Control	OH1078_22	*Kalmusia erioi*	MN473058.1	99%	100%
	Control	OH1078_12	*Phyllosticta catimbauensis*	NR_156631.1	99%	88%

	Control	OH2206_31	*Phyllosticta fallopiae*	AB454307.1	100%	99%
	Control	OH2208_4	*Phyllosticta capitalensis*	OL957169.1	100%	100%
Caryocar brasiliense	Liming	CB2790_3	*Colletotrichum* sp.	MK541034.1	92%	100%
	Liming	CB2790_5	*Diaporthe* sp.	EU552122.1	93%	100%
	Liming	CB2789_1	*Diaporthe* sp.	NR_111857.1	94%	100%
	Liming	CB2527_1	*Diaporthe* sp.	MH171064.1	95%	100%
	Liming	CB2789_3	*Fusarium* sp.	MH855630.1	95%	100%
	Liming	CB2790_11	*Diaporthe* sp.	MH855768.1	95%	100%
	Liming	CB2790_7	*Diaporthe* sp.	NR_168152.1	95%	100%
	Liming	CB2789_10	*Diaporthe* sp.	NR_137825.1	96%	100%
	Liming	CB2790_10	*Diaporthe* sp.	NR_137825.1	96%	100%
	Liming	CB2790_2	*Diaporthe* sp.	MH855768.1	96%	100%
	Liming	CB2789_1	*Diaporthe masirevicii*	KJ197276.1	97%	100%
	Liming	CB2789_12	*Diaporthe parapterocarpi*	NR_168152.1	97%	100%
	Liming	CB2789_14	*Diaporthe parapterocarpi*	NR_168152.1	97%	100%
	Liming	CB2790_6	*Diaporthe maytenicola*	NR_137826.1	97%	99%
	Liming	CB2755_3	*Diaporthe masirevicii*	KJ197276.1	98%	100%
	Liming	CB2789_11	*Cytospora* sp.	MK912135.1	98%	100%
	Liming	CB2789_15	*Colletotrichum boninense*	NR_165949.1	98%	97%
	Liming	CB2789_4	*Diaporthe novem*	MH864503.1	98%	100%
	Liming	CB2790_5	*Diaporthe anacardii*	NR_111841.1	98%	100%
	Liming	CB2790_8	*Diaporthe stewartii*	MH855768.1	98%	100%
	Liming	CB2755_3	*Diaporthe terebinthifolii*	NR_111862.1	99%	100%
	Liming	CB2789_6	*Diaporthe middletonii*	NR_147536.1	99%	100%
	Liming	CB2790_2	*Diaporthe middletonii*	NR_147536.1	99%	100%
	Liming	CB2527_70	*Colletotrichum plurivorum*	NR_160828.1	100%	100%
	Liming	CB2789_5	*Cytospora* sp.	MN854449.1	100%	100%
	Liming	OH874_20	*Anthostomelloides* sp.	NR_153510.1	88%	100%
	Liming	OH_1538_10	*Diaporthe* sp.	EU552122.1	95%	100%
	Liming	OH_1538_12	*Diaporthe* sp.	EU552122.1	95%	100%

Ouratea hex-asperma	Liming	OH_1538_18	*Diaporthe* sp.	EU552122.1	95%	100%
	Liming	OH_1538_22	*Diaporthe* sp.	EU552122.1	95%	100%
	Liming	OH_1538_3	*Diaporthe* sp.	EU552122.1	95%	100%
	Liming	OH2841_5	*Diaporthe* sp.	MH171064.1	95%	100%
	Liming	OH2841_1	*Bipolaris salviniae*	MH873897.1	99%	100%
	Liming	OH512_24	*Fusarium* sp.	MH862670.1	94%	100%
	Liming	OH2841_19	*Colletotrichum celtidis*	MW114362.1	100%	100%
	Liming	OH2841_3	*Colletotrichum chrysophilum*	NR_160821.1	100%	100%
	Liming	OH512_30	*Fusarium* sp.	MH862670.1	94%	100%
	Liming	OH512_4	*Fusarium pseudonygamai*	MH862656.1	100%	100%
Caryocar brasiliense	Nitrogen	CB1337_4	*Diaporthe* sp.	NR_147596.1	91%	100%
	Nitrogen	CB2534_6	*Diaporthe* sp.	EU552122.1	91%	100%
	Nitrogen	CB2536_10_0	*Diaporthe* sp.	MH855768.1	91%	100%
	Nitrogen	CB2536_12	*Phaeodiaporthe* sp.	KF570156.1	91%	100%
	Nitrogen	CB2534_10	*Diaporthe sp.*	EU552122.1	93%	100%
	Nitrogen	CB2534_8	*Diaporthe* sp.	EU552122.1	93%	100%
	Nitrogen	CB2536_3	*Diaporthe* sp.	JX862530.1	93%	100%
	Nitrogen	CB_1337_22	*Diaporthe* sp.	EU552122.1	94%	100%
	Nitrogen	CB_1337_2	*Diaporthe* sp.	EU552122.1	95%	100%
	Nitrogen	CB2534_1	*Diaporthe* sp.	MH855768.1	95%	100%
	Nitrogen	CB2536_11	*Diaporthe* sp.	EU552122.1	95%	100%
	Nitrogen	CB2536_13	*Diaporthe* sp.	EU552122.1	95%	100%
	Nitrogen	CB_1337_0	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	CB_1337_29	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	CB_1337_30	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	CB_1337_7	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	CB2534_1	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	CB2534_2	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	CB2534_3	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	CB2534_4	*Diaporthe* sp.	MH855768.1	96%	100%

	Nitrogen	CB2536_4	*Diaporthe stewartii*	MH855768.1	97%	100%
	Nitrogen	CB2536_10	*Diaporthe ocoteae*	NR_147596.1	98%	100%
	Nitrogen	CB2536_14	*Diaporthe stewartii*	MH855768.1	98%	100%
	Nitrogen	CB2536_15	*Diaporthe stewartii*	MH855768.1	98%	100%
	Nitrogen	CB_1337_3	*Phyllosticta capitalensis*	OL957169.1	99%	100%
	Nitrogen	CB_1337_8	*Diaporthe stewartii*	MH855768.1	99%	100%
	Nitrogen	CB1337_14	*Diaporthe miriciae*	NR_147535.1	99%	100%
	Nitrogen	CB2534_4	*Cytospora viridistroma*	MN172408.1	99%	100%
	Nitrogen	CB2534_7	*Diaporthe stewartii*	MH855768.1	99%	100%
	Nitrogen	CB2534_9	*Diaporthe stewartii*	MH855768.1	99%	100%
	Nitrogen	CB2536_5	*Diaporthe stewartii*	MH855768.1	99%	100%
	Nitrogen	CB2545_0	*Diaporthe stewartii*	MH855768.1	99%	100%
Ouratea hexasperma	Nitrogen	OH2611_20	*Dwiroopa* sp.	NR_164059.1	94%	100%
	Nitrogen	OH1943_7	*Diaporthe* sp.	NR_137826.1	95%	100%
	Nitrogen	OH800_15	*Diaporthe* sp.	EU552122.1	95%	100%
	Nitrogen	OH800_16	*Diaporthe* sp.	MH855768.1	95%	100%
	Nitrogen	OH800_16	*Diaporthe* sp.	MH855768.1	95%	100%
	Nitrogen	OH_800_25	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	OH_800_7	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	OH800_10	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen	OH_800_12	*Diaporthe stewartii*	MH855768.1	97%	100%
	Nitrogen	OH800_2	*Diaporthe vangueriae*	KJ869137.1	98%	100%
	Nitrogen+Phosphate	CB2358_8	*Diaporthe* sp.	EU552122.1	93%	100%
	Nitrogen+Phosphate	CB590_2	*Diaporthe* sp.	MH855768.1	93%	100%
	Nitrogen+Phosphate	CB2358_4	*Diaporthe* sp.	EU552122.1	94%	100%
	Nitrogen+Phosphate	CB590_9	*Diaporthe* sp.	EU552122.1	94%	100%
	Nitrogen+Phosphate	CB_590_4	*Diaporthe* sp.	MH855768.1	95%	100%
	Nitrogen+Phosphate	CB2358_3	*Diaporthe* sp.	MH858974.1	95%	100%
	Nitrogen+Phosphate	CB2358_10	*Dendrostoma* sp.	MN447229.1	96%	100%
	Nitrogen+Phosphate	CB590_3	*Diaporthe* sp.		96%	100%

Caryocar brasiliese	Nitrogen+Phosphate	CB2358_3	*Diaporthe stewartii*	NR_137825.1	97%	100%
	Nitrogen+Phosphate	CB590_3	*Diaporthe macadamiae*		98%	100%
	Nitrogen+Phosphate	CB590_5	*Diaporthe novem*	MH855768.1	98%	100%
	Nitrogen+Phosphate	CB590_8	*Diaporthe terebinthifolii*	NR_168240.1	98%	100%
	Nitrogen+Phosphate	CB_590_5	*Diaporthe stewartii*	MH864503.1	99%	100%
	Nitrogen+Phosphate	CB1876_4	*Diaporthe rosiphthora*	NR_111862.1	99%	100%
	Nitrogen+Phosphate	CB1876_6	*Curvularia dactyloctenicola*	MH855768.1	99%	100%
	Nitrogen+Phosphate	CB1876_7	*Cytospora viridistroma*	MT311197.1	99%	100%
	Nitrogen+Phosphate	CB1876_2	*Diaporthe terebinthifolii*	MF490815.1	99%	100%
	Nitrogen+Phosphate	CB2358_2	*Diaporthe stewartii*	MN172408.1	99%	100%
	Nitrogen+Phosphate	CB2358_7	*Diaporthe stewartii*	NR_111862.1	99%	100%
	Nitrogen+Phosphate	CB_610_1	*Pestalotiopsis telopeae*	MH855768.1	100%	100%
	Nitrogen+Phosphate	CB590_1	*Phyllosticta capitalensis*	MH855768.1	100%	99%
	Nitrogen+Phosphate	CB590_6	*Phyllosticta capitalensis*		100%	100%
				NR_147545.1		
				MH865128.1		
				MH865128.1		
Ouratea hexasperma	Nitrogen+Phosphate	OH1827_1	*Diaporthe* sp.	EU552122.1	92%	100%
	Nitrogen+Phosphate	OH610_2	*Diaporthe* sp.	MH855768.1	93%	100%
	Nitrogen+Phosphate	CB_610_13	*Seiridium* sp.	KT949914.1	95%	100%
	Nitrogen+Phosphate	CB_610_14	*Diaporthe* sp.	EU552122.1	95%	100%
	Nitrogen+Phosphate	OH_618_1	*Microdiplodia* sp.	DQ885897.1	95%	100%
	Nitrogen+Phosphate	OH_618_22	*Diaporthe* sp.	EU552122.1	95%	100%
	Nitrogen+Phosphate	OH_618_4	*Diaporthe* sp.	EU552122.1	95%	100%
	Nitrogen+Phosphate	OH_618_0	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen+Phosphate	OH_618_23	*Diaporthe* sp.	EU552122.1	96%	100%
	Nitrogen+Phosphate	OH1827_12	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen+Phosphate	OH1827_4	*Diaporthe* sp.	MH855768.1	96%	100%
	Nitrogen+Phosphate	OH610_3	*Diaporthe parapterocarpi*	NR_168152.1	98%	100%
	Nitrogen+Phosphate	OH1827_13	*Colletotrichum celtidis*	MW114362.1	100%	100%

	Nitrogen+Phosphate	OH1827_2	*Fusarium caatingaense*	MH668816.1	100%	100%
	Nitrogen+Phosphate	OH1827_6	*Phyllosticta capitalensis*	OL957169.1	100%	100%
	Nitrogen+Phosphate	OH610_4	*Phyllosticta capitalensis*	OL957169.1	100%	100%
Caryocar brasiliense	Phosphate	CB_2075_3	*Colletotrichum* sp.	AJ301948.1	92%	100%
	Phosphate	CB_2075_10	*Diaporthe* sp.	EU552122.1	93%	100%
	Phosphate	CB_323_11	*Colletotrichum* sp.	AJ301948.1	93%	100%
	Phosphate	CB_2075_1	*Diaporthe* sp.	EU552122.1	94%	100%
	Phosphate	CB_323_6	*Diaporthe* sp.	EU552122.1	94%	100%
	Phosphate	CB323_9	*Diaporthe* sp.	NR_147539.1	94%	90%
	Phosphate	CB_2075_13	*Diaporthe* sp.	MN447229.1	95%	100%
	Phosphate	CB_2075_4	*Diaporthe* sp.	MH855768.1	95%	100%
	Phosphate	CB_2075_5	*Diaporthe* sp.	EU552122.1	95%	100%
	Phosphate	CB_323_0	*Diaporthe* sp.	EU552122.1	95%	100%
	Phosphate	CB_323_2	*Diaporthe* sp.	EU552122.1	95%	100%
	Phosphate	CB_323_5	*Diaporthe* sp.	EU552122.1	95%	100%
	Phosphate	OH2075_8	*Diaporthe* sp.	NR_152458.1	95%	100%
	Phosphate	CB_2075_12	*Diaporthe* sp.	MH855768.1	96%	100%
	Phosphate	CB_2075_6	*Diaporthe* sp.	MH855768.1	96%	100%
	Phosphate	CB_2725_6	*Diaporthe* sp.	MH855768.1	96%	100%
	Phosphate	CB_323_12	*Diaporthe* sp.	EU552122.1	96%	100%
	Phosphate	CB_2075_2	*Diaporthe stewartii*	MH855768.1	97%	100%
	Phosphate	CB_2075_9	*Diaporthe stewartii*	MH855768.1	97%	100%
	Phosphate	CB_2725_8	*Diaporthe stewartii*	MH855768.1	97%	100%
	Phosphate	OH2075_11	*Diaporthe macintoshii*	NR_147539.1	97%	100%
	Phosphate	CB_323_13	*Alternaria indefessa*	MH861641.1	98%	100%
	Phosphate	CB300_2	*Diaporthe inconspicua*	NR_111849.1	98%	99%
	Phosphate	CB300_3	*Diaporthe masirevicii*	KJ197276.1	98%	100%
	Phosphate	CB_2075_7	*Ascochyta rabiei*	EU167600.1	99%	100%
	Phosphate	CB_2725_7	*Diaporthe stewartii*	MH855768.1	99%	100%
	Phosphate	CB323_1	*Cytospora viridistroma*	MN172408.1	99%	100%

	Phosphate	CB_323_7	*Ramulariopsis pseudoglycines*	NR_154439.1	100%	100%
Ouratea hexasperma	Phosphate	OH2075_15	*Diaporthe* sp.	EU552122.1	90%	100%
	Phosphate	OH248_40	*Diaporthe* sp.	EU552122.1	90%	100%
	Phosphate	OH248_5	*Diaporthe* sp.	EU552122.1	90%	100%
	Phosphate	OH2725_7	*Diaporthe* sp.	EU552122.1	90%	100%
	Phosphate	OH2075_14	*Diaporthe* sp.	NR_111857.1	91%	88%
	Phosphate	OH2075_2	*Diaporthe* sp.	EU552122.1	92%	100%
	Phosphate	OH2075_7	*Diaporthe* sp.	KT949914.1	92%	99%
	Phosphate	OH2725_12	*Diaporthe* sp.	MH855768.1	92%	100%
	Phosphate	OH2725_4	*Diaporthe* sp.	EU552122.1	92%	100%
	Phosphate	OH2725_22	*Diaporthe* sp.	EU552122.1	93%	100%
	Phosphate	OH2725_3	*Diaporthe* sp.	EU552122.1	93%	100%
	Phosphate	OH2725_30	*Diaporthe* sp.	JX862530.1	93%	100%
	Phosphate	OH2075_3	*Diaporthe* sp.	MH855768.1	94%	100%
	Phosphate	OH2725_6	*Diaporthe* sp.	MH855769.1	94%	100%
	Phosphate	OH2075_15	*Diaporthe* sp.	MH855768.1	95%	100%
	Phosphate	OH2075_5	*Diaporthe* sp.	NR_173373.1	95%	99%
	Phosphate	OH248_17	*Diaporthe* sp.	MH855768.1	95%	100%
	Phosphate	OH2725_14	*Diaporthe* sp.	EU552122.1	95%	100%
	Phosphate	OH248_1	*Diaporthe velutina*	NR_152470.1	97%	85%
	Phosphate	OH248_2	*Diaporthe foeniculina*	NR_145303.1	97%	100%
	Phosphate	OH2075_8	*Lasiodiplodia subglobosa*	NR_147350.1	99%	100%
	Phosphate	OH248_4	*Phyllosticta capitalensis*	OL957169.1	100%	100%
	Phosphate	OH2725_5	*Phyllosticta capitalensis*	MH865128.1	100%	100%

Taxons with an identity percentage below 97% were classified only at the genus level.

In addition to the difference between the number of endophytic fungal isolates recovered per treatment in the two host species, differences were noted in the taxonomic composition of the cultivable endophytic fungal community between the nutrient addition treatments. These differences can be seen from the taxonomic level of order since all isolates of the two host species belong to the phylum Ascomycota and mostly to the class *Sordariomycetes* (>80%). Among the endophytic fungi recovered from *C. brasiliense*, the order *Diaporthales* showed an abundance greater than 80% in all treatments. The other orders corresponded to < 20% of the isolates in all treatments for the endophytic fungal community in this host species. *Pleosporales* were found in the control (9.09%), nitrogen+phosphate (4.5%), and phosphate (7.1%) groups; *Glomerellales* were found in liming (12%) and phosphate (7.1%); *Botryosphaeriales* in the treatment with nitrogen (3.1%) and nitrogen+phosphate (9.1%); *Hypocreales* was exclusive to liming (4%), *Mycosphaerellales* from the phosphate treatment (3.5%) and *Amphisphaeriales* from the nitrogen+phosphate treatment (4.5%) (Figure 58).

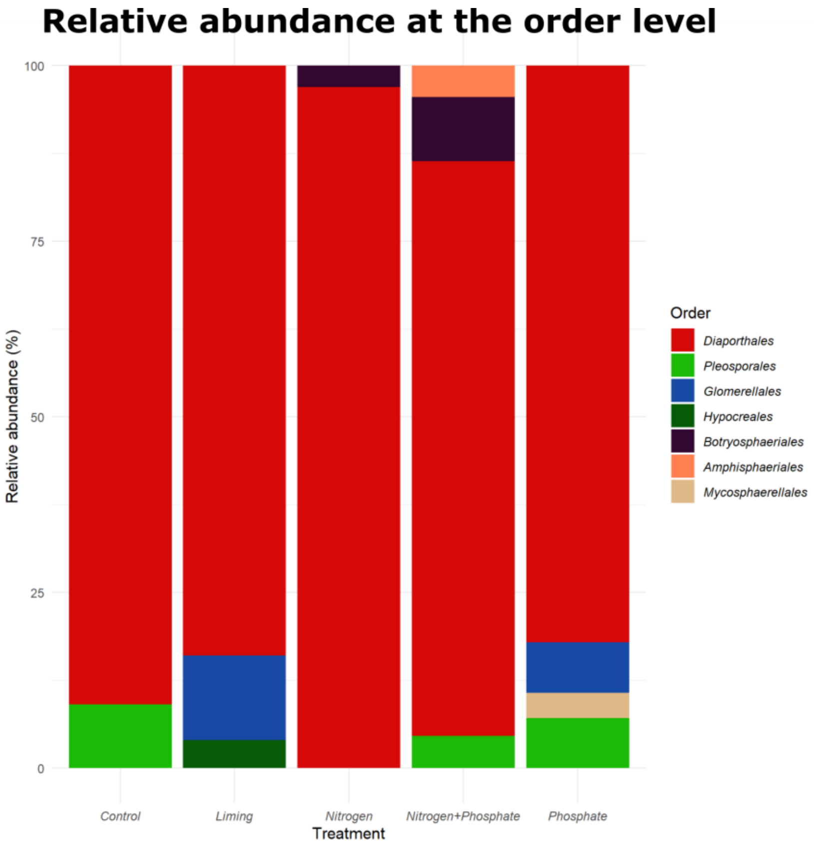


Figure 58. Order-level relative abundance of the cultivable endophytic fungal community associated with *Caryocar brasiliense* under different soil nutrient addition treatments.

The isolates of endophytic fungi recovered from the host *O. hexasperma* belong to eight orders and their distribution by nutrient addition treatment was quite heterogeneous, with the control and liming groups showing the highest number of orders (Figure 59). *Diaporthales* was dominant in the fungal community in all treatments and in the control group, but with a very different relative abundance depending on the treatment. In the control group, 43% of the isolates belonged to *Diaporthales*, while in the nitrogen treatment 100% of the isolates belonged to that order. *Pleoporales* was the second most abundant order in the control group (25%), followed by *Botryosphaeriales* (18.75%). The other orders in the control group corresponded to 6.3%. In liming, the second most abundant order was *Hypocreales* (23%), followed by *Glomerellales* (15.4%). *Botryosphaeriales* was the second most abundant group in the phosphate and nitrogen+phosphate treatments. *Coniochaetales* was exclusive to the control group, *Xylariales* from liming and *Amphisphaeriales* to the Nitrogen+phosphate group.

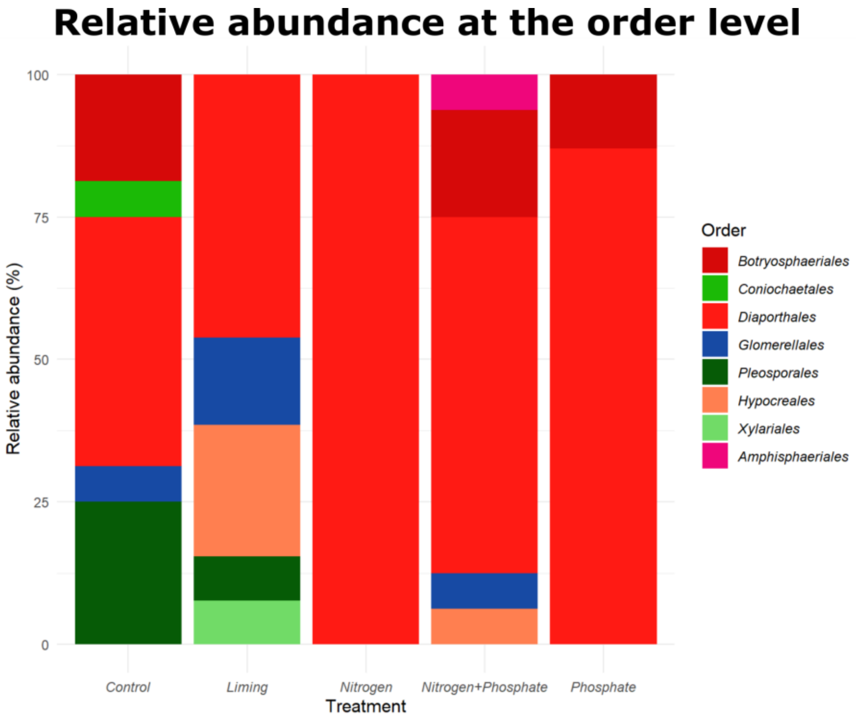


Figure 59. Order-level relative abundance of the cultivable endophytic fungal community associated with *Ouratea hexasperma* under different soil nutrient addition treatments.

Considering the taxonomic level of the family, the endophytic fungi isolated from the host *C. brasiliense* were distributed in ten families (Figure 60). Most of the isolates recovered for this host in the different treatments of addition of nutrients to the soil belong to *Diaporthaceae.* The control group had the lowest diversity of families, with only two families, *Diaporthaceae* and *Didymellaceae.* In contrast, the greatest diversity of families for this host among the different treatments was observed in the nitrogen+phosphate and phosphate groups, both with the isolates distributed in five fungal families. The *Pestalotiopsidaceae*, *Erythrogloeaceae*, and *Phyllostictaceae* families of the isolates recovered from the nitrogen+phosphate treatment, while *Nectriaceae* was exclusive to liming. *Cytosporaceae* was present in the four nutrient addition treatments.

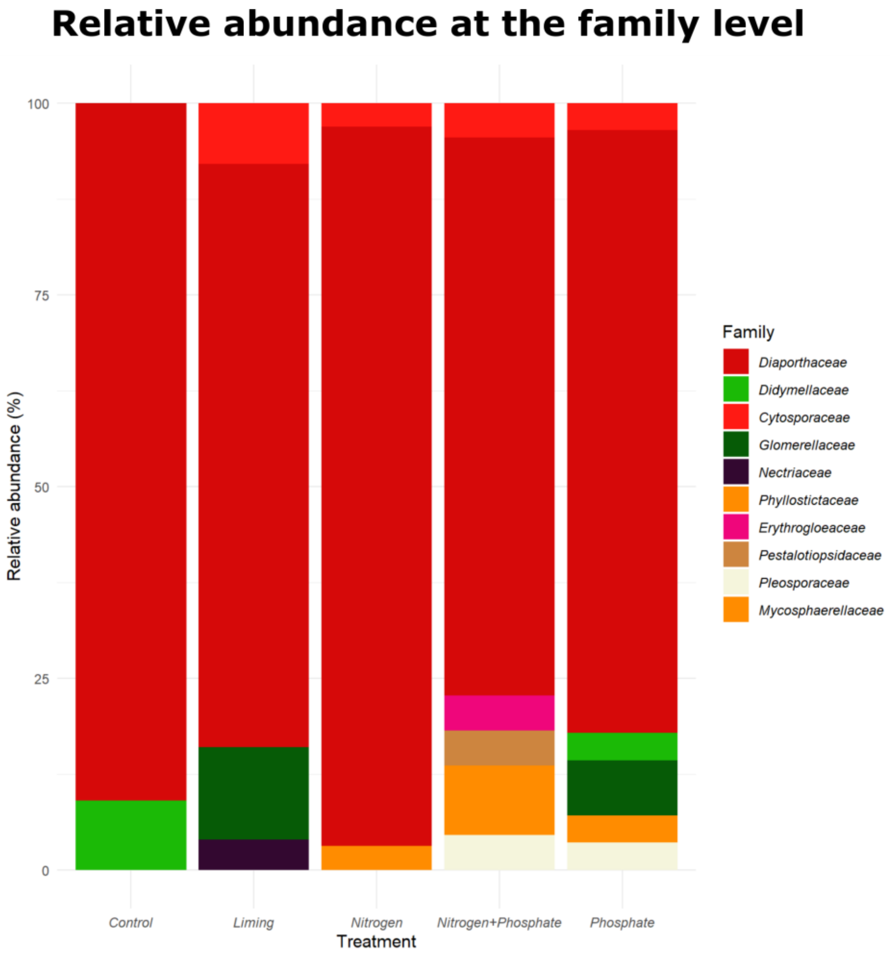


Figure 60. Family-level relative abundance of the cultivable endophytic fungal community associated with *Caryocar brasiliense* under different soil nutrient addition treatments.

The endophytic fungi isolated from the host *O. hexasperma* were distributed in 12 families and similar to the endophytic fungi isolated from the host *C. brasiliense, Diaporthaceae* was the dominant family in all treatments of addition of nutrients and control group (Figure 61). However, the control group in *O. hexasperma* had the highest number of fungal families when compared to the nutrient addition groups, with a total of seven families, four of them being exclusive to the control group (*Coniochaetaceae, Didymellaceae, Dedymosphaeriaceae,* and *Stilbosporaceae*). In contrast, nitrogen treatment showed the lowest diversity of families, with all fungal taxa belonging to *Diaporthaceae.* The isolates from the nitrogen+phosphate treatment were the second most diverse group in terms of the number of fungal families, with six families, while the liming isolates were the third most diverse group, with a total of five families, two of which were exclusive (*Pleosporaceae* and *Xylariaceae*).

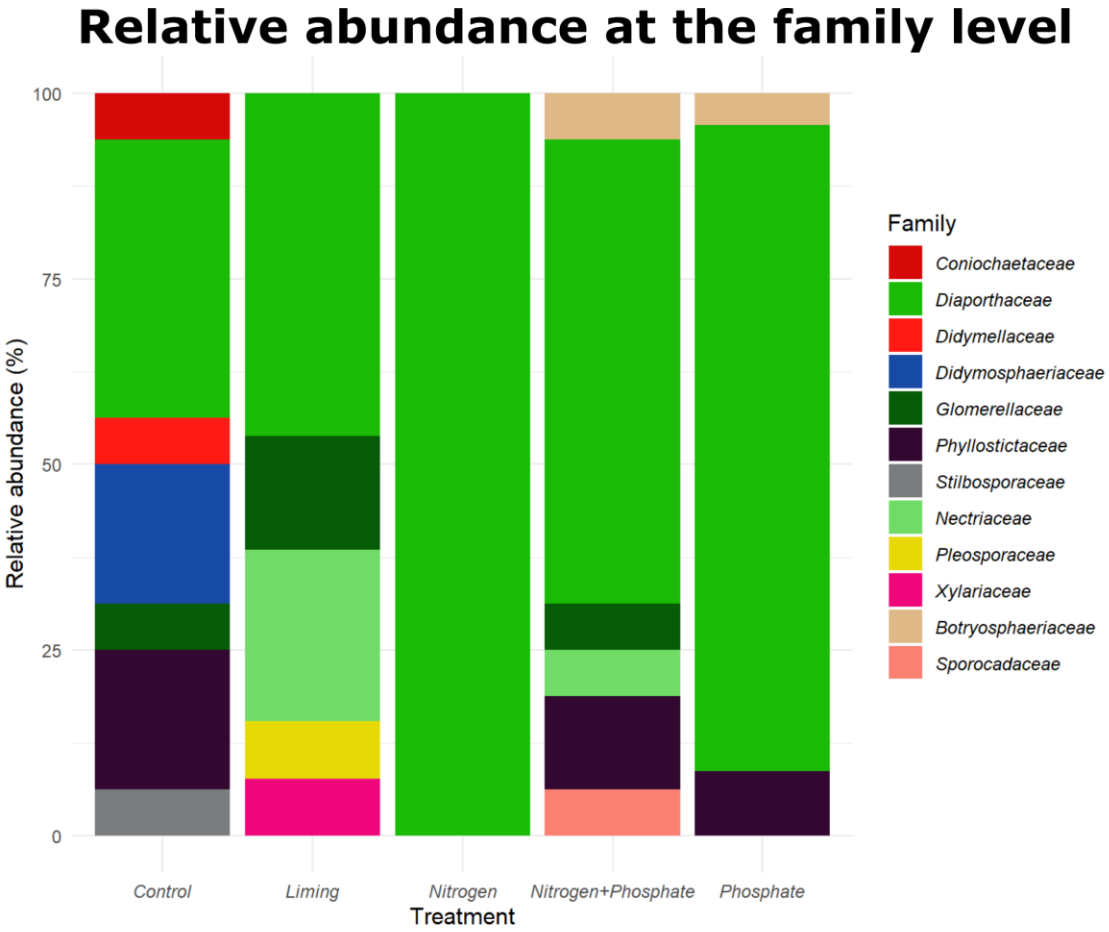


Figure 61. Family-level relative abundance of the cultivable endophytic fungal community associated with *Ouratea hexasperma* under different soil nutrient addition treatments.

In general, the fungal species isolated in both hosts and in all nutrient addition treatments present an equity value in all treatments, where no species presented a high dominance value in relation to the others. However, the outstanding feature observed and that differs between treatments in both hosts is the change in the pool of isolated fungal species depending on the nutrient addition treatment. *Diaporthe* species were dominant among the isolates of the host *C. brasiliense* in the different treatment regimes of nutrient addition to the soil (Figure 62). Furthermore, it is worth noting that more than 35% of the isolates recovered from this host were classified only as *Diaporthe* sp. Among the isolates identified at the species level, the control group had the lowest number of species, with five, namely *D. actinidae, D. masirevicii, D. rosae, D. schini,* and *Didymella keratinophila*. Liming presented the largest pool of fungal species, with a total of 12 species distributed among the genera *Diaporthe, Fusarium, Cytospora*, and *Colletotrichum*. Phosphate and nitrogen+phosphate treatments were the second most diverse in terms of the number of species found, both with 11 species, distributed among six different genera.

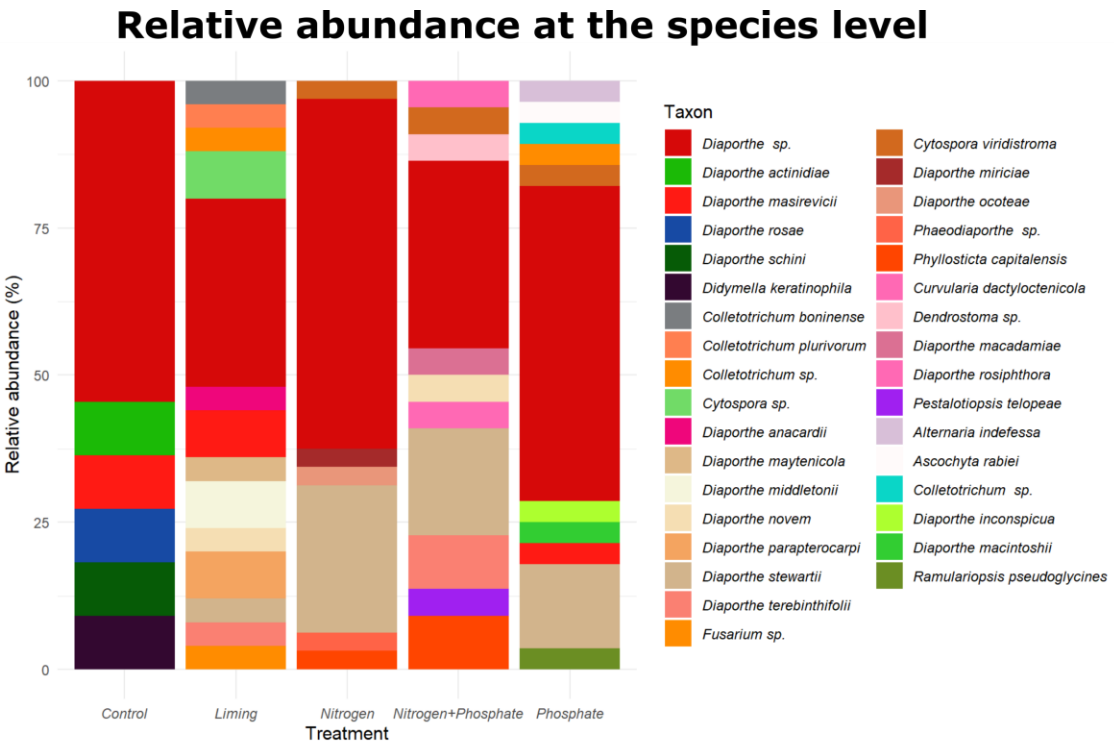


Figure 62. Species-level relative abundance of the cultivable endophytic fungal community associated with *Caryocar brasiliense* under different soil nutrient addition treatments.

Although a smaller number of endophytic fungi were recovered from *O. hexasperma*, a greater diversity of identified species was observed in this host, in all treatments, when compared to *C. brasiliense*. The isolates from the control group, in *O. hexasperma*, were distributed in 11 species belonging to eight genera, namely *Colletotrichum, Coniochaeta, Dendrothyrium, Diaporthe, Epicoccum, Kalmusia, Phyllosticta* and *Stilbospora* (Figure 63). The liming isolates were the second most diverse group, with seven species divided into five genera, with the genus *Fusarium* being the one with the highest number of species. In the treatment with nitrogen+phosphate, the identified isolates were classified into five species belonging to five genera. A smaller pool of species was observed in the nitrogen and phosphate treatments. In summary, these groups were dominated by *Diaporthe* spp.

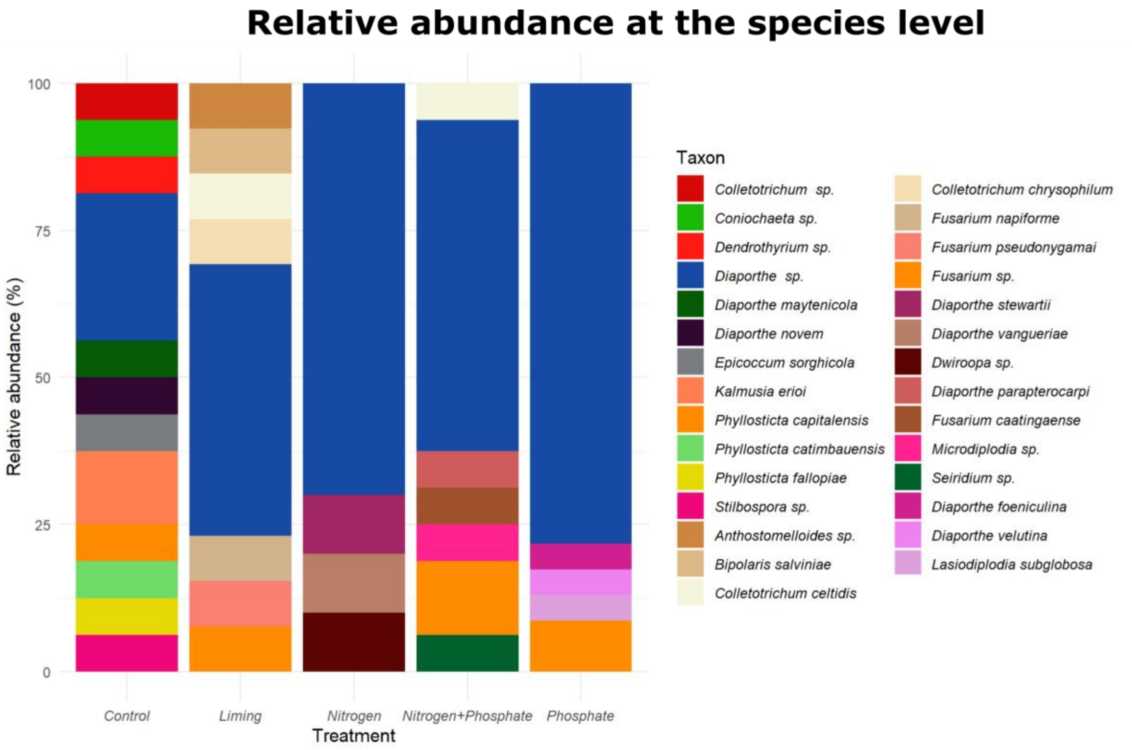


Figure 63. Species-level relative abundance of the cultivable endophytic fungal community associated with *Ouratea hexasperma* under different soil nutrient addition treatments.

As shown, the differences observed in the community of endophytic fungi between treatments were related to the *pool* of species found. In the host *C. brasiliense*, only *Diaporthe* not identified at the species level was common among all nutrient addiction treatments and the control group. In general, for this host, most of the reported species and/or genera were exclusive to the treatments (Figure 64). The species *D. actinidae, D. rosae, D. schini*, and *D. keratinophila* were exclusive to the control group. *Colletotrichum* spp. together with *D. anacardii, D. maytenicola*, and *D. parapterocarpi* were exclusive to liming; *D. miriciae, D. ocoteae*, and *Phaeodiaporthe* sp. were exclusive to nitrogen treatment; *Curvularia dactyloctenicola, Pestalotiopsis telopeae, and Diaporthe macadamiae* were exclusive to the nitrogen+phosphate treatment; *Alternaria indefensa, Ascochyta rabiei, D. inconspicua, D. macintoshii, D. masirevicii,* and *Ramulariopsis pseudoglycines* were exclusive to the phosphate treatment. Regarding the fungal species shared between treatments, D. masirevicii was the only species shared in the control group with the phosphate treatment. Regarding the species shared between treatments, *D. terebinthifolii* and *D. novem* were found in the treatment with nitrogen+phosphate and in liming. The species *D. stewartii* was present among the isolates from liming, treatment with nitrogen+phosphate, and treatment with phosphate. *Cytospora viridistroma* was present in the nitrogen, phosphate, and nitrogen+phosphate treatments; while *Dendrostoma sp.* was isolated from nitrogen+phosphate and phosphate treatments.

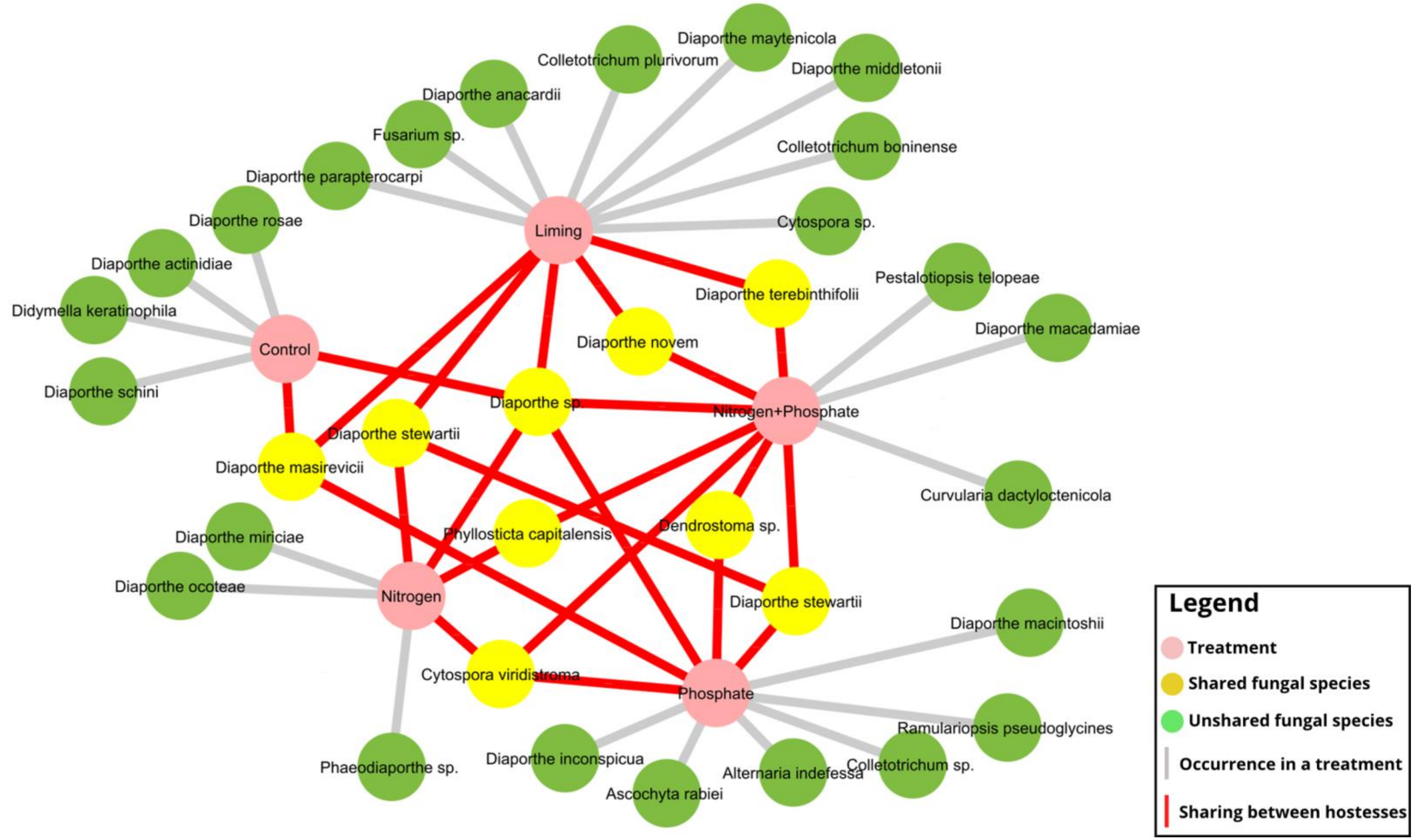


Figure 64. Architecture of the distribution network of endophytic fungi isolated from *Caryocar brasileinse* in different treatments of addition of nutrients to the soil. Pink nodes represent nutrient addition treatments; green nodes represent fungal taxa not shared between treatments; those in yellow show the shared fungal species. Gray edges indicate the occurrence of the taxon within a treatment; while those in red show species sharing.

Similar to what happened in the host *C. brasiliense*, the pool of species of endophytic fungi isolated from *O. hexasperma* varied depending on the nutrient addiction treatment to the soil (Figure 65). The species *Phyllosticta fallopiae, D. maytenicola, D. novem, Epicoccum sorghicola, Kalmusia* erioi, and the genera *Coniochaeta* sp., *Dendrothyrium* sp. *and Stilbospora* sp. were exclusive to the control group; *Anthostomelloides* sp., *Bipolaris salviniae, Colletotrichum chrysophilum, Fusarium napiforme*, and *F. pseudonygamai* were exclusive to liming*; D. stewartii, D. vangueriae* and *Dwiroopa sp*. were exclusive to nitrogen treatment; *D. parapterocarpi*, *F. caatingaense* and *Microdiplodia* sp. were exclusive to the nitrogen+phosphate treatment; and, finally, *D. Foeniculum, D. velutina*, and *Lasiodiplodia subglobosa* were exclusive to the phosphate treatment. Regarding the shared species, only unidentified *Diaporthe* were common among the four treatments and the control group. *Phyllosticta capitalensis* was found in the control group and the nitrogen+phosphate and phosphate treatments. C. celtidis was present in the nitrogen+phosphate and liming groups. The control group did not share any species with the nitrogen and liming treatments, except for unidentified *Diaporthe*.

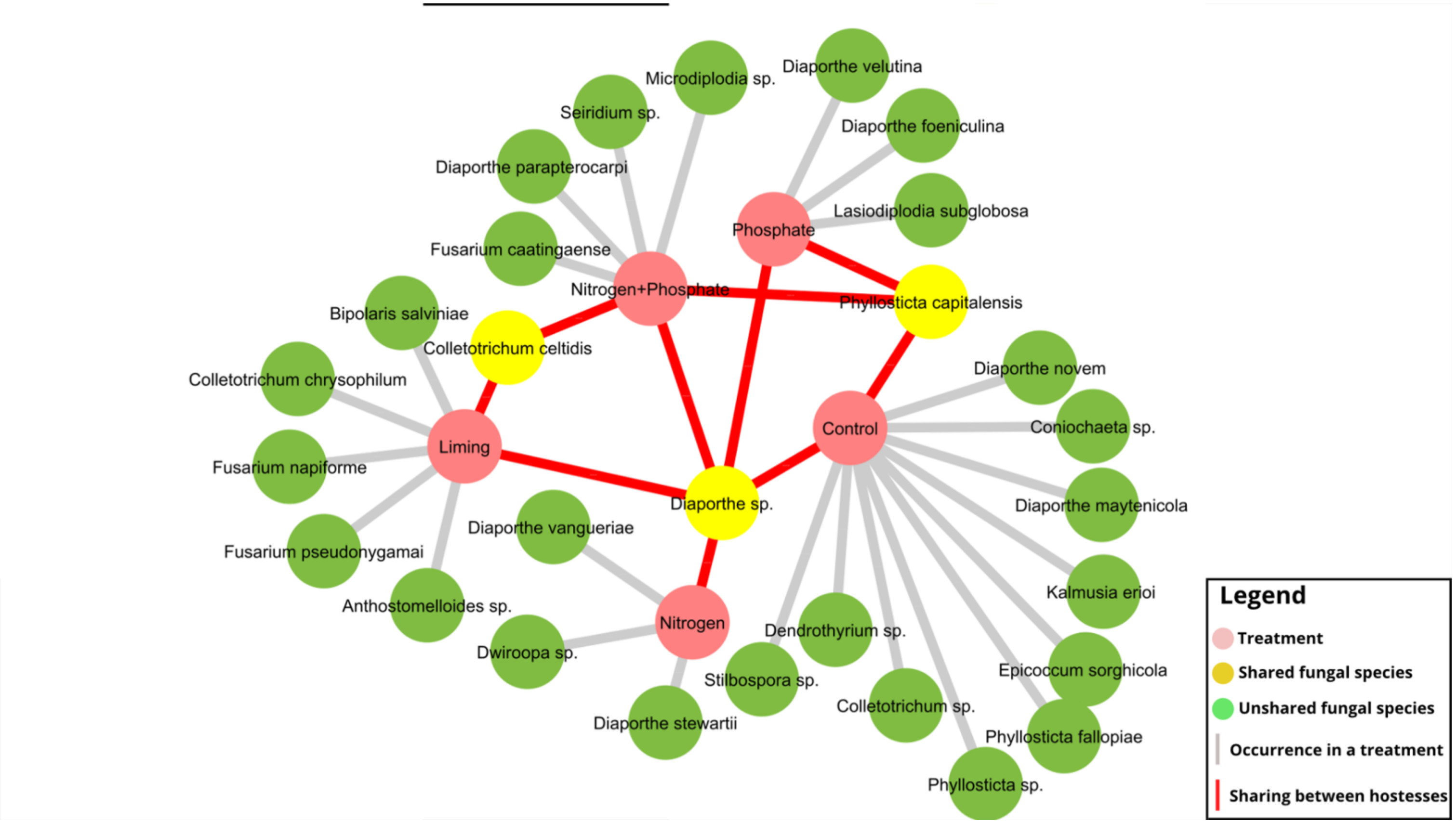


Figure 65. Architecture of the distribution network of endophytic fungi isolated from *Ouratea hexasperma* in different treatments of addition of nutrients to the soil. Pink nodes represent nutrient addition treatments; green nodes represent fungal taxa not shared between treatments; those in yellow show the shared fungal species. Gray edges indicate the occurrence of the taxon within a treatment; while those in red show species sharing.

There were no statistically significant differences in alpha diversity indices between treatments (p>0.05) for the two plant species. However, this does not mean that there are no differences. In *C. brasiliense*, the highest values of alpha diversity of the endophytic fungal community were observed in liming (H' 3.3), in the nitrogen+phosphate treatment (H' 2.9), in the phosphate treatment (H' 2.2), and control group (H' 2.0) (Figure 66a). The lowest alpha diversity value of the cultivable endophytic fungal community was observed in nitrogen treatment (H' 1.8). The 1st Order Jackknife Index showed the estimated richness of cultivable endophytic fungi species in *C. brasiliense* between treatments (Figure 66b). For the control group, the estimated richness was 6 species, thus, based on this index, 100% of the species were sampled. For liming, the estimated richness was 21 species, of which only 66.6% were recorded; for nitrogen treatment, only 61% of the estimated richness was recorded; for the treatment with nitrogen+phosphate only 51% of the estimated richness was recorded; while for the phosphate treatment, only 54.5% of the estimated richness was sampled.

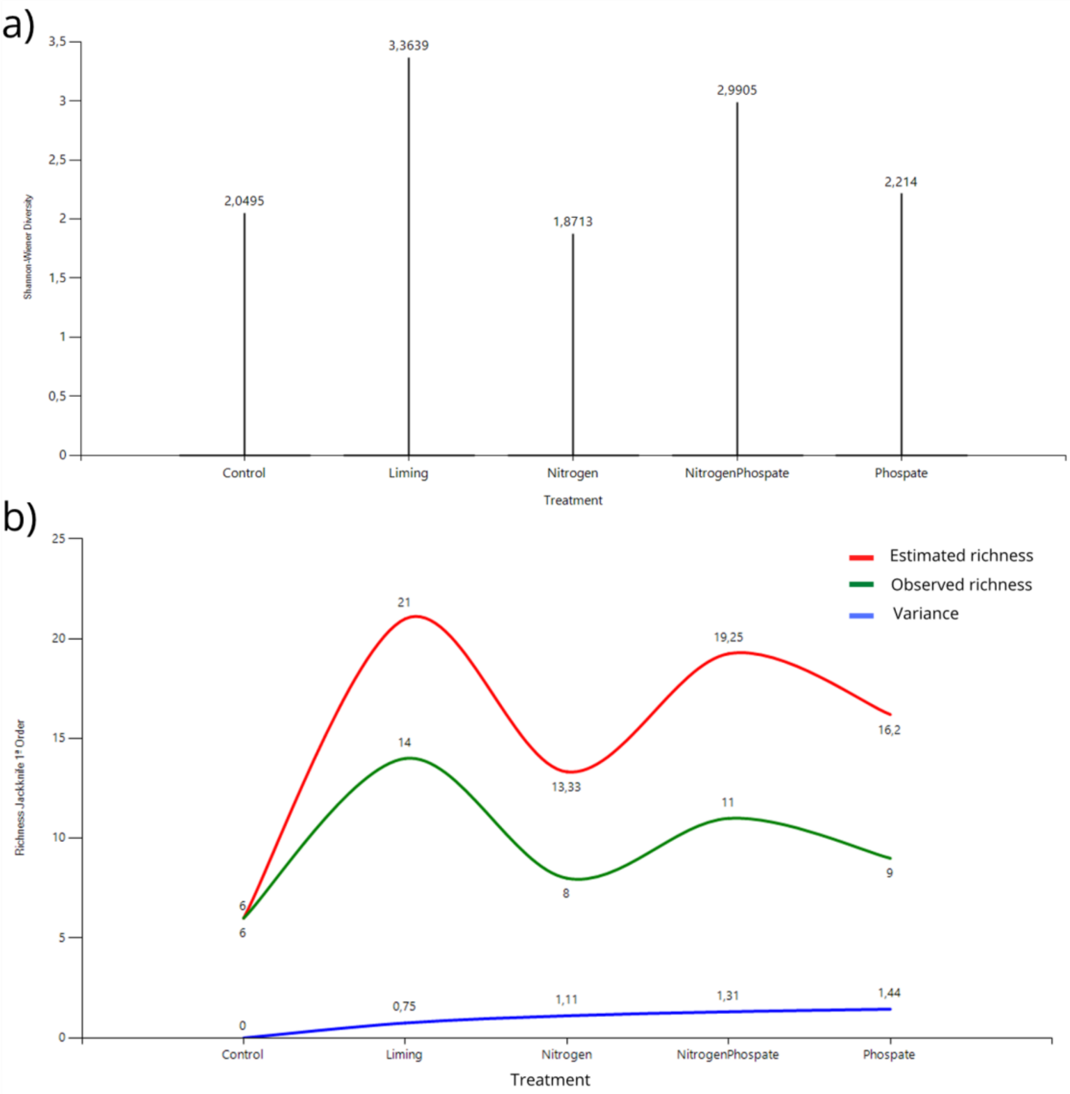


Figure 66. Metrics of alpha diversity and estimation of endophytic fungal community richness in *Caryocar brasiliese* in different nutrient addition treatments. In a) the Shannon Wiener diversity index is shown. In b) the estimate of the species richness of 1st Order Jackknife is presented.

In the host *O. hexasperma*, the highest values of alpha diversity of the cultivable fungal community among treatments were observed in the control group (H'3.3), followed by liming (H'2.5), nitrogen+phosphate treatment (H ' 1,3) (Figure 67a). The lowest value was observed in the treatment with phosphate (H'1). The Jackknife of 1st Order estimated the richness of cultivable fungi in the control and liming groups in 12 species; in the treatment with nitrogen in 6.6 species; in the treatment with nitrogen+phosphate in 12.25 species; and finally, in the phosphate treatment, with nine estimated fungal species (Figure 67b). Based on this index, 100% of the cultivable endophytic fungi species in the control group were demonstrated; 66% of the species were demonstrated in the liming treatment; 60% of the species in the nitrogen treatment were demonstrated; 56% of the species in the nitrogen+phosphate treatment were demonstrated; while only 55.5% of the species in the phosphate treatment were demonstrated.

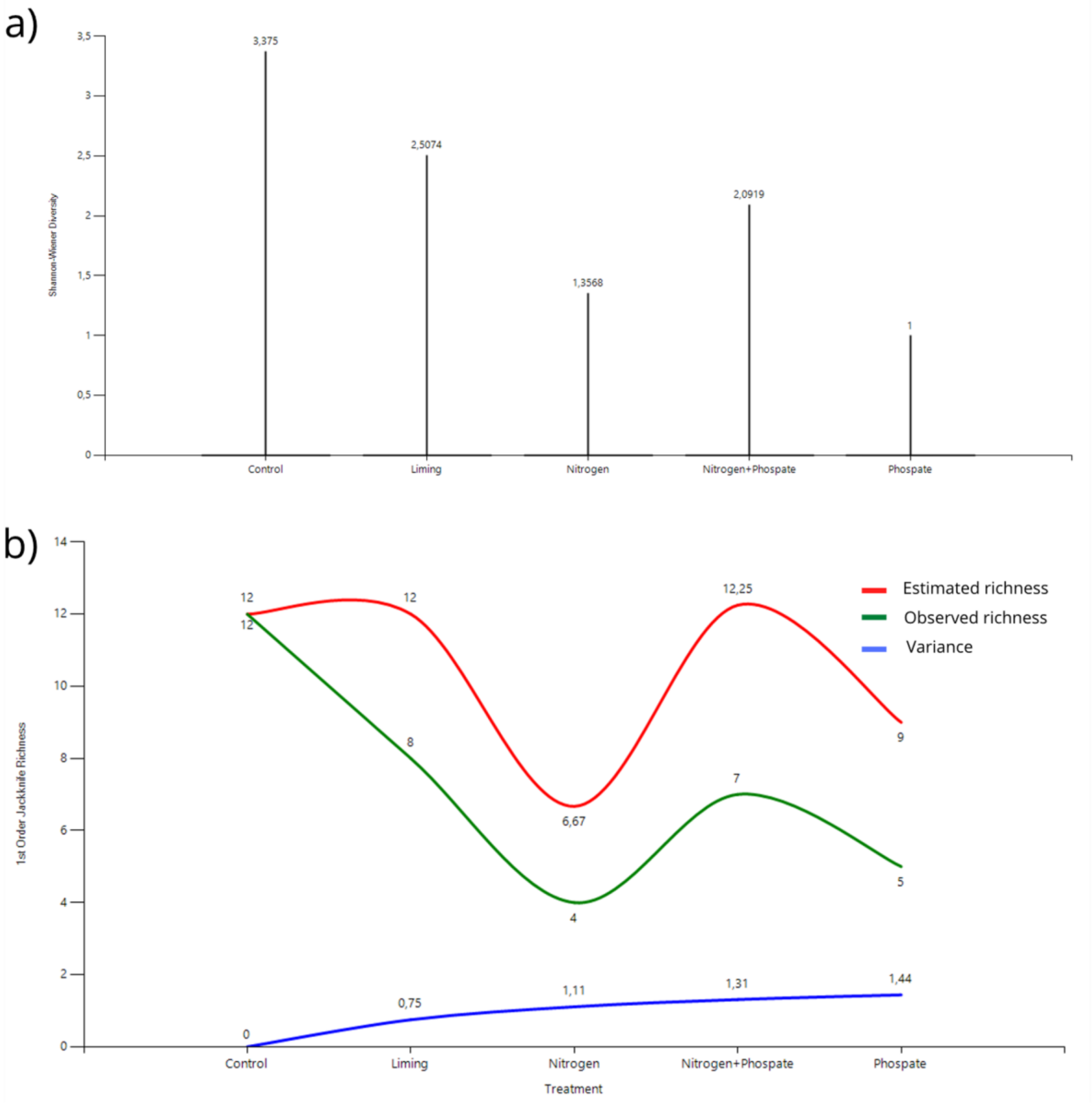


Figure 67. Metrics of alpha diversity and estimation of endophytic fungal community richness in *Ouratea hexasperma* in different nutrient addition treatments. In a) the Shannon Wiener diversity index is shown. In b) the estimate of the species richness of 1st Order Jackknife is presented.

The Simpson's evenness (D), an index that measures the proportion of individuals of a given species concerning the others present in the niche, showed that the abundance of endophytic fungi species between the two host plants and the different treatments present considerable variations, suggesting that soil treatments can influence dominance of certain species. In the host *C. brasiliense*, the highest equity values were observed in the treatments with liming (0.92 D) and nitrogen+phosphate (0.91 D), while the lowest value was observed in the treatment with nitrogen (0.69 D). (Figure 68a). In *O. hexasperma* the highest evenness value was observed in the control group (0.9 D). This finding suggests that the relative abundance of fungal species in this group is close to each other (Codominance) and that there is no significantly dominant group (Figure 68b). The lowest values for the community of this host were observed in the treatment with nitrogen (0.64 D) and the treatment with phosphate (0.46 D).

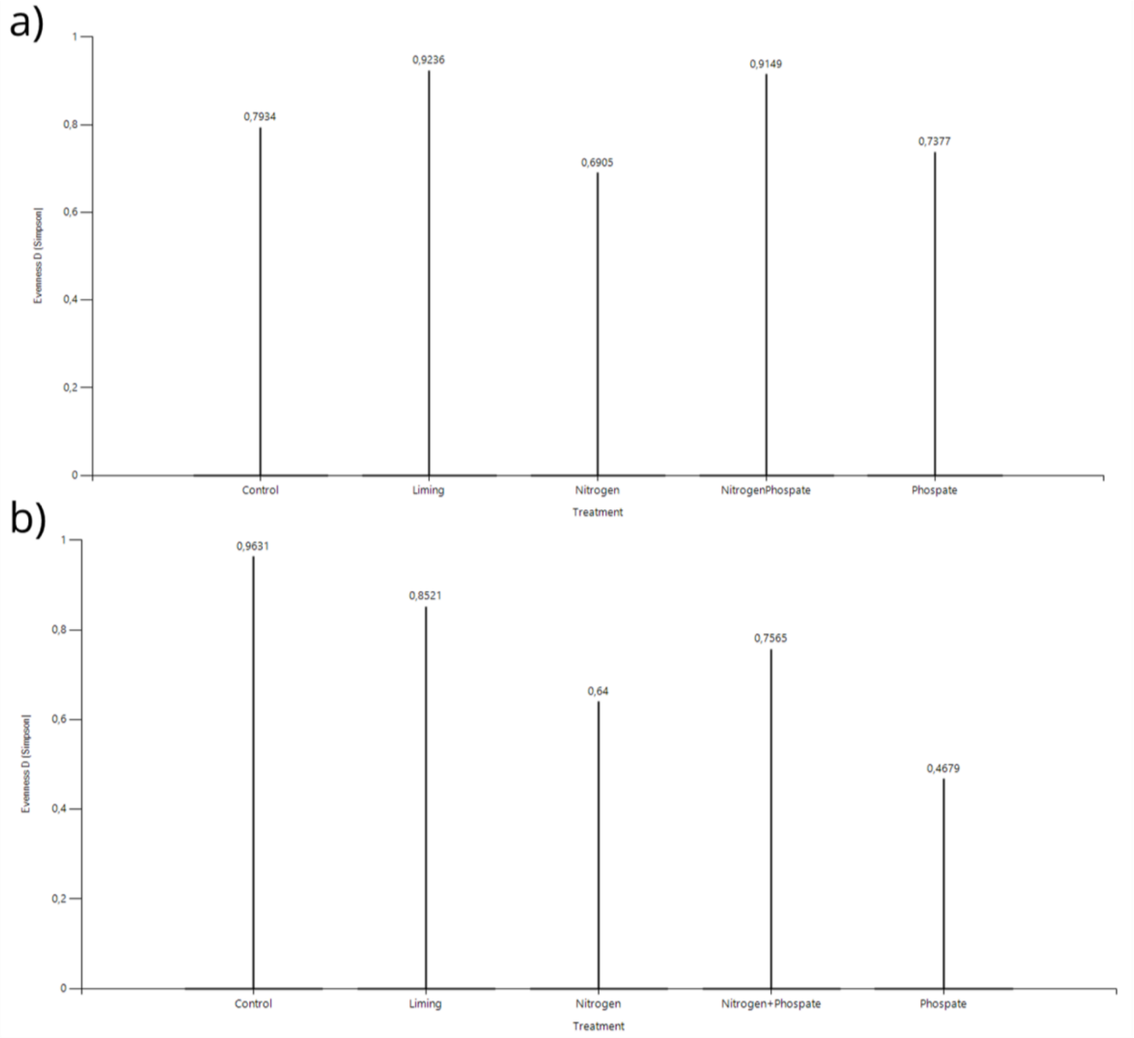


Figure 68. Simpson's equity index (D) of the endophytic fungal community in two host plant species under different soil nutrient addition treatments. In a) the values of D for the community of cultivable endophytic fungi of the host *Caryocar brasiliense* are shown; while in b) the value of D for the host community *Ouratea hexasperma* is shown. The closer the value of D is to 1, the more uniform is the abundance of species in the endophytic fungal community.

4.2. *Analysis of soil nutritional characteristics and foliar nutrients*

Soil characteristics varied between treatments with the addition of mineral fertilizers (Supplementary table 3). The analysis of principal components (PCA) of the physicochemical characteristics of the soil shows that the soil density (58.5%), shown as dry weight, and gravimetric content (27.9%) are the two main variables responsible for the dissimilarities between soils. submitted to different treatments with the addition of mineral fertilizers (Figure 69). Bulksoil from nitrogen+phosphate, phosphate and liming treatments are denser and more compact compared to the control group.

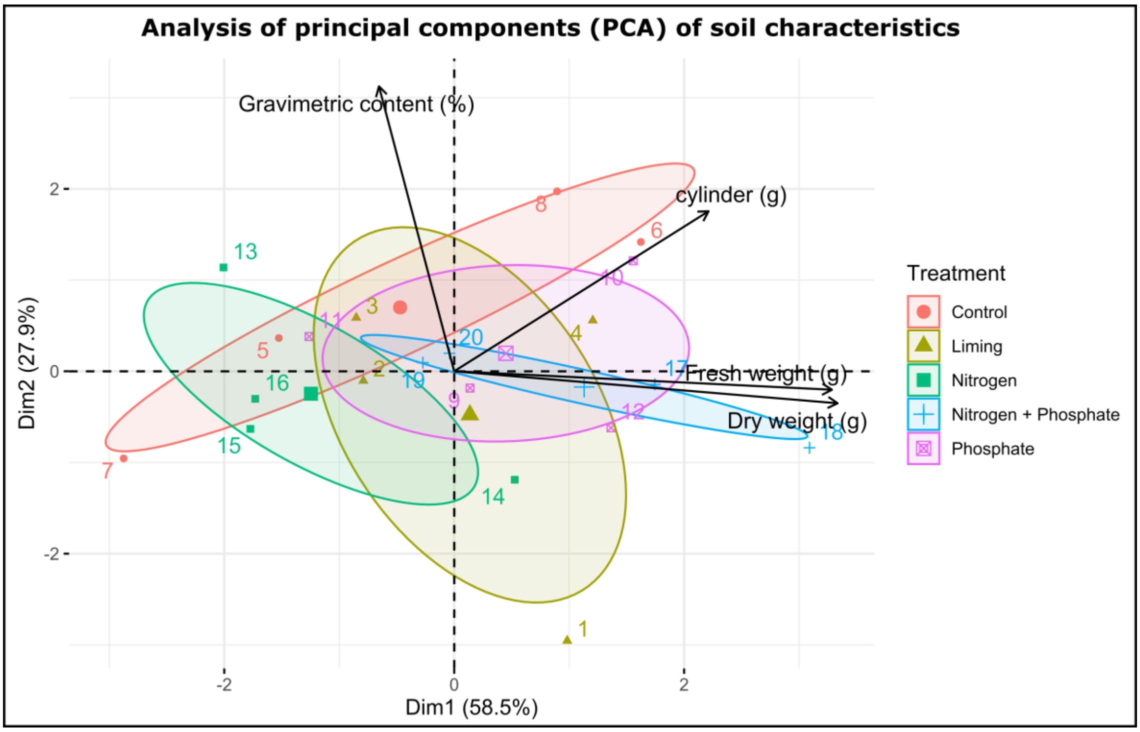


Figure 69. Ordenation produced by Principal Component Analysis (PCA) for soil physicochemical variables. The ellipses show the grouping of samples by treatment.

Leaf nutrient content, leaf area, and specific leaf area (AFE) varied depending on the treatment for both host species (Supplemental table 4). The PCA showed that in *C. brasiliense* the Ca+ (29.5%) and N (19.9%) content are the main variables responsible for the dissimilarities between the treatments for adding nutrients to the soil (Figure 70). The control group was grouped in an intermediate area, being correlated to high concentrations of aluminum (Al) and magnesium (Mg+), and a greater specific leaf area. In the treatment with nitrogen+phosphate and nitrogen, the leaves of *C. brasiliense* showed the highest concentrations of nitrogen (N), phosphate, and (P), however, they were related to low concentrations of sulfur (S), calcium (Ca+), lower leaf area and dry leaf weight. In contrast, the leaves of this plant species in the treatment with the addition of phosphate showed the highest values of Ca+ and S and the highest dry weight. In the liming treatment, the leaves were associated with high concentrations of Mg+ and Al, high values of weight, and leaf area (cm^2).

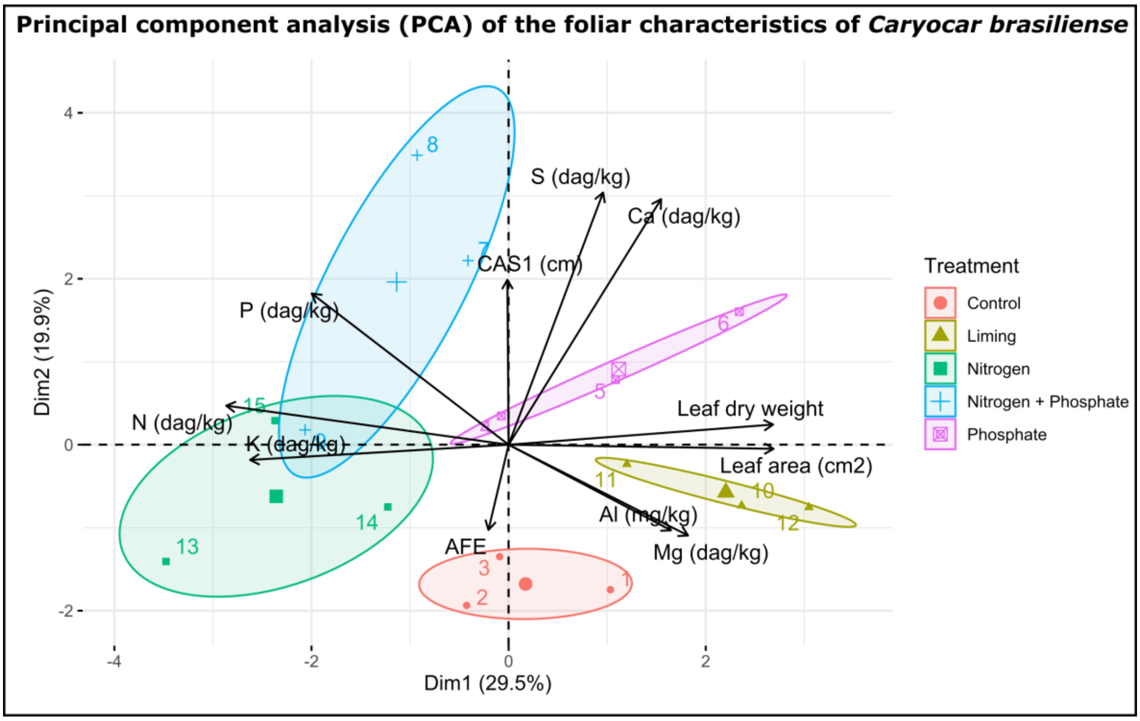


Figure 70. Ordenation produced by Principal Component Analysis (PCA) for variables of leaf nutrient concentration, specific leaf area (AFE) cm²/g, and dry leaf weight of *Caryocar brasiliense* under different treatments of addition of nutrients to the soil. The X-axis shows PC1 and the y shows PC2. The ellipses show the grouping of biological replicas by treatment. AFE: Specific foliar area; Al: Aluminium; Ca: Calcium; CAS1: Stem circumference; K: Potassium; Mg: Magnesium; P: phosphorus; S: sulfur.

In *O. hexasperma*, the main variables responsible for the dissimilarities of leaf characteristics between treatments were the concentration of Potassium (K) (34.5%) and Mg (27.2%) (Figure 71). The leaves of the control group were associated with greater leaf area (cm^2), greater leaf dry weight, greater stem circumference, and low concentrations of Al, Ca+, P, and S. In the treatment with liming, the leaves presented higher levels of Mg+ and AFE, and lower concentrations of Al, Ca+, P and S. In contrast, in the treatments with phosphate and nitrogen+phosphate, the highest concentrations of K, Al, P, Ca, S and lower concentrations of Mg+ and N, and of AFE were observed. The nitrogen treatment group was grouped in an intermediate region, being correlated with high leaf area (cm^2) and stem circumference and high levels of N, K, Al, P, Ca+, and S.

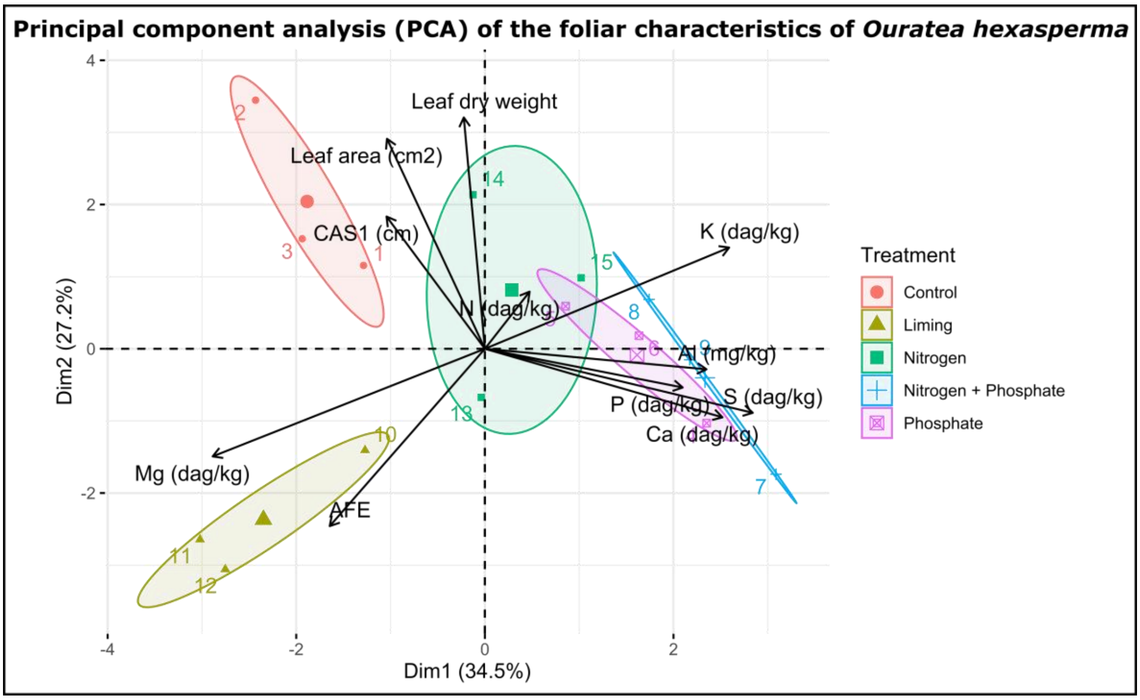


Figure 71. Ordenation produced by Principal Component Analysis (PCA) for variables of leaf nutrient concentration, specific leaf area (AFE) cm²/g, and dry leaf weight of *Ouratea hexasperma* under different treatments of addition of nutrients to the soil. The X-axis shows PC1 and the y shows PC2. The ellipses show the grouping of biological replicas by treatment. AFE: Specific foliar area; Al: Aluminium; Ca: Calcium; CAS1: Stem circumference; K: Potassium; Mg: Magnesium; P: phosphorus; S: sulfur.

4.3. *Metabarcoding*

For *C. brasiliense*, 6.013 OTU's were recorded, with only 2.916 receiving taxonomic attributions below kingdom (supplementary table 5). In *O. hexasperma*, 2.601 OTUs were recorded and of these, 1.959 received taxonomic attributions (supplementary table 6).

4.4. *Relative abundance*

The taxonomic classification of amplicons showed that, among the sequences with attribution at the phylum level, *Ascomycota* was the most abundant in the endophytic fungal community in both hosts under the different treatments of addition of nutrients to the soil (Figure 72a and Figure 73a). In the host species *C. brasiliense*, it should be considered that less than 50% of the amplicons in the control group received attribution at the phylum level, being classified only at the Fungi kingdom level. For liming, in addition to sampling bias, the number of amplificons classified at the phylum level was even lower than in the control group (<35%). Concerning other the phylum found in *C. brasiliense* in the different treatments, but in lower abundance, Basidiomycota was more abundant in the Nitrogen, Nitrogen+Phosphate, and Phosphate treatments (mean relative abundance of 4%) when compared to the control group (without the addition of nutrients to the soil) and liming (<0.9%) (Figure 72b). For *O. hexasperma*, more than 80% of the amplicons were classified at the phylum level in all treatments (sampling effort) (Figure 73b). Considering other less abundant phylum in *O. hexasperma*, *Basidiomycota* was more abundant in the control group (± 15%) compared to the other groups per treatment (<5%). These findings may be indicative of differences in the taxonomic composition of the foliar endophytic fungal community at the phylum level between soil nutrient addition treatments for both host species.

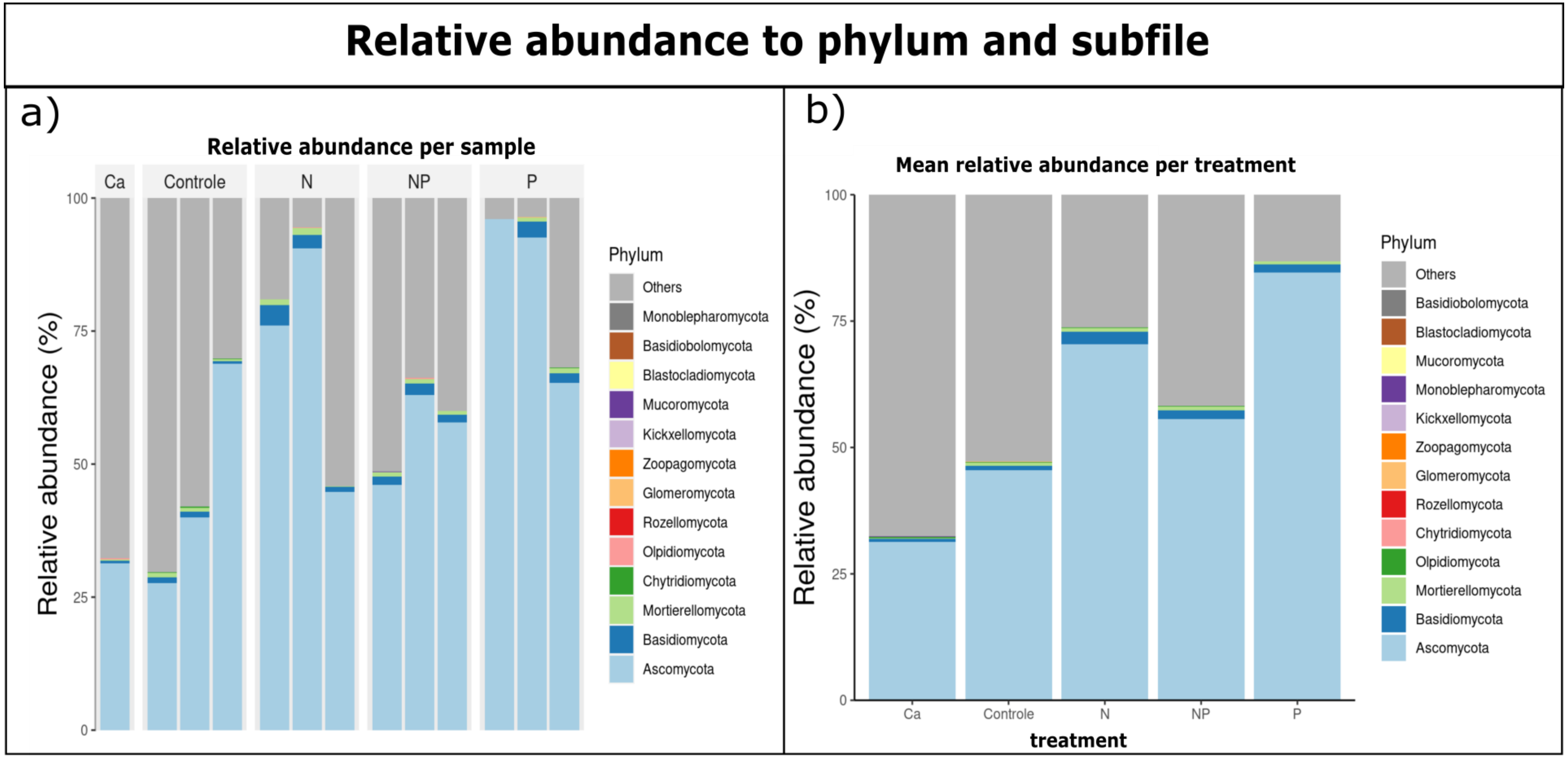


Figure 72. Relative abundance at phylum and subphylum levels of the foliar endophytic fungal community associated with *Caryocar brasiliense* under different nutrient addition treatments to the soil. In a) the relative abundance by sampling effort per treatment is presented; while in b) the mean relative abundance per treatment. Sequences classified only by kingdom level were grouped under "Other". Control: group without addition of nutrients to the soil; N: nitrogen treatment; NP: nitrogen+phosphate treatment; P: phosphate treatment; Ca: liming.

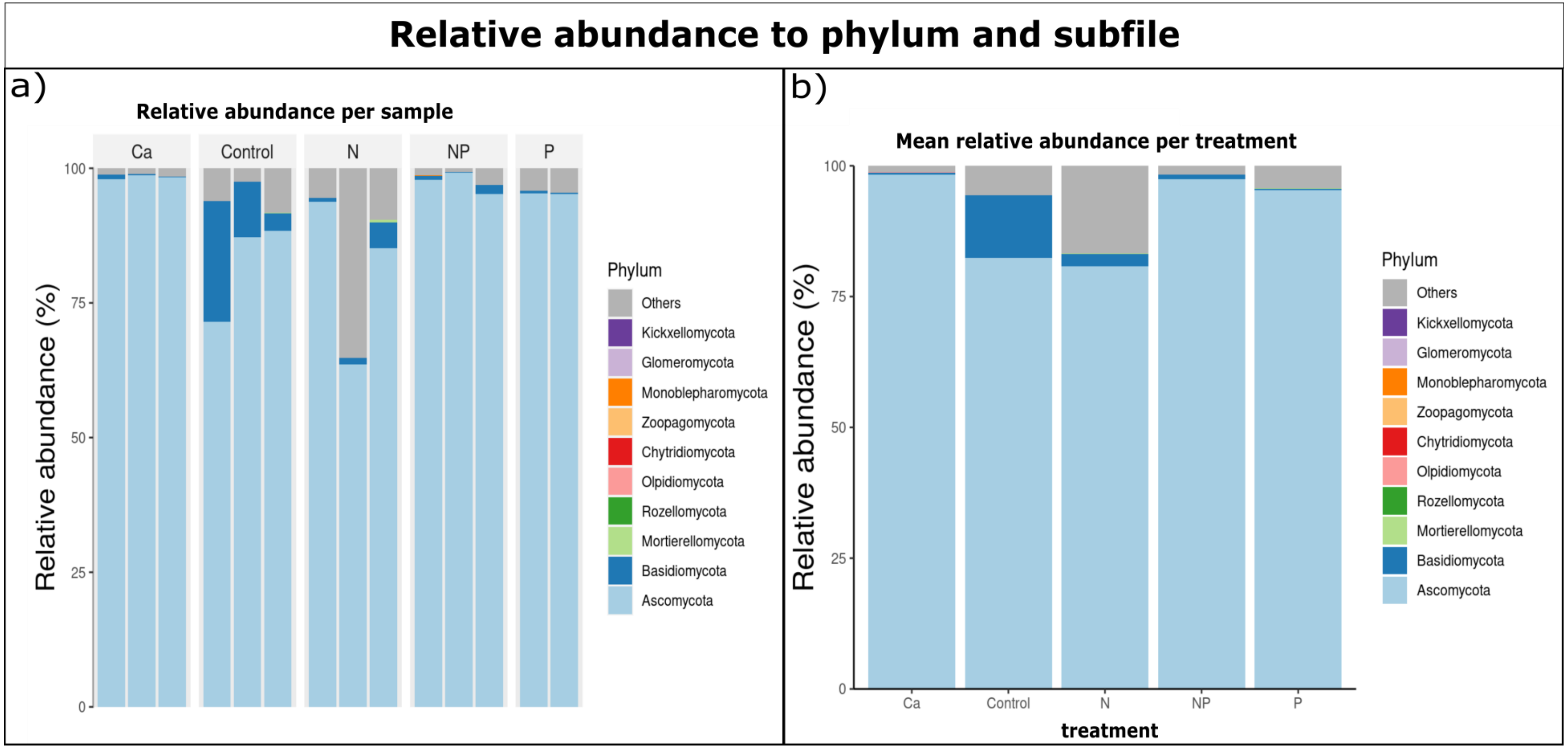


Figure 73. Relative abundance at phylum and subphylum levels of the foliar endophytic fungal community associated with *Ouratea hexasperma* under different nutrient addition treatments to the soil. In a) the relative abundance by sampling effort per treatment is presented; while in b) the mean relative abundance per treatment. Sequences classified only by kingdom level were grouped under "Other". Control: group without addition of nutrients to the soil; N: nitrogen treatment; NP: nitrogen+phosphate treatment; P: phosphate treatment; Ca: liming.

The dominant order among the classified sequences in *C. brasiliense* was *Capnodiales*, with an abundance of 48% in the Phosphate treatment, 42% in the nitrogen treatment, and 39% in the Nitrogen+Phosphate treatment, and 25% in the control group. The second most abundant order in the control group was *Helotiales*, while for the nitrogen treatment it was *Myriangiales* and for the phosphate treatment, it was *Xylariales*. In liming, the dominant order among the classified sequences were *Diaporthales* (7.5%), followed by *Capnodiales* (6.1%). Other orders were found among the different treatments, but in lower abundance (Figure 74)

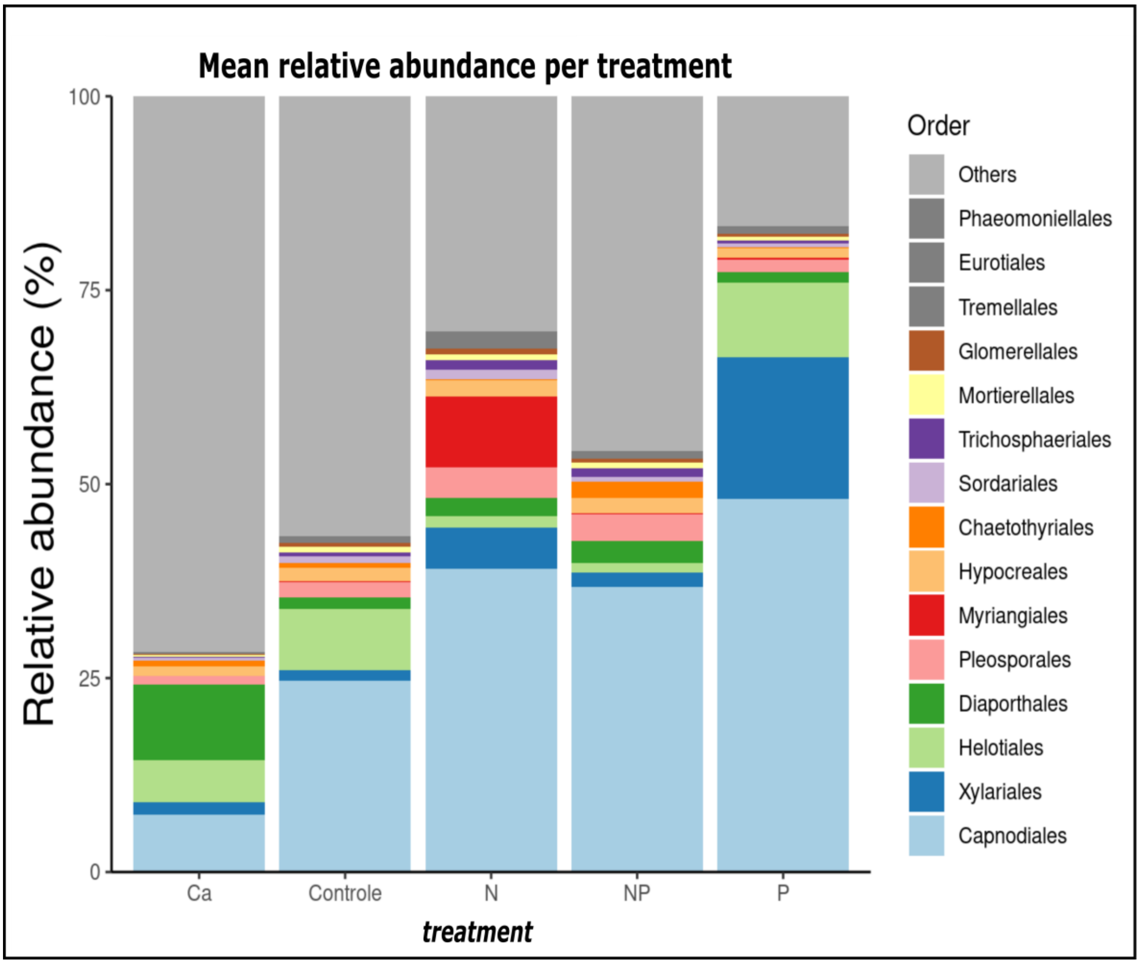


Figure 74. Order-level relative abundance of the leaf endophytic fungal community associated with *C. brasiliense* in different soil nutrient addition treatments. Sequences classified only at kingdom level were grouped into “Others”. Controle: control group without addition of nutrients to the soil; N: nitrogen treatment; NP: nitrogen+phosphate treatment; P: phosphate treatment; Ca: liming.

The mean relative abundance at the order level of the leaf endophytic fungal community in *O. hexasperma* showed significant differences between treatments (Figure 75). In the host *O. hexasperma*, the dominant order in the control and liming groups was *Pleosporales*, with a mean abundance of 39.5% and 37.5% respectively. In Phosphate treatment, *Xylariales* was dominant (45%), followed by *Capnodiales* (34.5%); while for the Nitrogen+Phosphate treatment, the dominant orders was *Capnodiales* (38.5%) followed by *Botryosphaeriales* (14.7%) and *Onygenales* (9.5%). For nitrogen treatment, it was *Xylariares* (23%). Other orders were found among the different treatments but in lower abundance.

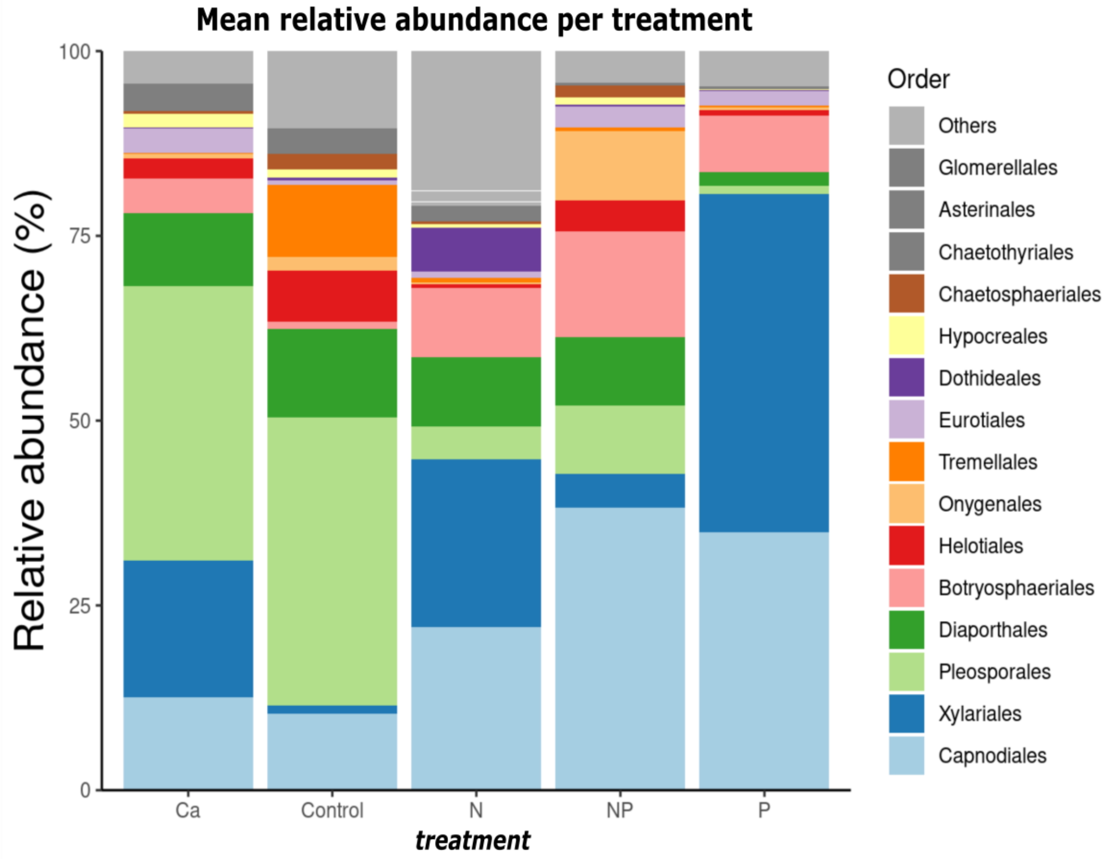


Figure 75. Order-level relative abundance of the leaf endophytic fungal community associated with *O. hexasperma* in different soil nutrient addition treatments. Sequences classified only at kingdom level were grouped into “Others”. Controle: control group without addition of nutrients to the soil; N: nitrogen treatment; NP: Nitrogen+Phosphate treatment; P: phosphate treatment; Ca: liming.

The 40 differentially abundant fungal families in the community of endophytic fungi of the host *C. brasiliense* are shown in Figure 76a. Overall, more than 45% of the amplicons were not classified at family level for the control group and for the Nitrogen treatments, Nitrogen+Phosphate and liming (Figure 76b). Among the identified groups, *Mycospharellaceae* was dominant in the control group and in the Nitrogen and Nitrogen+Phosphate treatments. In liming, *Diaporthaceae* was the most dominant family, while in phosphate treatment it was *Teratosphaeriaceae.*

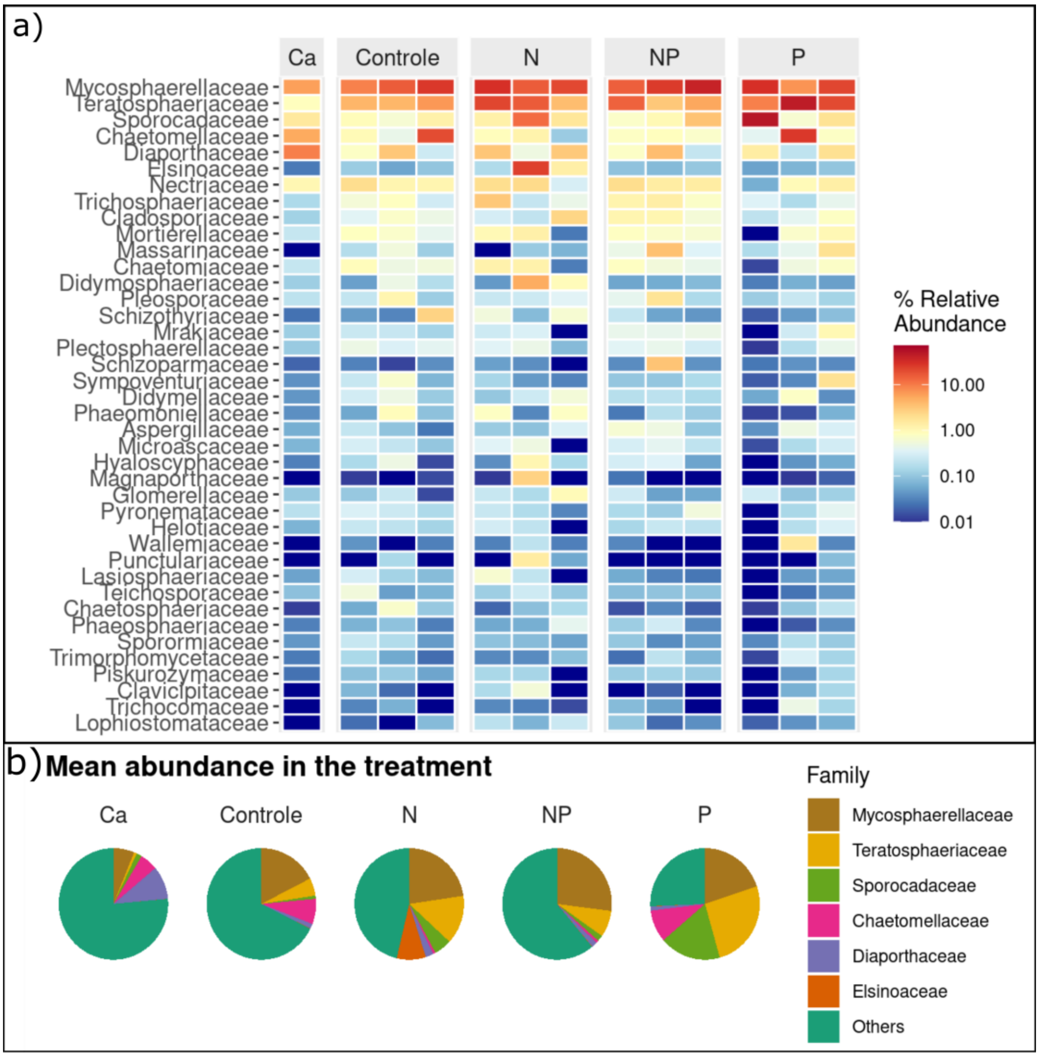


Figure 76. Data on the taxonomic composition of the endophytic fungal community at the family level for *C. brasiliense*. a) Heatmap of fungal family with significant differences ($p<0.05$) between the different treatments for adding nutrients to the soil. Relative abundance data were normalized by z-score per line. Darker red indicates greater abundance, while white indicates absence. In b) the mean of the most abundant fungal family per treatment (three individuals sampled per treatment) is presented. The family with less than 2% abundance and sequences classified only at kingdom level were grouped under “Others”.

Control: control group without addition of nutrients to the soil; N: nitrogen treatment; NP: Nitrogen+Phosphate Treatment; P: phosphate treatment; Ca: liming.

The relative abundance at the family level of the endophytic mycobiota in the host *O. hexasperma* differed between treatments of soil nutrient addition. The 40 families differentially between the different nutrient addition regimes to the soil are shown in Figure 77a. For the control group, *Didymosphaeriaceae* (36%) was dominant; in the nitrogen group and in the phosphate group it was *Sporocadaceae*; while for liming it was *Pleosporaceae* (Figura 77b).

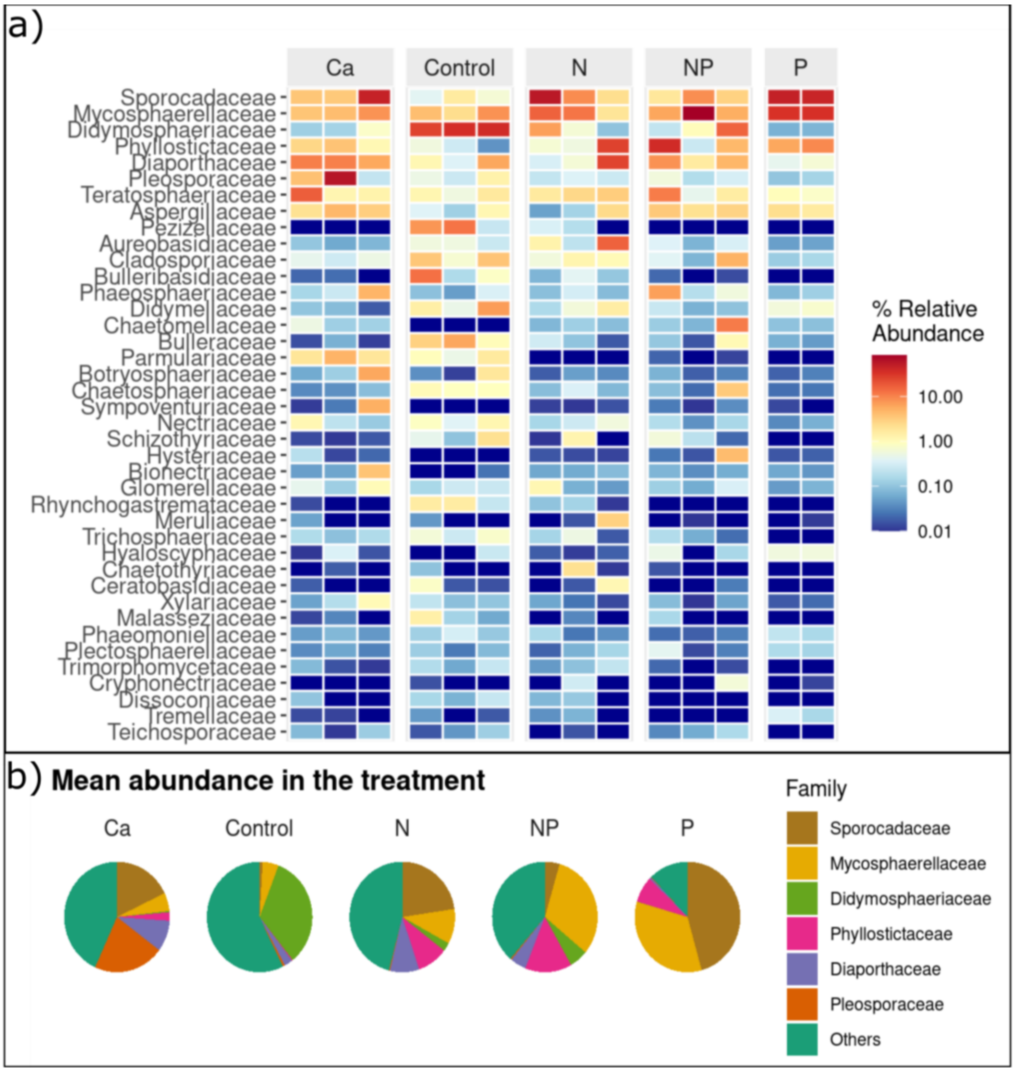


Figure 77. Data on the taxonomic composition of the endophytic fungal community at the family level for *O. hexasperma*. a) Heatmap of fungal family with significant differences (p<0.05) between the different treatments for adding nutrients to the soil. Relative abundance data were normalized by z-score per line. Darker red indicates greater abundance, while white indicates absence. In b) the mean of the most abundant fungal family per treatment (three individuals

sampled per treatment) is presented. The families with less than 2% abundance and sequences classified only at kingdom level were grouped under “Others”. Control: control group without addition of nutrients to the soil; N: nitrogen treatment; NP: Nitrogen+Phosphate Treatment; P: phosphate treatment; Ca: liming.

Paramycosphaerella was the genus with relatively high abundance among all treatments for the host *C. brasiliense* (Figure 78a), being dominant in the treatments Nitrogen, Nitrogen+Phosphate, control group and the second most abundant in the Phosphate treatment. Phosphate treatment presented a balanced mosaic concerning the abundance of genus, with *Neopestalotiopsi* being dominant (14.5%), followed by *Paramycosphaerella* (14%), *Neopharothecoidea* (14%), *Pilidium* (12%), and *Pseudoteratosphaeria* (12%) (Figure 78b). *Diaporthe* was dominant in liming (8%), followed by *Pilidium* (6%). In all treatments and the control group, the genus with an abundance less than 4% or not identified were grouped in “others” and corresponded to 36% of the taxa in the phosphate treatment, 72% in the control group, 68% in the nitrogen treatment, 82% in the Nitrogen+Phosphate treatment, 83% in the liming.

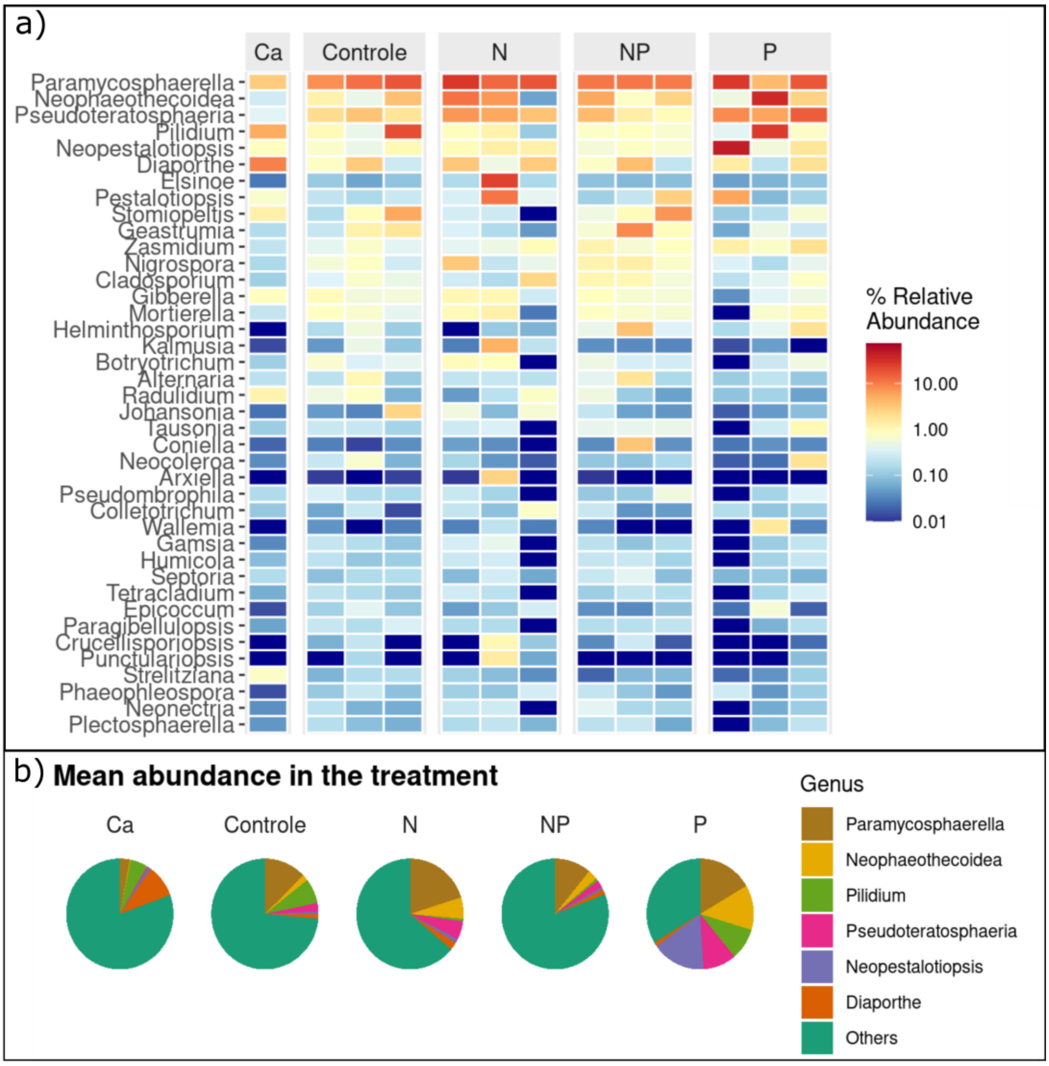


Figure 78. Data on the taxonomic composition of the endophytic fungal community at the genus level for *C. brasiliense*. a) Heatmap of fungal genus with significant differences ($p<0.05$) between the different treatments for adding nutrients to the soil. Relative abundance data were normalized by z-score per line. Darker red indicates greater abundance, while white indicates absence. In b) the mean of the most abundant fungal genus per treatment (three individuals sampled per treatment) is presented. The genus with less than 2% abundance and sequences classified only at kingdom level were grouped under "Others". Control: control group without addition of nutrients to the soil; N: nitrogen treatment; NP: Nitrogen+Phosphate Treatment; P: phosphate treatment; Ca: liming.

For the host *O. hexasperma*, the relative abundance at the genus level of the endophytic fungal community was heterogeneous between treatments (Figure 79a). *Kalmusia* (21%) was the dominant genus in the control group, followed by *Diaporthe* (2.5%). *Neopestalotiopsis* was dominant in liming and phosphate treatment, corresponding to an average abundance of 14% and 45%, respectively (Figure 79b). In the nitrogen treatment, *Pestalotiopsis* (21%) was dominant; while in Nitrogen+Phosphate, it was *Pseudocercospora* (27%). *Diaporthe* was the second most abundant genus in control, liming, and nitrogen treatment groups. *Pseudocercospora* showed considerable abundance in the phosphate treatment (32%). The genera with less than 2% of abundance were grouped with the unidentified sequences and corresponded between 15% to 74% of the abundance depending on the treatments.

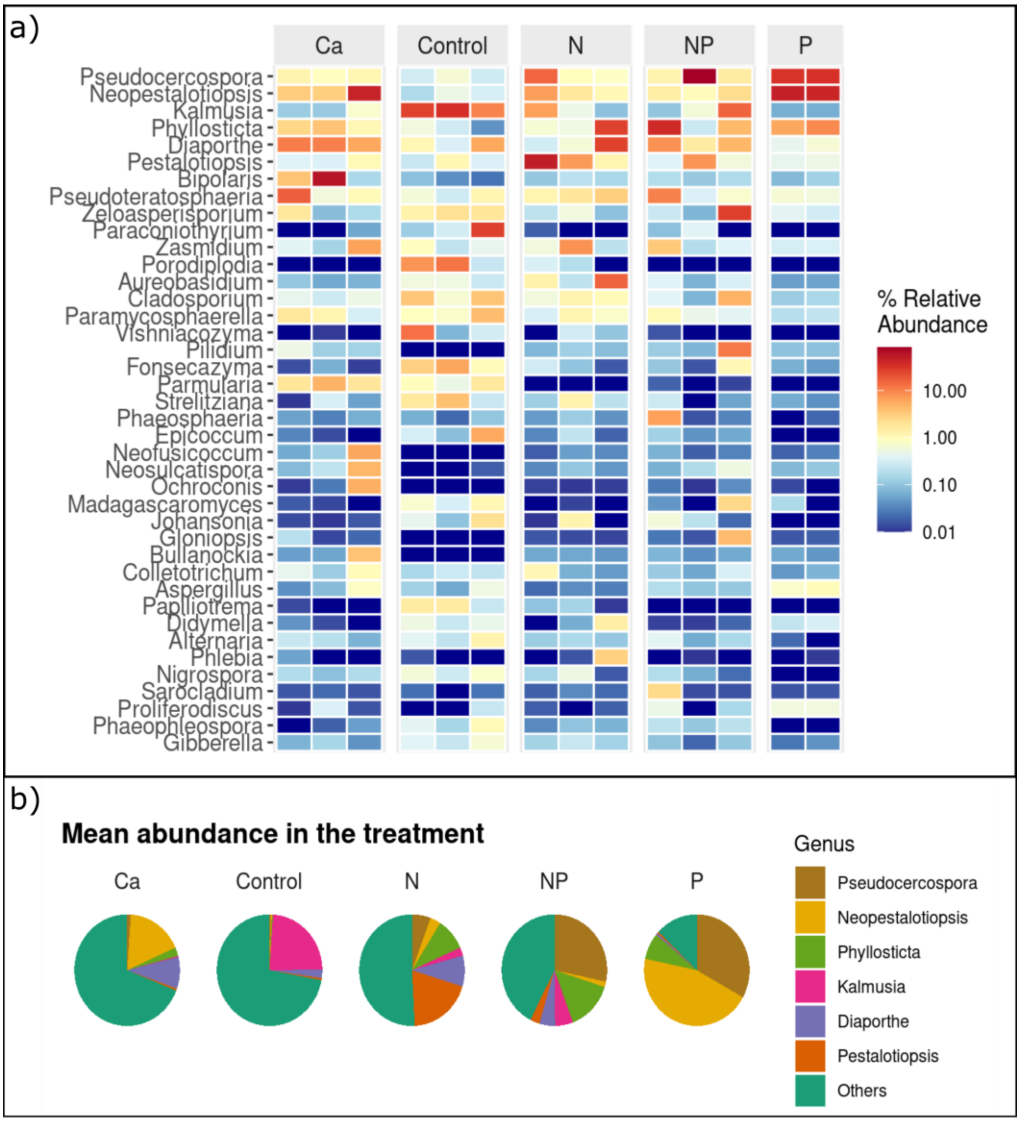


Figure 79. Data on the taxonomic composition of the endophytic fungal community at the genus level for *O. hexasperma*. a) Heatmap of fungal genus with significant differences ($p<0.05$) between the different treatments for adding nutrients to the soil. Relative abundance data were normalized by z-score per line. Darker red indicates greater abundance, while white indicates absence. In b) the mean of the most abundant fungal genus per treatment (three individuals sampled per treatment) is presented. The genus with less than 2% abundance and sequences classified only at kingdom level were grouped under “Others”. Control: control group without addition of nutrients to the soil; N: nitrogen

treatment; NP: Nitrogen+Phosphate Treatment; P: phosphate treatment; Ca: liming.

4.5. *Alpha and Beta diversity*

The pairwise comparison of the alpha diversity of endophytic fungi associated with *O. hexasperma* and *C. brasiliense* in different soil nutrient addition treatments did not show significant differences between treatments ($p > 0.05$). However, the community of endophytic fungi in the control group of *O. hexasperma* showed the highest values of alpha diversity when compared to the other groups; while the group sampled from the phosphate treatment showed the lowest alpha diversity indices (Figure 80). For the host *C. brasiliense*, the alpha diversity indices did not present discrepant variations, however, the group sampled from the nitrogen+phosphate treatment showed the highest value for phylogenetic diversity of Faith; while the phosphate treatment showed a lower value in Pielou evenness and Shannon entropy (Figure 81).

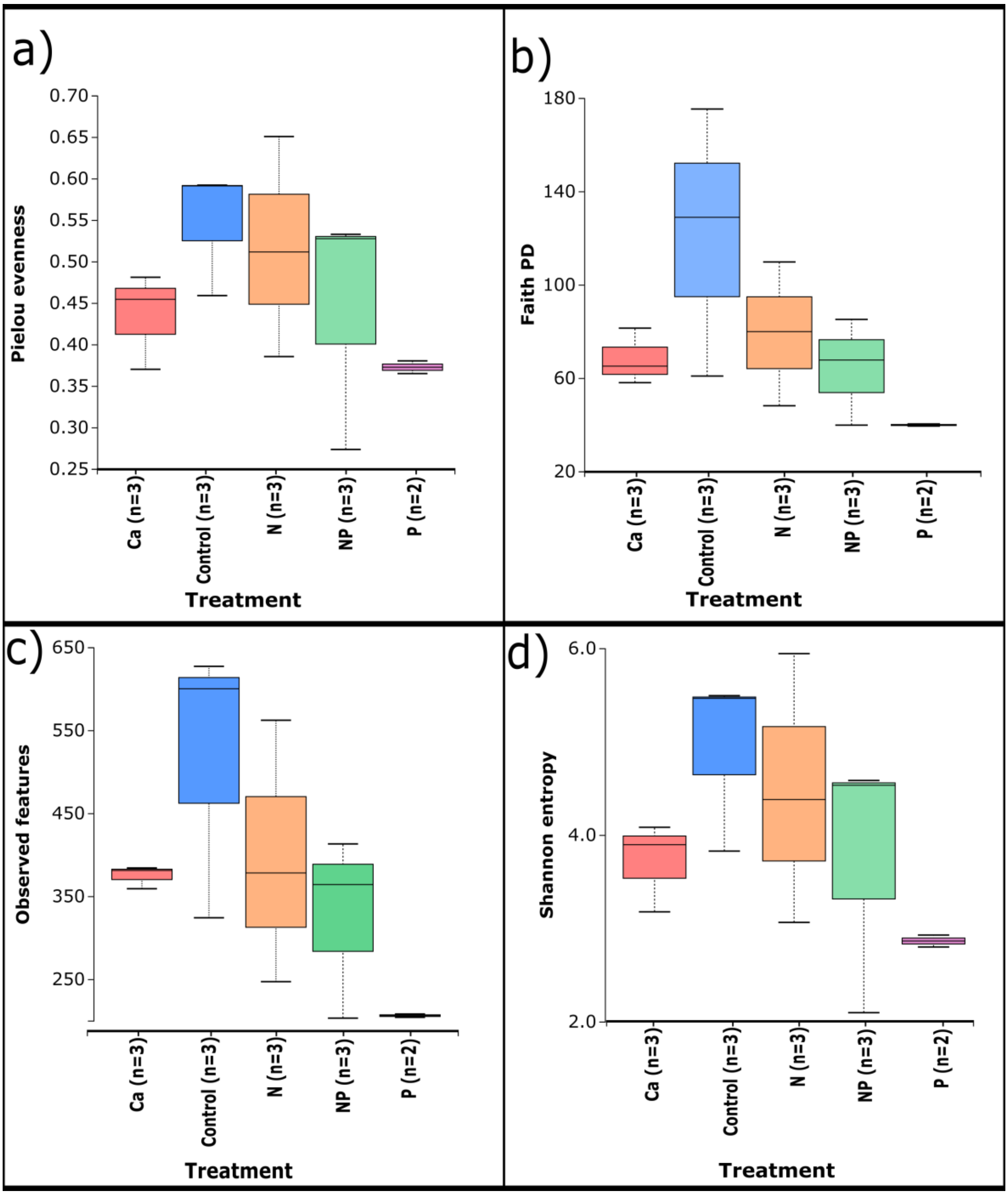


Figure 80. Alpha diversity indices of the endophytic fungal community in *O. hexasperma*. a) Pielou's evenness, b) Faith's phylogenetic diversity, c) observed features and d) Shannon entropy of the endophytic mycobiota of *O. hexasperma* under different long-term nutrient addition treatments. The control and nitrogen group are the richest in species. Ca: Liming; Control: Control; N: Nitrogen; NP: Nitrogen+Phosphate; P: Phosphate. The boxplots represent the inter-hip range (IQR) between the first and third quartiles (25th and 75th percentiles, respectively). The tails represent the lowest and highest values found; and the middle horizontal line inside the box represents the median.

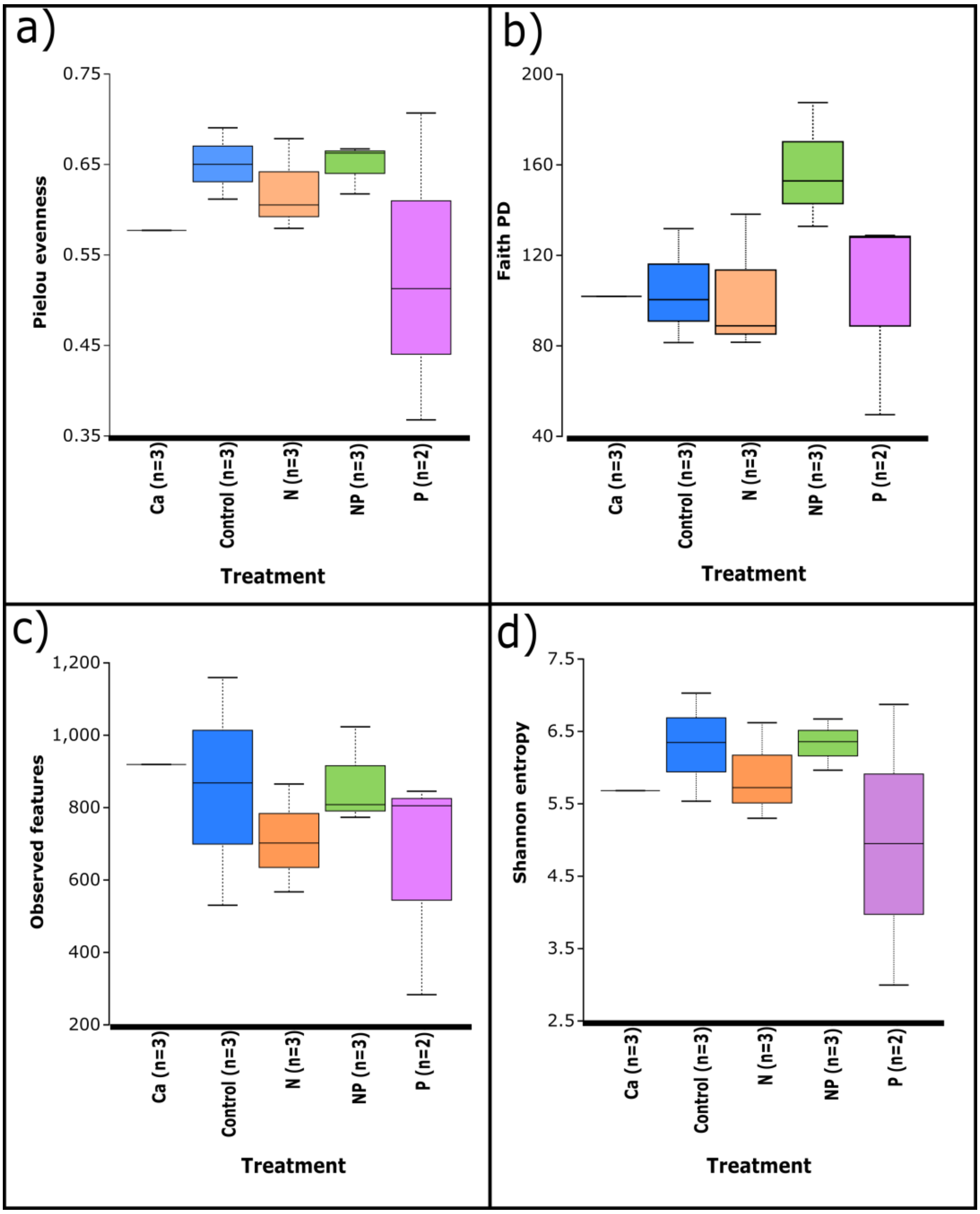


Figure 81. Alpha diversity indices of the community of endophytic fungi associated with *C. brasiliense*. a) Pielou equity, b) Faith phylogenetic diversity, c) observed features and d) Shannon entropy of the endophytic mycobiota of *C. brasiliense* under different long-term nutrient addition treatments. The control and nitrogen group are the richest in species. Ca: Liming; Control: Control; N: Nitrogen; NP: Nitrogen+Phosphate; P: Phosphate. The boxplots represent the inter-hip range (IQR) between the first and third quartiles (25th and 75th percentiles, respectively). The tails represent the lowest and highest values found; and the middle horizontal line inside the box represents the median.

For beta diversity, principal coordinate analysis (PCoA) of Bray Curtis dissimilarity weighted distances, Jaccard distance, Weighted unifrac, and Unweighted unifrac between the four treatments and the control group ($p < 0.04$ by PERMANOVA) suggest that there is a dissimilarity between the foliar endophytic fungal community per treatment for both hosts (Figure 82 and 83). The PERMANOVA statistical test, to assess whether the distance presented in the PCoA between treatments is significantly important, suggests that there are dissimilarities between treatments for all beta diversity indices ($p < 0.05$) when all treatments are compared together. However, when the leaf endophytic mycobiota between treatments was compared by pair, to identify in which groups were the dissimilarities indicated by the beta diversity metrics, no significant differences were found ($p > 0.05$).

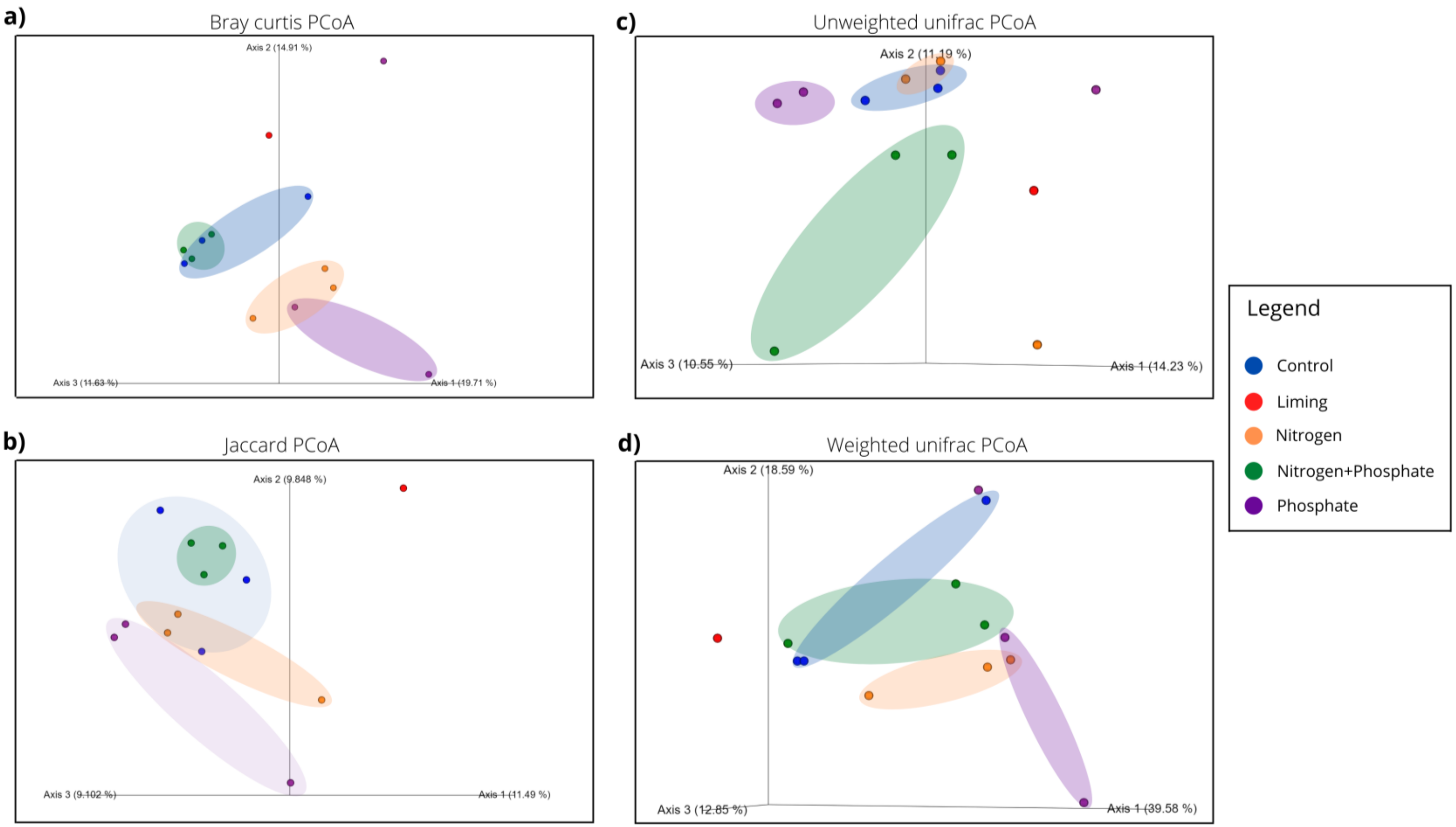


Figure 82. Beta diversity of the foliar endophytic fungal community in *C. brasiliense* under different soil nutrient addition treatments. Principal coordinate analysis (PCoA) of weighted distances a) Bray curtis dissimilarity, b) Jaccard distance, d) Weighted unifrac and unweighted c) Unweighted unifrac between the four treatments and the control group (p= 0.0001 by PERMANOVA). The colored dots indicate the endophytic fungal communities in the hosts sampled by treatment. The ellipses indicate the grouping of the endophytic microbial community by nutrient addition treatment. For each axis, in parentheses, the percentage of variations was reported.

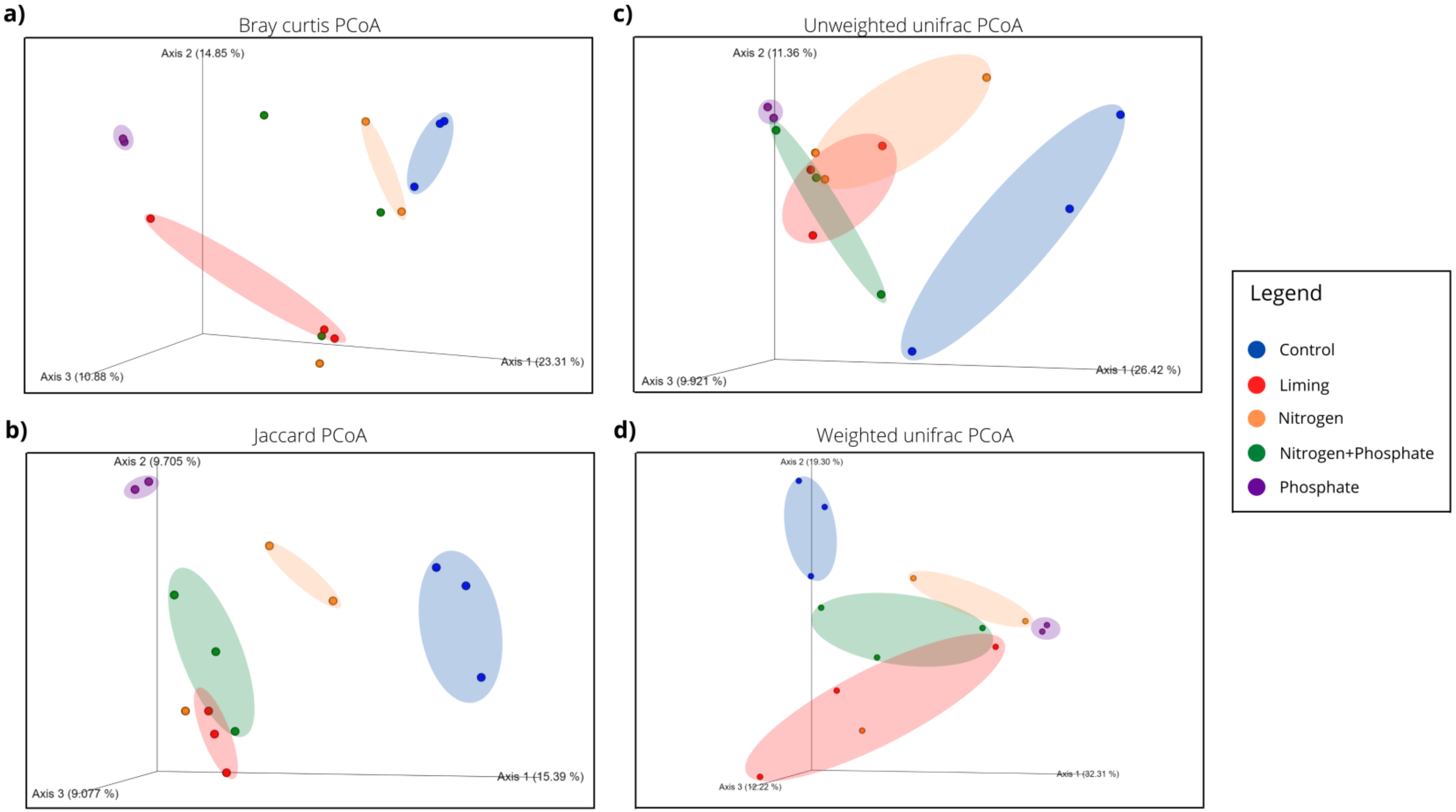


Figure 83. Beta diversity of the endophytic foliar fungal community in *O. hexasperma* under different treatments of soil nutrient addition. Principal coordinate analysis (PCoA) of weighted distances a) Bray curtis dissimilarity, b) Jaccard distance, d) Weighted unifrac and unweighted c) Unweighted unifrac between the four treatments and the control group (p= 0.004 by PERMANOVA). The colored dots indicate the endophytic fungal communities in the hosts sampled by treatment. Ellipses indicate the grouping of the endophytic microbial community by treatment. For each axis, in parentheses, the percentage of variations was reported.

4.6. *Differential abundance*

Differential abundance analyzes were performed to identify possible fungal taxa associated with differences between the fungal community in the different treatments after the evaluation of alpha and beta diversity metrics. The Ancom test showed that there is no statistically significant difference in the community of leaf endophytic fungi in *C. brasiliense* between the different treatments, reinforcing the results found in the alpha and beta diversity metrics. As for the community of endophytic fungi in *O. hexasperma*, the Ancom test showed which taxonomic groups showed significant variations in abundance between treatments (Figure 84). The class *Pezizomycetes*, the Order *Asterinales*, the family *Parmulariaceae*, and the genus *Parmularia* showed higher abundance values in the liming treatment and control group when compared to the others.

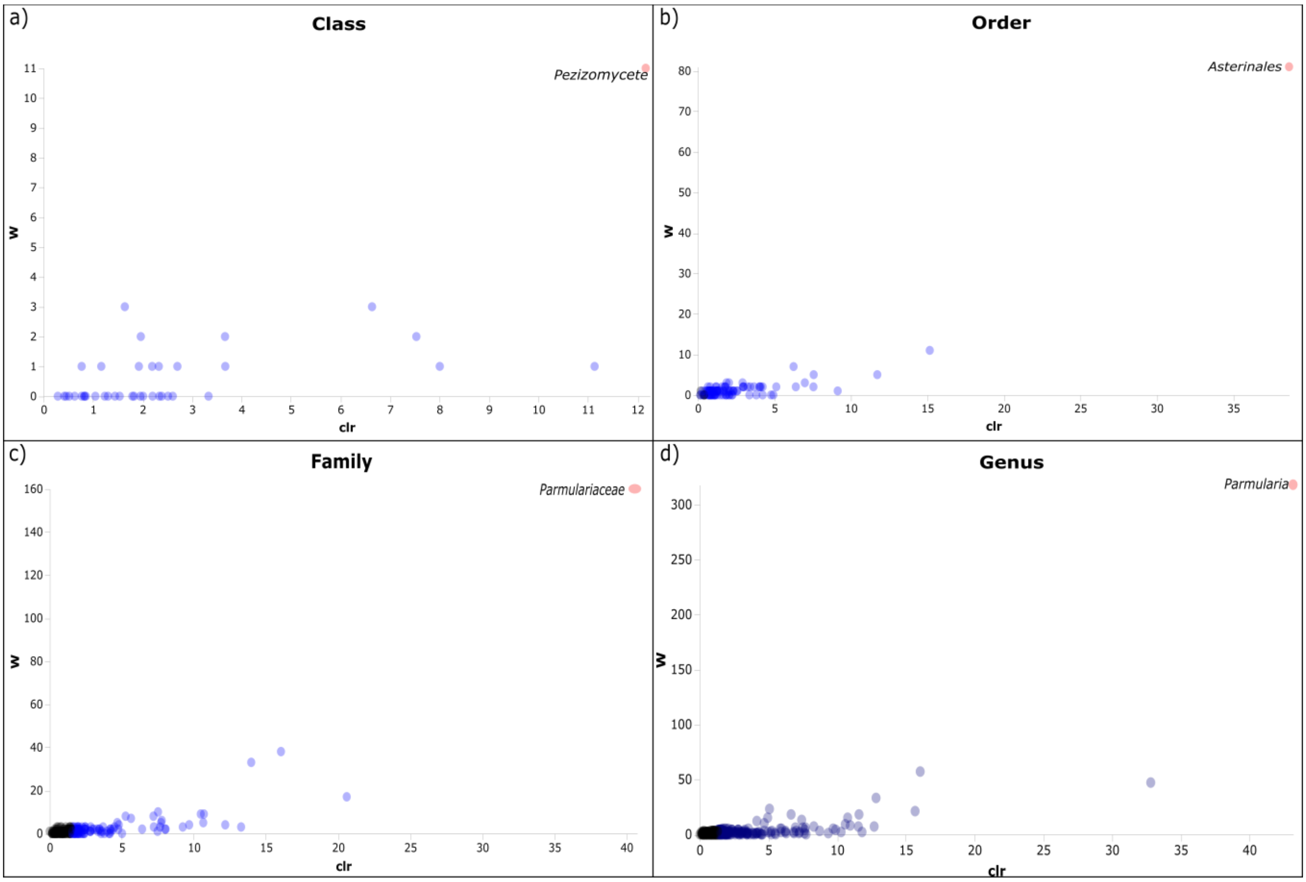


Figure 84. Vulcanoplot of differential abundance of leaf endophytic fungal community in *O. hexasperma* under different soil fertilization treatments. ANCOM generated volcanic plots showing differentially abundant characteristics among the nutrient addition treatments. The W is the ANCOM test statistic and demonstrates the number of times the null hypothesis is rejected by the analysis.

The higher the value of W, the greater the probability that a characteristic differs statistically. The clr shows the change in size between the groups compared by the test. The statistically significant characteristics found between treatments were labeled at the level of a) class, b) order, c) family and d) genus.

The *Metastasts* test showed the main groups that are not shown by the ANCOM test, but that contribute significantly to the dissimilarities between the communities of endophytic fungi associated with *C. brasiliense* and *O. hexasperma* in the different treatments of addition of nutrients to the soil. For *C. brasiliense, Chloridium* was the only genus significantly abundant among the treatments, with higher abundance in the phosphate treatment and lower abundance in the control group (Figure 85a). This finding may be indicative that the relative abundance of this genus in the community of endophytic fungi in *C. brasiliense* may be influenced by the addition of nutrients to the soil. For the host *O. hexasperma*, five genus showed significantly different abundances between the nutrient addition treatments, namely *Neosetophoma, Proliferodiscus, Pseudocercospora, Pilidium*, and *Neopestalotiopsis* (Figure 85b). The results of the metastast test show that *Pseudocercospora* is more abundant in the phosphate and nitrogen phosphate treatments, while *Neopestalotiopsis* is more abundant in the phosphate, liming, and nitrogen treatments. The genus *Pilidium* is more abundant in the nitrogen treatment when compared to the other treatments and the control group. These findings may indicate that the abundance of these genera in the endophytic mycobiota of the host *O. hexasperma* is significantly influenced by the addition of nutrients to the soil.

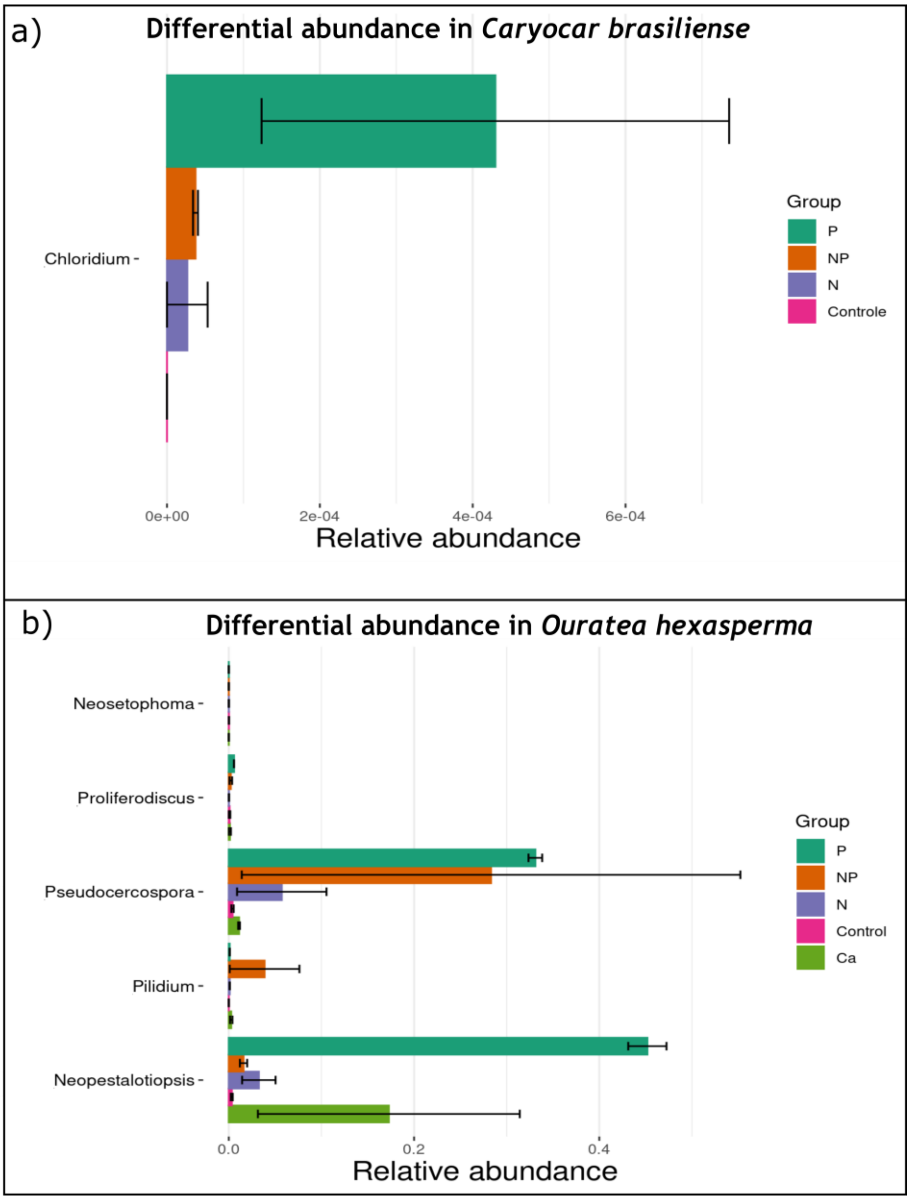


Figure 85. Differently abundant taxa (genus level) between the endophytic mycobiota of two Cerrado plant species under different soil nutrient addition treatments. On the Y axis, the main differentially abundant genera are shown; the X axis shows the relative abundance of each, respectively. Ca: Liming; Control: Control; N: Nitrogen; NP: Nitrogen+Phosphate; P: Phosphate.

5. DISCUSSION

The addition of mineral nutrients to the soil can positively or negatively impact the diversity of plant symbiotic fungi (Li et al., 2017). In our study, we evaluated how this endophyte variable influences the taxonomic structure of the leaf endophytic mycobiome of two native species of the Brazilian Cerrado. Using cultive-dependent and independent approaches, we observed the leaf mycobiome of *Caryocar brasiliense* and *Ouratea hexasperma* in different plots, where treatments were performed annually for 28 years with liming, nitrogen, nitrogen + phosphate, and phosphate. Our data provide extensive information on the effects of soil mineral fertilization on the leaf endophytic mycobiome, demonstrating that, similar to microorganisms associated with the rhizosphere region (Khan et al., 2017; Pietro-Souza et al., 2017; Parmar et al., 2018; El-Shafey et al., 2021), these anthropic variables impact their diversity, occurrence and abundance.

5.1. *Taxonomic attributions cultivation-dependent and metabarcoding*

Our results using culture-dependent and cultivation-independent methods showed that Ascomycota is the dominant phylum in the community of endophytic fungi associated with *C. brasiliese* and *O. hexasperma* in different treatments of addition of nutrients to the soil, which is in agreement with the results found in other studies (Yao et al., 2019; An et al., 2020; Du et al., 2020; Dang et al., 2021). Ascomycota is a phylum belonging to the kingdom of fungi with the largest number of species described so far, which have different lifestyles, being saprophytes, parasites, or symbionts (Muggia et al., 2020). The evolutionary success of ascomycetes, linked to the high number of species and ability to colonize a wide range of ecological niches, may be correlated with their high rate of chromosomal rearrangement and metabolic plasticity (Knapp et al., 2018; Rajeh et al., 2018; van Wyk et al., 2021), which allows these fungi to evolve quickly and adapt to the most varied environmental conditions (Shen et al., 2020).

The *metabarcoding* reported the occurrence of other phyla besides Ascomycota, namely *Basidiomycota, Glomeromycota, Monoblepharomycota, Mortierellomycota, Olpidiomycota, Chytridiomycota, Rozellomycota*, and *Zoopagomycota;* while the culture-dependent methods showed the occurrence of *Ascomycota* only. A study using culture-dependent and *metabarcoding* approaches to characterize the endophytic mycobiome of a grass species found similar results for culture-dependent methods (Durán et al., 2021).

The cultivation-dependent methods showed the occurrence of seven orders for *C. brasiliense* and eight orders for *O. hexasperma*, namely *Amphisphaeriales, Botryosphaeriales, Diaporthales, Glomerellales, Hypocreales, Pleoporales, Mycosphaerellales,* and *Xylariales*. The occurrence of these fungal orders is frequently reported in studies evaluating the endophytic mycobiome, already being associated with the mycobiome of plant species that occur in tropical (Yao et al., 2019) and temperate (Pawłowska et al., 2018; Durán et al., 2021). *Metabarcoding* showed the occurrence of more than 20 orders, with *Capnodiales* being dominant for the two hosts. Comparative phylogenetic analyzes suggest that this order evolved from an epiphytic ancestor and that throughout evolutionary processes it began to present an endophytic or phytopathogenic lifestyle, depending on environmental variables and host species (Abdollahzadeh et al., 2020). Furthermore, *Capnodiales* harbors *Mycospharellaceae,* here reported as the most abundant in *C. brasiliense* by metabarcoding. This family, together with *Sporocadaceae*, the most abundant in *O. hexasperma*, is extremely diverse in fungal species known to establish ecological relationships with woody plant species (Videira et al., 2017; Yao et al., 2019; Liu et al., 2019; Du et al., 2020).

Dependent cultivation methods showed that *Diaporthe* was dominant in the community of the two host species. Fungal species that co-occur between different ecological niches or between gradients of resource availability are generally generalist microorganisms, with high metabolic plasticity and capable of adapting to the most diverse conditions (Chen et al., 2021; Giovannoni et al., 2021). *Diaporthe* comprises species related to woody plant species in terrestrial ecosystems around the world (Dissanayake et al., 2020; Sun et al., 2021), either as a pathogen or as an endophytic (Gomes et al., 2013). Some species of this genus have sophisticated molecular mechanisms capable of dealing with the different defense mechanisms of the plant to establish colonization in its tissues (Mena et al., 2022), which would explain their co-occurrence between different treatments and hosts. For the *metabarcodig*, *Pseudocercospora* was more abundant in *O. hexasperma* and *Paramycosphaerella* was more abundant in *C. brasiliense.* Both these two genera belong to *Mycospharellaceae* (Videira et al., 2017) and are often reported as members of the endophytic fungal community (Yao et al., 2019; An et al., 2020; Du et al, 2020; Dang et al., 2021).

5.2. Dissimilarities shown by culture-dependent and metabarcoding methods

At the phylum level, *Ascomycota* was dominant in the endophytic fungal community in both hosts and in all treatments. However, the phylum

Basidiomycota decreased in abundance in all treatments for the host *O. hexasperma*. This finding goes against our hypotheses, as we did not expect to find variations in taxonomic structure at the phylum level (Pietro-Souza et al., 2017; Parmar et al., 2018).

Changes in the endophytic fungal community were observed at the order, family, genus, and species levels for both hosts in all treatments. The action of anthropic effects on microorganism communities can result in greater or lesser species diversity (Zheng et al., 2019; Semenov et al., 2022). For the host *O. hexasperma*, the diversity of endophytic fungi species was reduced in all treatments with added nutrients in relation to the control group; while for *C. brasiliense* this varied according to the treatment.

The lowest diversity values at taxonomic levels of order, family, genus, and species were observed in the nitrogen treatment for the mycobiota of both hosts. Diversity loss related to the addition of nitrogen to the soil has been reported in communities of mycorrhizal fungi associated with numerous plant species (Van Diepen et al., 2011; Liu et al., 2014; Liu et al., 2020). In communities of fungi associated with the rhizosphere, the addition of low concentrations of nitrogen to the soil increased diversity and equity (Wang et al., 2022). However, at higher doses, the reverse effect was observed. These authors also demonstrated, through metabolomic techniques, that the addition of nitrogen in high concentrations to the soil caused changes in the exudate profile produced by the plant, resulting in low production of long-chain organic acids (Wang et al., 2022), key compounds for communication between plants and microorganisms (Eichmann et al., 2021). Taking this information as a guideline, one of the possible explanations for the loss of diversity of cultivable fungal species in the treatment with nitrogen may be related to the alterations caused by this macronutrient in the phytochemical profile of the host plant, so that these key molecules for the plant interaction -the endophytic fungus is produced at low concentrations, resulting in loss of diversity

Positive and negative changes in the diversity of cultivable endophytic fungi species were observed between the two hosts at liming, with a positive effect on the community associated with *C. brasiliense,* and a negative effect on the community associated with *O. hexasperma*. Cerrado soils are acidic and rich in aluminum, and liming modify these characteristics (Tsuioshi, 2005), making the soil more basic and with lower aluminum concentrations (Rahman et al., 2018). In-plant species, the effects of changes in soil pH caused by liming treatment can cause a reduction in shoot biomass, lower xylem nutrient availability, and a decrease in phytohormone production (Villela D & Haridasaz, 1994; Rothwell et al., 2015). Therefore, liming may have altered the phytochemistry of *O. hexasperma*, resulting in a lower synthesis of key molecules for plant-endophytic fungus communication and establishment of colonization, resulting in lower diversity.

Contrary to the effect observed in the endophytic fungal community of *O. hexasperma* in the liming treatment, the host *C. brasiliense* presented a greater number of fungal species. It is known that under conditions of anthropic environmental variations, including stress caused by the entry of cations into the soil, some plant species change their phytochemistry and start to establish symbiotic relationships with the fungus to minimize the stress caused by these variations (Khan et al., 2017; Pietro-Souza et al., 2017; Parmar et al., 2018; El-Shafey et al., 2021). Thus, we can suggest that under the liming treatment, the host *C. brasiliense* may be altering its phytochemistry to stimulate the colonization of its tissues by endophytic fungi to minimize the impacts caused by this anthropic variation.

Changes at the local level (the portion with or without the addition of nutrients) caused by the addition of nutrients to the soil must also be considered to explain these variations in the number of fungal species observed per treatment. For this, we must consider two fundamental factors, which are the environmental changes on a macroscale and the form of transmission of endophytic fungi. Environmental variations on a macroenvironmental scale can cause local changes that impact the number of resources present in the macroenvironment (Zheng et al., 2019), which reflects on the diversity of fungi and the dispersion of these microorganisms (Nara, 2009; Parmar et al., 2018; Van et al., 2018). Some foliar endophytic fungi come from the environment through horizontal transmission (Govinda et al., 2011). Thus, we can hypothesize that the addition of nutrients to the soil causes changes in the macroenvironment level (with or without the addition of nutrients), reflecting the diversity of the soil mycobiome (Zheng et al., 2019; Semenov et al. 2022), which, in turn, impacts the dispersion of these microorganisms (Parmar et al., 2018; Van et al., 2018).

Therefore, if the impacts caused by the addition of nutrients to the soil are negative on the community of fungi present in the soil in terms of occurrence and abundance, the lower the fungus propagule will be, which results in a lower foliar inoculum, resulting in lower colonization rates, the which results in less diversity. The reverse situation can also occur. However, it should also be considered that intrinsic variations in isolation methods may be related to a lower observed diversity, such as isolation conditions, antagonistic relationships in the culture medium, and type of substrate used, among others (Hanišáková et al., 2022).

The beta diversity metrics show the dissimilarities in the endophytic fungal community for the two host species in the different treatments. The correlation methods obtained from the data from the cultivation-dependent methods, relating leaf nutrients with the occurrence, with the metabarcoding, metastatic test, show that certain taxa are influenced by the concentration of certain leaf nutrients, which in turn are dictated by the availability of these nutrients in the soil. Thus, we show that the foliar endophytic fungi community is influenced by anthropization caused by the addition of chemical fertilizers to the soil.

CONCLUSIONS

This study provides one of the first reports on the evaluation of the effects of mineral fertilization on the foliar endophytic fungal community of two plant species from the Brazilian Neotropical savanna, using culture-dependent methods and high-throughput DNA sequencing.

The species diversity of the endophytic mycobiome was positively or negatively influenced depending on the type of mineral fertilizer and host identity. Our data, therefore, suggest that the taxonomic structure of the endophytic mycobiome responds in different ways to the anthropization of the ecosystem.

BIBLIOGRAPHIC REFERENCES

1. Abdollahzadeh J, Groenewald JZ, Coetzee MPA, Wingfield MJ, Crous PW. Evolution of lifestyles in Capnodiales. Stud Mycol. 2020; 5; 95:381-414. doi: 10.1016/j.simyco.2020.02.004.
2. An C, Ma S, Shi X, Xue W, Liu C, Ding H. Diversity and Antimicrobial Activity of Endophytic Fungi Isolated from *Chloranthus japonicus* Sieb in Qinling Mountains, China. *Int J Mol Sci*. 2020; 19;21(17):5958. doi: 10.3390/ijms21175958. Du W, Yao Z, Li J, Sun C, Xia J, Wang B, Shi D, Ren L. Diversity and antimicrobial activity of endophytic fungi isolated from Securinega suffruticosa in the Yellow River Delta. PLoS One. 2020 Mar 10;15(3):e0229589. doi: 10.1371/journal.pone.0229589. PMID: 32155163; PMCID: PMC7064225.
3. Chen P, Zhou H, Huang Y, Xie Z, Zhang M, Wei Y, Li J, Ma Y, Luo M, Ding W, Cao J, Jiang T, Nan P, Fang J, Li X. Revealing the full biosphere structure and versatile metabolic functions in the deepest ocean sediment of the Challenger Deep. *Genome Biol*. 2021; 13;22(1):207. doi: 10.1186/s13059-021-02408-w.
4. Chiu CH, Paszkowski U. Mechanisms and Impact of Symbiotic Phosphate Acquisition. *Cold Spring Harb Perspect Biol*. 2019; 3;11(6):a034603. doi: 10.1101/cshperspect.a034603. Erratum in: Cold Spring Harb Perspect Biol. 2019 Jun 3;11(6).
5. Dang H, Zhang T, Wang Z, Li G, Zhao W, Lv X, Zhuang L. Differences in the endophytic fungal community and effective ingredients in root of three *Glycyrrhiza* species in Xinjiang, China. *PeerJ.* 2021; 9;9:e11047. doi: 10.7717/peerj.11047.
6. Dissanayake AJ, Chen YY, Liu JJ. Unravelling *Diaporthe* Species Associated with Woody Hosts from Karst Formations (Guizhou) in China. *J Fungi* (Basel). 2020 Oct 27;6(4):251. doi: 10.3390/jof6040251.
7. Du W, Yao Z, Li J, Sun C, Xia J, Wang B, Shi D, Ren L. Diversity and antimicrobial activity of endophytic fungi isolated from Securinega suffruticosa in the Yellow River Delta. Plos One. 2020; 10;15(3):e0229589. doi: 10.1371/journal.pone.0229589.
8. Du W, Yao Z, Li J, Sun C, Xia J, Wang B, Shi D, Ren L. Diversity and antimicrobial activity of endophytic fungi isolated from Securinega suffruticosa in the Yellow River Delta. Plos One. 2020; 10; 15(3):e0229589. doi: 10.1371/journal.pone.0229589.
9. Durán M, San Emeterio L, Canals RM. Comparison of Culturing and Metabarcoding Methods to Describe the Fungal Endophytic Assemblage of Brachypodium rupestre Growing in a Range of Anthropized Disturbance Regimes. Biology (Basel). 2021; 29;10(12):1246. doi: 10.3390/biology10121246.
10. Eichmann R, Richards L, Schäfer P. Hormones as go-betweens in plant microbiome assembly. Plant J. 2021 Jan;105(2):518-541. doi: 10.1111/tpj.15135.
11. El-Shafey NM, Marzouk MA, Yasser MM, Shaban SA, Beemster GTS, AbdElgawad H. Harnessing Endophytic Fungi for Enhancing Growth, Tolerance and Quality of Rose-Scented Geranium (*Pelargonium*

graveolens (L'Hér) Thunb.) Plants under Cadmium Stress: A Biochemical Study. *J Fungi* (Basel). 2021 Dec 3;7(12):1039. doi: 10.3390/jof7121039.

12. Fang K, Miao YF, Chen L, Zhou J, Yang ZP, Dong XF, Zhang HB. Tissue-Specific and Geographical Variation in Endophytic Fungi of *Ageratina adenophora* and Fungal Associations With the Environment. *Front Microbiol*. 2019; 18; 10:2919. doi: 10.3389/fmicb.2019.02919.
13. Giovannoni M, Larini I, Scafati V, Scortica A, Compri M, Pontiggia D, Zapparoli G, Vitulo N, Benedetti M, Mattei B. A novel Penicillium sumatraense isolate reveals an arsenal of degrading enzymes exploitable in algal bio-refinery processes. *Biotechnol Biofuels*. 2021; 13;14(1):180. doi: 10.1186/s13068-021-02030-9.
14. Golias HC, Polonio JC, Dos Santos Ribeiro MA, Polli AD, da Silva AA, Bulla AM, Volpato H, Nakamura CV, Meurer EC, Azevedo JL, Pamphile JA. Tibouchina granulosa (Vell.) Cogn (Melastomataceae) as source of endophytic fungi: isolation, identification, and antiprotozoal activity of metabolites from *Phyllosticta capitalensis*. *Braz J Microbiol*. 2020; 51(2):557-569. doi: 10.1007/s42770-019-00221-z.
15. Gomes RR, Glienke C, Videira SI, Lombard L, Groenewald JZ, Crous PW. Diaporthe: a genus of endophytic, saprobic and plant pathogenic fungi. *Persoonia*. 2013; 31:1-41. doi: 10.3767/003158513X666844.
16. Govinda Rajulu MB, Thirunavukkarasu N, Suryanarayanan TS, Ravishankar JP, El Gueddari NE, and Moerschbacher BM. Chitinolytic enzymes from endophytic fungi. *Fungal Diversity*. 2011; *47*(1), 43-53.
17. Hanišáková N, Vítězová M, Rittmann SKR. The Historical Development of Cultivation Techniques for Methanogens and Other Strict Anaerobes and Their Application in Modern Microbiology. *Microorganisms*. 2022; 10; 10(2):412. doi: 10.3390/microorganisms10020412.
18. Hong G, Miller HB, Allgood S, Lee R, Lechtzin N, Zhang SX. Use of Selective Fungal Culture Media Increases Rates of Detection of Fungi in the Respiratory Tract of Cystic Fibrosis Patients. *J Clin Microbiol*. 2017; 55(4): 1122-1130. doi: 10.1128/JCM.02182-16.
19. Hubbell SP. *The Unified Neutral Theory of Biodiversity and Biogeography.* Princeton: Princeton University Press. 2001.
20. Khan AR, Ullah I, Waqas M, Park GS, Khan AL, Hong SJ, Ullah R, Jung BK, Park CE, Ur-Rehman S, Lee IJ, Shin JH. Host plant growth promotion and cadmium detoxification in Solanum nigrum, mediated by endophytic fungi. *Ecotoxicol Environ Saf*. 2017; 136:180-188. doi: 10.1016/j.ecoenv.2016.03.014.
21. Knapp DG, Németh JB, Barry K, Hainaut M, Henrissat B, Johnson J, Kuo A, Lim JHP, Lipzen A, Nolan M, Ohm RA, Tamás L, Grigoriev IV, Spatafora JW, Nagy LG, Kovács GM. Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. Sci Rep. 2018; 20; 8(1):6321. doi: 10.1038/s41598-018-24686-4.
22. Li HL, Ma B, Zhang XL, Zhang QQ, Guo XH, Fan P, Gong J. 滨海湿地植物芦苇可培养内生真菌的多样性. *Ying Yong Sheng Tai Xue Bao*. 2016; 27(7):2066-2074. Chinese. doi: 10.13287/j.1001-9332.201607.014.
23. Li L, Fan F, Song A, Yin C, Cui P, Li Z, Liang Y. Microbial composition and diversity are associated with plant performance: a case study on long-term

fertilization effect on wheat growth in an Ultisol. *Appl Microbiol Biotechnol*. 2017; 101(11):4669-4681. doi: 10.1007/s00253-017-8147-2.

24. Liu F, Bonthond G, Groenewald JZ, Cai L, Crous PW. Sporocadaceae, a family of coelomycetous fungi with appendage-bearing conidia. Stud Mycol. 2019; 92:287-415. doi: 10.1016/j.simyco.2018.11.001.
25. Liu J, Zhang J, Li D, Xu C, Xiang X. Differential responses of arbuscular mycorrhizal fungal communities to mineral and organic fertilization. *Microbiologyopen*. 2020; 9(1):e00920. doi: 10.1002/mbo3.920.
26. Liu J, Zhang J, Li D, Xu C, Xiang X. Differential responses of arbuscular mycorrhizal fungal communities to mineral and organic fertilization. *Microbiologyopen*. 2020; 9(1):e00920. doi: 10.1002/mbo3.920.
27. Liu W, Jiang S, Zhang Y, Yue S, Christie P, Murray PJ, Li X, Zhang J. Spatiotemporal changes in arbuscular mycorrhizal fungal communities under different nitrogen inputs over a 5-year period in intensive agricultural ecosystems on the North China Plain. *FEMS Microbiol Ecol*. 2014; 90(2):436-53. doi: 10.1111/1574-6941.12405.
28. Luo Y, Wang Z, He Y, Li G, Lv X, Zhuang L. High-throughput sequencing analysis of the rhizosphere arbuscular mycorrhizal fungi (AMF) community composition associated with Ferula sinkiangensis. *BMC Microbiol*. 2020; 3; 20(1):335. doi: 10.1186/s12866-020-02024-x.
29. Mei L, Zhu M, Zhang DZ, Wang YZ, Guo J, Zhang HB. Geographical and temporal changes of foliar fungal endophytes associated with the invasive plant Ageratina adenophora. *Microb Ecol*. 2014; 67(2): 402-9. doi: 10.1007/s00248-013-0319-8.
30. Mena E, Garaycochea S, Stewart S, Montesano M, Ponce De León I. Comparative genomics of plant pathogenic *Diaporthe* species and transcriptomics of Diaporthe caulivora during host infection reveal insights into pathogenic strategies of the genus. BMC Genomics. 2022; 3;23(1):175. doi: 10.1186/s12864-022-08413-y.
31. Muggia L, Ametrano CG, Sterflinger K, Tesei D. An Overview of Genomics, Phylogenomics and Proteomics Approaches in Ascomycota. Life (Basel). 2020; 17;10(12):356. doi: 10.3390/life10120356.
32. Nara K. Spores of ectomycorrhizal fungi: ecological strategies for germination and dormancy. *New Phytol*. 2009 Jan;181(2):245-248. doi: 10.1111/j.1469-8137.2008.02691.x.
33. Parmar S, Li Q, Wu Y, Li X, Yan J, Sharma VK, Wei Y, Li H. Endophytic fungal community of Dysphania ambrosioides from two heavy metal-contaminated sites: evaluated by culture-dependent and culture-independent approaches. *Microb Biotechnol*. 2018; 11(6):1170-1183. doi: 10.1111/1751-7915.13308.
34. Pawłowska J, Wilk M, Sliwińska-Wyrzychowska A, Mętrak M, Wrzosek M. The diversity of endophytic fungi in the above-ground tissue of two Lycopodium species in Poland. Symbiosis. 2014; 63(2):87-97. doi: 10.1007/s13199-014-0291-1.
35. Peay KG, Schubert MG, Nguyen NH, Bruns TD. Measuring ectomycorrhizal fungal dispersal: macroecological patterns driven by microscopic propagules. *Mol Ecol*. 2012 Aug;21(16):4122-36. doi: 10.1111/j.1365-294X.2012.05666.x.
36. Pietro-Souza W, Mello IS, Vendruscullo SJ, Silva GFD, Cunha CND, White JF, Soares MA. Endophytic fungal communities of Polygonum

acuminatum and Aeschynomene fluminensis are influenced by soil mercury contamination. *Plos One*. 2017; 25; 12(7):e0182017. doi: 10.1371/journal.pone.0182017.

37. Rahman MA, Lee SH, Ji HC, Kabir AH, Jones CS, Lee KW. Importance of Mineral Nutrition for Mitigating Aluminum Toxicity in Plants on Acidic Soils: Current Status and Opportunities. *Int J Mol Sci*. 2018; 8;19(10):3073. doi: 10.3390/ijms19103073.
38. Rajeh A, Lv J, Lin Z. Heterogeneous rates of genome rearrangement contributed to the disparity of species richness in Ascomycota. BMC Genomics. 2018; 24; 19(1):282. doi: 10.1186/s12864-018-4683-0.
39. Rajeh A, Lv J, Lin Z. Heterogeneous rates of genome rearrangement contributed to the disparity of species richness in Ascomycota. BMC Genomics. 2018; 24;19(1):282. doi: 10.1186/s12864-018-4683-0.
40. Rodrigues CM, Takita MA, Silva NV, Ribeiro-Alves M, Machado MA. Comparative genome analysis of *Phyllosticta citricarpa* and *Phyllosticta capitalensis*, two fungi species that share the same host. BMC *Genomics*. 2019; 5; 20(1):554. doi: 10.1186/s12864-019-5911-y.
41. Rothwell SA, Elphinstone ED, Dodd IC. Liming can decrease legume crop yield and leaf gas exchange by enhancing root to shoot ABA signalling*. J Exp Bot*. 2015; 66(8):2335-45. doi: 10.1093/jxb/erv042.
42. Semenov MV, Krasnov GS, Semenov VM, van Bruggen A. Mineral and Organic Fertilizers Distinctly Affect Fungal Communities in the Crop Rhizosphere. *J Fungi* (Basel). 2022; 1;8(3):251. doi: 10.3390/jof8030251.
43. Shen XX, Steenwyk JL, LaBella AL, Opulente DA, Zhou X, Kominek J, Li Y, Groenewald M, Hittinger CT, Rokas A. Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. Sci Adv. 2020; 4;6(45):eabd0079. doi: 10.1126/sciadv.abd0079.
44. Soonvald L, Loit K, Runno-Paurson E, Astover A, Tedersoo L. Characterising the effect of crop species and fertilisation treatment on root fungal communities. *Sci Rep*. 2020; 30;10(1):18741. doi: 10.1038/s41598-020-74952-7.
45. Sun W, Huang S, Xia J, Zhang X, Li Z. Morphological and molecular identification of *Diaporthe* species in south-western China, with description of eight new species. *MycoKeys*. 2021; 14;77:65-95. doi: 10.3897/mycokeys.77.59852.
46. Tsuioshi Y. The Cerrado of Brazil: A Success Story of Production on Acid Soils. *Soil Science & Plant Nutrition*. 2005; 51:5, 617-620, DOI: 10.1111/j.1747-0765.2005.tb00076.x.
47. van den Brink J, de Vries RP. Fungal enzyme sets for plant polysaccharide degradation. Appl Microbiol Biotechnol. 2011; 91(6):1477-92. doi: 10.1007/s00253-011-3473-2. Epub 2011 Jul 23.
48. Van Diepen LT, Lilleskov EA, Pregitzer KS. Simulated nitrogen deposition affects community structure of arbuscular mycorrhizal fungi in northern hardwood forests. *Mol Ecol*. 2011; 20(4):799-811. doi: 10.1111/j.1365-294X.2010.04969.x.
49. Van Geel M, Jacquemyn H, Plue J, Saar L, Kasari L, Peeters G, van Acker K, Honnay O, Ceulemans T. Abiotic rather than biotic filtering shapes the arbuscular mycorrhizal fungal communities of European seminatural grasslands. *New Phytol*. 2018; 220(4):1262-1272. doi: 10.1111/nph.14947.

50. van Wyk S, Wingfield BD, De Vos L, van der Merwe NA, Steenkamp ET. Genome-Wide Analyses of Repeat-Induced Point Mutations in the Ascomycota. Front Microbiol. 2021; 1; 11:622368. doi: 10.3389/fmicb.2020.622368.
51. Videira SIR, Groenewald JZ, Nakashima C, Braun U, Barreto RW, de Wit PJGM, Crous PW. Mycosphaerellaceae - Chaos or clarity? Stud Mycol. 2017; 87:257-421. doi: 10.1016/j.simyco.2017.09.003.
52. Villela D & Haridasaz M. Response of the ground layer community of a cerrado vegetation in central Brazil to liming and irrigation. *Plant and Soil*. 1994; 163. 25-31. 10.1007/BF00033937.
53. Wang G, Koziol L, Foster BL, Bever JD. Microbial mediators of plant community response to long-term N and P fertilization: Evidence of a role of plant responsiveness to mycorrhizal fungi. *Glob Chang Biol*. 2022; 28(8):2721-2735. doi: 10.1111/gcb.16091.
54. Wang J, Liao L, Wang G, Liu H, Wu Y, Liu G, Zhang C. N-induced root exudates mediate the rhizosphere fungal assembly and affect species coexistence. Sci *Total Environ*. 2022; 15; 804:150148. doi: 10.1016/j.scitotenv.2021.150148.
55. Yao H, Sun X, He C, Maitra P, Li XC, Guo LD. Phyllosphere epiphytic and endophytic fungal community and network structures differ in a tropical mangrove ecosystem. *Microbiome*. 2019; 9;7(1):57. doi: 10.1186/s40168-019-0671-0.
56. Yao H, Sun X, He C, Maitra P, Li XC, Guo LD. Phyllosphere epiphytic and endophytic fungal community and network structures differ in a tropical mangrove ecosystem. *Microbiome*. 2019; 9; 7(1):57. doi: 10.1186/s40168-019-0671-0.
57. Zheng Q, Hu Y, Zhang S, Noll L, Böckle T, Dietrich M, Herbold CW, Eichorst SA, Woebken D, Richter A, Wanek W. Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity. *Soil Biol Biochem*. 2019; 136:107521. doi: 10.1016/j.soilbio.2019.107521.
58. Zheng Y, Chen L, Luo CY, Zhang ZH, Wang SP, Guo LD. Plant Identity Exerts Stronger Effect than Fertilization on Soil Arbuscular Mycorrhizal Fungi in a Sown Pasture. *Microb Ecol*. 2016; 72(3): 647-658.

CONSIDERAÇÕES FINAIS

Este estudo é um dos primeiros a utilizar *metabarcoding* para caracterizar o micobioma endofítico foliar de diferentes espécies de plantas do Cerrado brasileiro e, portanto, fornece um inventário mais completo da diversidade, composição e estrutura taxonômica dessa comunidade. Nossos dados mostram que esta comunidade é altamente diversificada em diferentes níveis taxonômicos, sendo composta por espécies de inúmeros filos, classes, ordens e gêneros em diferentes proporções. Além disso, fazemos o relato inédito de filos não antes conhecidos como membros do micobioma endofítico de espécies nativas desse bioma.

O micobioma endofítico associado aos hospedeiros com fenologia foliar sazonal apresentou as comunidades fúngicas endofíticas mais diversas quando comparados àqueles com fenologia perene. Em contrapartida, a comunidade perene, embora diversa, apresentou grupos taxonômicos dominantes. Esses achados levantam inúmeras questões sobre os fatores que determinam a diversidade e o grau de especialização dos fungos endofíticos, e podem orientar futuros estudos envolvendo esses aspectos.

A identidade taxonômica da planta hospedeira foi decisiva para a estruturação do micobioma endofítico, tanto em relação à diversidade de espécies quanto à abundância de determinados grupos. Além de dissimilaridades a níveis de ordem e família, mostramos que a ocorrência e abundância de certos gêneros, principalmente de gêneros leveduriformes, foi significativamente influenciada pela identidade da planta hospedeira. Portanto, nossos dados suportam que o fator de identidade da planta hospedeira desempenha papel de filtro ambiental sobre a comunidade de fungos endofíticos de plantas nativas do Cerrado sob as mesmas condições ambientais.

Nós mostramos que o micobioma endofítico responde de diferentes maneiras à antropização causada pela adição de fertilizantes minerais ao solo: positivamente, quando há aumento da diversidade, e negativamente, quando há perda de diversidade. Observamos que essas diferentes respostas dependem de dois fatores principais, que são a identidade da planta hospedeira e o tipo de nutriente adicionado ao solo. Assim, atribuímos essas diferentes respostas ao fenótipo da planta hospedeira (genótipo + fatores ambientais).

Nós também fornecemos uma coleção com 284 isolados, purificados por meio de ponta de hifa, depositados em coleção e identificados em nível de espécie e gênero. Esses isolados representam um importante recurso genético para estudos futuros, principalmente para o estudo de bioprospecção de fungos endofíticos e para estudos que visem melhor compreender a relação entre fungos endofíticos e a planta hospedeira. Além disso, isolados classificados apenas em nível de gênero podem ser espécies novas e devem ser mais estudados a fim de serem classificados em nível de espécie e apresentados para a comunidade científica como novos componentes da lista de espécies de fungos que ocorrem no Cerrado.

A utilização da metodologia hifenizada, com a utilização conjunta de métodos independentes de cultura e dependentes de cultura, mostrou-se ser uma maneira mais abrangente para estudar a comunidade fúngica endofítica, uma vez que os métodos independentes de cultura nos forneceram dados mais próximos da diversidade real, enquanto os dependentes de cultivo nos forneceram isolados que podem ser estudados para as mais diversas aplicações biotecnológicas, farmacêuticas, etc.

Por fim, nosso trabalho traz importantes contribuições para a construção do conhecimento sobre a diversidade, composição e estrutura taxonômica do micobioma endofítico foliar de espécies vegetais nativas do Cerrado brasileiro, reforçam ainda mais a importância do Cerrado como reservatório de espécies e de sua preservação.

PERSPECTIVAS

O presente trabalho resultou no depósito de 284 isolados na Coleção de Cultura da Universidade de Brasília (CCUB). Muitos desses isolados foram classificados apenas em nível de gênero e podem ser novas espécies dentro de seus respectivos gêneros. Esperamos continuar a identificação destes, visando classificá-las em nível de espécie e descrever novas espécies, caso sejam identificadas. Além disso, esses micro-organismos representam um importante recurso genético para estudos futuros, tanto para melhor compreender o estilo de vida endofítico, por meio de técnicas de sequenciamento de genoma e genômica comparativa, quanto para explorar seu potencial de síntese de metabólitos bioativos.

Nos próximos meses, começaremos a anotar o genoma de seis isolados, sendo um isolado para cada espécie hospedeira. Para isso, utilizaremos uma abordagem exploratória seguida da anotação do genoma por completo. Primeiramente, faremos o esboço genômico (rascunho), visando o conhecimento prévio do tamanho do genoma e uma descrição preliminar do mesmo, e com base nos dados gerados direcionaremos nossos esforços para anotá-lo por completo. Não se limitando a estes seis isolados, também planejamos selecionar uma espécie fúngica específica, bem delimitada por filogenia multigênica e que esteve presente em todas as espécies hospedeiras ou em todos os tratamentos de adição de fertilizantes, e realizaremos a anotação do genoma desta, visando melhor compreender a sua onipresença entre as hospedeiras ou tratamentos.

Utilizando abordagens de genômica comparativa, pretendemos comparar o genoma das nossas espécies com o genoma de espécies com diferentes estilos de vida dentro do mesmo gênero, ou mesmo da mesma espécie se encontrarmos o genoma depositado em bases de dados publicamente acessíveis. Desta forma, pretendemos elucidar os mecanismos responsáveis pelo seu estilo de vida simbiótico e melhor caracterizá-los, esclarecendo assim inúmeras lacunas ainda não preenchidas sobre fungos endofíticos.

Visando aplicações biotecnológicas e conhecimento do arsenal químico produzido por nossos isolados, pretendemos realizar o estudo de seu secretoma. Este experimento em particular já foi iniciado e está em progresso, uma vez que já realizamos vários experimentos pilotos para a caracterização preliminar dos principais metabólitos produzidos por esses microrganismos. Utilizando o equipamento de Cromatógrafo Líquido Eksigent Ekspert 100-XL acoplado a um Espectrômetro AB ScieTripleTOF 5600+ (no modo positivo e negativo) obtivemos o espectro de massa do extrato bruto da extração líquido-líquido com acetato de etila do caldo fermentado para um dos nossos isolados (Figura 84). Comparamos os dados de massa de alta resolução de íons principais em bancos de dados públicos (massbank e metlin) e anotados em *in silico* de 176 peptídeos e 403 metabólitos, muitos dos quais descritos na literatura com atividade biológica.

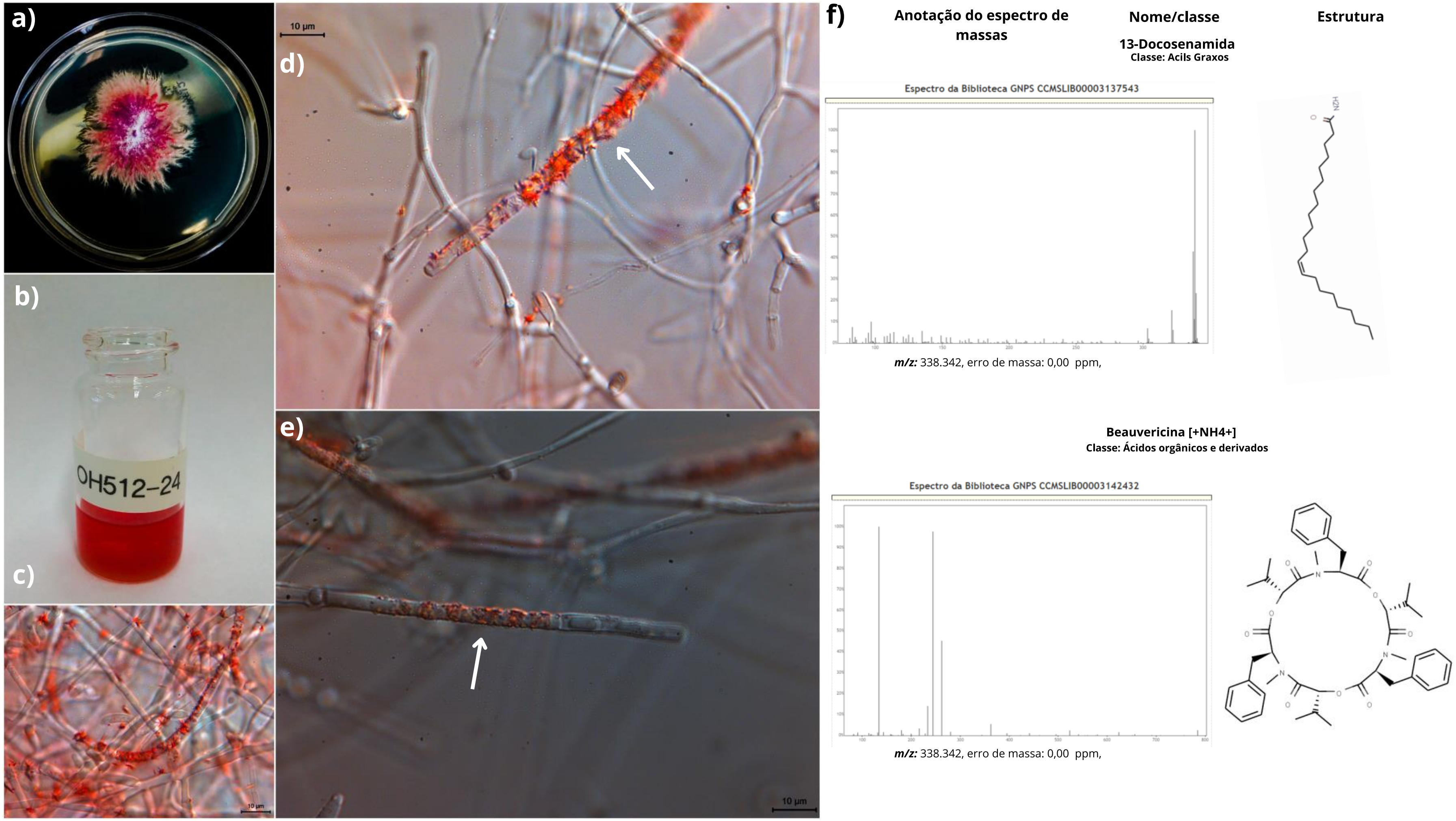


Figura 84. Isolado submetido a metodologia hifenada para estudo do secretoma. A) *Fusarium* sp. crescido em PDA durante dois dias a 25ºC sob escuro. b) extrato bruto obtido por extração líquido-líquido com acetato de etila do caldo batata dextrose

fermentado por 15 dias a 25ºC sob agitação a 100rpm. Em c), d) e e) é mostrada a microscopia de luz para visualização de metabólitos de cor avermelhada que cristalizam em torno das hifas fúngicas. As setas em d) e e) apontam para esses cristais. Em f) é apresentada a anotação *in silico* de alguns metabólitos, onde são fornecidas a relação massa-carga, erro do equipamento, espectro de fragmentação, classe do metabólito, fórmula química e provável estrutura da molécula.

Em conjunto com a pesquisadora Dra Patrícia Cardoso Cortelo, pretendemos fracionar os compostos majoritários presentes e identificá-los. Além disso, em parceria com a doutorando Alexandra Martins, pretendemos comparar o excretoma dos nossos isolados com o extrato bruto obtido a partir do tecido foliar das seis plantas hospedeiras aqui estudadas, relatando os metabólitos secundários produzidos por ambos os reinos, mostrando o que eles compartilham e o que não compartilham.

Por fim, esperamos que os dados gerados por nossos futuros experimentos contribuam para um melhor entendimento da relação endofítico-planta hospedeira e também reforcem a importância desses micro-organismos em nível ecossistêmico e também para explorar seu potencial biotecnológico. Esperamos também contribuir para a construção do conhecimento sobre a evolução microbiana e para o fortalecimento da pesquisa e da ciência em nosso país.

SUPPLEMENTARY MATERIAL

Supplementary table 1. General data on the plant species sampled

Specie	Treatment	Plot	Subplot	Individual	Phenology	Height (m)	CAS1 (cm)	leaf dry weight	Leaf Area (cm^2)	Specific Leaf Area (SLA)	N (dag/kg)	P (dag/kg)	K (dag/kg)	Ca (dag/kg)	Mg (dag/kg)	S (dag/kg)	Al (mg/kg)
Dalbergia miscolobium	Control	1 C	1	18	Brevideciduous	3	33	0,077	7,77	100,84	1,894	0,067	0,26	0,21	0,157	0,084	117,056
Dalbergia miscolobium	Control	11 C	4	1044	Brevideciduous	3	23	0,145	16,28	112,27	2,006	0,06	0,3	0,205	0,146	0,084	87,142
Dalbergia miscolobium	Control	21 C	3	2226	Brevideciduous	3	23	0,118	11,82	100,18	2,068	0,064	0,306	0,146	0,117	0,088	131,685
Leptolobium dasycarpum	Control	21 C	7	2293	Deciduous	1,5	13	1,531	95,84	62,60	1,769	0,062	0,333	0,141	0,052	0,065	162,309
Leptolobium dasycarpum	Control	21 C	7	2299	Deciduous	1,5	12	1,531	94,34	61,62	1,782	0,06	0,33	0,14	0,055	0,069	127,176
Leptolobium dasycarpum	Control	21 C	8	2304	Deciduous	1,6	13	3,065	154,08	50,27	1,832	0,063	0,337	0,243	0,12	0,078	208,860
Qualea parviflora	Control	1 C	3	65	Deciduous	2	21	1,038	72,10	69,46	1,333	0,06	0,301	0,324	0,209	0,09	12.719,567
Qualea parviflora	Control	11 C	1	971	Deciduous	2,3	16	1,932	192,55	99,66	1,283	0,055	0,326	0,293	0,163	0,079	12.861,361
Qualea parviflora	Control	11 C	9	1131	Deciduous	2,2	17	1,342	94,53	70,44	1,209	0,053	0,31	0,328	0,151	0,072	13.452,386
Styrax ferrugineus	Control	1 C	7	134	Evergreen	1,7	11	4,388	220,35	50,22	1,458	0,066	0,268	0,355	0,197	0,093	300,061
Styrax ferrugineus	Control	5 C	6	1697	Evergreen	1,5	11	3,118	201,18	64,52	1,283	0,061	0,285	0,341	0,187	0,085	173,486
Styrax ferrugineus	Control	5 C	8	1753	Evergreen	1,5	12	2,627	206,96	78,78	1,346	0,061	0,289	0,343	0,212	0,093	301,420
Caryocar brasiliense	Control	5 C	2	1629	Brevideciduous	2	25	8,942	662,80	74,12	1,283	0,066	0,291	0,389	0,184	0,08	322,304
Caryocar brasiliense	Control	5 C	9	1765	Brevideciduous	2	20	5,661	390,73	69,02	1,221	0,065	0,25	0,321	0,174	0,074	311,086
Caryocar brasiliense	Control	11 C	2	996	Brevideciduous	3,8	26	7,39	502,02	67,93	1,333	0,065	0,309	0,447	0,237	0,083	290,060
Ouratea hexasperma	Control	11 C	6	1078	Evergreen	1	15	3,483	200,93	57,69	1,072	0,048	0,399	0,71	0,199	0,067	79,589
Ouratea hexasperma	Control	21 C	2	2208	Evergreen	1,4	15	5,001	282,23	56,44	1,209	0,051	0,294	0,493	0,241	0,081	80,058
Ouratea hexasperma	Control	21 C	5	2226	Evergreen	1,5	17	3,558	233,39	65,60	1,333	0,053	0,371	0,575	0,263	0,082	103,176

Al: Aluminium; Ca: Calcium; CAS1: Stem circumference; K: Potassium; Mg: Magnesium; P: phosphorus; S: sulfur.

Supplementary table 2. Taxonomic attribution of fungal ITS sequences obtained from the six species of host plants

OTU	**CB 1629C**	**CB 1765C**	**CB 996C**	**DM 18**	**LD 2293**	**LD 2299**	**LD 2304**	**OH 1078**	**OH 2208**	**OH 2226**	**QP 1131**	**QP 65**	**Q P971**	**SF 134**	**SF 1697**	**SF 1753**
Acicuseptoria	0,0	0,0	0,0	0,0	0,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Acidiella	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Acremonium	0,0	0,0	0,0	0,0	15,0	29,0	9,0	21,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0
Acrocalymma	15,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Acrophialophora	0,0	0,0	0,0	0,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Agaricales	6,0	0,0	0,0	0,0	0,0	12,0	18,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Agaricomycetes	16,0	70,0	6,0	0,0	14,0	4,0	0,0	0,0	0,0	6,0	0,0	6,0	0,0	0,0	0,0	0,0
Agaricus	6,0	3,0	0,0	0,0	3,0	7,0	0,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0
Ajellomycetaceae	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Aleuria	9,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Allophoma	0,0	0,0	10,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Alternaria	226,0	1172,0	134,0	67,0	2906,0	3087,0	2162,0	383,0	235,0	1354,0	43,0	208,0	53,0	34,0	62,0	221,0
Amphisphaeria	0,0	22,0	0,0	0,0	4,0	20,0	6,0	0,0	0,0	56,0	0,0	0,0	2,0	3,0	0,0	9,0
Amphisphaeriaceae	4,0	24,0	3,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0
Angustimassarina	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Anthostomella	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Aphanoascus	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Apiosordaria	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0
Apiospora	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Apiosporaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0
Apiotrichum	17,0	0,0	6,0	9,0	0,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Aplosporella	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Apodus	56,0	6,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Archaeorhizomyces	48,0	39,0	0,0	0,0	2,0	0,0	24,0	10,0	2,0	56,0	0,0	0,0	0,0	0,0	0,0	15,0
Archaeorhizomycetes	58,0	32,0	0,0	0,0	14,0	0,0	20,0	71,0	28,0	36,0	0,0	0,0	0,0	0,0	0,0	4,0
Archaeorhizomycetes	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0
Arthrobotrys	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Arthrocatena	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Arthrographis	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	20,0	0,0	0,0	0,0	0,0	0,0	0,0
Articulospora	0,0	2,0	0,0	0,0	0,0	7,0	6,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Arxiella	13,0	0,0	14,0	0,0	0,0	0,0	0,0	11,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Ascobolus	12,0	4,0	0,0	0,0	0,0	0,0	0,0	5,0	8,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0
Ascomycota	89,0	330,0	31,0	7,0	61,0	11,0	41,0	44,0	3,0	268,0	0,0	10,0	3,0	0,0	2,0	39,0
Aspergillaceae	12,0	46,0	19,0	1882,0	24,0	6006,0	4219,0	182,0	64,0	475,0	1005,0	2630,0	2191,0	1817,0	1821,0	2133,0
Aspergillus	96,0	0,0	0,0	20,0	52,0	393,0	366,0	122,0	62,0	580,0	1478,0	109,0	1084,0	12,0	19,0	841,0
Atractiella	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Atrocalyx	0,0	16,0	0,0	0,0	0,0	0,0	11,0	0,0	11,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0
Aurantiosacculus	0,0	0,0	0,0	0,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Aureobasidium	33,0	22,0	76,0	258,0	64,0	43,0	52,0	534,0	610,0	271,0	70,0	17,0	6,0	0,0	0,0	10,0
Auriculariales	2,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	25,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Auriculoscypha	41,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0
Australosphaerella	14,0	0,0	53,0	0,0	0,0	0,0	0,0	0,0	0,0	25,0	0,0	0,0	0,0	0,0	0,0	0,0
Auxarthron	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0
Bacidina	0,0	0,0	0,0	0,0	0,0	16,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Bannoa	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0
Basidiomycota	0,0	2,0	13,0	11,0	0,0	36,0	27,0	355,0	1287,0	68,0	20,0	17,0	28,0	8,0	20,0	22,0
Betamyces	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	18,0	0,0	0,0	0,0	0,0	0,0	0,0
Bionectria	0,0	0,0	4,0	0,0	0,0	0,0	4,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Bionectriaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	6,0	0,0	2,0	0,0	0,0
Bipolaris	11,0	0,0	0,0	0,0	298,0	35,0	29,0	88,0	44,0	27,0	0,0	8,0	0,0	477,0	105,0	0,0
Bisifusarium	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Bjerkandera	0,0	0,0	0,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Blastobotrys	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Blumeria	0,0	0,0	0,0	0,0	0,0	0,0	0,0	250,0	0,0	17,0	0,0	0,0	0,0	0,0	0,0	0,0
Boeremia	0,0	0,0	0,0	0,0	0,0	19,0	13,0	53,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Boliniales	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Botryotinia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Botryotrichum	804,0	350,0	494,0	0,0	0,0	0,0	0,0	0,0	0,0	17,0	0,0	5,0	0,0	0,0	0,0	0,0
Brycekendrickomyces	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	27,0	0,0
Bullanockia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	222,0
Bulleribasidium	0,0	0,0	0,0	0,0	0,0	2,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Bulleromyces	0,0	3,0	3,0	0,0	0,0	28,0	16,0	0,0	3,0	19,0	0,0	0,0	0,0	0,0	0,0	0,0
Cadophora	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Caliciaceae	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Canariomyces	0,0	9,0	0,0	0,0	6,0	0,0	0,0	120,0	18,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0
Candida	3,0	7,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0
Cantharellales	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Capnodiales	595,0	338,0	4557,0	168,0	36276,0	12619,0	15189,0	1510,0	181,0	2713,0	343,0	677,0	232,0	71,0	146,0	154,0
Capnodium	23,0	9,0	31,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Castanediella	0,0	0,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Catenulostroma	50,0	0,0	35,0	0,0	7,0	10,0	21,0	14,0	0,0	68,0	0,0	0,0	0,0	8,0	0,0	4,0
Cephaliophora	40,0	23,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cephalotrichum	40,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ceramothyrium	0,0	0,0	0,0	0,0	0,0	0,0	0,0	70,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ceratobasidiaceae	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ceratobasidium	5,0	0,0	0,0	12,0	0,0	0,0	0,0	24,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cercophora	60,0	20,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Chaetomellaceae	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Chaetomiaceae	36,0	48,0	7,0	0,0	30,0	58,0	28,0	3,0	13,0	16,0	0,0	0,0	0,0	0,0	0,0	0,0
Chaetomium	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Chaetosphaeriaceae	68,0	751,0	124,0	43,0	0,0	37,0	42,0	66,0	13,0	824,0	39,0	628,0	18,0	8,0	6,0	18,0
Chaetosphaeriales	6,0	39,0	4,0	56,0	16,0	45,0	37,0	729,0	1126,0	1576,0	59,0	577,0	62,0	22,0	31,0	47,0
Chaetothyriaceae	0,0	4,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Chaetothyriales	123,0	25,0	1328,0	0,0	9,0	3,0	2,0	108,0	0,0	10,0	0,0	4,0	2,0	3,0	0,0	2,0
Chaetothyriales	0,0	11,0	28,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Chaetothyrium	9,0	0,0	25,0	0,0	0,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Chlamydocillium	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Chloridium	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0
Chytridiomycota	14,0	63,0	13,0	0,0	0,0	6,0	0,0	2,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Cinereomyces	7,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cladobotryum	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cladorrhinum	28,0	43,0	14,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cladosporium	415,0	762,0	566,0	164,0	549,0	377,0	440,0	3445,0	754,0	4082,0	64,0	230,0	55,0	35,0	77,0	80,0

Classicula	0,0	0,0	21,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Clavaria	3,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Clavicipitaceae	10,0	12,0	0,0	0,0	23,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0
Clavulinaceae	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Clavulinopsis	0,0	0,0	2,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Clitocybula	0,0	0,0	0,0	0,0	187,0	0,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0
Clitopilus	0,0	11,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0
Clonostachys	35,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Clypeosphaerella	0,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cochliobolus	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Collariella	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Colletotrichum	70,0	248,0	16,0	10,0	370,0	160,0	453,0	139,0	273,0	238,0	19,0	32,0	11,0	7,0	51,0	127,0
Condenascus	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0
Coniella	35,0	13,0	44,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Coniocessia	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Coniochaeta	5,0	0,0	2,0	3,0	0,0	0,0	6,0	8,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	3,0
Conioscypha	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	12,0
Coniosporium	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Coniothyriaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	15,0	6,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0
Coniothyrium	0,0	0,0	0,0	0,0	0,0	4,0	9,0	0,0	3,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0
Conocybe	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Coprinellus	0,0	3,0	0,0	0,0	0,0	6,0	0,0	3,0	9,0	25,0	0,0	0,0	0,0	0,0	0,0	4,0
Coprinopsis	24,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Corticiales	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Corticifraga	0,0	0,0	28,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	13,0	0,0	0,0
Cortinarius	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Corynascus	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Corynespora	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0
Crucellisporiopsis	78,0	236,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	17,0	0,0	0,0	0,0	0,0	3,0	0,0
Cryphonectriaceae	4,0	16,0	0,0	0,0	6,0	67,0	0,0	0,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0
Cryptococcus	16,0	8,0	0,0	0,0	2,0	0,0	0,0	31,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cucurbitariaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0
Curvularia	14,0	13,0	3,0	0,0	293,0	139,0	85,0	9,0	7,0	63,0	0,0	0,0	0,0	0,0	0,0	3,0

Cutaneotrichosporon	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0
Cyanodermella	11,0	87,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0
Cylindrocarpon	85,0	38,0	33,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cylindrocladiella	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Cyphellophora	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	2,0	0,0
Cystofilobasidium	0,0	0,0	0,0	0,0	0,0	0,0	0,0	42,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0
Cytospora	15,0	16,0	4,0	0,0	0,0	0,0	11,0	0,0	0,0	593,0	0,0	14,0	0,0	0,0	0,0	0,0
Dactylonectria	196,0	134,0	96,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Daldinia	0,0	0,0	3,0	0,0	0,0	16,0	2,0	0,0	10,0	43,0	0,0	0,0	0,0	0,0	0,0	0,0
Debaryomyces	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0
Dendrophoma spp.	0,0	16,0	0,0	78,0	0,0	62,0	33,0	40,0	24,0	73,0	60,0	2261,0	34,0	20,0	22,0	39,0
Dendryphion	0,0	25,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Dermateaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Devriesia	0,0	0,0	2,0	3,0	0,0	0,0	0,0	44,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0
Diaporthaceae	0,0	128,0	0,0	22,0	802,0	1261,0	1128,0	0,0	27,0	67,0	0,0	38,0	5,0	0,0	17,0	0,0
Diaporthales	0,0	15,0	0,0	0,0	28,0	69,0	43,0	2,0	0,0	2,0	3,0	0,0	7,0	3,0	0,0	0,0
Diaporthe	912,0	3290,0	331,0	860,0	37675,0	39319,0	33738,0	1088,0	373,0	6093,0	345,0	522,0	305,0	325,0	1658,0	2621,0
Dictyochaeta	0,0	0,0	0,0	10,0	0,0	34,0	25,0	735,0	827,0	169,0	30,0	12,0	22,0	0,0	11,0	16,0
Didymella	128,0	76,0	0,0	15059,0	254,0	319,0	169,0	522,0	268,0	506,0	128,0	93,0	108,0	53,0	141,0	99,0
Didymellaceae	45,0	3,0	0,0	0,0	740,0	276,0	480,0	31,0	65,0	200,0	31,0	0,0	27,0	0,0	0,0	0,0
Didymosphaeriaceae	0,0	0,0	5,0	0,0	0,0	0,0	0,0	1,0	0,0	17,0	0,0	0,0	0,0	0,0	0,0	0,0
Dioszegia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	32,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Diplodia	2,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0
Dipodascaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0
Dipodascus	10,0	7,0	0,0	0,0	0,0	0,0	2,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Diutina	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0
Dothideales	0,0	0,0	15,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Dothideomycetes	110,0	540,0	2414,0	6,0	0,0	8,0	40,0	171,0	472,0	12,0	4,0	17,0	8,0	5,0	3,0	6,0
Elsinoaceae	3,0	0,0	2,0	0,0	4,0	0,0	0,0	0,0	0,0	80,0	0,0	0,0	0,0	0,0	0,0	0,0
Elsinoe	126,0	57,0	114,0	0,0	4,0	0,0	0,0	0,0	0,0	18,0	0,0	0,0	0,0	0,0	0,0	0,0
Emericellopsis	12,0	8,0	5,0	0,0	0,0	0,0	11,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Engyodontium	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Entoloma	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Epicoccum	149,0	407,0	120,0	32,0	4671,0	1219,0	1976,0	294,0	108,0	6445,0	69,0	65,0	46,0	17,0	53,0	47,0
Erythrobasidium	0,0	11,0	19,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Eurotiales	67,0	61,0	13,0	5,0	105,0	72,0	28,0	66,0	14,0	59,0	0,0	11,0	0,0	3,0	0,0	7,0
Eurotiomycetes	3,0	0,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Euteratosphaeria	71,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Exidiaceae	17,0	4,0	0,0	0,0	0,0	0,0	0,0	78,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Exobasidiales	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Exopassalora	0,0	2,0	437,0	2,0	0,0	0,0	0,0	62,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Exophiala	32,0	0,0	3,0	0,0	0,0	2,0	10,0	16,0	7,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0
Exutisphaerella	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	16,0	0,0	0,0	0,0	0,0
Fasciatispora	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0
Favolus	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	71,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Fellomyces	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	16,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Fibulochlamys	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Filobasidium	49,0	22,0	18,0	8,0	0,0	60,0	42,0	344,0	9,0	34,0	0,0	0,0	0,0	0,0	0,0	3,0
Flabellascoma	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Fonsecazyma	0,0	195,0	96,0	31,0	4,0	45,0	27,0	0,0	6833,0	1107,0	46,0	80,0	31,0	0,0	39,0	40,0
Funalia	0,0	0,0	0,0	0,0	0,0	0,0	103,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Fungi	13,0	24,0	3,0	0,0	0,0	3,0	11,0	27,0	9,0	5,0	0,0	0,0	0,0	0,0	4,0	0,0
Fungi	81796,0	61792,0	36709,0	2798,0	6592,0	50028,0	36689,0	6203,0	2895,0	9343,0	144329,0	10682,0	129624,0	701,0	1655,0	2038,0
Funneliformis	0,0	42,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Fusarium	204,0	83,0	166,0	0,0	0,0	0,0	0,0	48,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Fusculina	0,0	8,0	0,0	0,0	0,0	0,0	15,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Fusicolla	186,0	47,0	63,0	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	4,0
Gamsia	260,0	181,0	118,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ganoderma	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0
Geastrumia	263,0	1348,0	2151,0	0,0	9,0	19,0	0,0	41,0	0,0	10,0	0,0	5,0	0,0	0,0	0,0	0,0
Gelasinospora	0,0	150,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	11,0
Geopora	0,0	9,0	0,0	0,0	20,0	5,0	0,0	282,0	52,0	160,0	0,0	0,0	0,0	0,0	0,0	0,0
Geosmithia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0
Gerronema	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Gibberella	1125,0	604,0	716,0	45,0	169,0	83,0	140,0	366,0	257,0	717,0	23,0	36,0	24,0	0,0	15,0	41,0
Gliocephalotrichum	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0
Gliomastix	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0
Glomerellaceae	57,0	0,0	0,0	0,0	0,0	0,0	16,0	0,0	9,0	39,0	0,0	0,0	5,0	0,0	22,0	47,0
Gloniopsis	10,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	10,0	0,0	60,0	0,0	0,0	4,0	0,0
Gnomoniaceae	0,0	0,0	0,0	5,0	0,0	14,0	6,0	0,0	8,0	19,0	6,0	0,0	4,0	6,0	230,0	86,0
Goffeauzyma	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Golubevia	0,0	0,0	0,0	0,0	0,0	13,0	0,0	0,0	4,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0
Gomphillaceae	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Gonatophragmium	0,0	59,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Gymnoascus	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Gymnostellatospora	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Gyroporus	22,0	0,0	2,0	0,0	0,0	0,0	17,0	0,0	0,0	18,0	0,0	0,0	0,0	0,0	0,0	0,0
Hannaella	19,0	7,0	0,0	2,0	24,0	0,0	7,0	284,0	95,0	591,0	0,0	0,0	0,0	0,0	11,0	0,0
Hanseniaspora	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0
Hansfordia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Helminthosporium	189,0	581,0	140,0	0,0	0,0	0,0	35,0	0,0	43,0	33,0	0,0	0,0	0,0	3,0	0,0	16,0
Helotiaceae	36,0	38,0	27,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Helotiales	238,0	4,0	3,0	0,0	3,0	21,0	13,0	0,0	0,0	2,0	0,0	0,0	2,0	0,0	185,0	7,0
Hermetothecium	14,0	0,0	80,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Herpotrichiellaceae	0,0	0,0	3,0	0,0	0,0	0,0	0,0	14,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	3,0
Hirsutella	3,0	0,0	0,0	0,0	0,0	0,0	0,0	41,0	0,0	2,0	0,0	0,0	4,0	0,0	0,0	0,0
Holtermanniella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	52,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Hormonema	4,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Humicola	227,0	107,0	140,0	0,0	0,0	5,0	36,0	21,0	0,0	73,0	0,0	0,0	4,0	0,0	0,0	0,0
Hyaloscypha	0,0	0,0	0,0	0,0	0,0	0,0	2,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Hyaloscyphaceae	14,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Hydnodontaceae	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Hydropisphaera	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0
Hymenochaete	0,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Hyphopichia	5,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0
Hypochnicium	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Hypocreaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0

Hypocreales	41,0	17,0	35,0	0,0	0,0	6,0	5,0	5,0	9,0	8,0	0,0	5,0	4,0	0,0	0,0	0,0
Hypocreales	0,0	0,0	0,0	0,0	0,0	12,0	22,0	10,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Hypomontagnella	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Hypoxylon	0,0	14,0	0,0	2,0	0,0	0,0	20,0	21,0	33,0	49,0	0,0	0,0	4,0	0,0	0,0	46,0
Hysteriales	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Hyweljonesia	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	19,0	0,0	0,0	0,0	0,0
Ilyonectria	0,0	0,0	0,0	5,0	0,0	18,0	0,0	0,0	0,0	19,0	2,0	0,0	0,0	0,0	0,0	0,0
Inocybaceae	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Iodophanus	0,0	20,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Issatchenkia	5,0	0,0	0,0	0,0	5,0	0,0	8,0	17,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0
Jattaea	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Johansonia	0,0	0,0	35,0	0,0	2,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Kalmusia	51,0	493,0	119,0	124,0	18,0	433,0	228,0	24997,0	38401,0	11035,0	245,0	507,0	183,0	107,0	244,0	231,0
Kazachstania	0,0	0,0	0,0	0,0	0,0	0,0	19,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Knufia	0,0	0,0	0,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Kockovaella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	18,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0
Kondoa	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Kramasamuha	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0
Kuehneromyces	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0
Kurtzmanomyces	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Kwoniella	0,0	0,0	0,0	4,0	0,0	7,0	6,0	89,0	580,0	5,0	5,0	5,0	4,0	0,0	5,0	7,0
Lamproconiaceae	0,0	0,0	0,0	61,0	0,0	140,0	473,0	8105,0	20980,0	449,0	169,0	69,0	152,0	55,0	86,0	185,0
Lapidomyces	0,0	0,0	0,0	0,0	0,0	0,0	0,0	35,0	16,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Lasiodiplodia	0,0	0,0	0,0	16,0	17,0	0,0	17,0	27,0	13,0	1972,0	14,0	9,0	12,0	0,0	16,0	8,0
Lasionectria	204,0	100,0	92,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Lasiosphaeriaceae	28,0	25,0	0,0	0,0	4,0	0,0	0,0	35,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0
Lecanicillium	19,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Lecanoromycetes	0,0	0,0	0,0	0,0	21,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Lectera	16,0	31,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0
Leiorreuma	0,0	0,0	0,0	0,0	4,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Leohumicola	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Leotiomycetes	7,0	0,0	0,0	0,0	0,0	5,0	0,0	2,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0

Lepiota	0,0	27,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Lepteutypa	5,0	6,0	0,0	0,0	6,0	0,0	0,0	3,0	0,0	56,0	0,0	0,0	0,0	0,0	0,0	0,0
Leptodiscella	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Leptosphaeria	20,0	7,0	23,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Leptospora	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0
Leucothecium	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	17,0	0,0	0,0	0,0	0,0	0,0	0,0
Liberomyces	9,0	795,0	11,0	0,0	0,0	0,0	0,0	21,0	24,0	10,0	0,0	12,0	0,0	0,0	0,0	0,0
Longipedicellata	0,0	0,0	0,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Lophiostomataceae	26,0	0,0	90,0	0,0	195,0	25,0	20,0	0,0	0,0	98,0	2,0	0,0	0,0	0,0	0,0	0,0
Lophiotremataceae	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Lophotrichus	45,0	29,0	0,0	0,0	0,0	182,0	151,0	32,0	10,0	37,0	9,0	22,0	14,0	0,0	9,0	12,0
Macalpinomyces	0,0	0,0	0,0	0,0	0,0	0,0	4,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Madagascaromyces	0,0	0,0	0,0	357,0	18,0	1185,0	687,0	680,0	347,0	1254,0	923,0	80857,0	5175,0	209,0	403,0	437,0
Magnaporthaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0
Magnaporthe	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Magnibotryascoma	64,0	48,0	71,0	0,0	19,0	77,0	5,0	7,0	47,0	132,0	0,0	25,0	0,0	15,0	8,0	13,0
Malassezia	0,0	0,0	0,0	0,0	91,0	151,0	14,0	1303,0	144,0	63,0	0,0	0,0	0,0	0,0	0,0	0,0
Malasseziaceae	0,0	0,0	0,0	0,0	4,0	0,0	3,0	29,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Mariannaea	0,0	0,0	0,0	4,0	0,0	7,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Mastigosporella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	201,0	65,0	91,0	0,0	0,0	0,0
Melanodiplodia	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Melanommataceae	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Metarhizium	74,0	11,0	8,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Meyerozyma	0,0	7,0	7,0	0,0	0,0	10,0	10,0	7,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Microascales	7,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Microascus	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Microcyclospora	16,0	10,0	73,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Microdochiaceae	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Microdochium	54,0	57,0	35,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0
Microsphaera	0,0	0,0	0,0	0,0	0,0	17,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Microsporomycetaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Mirandina	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Moellerodiscus	0,0	71,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Moesziomyces	0,0	0,0	0,0	0,0	4,0	21,0	3,0	126,0	65,0	119,0	0,0	0,0	0,0	0,0	4,0	0,0
Mollisia	0,0	0,0	0,0	0,0	5,0	4,0	6,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Monascus	6,0	0,0	0,0	0,0	0,0	0,0	36,0	0,0	2,0	24,0	0,0	0,0	0,0	0,0	0,0	4,0
Monoblepharidales	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0
Monocillium	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0
Montagnula	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Morenoina	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	26,0	0,0	0,0	0,0	0,0
Morosphaeriaceae	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Mortierella	979,0	695,0	493,0	31,0	0,0	38,0	47,0	27,0	20,0	71,0	0,0	0,0	0,0	5,0	3,0	0,0
Mortierellaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Mortierellales	5,0	0,0	0,0	0,0	0,0	13,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Mortierellomycota	0,0	0,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Multiseptospora	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Muscodor	0,0	0,0	3,0	0,0	7,0	50,0	12,0	57,0	54,0	9,0	2,0	0,0	5,0	0,0	0,0	12,0
Muyocopron	0,0	0,0	0,0	0,0	0,0	0,0	0,0	8,0	49,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Mycoacia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	26,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0
Mycofalcella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Mycosphaerellaceae	619,0	541,0	803,0	282,0	1243,0	733,0	843,0	286,0	118,0	667,0	445,0	8824,0	2332,0	476,0	460,0	215,0
Myriangiales	37,0	35,0	95,0	2,0	0,0	9,0	0,0	0,0	8,0	0,0	9,0	4,0	0,0	0,0	0,0	0,0
Myrmecridium	4,0	0,0	0,0	0,0	0,0	0,0	3,0	4,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Naganishia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Neoascochyta	3,0	0,0	0,0	4,0	0,0	0,0	0,0	118,0	0,0	15,0	0,0	0,0	0,0	0,0	4,0	0,0
Neoceratosperma	0,0	0,0	0,0	44,0	0,0	65,0	43,0	52,0	17,0	100,0	31,0	888,0	78,0	281,0	515,0	28,0
Neocoleroa	268,0	729,0	83,0	0,0	4,0	24,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Neocosmospora	139,0	84,0	66,0	26,0	79,0	55,0	31,0	68,0	30,0	70,0	2,0	15,0	0,0	0,0	6,0	21,0
Neocucurbitaria	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Neodevriesia	0,0	0,0	0,0	0,0	0,0	17,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0
Neodidymella	0,0	0,0	0,0	37,0	57,0	11,0	28,0	347,0	103,0	576,0	0,0	0,0	0,0	12,0	38,0	0,0
Neofusicoccum	0,0	4,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	7,0	5,0	249,0
Neomassarina	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Neonectria	223,0	73,0	73,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Neopestalotiopsis	854,0	503,0	1218,0	140,0	510,0	282,0	255,0	151,0	553,0	344,0	2274,0	99,0	2391,0	1516,0	152,0	1925,0

Neophaeomoniella	0,0	0,0	28,0	0,0	0,0	0,0	0,0	0,0	2,0	92,0	8,0	0,0	14,0	0,0	0,0	0,0
Neophaeothecoidea	1451,0	485,0	4630,0	618,0	0,0	30,0	17,0	68,0	13,0	115,0	36,0	22,0	31,0	5,0	19,0	21,0
Neosetophoma	6,0	59,0	0,0	0,0	0,0	60,0	3,0	12,0	13,0	18,0	0,0	0,0	0,0	0,0	0,0	0,0
Neosulcatispora	22,0	15,0	17,0	13,0	84,0	36,0	51,0	0,0	11,0	24,0	8,0	34,0	10,0	8,0	8,0	251,0
Neurospora	0,0	0,0	0,0	0,0	0,0	0,0	15,0	0,0	3,0	34,0	0,0	4,0	0,0	0,0	0,0	0,0
Nigrograna	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	45,0
Nigroporus	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	17,0	0,0	0,0	0,0	0,0	0,0	0,0
Nigrospora	688,0	872,0	327,0	41,0	2926,0	1273,0	1325,0	611,0	274,0	780,0	72,0	49,0	69,0	34,0	37,0	67,0
Nothophoma	0,0	30,0	0,0	0,0	0,0	0,0	184,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Occultifur	0,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ochroconis	0,0	0,0	3,0	0,0	0,0	18,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	97,0
Olpidium	43,0	4,0	24,0	0,0	0,0	63,0	51,0	2,0	0,0	10,0	0,0	0,0	2,0	0,0	0,0	9,0
Ophiobolus	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ophiocordyceps	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	3,0	0,0	0,0	0,0	0,0
Ophiocordycipitaceae	0,0	0,0	0,0	0,0	3,0	0,0	0,0	12,0	5,0	20,0	0,0	0,0	0,0	0,0	0,0	0,0
Ophionectria	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ophiosphaerella	14,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Orbilia	0,0	0,0	4,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Orbiliaceae	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Orbiliales	0,0	17,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ostropales	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Pallidocercospora	0,0	0,0	13,0	0,0	0,0	0,0	0,0	16,0	0,0	26,0	0,0	112,0	0,0	0,0	0,0	0,0
Panaeolus	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Papiliotrema	3,0	8,0	0,0	20,0	0,0	77,0	57,0	1488,0	1745,0	255,0	37,0	31,0	60,0	7,0	31,0	37,0
Paraboeremia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0
Paracamarosporium	6,0	0,0	0,0	10,0	10,0	26,0	0,0	0,0	0,0	866,0	0,0	0,0	0,0	0,0	0,0	0,0
Paraconiothyrium	0,0	0,0	0,0	43,0	43,0	111,0	49,0	112,0	327,0	27094,0	78,0	51,0	26,0	24,0	65,0	43,0
Paracremonium	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0
Paragibellulopsis	265,0	177,0	378,0	0,0	0,0	0,0	11,0	22,0	0,0	19,0	2,0	0,0	0,0	0,0	0,0	0,0
Paramycosphaerella	9297,0	13056,0	21647,0	7836,0	24392,0	9348,0	10235,0	871,0	846,0	4627,0	360,0	2275,0	433,0	460,0	1648,0	824,0
Paramyrothecium	23,0	5,0	0,0	0,0	0,0	24,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Parapenidiella	28,0	9,0	17,0	0,0	4,0	0,0	16,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0

Paraphaeosphaeria	0,0	8,0	13,0	0,0	206,0	16,0	7,0	6,0	0,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0
Paraphoma	7,0	8,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Parapyrenochaeta	4,0	0,0	61,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	2,0	0,0	0,0	0,0	0,0
Parateratosphaeria	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	22,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Parmularia	0,0	71,0	0,0	516,0	74,0	1701,0	984,0	912,0	582,0	1885,0	666,0	531,0	418,0	93563,0	73141,0	80019,0
Peltaster	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Penicillifer	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	20,0	0,0	4,0	0,0	0,0	0,0	0,0
Penicillium	136,0	53,0	11,0	11,0	16,0	83,0	59,0	51,0	12,0	152,0	4,0	0,0	0,0	0,0	0,0	7,0
Penidiella	0,0	3,0	0,0	0,0	26,0	34,0	27,0	0,0	4,0	19,0	0,0	0,0	0,0	15,0	0,0	0,0
Peniophora	25,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Peniophoraceae	0,0	19,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Periconia	7,0	8,0	11,0	0,0	0,0	13,0	28,0	15,0	0,0	33,0	5,0	0,0	0,0	0,0	2,0	0,0
Peroneutypa	0,0	0,0	0,0	0,0	0,0	0,0	0,0	33,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0
Pestalotiopsis	239,0	160,0	294,0	41,0	3,0	525,0	0,0	235,0	1284,0	361,0	25,0	19,0	14,0	26,0	4,0	38,0
Pezicula	154,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	26,0	3,0	0,0	7,0
Phaeoacremonium	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	21,0
Phaeococcomyces	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Phaeodothis	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Phaeomoniellaceae	22,0	219,0	52,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0
Phaeomoniellales	6,0	272,0	108,0	0,0	0,0	0,0	0,0	7,0	119,0	10,0	0,0	0,0	0,0	0,0	4,0	0,0
Phaeophleospora	124,0	247,0	109,0	1004,0	14960,0	7529,0	6263,0	391,0	159,0	1172,0	168,0	3045,0	197,0	93,0	203,0	168,0
Phaeosphaeria	10,0	0,0	0,0	0,0	0,0	11,0	308,0	88,0	23,0	110,0	0,0	0,0	0,0	0,0	0,0	0,0
Phaeosphaeriaceae	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	136,0	0,0	0,0	0,0	0,0	0,0	0,0
Phanerochaete	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Phialemoniopsis	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	7,0
Phialocephala	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0
Phialomyces	0,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Phialoseptomonium	0,0	8,0	0,0	142,0	0,0	361,0	243,0	265,0	145,0	460,0	229,0	124,0	128,0	86,0	36476,0	137,0
Phlebia	0,0	0,0	0,0	44,0	0,0	0,0	0,0	15,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0
Phyllosticta	5,0	5,0	6,0	339,0	3,0	19,0	746,0	536,0	303,0	44,0	241,0	81,0	142,0	45,0	196,0	53,0
Pichia	0,0	6,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0

Pilidium	1155,0	471,0	24713,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	485,0	0,0	0,0	26,0	0,0
Plectosphaerella	205,0	92,0	78,0	9,0	0,0	44,0	96,0	91,0	30,0	48,0	21,0	0,0	27,0	5,0	4,0	11,0
Plectosphaerellaceae	55,0	25,0	0,0	0,0	0,0	16,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0
Pleosporaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0
Pleosporales	97,0	206,0	90,0	38,0	1217,0	172,0	220,0	1360,0	538,0	2844,0	0,0	50,0	3,0	0,0	1078,0	21,0
Pleosporales	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Podosphaera	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Podospora	0,0	0,0	0,0	0,0	0,0	15,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Polyporales	0,0	0,0	0,0	0,0	35,0	10,0	27,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Polytolypa	17,0	15,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Porodiplodia	0,0	0,0	0,0	66,0	0,0	183,0	150,0	7525,0	13815,0	269,0	100,0	68,0	89,0	36,0	92,0	95,0
Postia	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Powellomycetaceae	0,0	2,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Preussia	268,0	171,0	54,0	4,0	0,0	68,0	0,0	2,0	319,0	47,0	0,0	13,0	4,0	0,0	8,0	14,0
Proliferodiscus	83,0	284,0	16,0	0,0	0,0	0,0	43,0	5,0	0,0	256,0	35,0	0,0	24,0	14,0	0,0	0,0
Pseudeurotium	0,0	0,0	0,0	0,0	0,0	14,0	9,0	0,0	5,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0
Pseudoascochyta	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0
Pseudocercospora	22,0	13,0	39,0	38,0	170,0	5252,0	123,0	277,0	721,0	303,0	1374,0	938,0	1245,0	0,0	1241,0	3453,0
Pseudocoleophoma	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	19,0	0,0	0,0	0,0	0,0	0,0	0,0
Pseudodinemasporium	0,0	0,0	0,0	0,0	0,0	0,0	0,0	158,0	147,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Pseudofusicoccum	0,0	14,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	35,0
Pseudogymnoascus	110,0	21,0	47,0	0,0	11,0	29,0	14,0	125,0	26,0	34,0	2,0	4,0	0,0	0,0	12,0	4,0
Pseudolophiostoma	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Pseudombrophila	361,0	172,0	180,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Pseudopithomyces	0,0	0,0	32,0	0,0	6,0	52,0	0,0	81,0	31,0	220,0	0,0	0,0	0,0	0,0	3,0	0,0
Pseudoramichloridium	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	28,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Pseudoteratosphaeria	2365,0	2875,0	2137,0	847,0	1236,0	518,0	1192,0	587,0	293,0	1283,0	168,0	1883,0	586,0	54,0	749,0	166,0
Pseudozasmidium	0,0	0,0	0,0	22,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Punctulariopsis	0,0	154,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	6,0
Pyrenochaeta	4,0	0,0	0,0	0,0	0,0	26,0	8,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0
Pyrenochaetopsis	35,0	28,0	25,0	0,0	4,0	10,0	7,0	0,0	0,0	19,0	3,0	0,0	0,0	0,0	8,0	0,0
Pyronemataceae	0,0	66,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Pyxidiophorales	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rachicladosporium	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0
Radulidium	607,0	833,0	81,0	0,0	42,0	9,0	10,0	0,0	0,0	145,0	0,0	3,0	0,0	0,0	0,0	0,0
Ramboldia	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ramimonilia	21,0	14,0	110,0	0,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	6,0	0,0	0,0	0,0	0,0
Ramophialophora	15,0	3,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ramularia	0,0	0,0	2,0	0,0	0,0	9,0	6,0	149,0	6,0	7,0	0,0	3,0	4,0	4,0	0,0	0,0
Ramulariopsis	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0
Remispora	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Retroconis	11,0	13,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhizophagus	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhizophlyctidaceae	24,0	35,0	70,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhizophlyctis	0,0	0,0	0,0	0,0	0,0	20,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhizophydiales	18,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhizophydiales	288,0	123,0	132,0	11,0	0,0	0,0	13,0	51,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0
Rhodosporidiobolus	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhodotorula	8,0	40,0	0,0	0,0	0,0	5,0	14,0	11,0	17,0	9,0	0,0	298,0	0,0	0,0	0,0	0,0
Rhodoveronaea	0,0	6,0	0,0	0,0	2,0	10,0	6,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhytidhysteron	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rhytismataceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rickiopora	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Roussoella	0,0	17,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Rozellomycota	0,0	5,0	0,0	0,0	7,0	18,0	18,0	16,0	0,0	5,0	0,0	7,0	0,0	0,0	0,0	0,0
Rozellomycotina	0,0	0,0	0,0	0,0	0,0	24,0	7,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0
Rozellomycotina	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Ruinenia	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Russula	2,0	14,0	0,0	0,0	12,0	14,0	10,0	386,0	47,0	93,0	0,0	2,0	0,0	2,0	0,0	0,0
Russulales	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Saccharomycetales	8,0	0,0	0,0	0,0	0,0	3,0	3,0	0,0	0,0	15,0	3,0	0,0	0,0	0,0	0,0	0,0
Saitozyma	168,0	60,0	26,0	27,0	16,0	18,0	25,0	162,0	64,0	267,0	6,0	10,0	4,0	0,0	10,0	5,0
Sampaiozyma	50,0	17,0	0,0	2,0	0,0	242,0	151,0	22,0	26,0	88,0	0,0	21,0	6,0	0,0	0,0	0,0
Sarcosomataceae	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Sarocladium	9,0	0,0	5,0	0,0	0,0	0,0	136,0	22,0	10,0	27,0	0,0	0,0	0,0	0,0	0,0	0,0

Schizophyllum	23,0	7,0	0,0	0,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0
Schizothecium	167,0	33,0	73,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0
Sclerotinia	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Scopulariopsis	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0
Scutellinia	2,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Scytalidium	0,0	0,0	0,0	0,0	0,0	17,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Sebacina	24,0	15,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Sebacinales	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0
Seiridium	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Selenodriella	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Septobasidium	26,0	12,0	68,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Septoria	104,0	169,0	197,0	35,0	52,0	121,0	118,0	96,0	47,0	121,0	24,0	67,0	22,0	17,0	34,0	47,0
Serendipita	0,0	2,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0
Serendipitaceae	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Setophoma	14,0	10,0	11,0	40,0	8,0	0,0	0,0	13,0	6,0	60,0	0,0	0,0	0,0	0,0	0,0	0,0
Sidera	0,0	0,0	0,0	0,0	0,0	9,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Similiphoma	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,0	0,0	0,0	0,0	0,0	0,0	0,0
Simplicillium	13,0	0,0	0,0	7,0	13,0	30,0	62,0	16,0	11,0	61,0	7,0	0,0	0,0	0,0	11,0	0,0
Skeletocutis	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Solicoccozyma	102,0	114,0	63,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Sordariales	30,0	2,0	0,0	8,0	6,0	25,0	43,0	160,0	22,0	3,0	0,0	13,0	20,0	0,0	4,0	0,0
Sordariomycetes	9,0	13,0	0,0	0,0	0,0	39,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Sordariomycetes	81,0	45,0	13,0	192,0	45,0	78,0	174,0	997,0	1050,0	240,0	47,0	258,0	49,0	26,0	35,0	52,0
Spadicoides	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0
Spegazzinia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Sphaerosporella	0,0	0,0	0,0	0,0	0,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Spiromastix	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Spissiomyces	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	3,0
Spizellomyces	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Spizellomycetales	56,0	35,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Sporobolomyces	0,0	22,0	0,0	0,0	0,0	12,0	0,0	50,0	2,0	24,0	0,0	0,0	0,0	0,0	0,0	0,0
Sporocadaceae	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Stachybotryaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0

Stachybotrys	24,0	11,0	24,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Stagonospora	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Stagonosporopsis	0,0	0,0	0,0	0,0	0,0	0,0	0,0	26,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Steccherinum	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Stemphylium	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0
Stephanonectria	13,0	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Stephanosporaceae	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Stictidaceae	0,0	0,0	44,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Stolonocarpus	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Stomiopeltis	197,0	966,0	6484,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Strelitziana	81,0	175,0	195,0	31,0	4,0	61,0	49,0	1690,0	4410,0	260,0	31,0	33,0	17,0	17,0	176,0	43,0
Striatibotrys	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Symmetrospora	0,0	0,0	0,0	0,0	0,0	12,0	24,0	21,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Syncephalis	2,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Talaromyces	37,0	67,0	0,0	11,0	0,0	84,0	75,0	14,0	16,0	45,0	5,0	7,0	0,0	0,0	0,0	8,0
Taphrina	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Tausonia	277,0	244,0	158,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Teichospora	582,0	0,0	10,0	286,0	21,0	0,0	0,0	8,0	0,0	0,0	0,0	15,0	0,0	0,0	0,0	0,0
Teichosporaceae	0,0	3,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	7,0
Teratoramularia	0,0	0,0	0,0	0,0	0,0	0,0	0,0	20,0	11,0	46,0	0,0	0,0	0,0	0,0	0,0	0,0
Teratosphaeriaceae	779,0	544,0	1397,0	61,0	143,0	58,0	94,0	367,0	247,0	358,0	3,0	98,0	26,0	5,0	36,0	29,0
Teratosphaericola	0,0	11,0	19,0	0,0	15,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Tetracladium	233,0	168,0	130,0	0,0	0,0	0,0	0,0	9,0	0,0	13,0	0,0	0,0	0,0	0,0	0,0	0,0
Tetraplosphaeriaceae	0,0	12,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Thanatephorus	3,0	0,0	7,0	0,0	0,0	0,0	0,0	0,0	18,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Thelebolus	49,0	70,0	38,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Thelephoraceae	32,0	36,0	6,0	0,0	42,0	14,0	4,0	225,0	112,0	142,0	0,0	0,0	0,0	0,0	4,0	0,0
Thelonectria	0,0	0,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Thermomyces	0,0	2,0	0,0	0,0	0,0	0,0	15,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0
Thozetella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	38,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Tilletiopsis	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Tolypocladium	0,0	0,0	0,0	0,0	5,0	0,0	8,0	8,0	6,0	421,0	7,0	6,0	8,0	0,0	0,0	9,0
Torula	0,0	8,0	0,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Toxicocladosporium	12,0	21,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Trametes	13,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Trechispora	2,0	0,0	0,0	0,0	7,0	20,0	9,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Trechisporales	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Tremella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	11,0	0,0	0,0	15,0	0,0	26,0	0,0	0,0	0,0
Tremellales	49,0	0,0	27,0	0,0	0,0	0,0	0,0	2856,0	0,0	0,0	2,0	0,0	3,0	21,0	0,0	0,0
Tremellomycetes	0,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	10,0	2,0	5,0	0,0	0,0	0,0	0,0	0,0
Trichobolus	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Trichoderma	36,0	49,0	7,0	0,0	6,0	18,0	38,0	166,0	26,0	50,0	4,0	11,0	0,0	0,0	11,0	26,0
Tricholoma	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Trichomerium	13,0	26,0	106,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Trichosporon	0,0	0,0	0,0	0,0	0,0	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Trichothecium	0,0	0,0	0,0	0,0	15,0	21,0	13,0	0,0	0,0	9,0	0,0	0,0	0,0	0,0	0,0	4,0
Trimorphomycetaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	246,0	162,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Triposporium	13,0	167,0	0,0	0,0	16,0	0,0	0,0	24,0	39,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0
Tubeufiaceae	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	14,0	0,0	0,0	0,0	12,0	98,0	21,0
Typhula	15,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Udeniozyma	0,0	0,0	0,0	0,0	0,0	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Uncobasidium	3,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Uwebraunia	2,0	0,0	0,0	0,0	20,0	0,0	0,0	139,0	76,0	258,0	0,0	0,0	0,0	0,0	16,0	3,0
Valsonectria	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Venturiales	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0
Veronaea	0,0	0,0	0,0	31,0	0,0	0,0	0,0	0,0	0,0	3,0	0,0	3,0	0,0	0,0	8,0	0,0
Verrucocladosporium	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0
Verticillium	15,0	15,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Vishniacozyma	32,0	36,0	6,0	47,0	7,0	67,0	100,0	12434,0	82,0	315,0	76,0	60,0	69,0	20,0	44,0	54,0
Volutella	0,0	2,0	0,0	0,0	3,0	0,0	0,0	12,0	14,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Waitea	0,0	0,0	0,0	0,0	0,0	0,0	0,0	731,0	0,0	16,0	0,0	0,0	0,0	0,0	0,0	0,0
Wallemia	47,0	15,0	35,0	14,0	0,0	13,0	16,0	49,0	17,0	140,0	6,0	5,0	0,0	2,0	15,0	0,0
Westerdykella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0
Wickerhamomyces	0,0	9,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	3,0
Wojnowiciella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	5,0	0,0	0,0	0,0	0,0	0,0	0,0

Xenocamarosporium	0,0	0,0	29,0	0,0	10,0	6,0	0,0	123,0	400,0	22,0	7,0	0,0	6,0	0,0	8,0	0,0
Xenocylindrocladium	6,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Xenocylindrosporium	42,0	762,0	28,0	5,0	65,0	8,0	25,0	141,0	323,0	26,0	0,0	12,0	0,0	0,0	0,0	2,0
Xenopenidiella	0,0	0,0	0,0	0,0	16,0	19,0	0,0	0,0	0,0	24,0	0,0	0,0	0,0	0,0	0,0	0,0
Xenophacidiella	33,0	0,0	22,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Xenosonderhenia	0,0	17,0	0,0	76,0	0,0	266,0	158,0	160,0	84,0	291,0	137,0	80,0	128,0	13380,0	525,0	236,0
Xenoteratosphaeria	93,0	0,0	54,0	13,0	50,0	28,0	45,0	30,0	0,0	28,0	0,0	52,0	11,0	4,0	0,0	0,0
Xylaria	6,0	7,0	9,0	0,0	0,0	0,0	0,0	128,0	0,0	8,0	0,0	0,0	0,0	0,0	0,0	0,0
Xylariaceae	3,0	10,0	0,0	0,0	0,0	2,0	0,0	0,0	3,0	2,0	0,0	0,0	0,0	0,0	3,0	0,0
Xylonomycetes	4,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Zasmidium	472,0	804,0	475,0	170,0	823,0	487,0	654,0	843,0	191,0	484,0	37,0	733,0	77,0	31,0	222,0	440,0
Zeloasperisporium	0,0	0,0	244,0	138,0	4,0	19,0	27,0	1238,0	2401,0	2057,0	24,0	468,0	22,0	0,0	63,0	16,0
Zoopagomycota	11,0	2,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
Zopfiella	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	11,0	0,0	0,0	0,0	0,0	0,0	0,0
Zymoseptoria	0,0	0,0	0,0	0,0	0,0	0,0	0,0	10,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

CB: *Caryocar brasiliense*, DM: *Dalbergia miscolobium*; LD: *Leptolobium dasycarpum*; QP: *Qualea parviflora*; OH: *Ouratea hexasperma*; SF: *Styrax ferrugineus*.

Suplementary table 3. Soil characteristics between mineral fertilizer addition treatments

Plot	Treatment	Fresh weight (g)	Dry weight (g)	Cylinder (g)	gravimetric content (%)
12Ca	Liming	37,32	33,26	14,73	21,91
17Ca	Liming	34,49	30,23	14,62	27,29
20Ca	Liming	34,6	30,17	14,67	28,58
3Ca	Liming	37,4	32,84	16,06	27,18
11C	Control	32,28	28,52	14,92	27,65

1C	Control	37,34	32,9	16,94	27,82
21C	Control	29,53	26,38	14,14	25,74
5C	Control	36,39	31,91	16,58	29,22
15P	Phosphate	36,4	31,82	14,87	27,02
19P	Phosphate	38,89	33,77	15,94	28,72
4P	Phosphate	32,61	28,84	15,12	27,48
9P	Phosphate	40,48	34,86	14,25	27,27
10N	Nitrogen	32,71	28,44	14,21	30,01
14N	Nitrogen	36,34	32,14	15,16	24,73
2N	Nitrogen	32,61	28,71	14,1	26,69
7N	Nitrogen	31,88	28,26	14,66	26,62
13NP	Nitrogen+Phosphate	38,51	33,87	16,01	25,98
16NP	Nitrogen+Phosphate	42,51	37,01	15,51	25,58
6NP	Nitrogen+Phosphate	33,82	30,07	15,79	26,26
8NP	Nitrogen+Phosphate	34,94	30,83	15,53	26,86

Suplementary table 4. general data of the host plant species between treatments of addition of mineral nutrients to the soil

Host Specie	Treatment	Portion	Subplot	Individual	Height (m)	CAS1 (cm)	Leaf dry weight	Leaf area (cm2)	Specific leaf area (SLA)	N (dag/kg)	P (dag/kg)	K (dag/kg)	Ca (dag/kg)	Mg (dag/kg)	S (dag/kg)	Al (mg/kg)
Caryocar brasiliense	Control	5 C	2	1629	2	25	8,942	662,80	74,12	1,283	0,066	0,291	0,389	0,184	0,08	322,304
Caryocar brasiliense	Control	5 C	9	1765	2	20	5,661	390,73	69,02	1,221	0,065	0,25	0,321	0,174	0,074	311,086
Caryocar brasiliense	Control	11 C	2	996	3,8	26	7,39	502,02	67,93	1,333	0,065	0,309	0,447	0,237	0,083	290,060
Ouratea hexasperma	Control	11 C	6	1078	1	15	3,483	200,93	57,69	1,072	0,048	0,399	0,71	0,199	0,067	79,589

Ouratea hexasperma	Control	21 C	2	2208	1,4	15	5,001	282,23	56,44	1,209	0,051	0,294	0,493	0,241	0,081	80,058
Ouratea hexasperma	Control	21 C	5	2226	1,5	17	3,558	233,39	65,60	1,333	0,053	0,371	0,575	0,263	0,082	103,176
Caryocar brasiliense	Phosphate	15 P	8	300	3,4	32	5,423	342,91	63,23	1,072	0,054	0,31	0,837	0,058	0,195	277,038
Caryocar brasiliense	Phosphate	15 P	9	323	2,8	28	6,442	480,70	74,62	1,059	0,064	0,273	0,975	0,123	0,27	310,836
Caryocar brasiliense	Phosphate	9P	1	2077	2	19	10,201	667,30	65,42	1,283	0,07	0,18	0,992	0,103	0,246	223,676
Caryocar brasiliense	Nitrogen+Phosphate	13 NP	2	590	2,5	17	6,615	437,06	66,07	1,52	0,078	0,268	1,2	0,152	0,279	281,047
Caryocar brasiliense	Nitrogen+Phosphate	13 NP	4	614	6	54	6,586	442,61	67,20	1,495	0,08	0,323	0,974	0,155	0,336	289,137
Caryocar brasiliense	Nitrogen+Phosphate	8 NP	1	2358	2,5	12	3,697	268,58	72,65	1,47	0,077	0,252	0,77	0,178	0,199	267,470
Caryocar brasiliense	Liming	20 Ca	2	2755	2,5	18	6,88	525,14	76,33	1,209	0,063	0,221	0,765	0,41	0,278	387,171
Caryocar brasiliense	Liming	20 Ca	4	2789	2,8	23	5,754	423,77	73,65	1,184	0,062	0,213	0,797	0,404	0,24	246,154
Caryocar brasiliense	Liming	20 Ca	5	2790	2,5	14	8,653	535,00	61,83	1,121	0,063	0,204	0,801	0,418	0,181	361,456
Caryocar brasiliense	Nitrogen	2 N	2	1337	4,4	13	4,845	346,49	71,52	1,707	0,072	0,339	0,188	0,094	0,115	236,664
Caryocar brasiliense	Nitrogen	10 N	4	2531	2,9	14	6,011	404,34	67,27	1,582	0,07	0,354	0,61	0,236	0,179	379,896
Caryocar brasiliense	Nitrogen	10 N	4	2536	2,7	24	5,531	380,84	68,86	1,57	0,077	0,292	0,493	0,206	0,159	167,717
Ouratea hexasperma	Phosphate	15 P	5	248	1,3	14	2,789	159,10	57,04	1,209	0,064	0,387	1,794	0,098	0,238	83,855
Ouratea hexasperma	Phosphate	9P	1	2527	1,1	13	3,828	205,39	53,66	0,897	0,047	0,353	1,498	0,105	0,174	122,270
Ouratea hexasperma	Phosphate	19 P	9	2725	1,6	15	3,326	197,24	59,30	1,209	0,075	0,381	1,304	0,114	0,196	116,560
Ouratea hexasperma	Nitrogen+Phosphate	13 NP	3	610	0,8	11	2,801	176,76	63,11	1,209	0,074	0,392	1,166	0,11	0,218	257,205
Ouratea hexasperma	Nitrogen+Phosphate	13 NP	4	618	1,2	16	3,478	213,18	61,29	1,221	0,07	0,397	1,376	0,111	0,183	183,265
Ouratea hexasperma	Nitrogen+Phosphate	6 NP	3	1827	0,8	13	3,312	203,33	61,39	1,072	0,048	0,448	1,508	0,118	0,221	204,681
Ouratea hexasperma	Liming	17 Ca	3	874	0,9	12	2,848	178,48	62,67	1,059	0,046	0,352	0,923	0,37	0,111	100,045
Ouratea hexasperma	Liming	20 Ca	9	1536	1,15	15	2,55	189,34	74,25	1,022	0,052	0,218	0,811	0,517	0,156	95,717
Ouratea hexasperma	Liming	20 Ca	9	2891	1,1	13	2,399	173,23	72,21	1,134	0,053	0,213	0,802	0,489	0,12	99,818
Ouratea hexasperma	Nitrogen	14 N	8	800	1,2	15	2,574	167,55	65,09	1,458	0,059	0,37	0,631	0,156	0,156	110,540
Ouratea hexasperma	Nitrogen	7 N	2	1943	1,5	15	4,245	235,55	55,49	1,209	0,05	0,386	0,67	0,227	0,174	153,216

Ouratea hexasperma	Nitrogen	10 N	2	2611	1,2	15	3,558	203,75	57,27	1,458	0,06	0,388	0,712	0,197	0,221	161,560

Al: Aluminium; Ca: Calcium; CAS1: Stem circumference; K: Potassium; Mg: Magnesium; P: phosphorus; S: sulfur.

Suplementary table 5. Taxonomic attribution of fungal ITS sequences obtained from *Caryocar brasiliense* in different treatments of addition of nutrients to the soil

Phylum	Class	Order	Family	Genus	Species	CB1337N	CB1629C	CB1765C	CB2077P	CB2358NP	CB2531N	CB2536N	CB2755CA	CB300P	CB323P	CB590NP	CB614NP	CB996C
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Paramycosphaerella	34220	8196	12265	35277	10662	14715	18723	3932	5098	17565	13893	11923	20170
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		1087	906	466	517	917	1163	114	6424	38821	866	1067	823	24677
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae		Neopestalotiopsis	1211	857	503	61590	725	1613	1323	1177	832	2000	1091	788	1219
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Neophaeothecoidea	6314	447	281	278	4945	5259	13	174	23046	1502	625	1704	2244
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	6493	1526	2274	5495	3275	3403	1047	172	3731	7901	834	632	887
Ascomycota	Dothideomycetes	Myriangiales	Elsinoaceae	Elsinoe		194	126	57	66	109	29177	157	35	101	109	105	97	114
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae		Pestalotiopsis	323	145	97	7614	143	7029	367	121	112	148	157	3236	252
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Neophaeothecoidea	4184	130	63	88	132	262	0	54	13289	231	152	151	189

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	3495	136	85	94	1146	1631	0	103	7829	706	169	467	1031
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	788	965	763	644	2541	849	436	63	657	2197	1403	219	1077
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	229	140	727	102	406	219	0	204	176	128	207	5669	3606
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		1108	285	67	164	4119	2774	77	87	992	307	490	633	573
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	1174	401	274	1590	659	1066	989	109	628	3309	333	280	615
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		117	96	100	55	75	153	2	87	87	101	153	10001	115
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	325	121	249	64	176	140	32	191	122	173	5582	691	1554
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	344	405	745	258	899	195	2150	162	495	808	1453	678	567
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	558	353	80	1371	461	1658	254	32	2394	1386	204	94	197
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	54	0	0	0	95	0	0	7562	79	52	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		116	66	33	83	672	122	0	35	91	122	88	6322	90
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	66	94	63	104	0	6324	56	810	0	0	93	0	42

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	3402	166	1024	88	447	101	902	91	85	0	1065	59	136
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia		36	51	493	19	44	5760	207	18	70	0	48	38	119
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae		Nigrospora	3256	257	176	277	994	143	115	157	84	173	488	475	139
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			131	150	228	187	74	153	15	425	986	67	3974	97	66
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	346	92	165	1725	93	296	0	34	375	2129	429	122	439
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Alternaria	268	222	1172	149	470	274	194	257	293	116	2515	175	130
Ascomycota	Dothideomycetes	Capnodiales	Schizothyriaceae		Johansonia	679	53	34	23	258	94	653	31	65	95	71	48	3124
Ascomycota	Sordariomycetes	Diaporthales	Schizoparmaceae	Coniella		61	35	13	34	42	44	0	26	57	38	4659	45	44
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gibberella	657	592	266	0	437	567	0	583	122	224	401	408	350
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Mrakiaceae	Tausonia		319	277	244	0	509	377	0	125	376	1083	576	528	158
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			50	37	23	42	44	80	0	21	52	58	53	4023	65
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		Botryotrichum	867	489	183	0	425	726	0	123	252	417	383	288	302

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	652	685	56	64	0	825	41	33	506	84	67	420	839
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	217	187	656	780	0	242	0	151	231	1725	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	59	82	733	584	109	88	934	457	40	351	599	48	38
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	56	431	668	92	476	157	487	1264	139	57	153	51	67
Basidiomycota	Tremellomycetes	Tremellales			3606	32	0	0	40	33	0	27	0	25	216	47	27
Ascomycota	Dothideomycetes	Capnodiales			64	38	27	43	41	44	0	28	68	2641	730	37	101
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		173	106	82	200	174	216	130	777	257	331	107	487	288
Ascomycota	Dothideomycetes				64	22	79	21	40	56	4	1747	31	32	68	70	1044
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	136	152	173	598	335	97	291	105	60	700	314	176	131
Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Arxiella	13	13	0	0	12	3162	0	6	0	9	0	0	14
Ascomycota	Eurotiomycetes	Chaetothyriales			26	0	21	37	14	18	0	26	49	0	2924	0	28
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	83	185	181	80	48	51	115	215	36	106	1870	40	18

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			379	294	0	270	0	0	0	0	811	706	325	148	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae		Pseudombrophila	291	355	172	0	123	161	0	207	188	399	139	627	180
Ascomycota	Eurotiomycetes	Chaetothyriales				34	0	0	0	15	32	0	0	0	34	2549	32	29
Ascomycota	Dothideomycetes	Capnodiales				162	42	133	54	124	73	48	18	1262	245	330	50	142
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae		Helminthosporium	0	86	0	0	298	0	71	0	0	1979	0	0	84
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Septoria		97	104	169	96	275	333	59	214	153	77	526	97	197
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	119	58	91	54	45	78	110	1491	0	0	223	58	53
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			91	0	0	0	0	185	0	0	1792	0	0	0	286
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gibberella	352	187	136	0	275	388	0	360	66	104	210	84	177
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	110	212	313	157	235	215	96	62	390	285	130	124
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Neophaeothecoidea	0	0	0	156	417	133	0	0	794	337	0	296	187
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Geastrumia	13	21	8	12	126	29	0	0	20	22	2008	28	32

Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia		0	0	0	0	0	0	0	0	2317	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Gamsia		341	261	181	0	161	482	0	45	162	239	129	199	101
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae		Helminthosporium	0	0	0	159	0	0	0	0	0	0	2133	0	0
Ascomycota	Dothideomycetes	Pleosporales				47	28	118	19	579	183	246	701	115	62	107	0	41
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Stomiopeltis	98	31	214	28	108	86	5	1219	55	69	73	0	220
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		Paragibellulopsis	195	266	177	0	165	196	0	69	97	201	246	208	376
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	41	95	0	478	43	65	44	1238	35	0	133	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Geastrumia	30	15	0	0	19	18	0	13	20	20	1966	0	19
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	0	0	82	146	98	0	1069	0	461	101	105	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Neonectria	287	226	73	0	458	313	0	50	86	129	202	159	73
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola	grisea	305	215	109	8	210	308	0	49	115	211	223	120	140
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Phaeophleospora	152	113	247	347	262	118	244	19	62	131	138	50	109

Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	104	0	35	0	0	0	0	203	111	1304	164	42
Ascomycota	Dothideomycetes	Capnodiales			1485	0	36	40	102	33	0	27	0	84	68	51	0
Ascomycota	Dothideomycetes				672	30	154	0	27	37	0	92	30	56	62	40	719
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	16	0	0	0	0	0	0	370	62	1388	42	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	234	170	129	0	186	251	0	74	84	217	250	153	102
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	451	201	28	82	89	69	0	0	96	0	586	174	73
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	48	91	965	0	0	0	0	0	62	0	107	113	449
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	262	0	0	630	117	253	58	0	125	182	0	0	167
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	33	0	22	0	11	33	0	1526	23	38	55	26	26
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae	Punctulariopsis	8	0	0	0	0	1536	35	4	9	93	0	0	6
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	0	0	0	0	0	0	0	0	0	1652	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		142	18	46	159	15	210	125	235	7	319	199	53	77

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	0	1542	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	73	98	275	47	431	0	150	22	353	0	36	43	0
Ascomycota	Sordariomycetes	Hypocreales			175	205	100	0	141	209	0	43	140	128	89	200	92
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	154	153	119	30	173	129	74	85	262	96	102	55	59
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	194	170	133	0	156	206	0	58	79	165	141	99	88
Ascomycota	Dothideomycetes	Myriangiales			631	37	0	57	0	0	26	0	68	164	401	0	95
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		155	231	78	0	177	183	0	33	84	112	137	159	112
Ascomycota	Dothideomycetes	Capnodiales			20	0	0	0	99	31	0	25	26	511	552	23	158
Basidiomycota	Tremellomycetes	Tremellales			360	0	195	26	28	0	280	0	103	120	152	0	96
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		568	17	13	10	504	45	0	0	35	21	62	31	49
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	140	146	119	0	154	187	0	41	0	184	139	147	58
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dactylonectria	161	196	134	0	155	197	0	29	63	119	94	63	96
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma	42	166	38	17	27	42	18	36	400	143	263	81	26

Basidiomycota	Tremellomycetes	Filobasidiales	Piskurozymaceae		Solicoccozyma	176	99	112	3	132	160	0	31	61	153	174	123	63
Ascomycota	Eurotiomycetes	Chaetothyriales				15	0	0	0	0	13	0	0	0	17	1217	11	13
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Stomiopeltis	0	24	0	0	22	0	0	0	0	0	31	21	1182
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Stomiopeltis	32	0	0	17	30	0	0	284	17	0	864	31	0
Ascomycota	Dothideomycetes	Myriangiales	Elsinoaceae			0	3	0	0	0	3	1199	0	0	0	0	20	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	60	0	0	389	51	34	0	408	73	0	179	0
Ascomycota	Dothideomycetes	Capnodiales				516	0	43	0	0	0	16	0	49	212	0	0	340
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		Plectosphaerella	130	149	45	0	103	113	74	55	74	77	202	65	78
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium		100	105	49	0	154	128	0	46	46	72	181	144	139
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae		Nigrospora	194	0	0	48	141	0	70	0	0	63	498	93	55
Ascomycota	Eurotiomycetes	Phaeomoniellales				61	6	272	0	6	41	24	7	78	108	433	17	108
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Australosphaerella	40	0	0	0	0	149	126	0	535	249	0	0	53

Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	138	112	94	0	146	175	0	40	54	125	72	92	79
Ascomycota	Dothideomycetes	Capnodiales	Capnodiaceae		Capnodium	23	23	9	844	22	38	0	9	35	30	24	36	31
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Neocoleroa	55	54	106	0	0	32	0	27	0	847	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Neocoleroa	82	98	390	16	114	0	17	0	33	154	94	64	40
Ascomycota	Dothideomycetes	Myriangiales				969	0	0	0	0	82	0	0	0	0	0	35	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Xenophacidiella	447	33	0	0	31	20	0	10	414	17	64	19	22
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	1075	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		47	248	0	0	15	40	0	593	47	0	42	0	38
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae		Nigrospora	76	193	0	46	0	30	58	41	45	85	300	123	57
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gibberella	142	162	73	0	101	87	14	37	50	73	92	109	109
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		Crucellisporiopsis	0	0	0	0	41	496	108	10	0	25	350	19	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae			678	22	91	13	8	9	0	12	19	21	31	92	48

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Exopassalora	0	0	0	10	0	26	0	0	30	14	537	0	420
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metarhizium	robertsii	165	66	4	0	0	681	0	2	21	53	15	0	8
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	128	68	72	0	107	228	0	30	35	112	74	100	47
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusicolla		104	150	47	0	126	166	0	43	64	82	87	62	63
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae			52	0	46	23	151	49	148	28	110	42	318	0	19
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		Botryotrichum	121	185	66	0	81	169	0	36	106	72	27	30	87
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	14	0	0	0	0	0	0	919	0	0	24	0	14
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Stomiopeltis	0	0	0	0	0	0	0	0	0	168	0	0	803
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Parapenidiella	520	28	9	15	15	23	0	0	19	23	19	269	17
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	92	23	30	100	43	0	342	156	14	33	107	0	16
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	75	0	0	0	825	0	0	45	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	51	90	74	188	0	118	88	74	33	131	90	0	0

Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis		Liberomyces	46	9	795	17	0	17	0	0	8	14	11	0	11
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis		Microcyclospora	24	16	10	0	260	23	0	14	423	23	23	11	73
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		81	100	145	45	50	67	53	48	81	91	32	55	48
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	0	0	892	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae		Helminthosporium	0	0	379	0	0	129	0	0	153	0	0	221	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae		Tetracladium	126	111	115	0	43	59	0	57	40	114	102	67	41
Ascomycota	Dothideomycetes	Capnodiales				20	14	0	25	17	0	0	82	30	187	137	40	309
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	102	0	0	207	0	130	125	0	0	279	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		Botryotrichum	183	110	98	0	81	184	0	0	0	91	0	0	88
Ascomycota	Dothideomycetes	Pleosporales				45	0	23	10	43	66	24	139	31	24	401	0	27
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Pseudocercospora	0	0	0	0	0	8	779	40	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	818	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		30	15	14	18	13	30	15	0	0	0	0	675	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	0	157	165	33	0	53	123	274	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	0	0	0	792	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	101	92	29	19	80	89	19	36	57	69	99	54	46
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Lophotrichus	71	41	29	19	80	57	5	40	23	50	332	30	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	30	40	187	0	0	96	52	93	174	95	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			13	15	0	21	0	16	0	0	8	0	0	11	680
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		24	570	0	0	0	60	0	0	9	0	9	80	8
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	27	0	229	0	0	0	0	20	0	475	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		239	26	0	25	0	81	192	0	57	69	29	32	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	59	0	106	0	0	0	0	75	510	0	0

Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Neophaeomoniella	0	0	0	0	0	0	741	0	0	0	6	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium	44	0	422	0	0	0	41	34	0	0	139	24	28
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	60	31	0	0	92	206	92	56	0	47	58	23	64
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	723	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		632	0	0	15	0	0	0	0	0	33	0	20	19
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	74	0	0	31	44	0	0	0	0	567	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Proliferodiscus	19	81	285	0	211	10	34	8	15	9	0	21	16
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	285	421	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Planistromellaceae	Ramimonilia	15	21	0	13	16	0	20	56	205	0	272	22	59
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	250	0	0	443	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cladorrhinum	686	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		13	0	326	0	0	48	121	8	45	0	0	0	121

Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		Plectosphaerella	68	56	47	9	123	121	0	0	43	106	106	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae		Nigrospora	0	0	671	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	solani	98	99	34	0	76	100	0	17	28	60	70	54	27
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Stomiopeltis	0	0	0	0	0	0	0	0	0	0	0	535	123
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae		Tetracladium	88	34	21	0	43	51	0	25	72	94	76	96	38
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae		Talaromyces	23	0	0	0	0	17	0	0	429	110	50	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Cylindrocarpon	84	85	38	0	50	93	0	0	26	55	75	79	33
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Paramycosphaerella	0	0	0	0	0	614	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		Colletotrichum	74	36	68	25	121	27	0	104	105	22	0	21	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		Schizothecium	81	126	33	0	39	97	0	37	40	46	17	16	67
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	49	544	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		Colletotrichum	0	0	0	0	0	0	575	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	8	0	0	0	0	0	8	0	556
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	564	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium	36	0	342	0	23	30	30	0	0	41	58	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	6	0	0	0	0	0	202	0	7	7	327	4	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	65	425	15	11	0	0	0	0	14	0	16	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	0	0	0	0	0	0	0	0	91	455	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	0	0	0	0	31	105	0	19	322	0	0	0	67
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	16	396	53	0	0	25	0	0	0	51	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	65	74	66	0	56	67	7	11	28	56	56	22	30
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	28	0	28	0	0	17	199	52	60	0	0	144
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	0	0	7	0	0	34	0	0	0	465	4	0	9
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	0	42	379	32	0	0	0	0	0	21	0	0	40

Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Filobasidium	27	49	21	0	29	226	7	10	19	14	66	27	18
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Tetracladium	65	88	33	0	27	78	0	0	34	49	44	35	42
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	495	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Thelebolaceae	Thelebolus	73	49	70	0	29	61	0	10	24	57	53	22	38
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	61	0	0	0	323	0	0	0	23	23	0	54
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	59	32	0	0	47	86	0	43	19	39	58	74	21
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	6	15	3	0	0	0	0	0	388	42	12	9	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	103	17	11	0	0	28	11	0	64	9	144	25	62
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae	Wickerhamomyces	0	0	9	0	14	35	0	0	414	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	471	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	470	0	0	0	0	0	0	0	0
Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia	37	47	0	0	39	237	30	5	0	36	0	0	35
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	53	24	20	171	0	50	74	15	12	0	18	10	16

Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	0	0	0	0	0	18	46	0	358	0	26	0	13
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	79	57	48	0	38	67	0	18	0	60	39	22	22
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	447	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		12	0	0	136	29	0	240	0	0	4	13	11	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		15	0	0	0	417	12	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	440	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	59	0	0	0	0	0	166	0	161	0	21	32	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Crucellisporiopsis	0	21	0	0	0	412	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	0	432	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	228	204	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	11	15	0	5	274	10	5	0	12	11	74	13	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	424	0	0	0	0

Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis		Triposporium	40	0	167	6	0	15	4	0	56	133	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	66	0	0	0	0	0	0	0	0	81	0	263	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		Cladosporium	0	0	0	0	0	0	330	0	0	78	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae		Pseudogymnoascus	62	70	21	0	48	40	0	20	26	29	34	32	25
Olpidiomycota	Olpidiomycetes	Olpidiales	Olpidiaceae	Olpidium		7	23	4	3	19	16	0	256	15	11	23	12	17
Ascomycota						0	0	0	0	0	148	0	0	0	0	160	92	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	45	0	344	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia		36	7	8	0	11	21	225	0	0	0	44	31	0
Ascomycota						16	8	5	3	316	8	0	0	5	6	15	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Neocosmospora	62	47	16	0	41	70	0	17	19	27	31	26	19
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Stomiopeltis	0	0	0	0	0	0	0	0	0	357	0	17	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	65	0	0	307	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis		Parapyrenochaeta	6	4	0	0	10	284	0	0	0	0	5	0	61

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	370	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	67	69	16	0	19	73	0	11	23	26	0	26	36
Ascomycota	Dothideomycetes	Capnodiales			35	0	0	0	34	96	12	8	16	0	0	143	17
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	0	0	0	0	0	0	0	0	360	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	359	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Crucellisporiopsis	0	0	0	0	0	358	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	357	0	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Chrysozymaceae	Sampaiozyma	0	0	0	0	22	0	0	0	0	11	296	27	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		0	32	36	0	114	0	81	54	0	0	31	0	6
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora neriicola	0	0	13	0	0	0	336	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	13	336	0	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	79	0	0	0	0	0	253	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	33	92	33	8	46	15	9	24	0	25	20	15	11
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Issatchenkia	orientalis	11	5	0	0	0	35	0	0	213	10	37	16	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	0	0	0	0	0	0	0	0	231	50	45	0	0
Ascomycota	Eurotiomycetes	Eurotiales				39	44	61	0	12	0	37	31	0	25	53	0	13
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Pseudocercospora	0	22	0	45	0	87	55	0	45	0	0	20	39
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	13	0	0	81	0	0	46	0	0	172	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		0	0	0	0	0	243	0	0	0	0	69	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Stomiopeltis	0	0	0	0	0	0	0	0	0	0	0	0	312
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	311	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae		Tetracladium	59	0	0	0	26	42	0	0	48	76	58	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	0	0	0	0	0	0	0	0	0	309	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	309
Ascomycota	Sordariomycetes				255	8	0	6	4	8	0	0	0	0	0	9	13
Olpidiomycota	Olpidiomycetes	Olpidiales	Olpidiaceae	Olpidium	8	20	0	10	12	0	0	8	0	7	202	25	7
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		66	0	0	0	190	0	0	0	0	41	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	7	0	0	0	0	0	46	27	7	0	8	0	201
Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	Microdochium	39	47	58	0	18	36	0	0	0	23	22	15	35
Ascomycota	Eurotiomycetes	Eurotiales			22	23	0	0	50	20	39	10	0	18	110	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	68	33	0	26	0	89	6	60	0	9	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	291	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	55	0	54	0	7	54	0	0	0	0	47	68	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		61	6	0	0	50	0	150	0	12	0	0	3	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	0	0	0	0	280	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	203	0	74	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosulcatispora	16	22	0	13	64	17	95	14	0	10	0	7	17
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	0	128	48	0	71	0	0	0	0	0	0	23	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	270	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	0	0	270
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	0	269	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			30	0	0	12	0	209	0	0	0	0	0	0	17
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae		37	24	35	0	6	28	0	0	0	0	49	15	70
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		39	42	16	0	36	51	0	8	11	23	11	13	13
Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Schizophyllum	8	0	7	0	218	7	0	6	0	0	8	9	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	4	5	5	105	16	11	53	0	12	9	37	0	6
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	47	35	28	0	20	23	0	7	0	37	23	16	25

Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	0	17	0	15	10	11	37	0	29	12	105	11	14
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Meyerozyma	5	0	7	0	138	9	0	0	32	13	45	0	7
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	0	0	97	158
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	34	45	0	0	26	12	11	0	11	0	93	21	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	43	0	67	0	77	0	0	8	0	14	25	18	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	97	0	16	0	0	12	22	0	38	44	22
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	199	40	0	11	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	0	250
Ascomycota	Dothideomycetes	Capnodiales			0	235	3	0	4	0	0	0	6	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Euteratosphaeria	35	71	0	7	32	11	0	0	12	22	47	0	10
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Neodidymella	0	0	0	0	0	0	216	0	0	0	28	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Exopassalora	23	0	0	0	0	0	0	0	0	0	0	219	0

Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	128	0	109	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Crucellisporiopsis	0	0	236	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	7	0	0	0	0	0	0	0	0	186	0	21	21
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	0	19	0	0	147	0	47	0	0	0	0	7	14
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	0	234	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales			218	0	6	0	0	0	0	0	0	9	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	108	0	125	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	0	0	0	0	152	0	0	0	77	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	229	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			3	10	0	0	25	35	0	0	138	0	4	0	13
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	0	0	0	0	228	0	0
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae	Punctulariopsis	0	0	0	0	0	226	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum		0	89	0	0	0	0	0	0	76	0	0	60	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	sackstonii	16	26	0	0	0	0	46	113	0	0	20	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria		0	0	0	0	0	0	221	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Stachybotrys		35	24	11	0	22	23	5	12	13	17	15	19	24
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Catenulostroma		25	28	0	17	0	7	7	0	0	112	0	0	22
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa		0	80	0	0	4	18	0	0	0	0	22	71	22
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	216	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	119	0	0	0	0	0	0	0	96	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium		0	0	92	0	0	0	0	0	0	0	121	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia		0	0	0	0	0	0	11	0	0	0	180	21	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum		34	0	76	13	38	0	41	0	0	9	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		9	0	0	10	9	14	9	79	0	0	76	0	5

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	0	0	0	0	0	208	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	0	0	0	0	0	208	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		0	0	0	0	0	0	0	0	0	207	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium		0	0	0	0	0	0	0	0	0	0	206	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	gamsii	29	31	33	0	23	35	0	8	0	19	26	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cyanodermella		0	0	2	3	0	0	0	0	2	4	193	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria		7	0	152	0	0	9	0	0	0	0	0	0	32
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana		8	0	0	0	0	20	21	136	0	0	0	0	14
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae			55	0	28	0	0	115	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes					3	3	0	0	3	0	0	2	187	0	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora		0	0	0	0	0	0	50	0	0	147	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana		78	0	20	0	8	0	0	62	0	3	0	5	15

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	30	0	0	0	28	30	0	0	72	31	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	0	0	0	0	0	0	0	0	0	191	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Xenoteratosphaeria	0	0	0	0	0	0	0	0	0	191	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		Cercophora	18	60	11	0	0	100	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	0	0	188
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae			10	36	38	0	7	12	0	7	14	12	10	14	27
Ascomycota	Sordariomycetes	Chaetosphaeriales				3	6	0	4	0	10	0	0	0	0	4	154	4
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Neocosmospora	0	0	40	0	0	0	0	0	92	20	32	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Apodus		22	56	6	0	6	37	0	15	18	13	0	0	9
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	0	0	0	182	0	0	0	0	0	0	0	0	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae		Septobasidium	0	26	0	5	0	0	0	0	0	0	34	99	15
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae		Helminthosporium	0	0	0	0	0	0	0	0	0	0	179	0	0

Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	0	155	0	0	0	0	0	0	16	0	7	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	0	0	178	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	4	6	0	0	161	0	3	3	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	11	0	0	0	166	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cyanodermella	8	11	87	0	0	10	37	0	23	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	0	0	0	0	0	8	0	168
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Madagascaromyces	160	0	0	10	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	118	56	0
Ascomycota	Dothideomycetes	Asterinales	Parmulariaceae	Parmularia	0	0	69	0	33	6	29	27	3	0	0	5	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	172	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	114	57	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		36	55	25	0	0	54	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		115	0	0	0	0	20	0	0	0	0	14	7	12
Ascomycota	Sordariomycetes				5	3	0	0	2	6	0	139	5	0	8	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris	0	0	0	0	0	0	167	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	167	0	0	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	0	0	166	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	97	0	0	0	0	18	51	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	0	0	0	135	31	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	32	0	0	0	0	0	0	0	0	0	133	0	0
Ascomycota	Leotiomycetes	Helotiales			5	151	0	0	0	3	0	0	0	0	0	6	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	164	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	0	0	0	0	161	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	9	0	0	0	0	0	134	0	0	17	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	160	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	17	26	32	0	11	0	8	8	0	0	31	19	6
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		153	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	76	0	0	0	38	0	0	6	27	0	0	10
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	0	0	0	0	0	0	0	0	0	0	157
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae	Gloniopsis	2	10	0	0	0	0	12	0	132	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	18	0	0	0	0	137	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	69	0	0	57	0	0	0	29	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	0	0	0	0	155	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Pezicula	0	154	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae	Punctulariopsis	0	0	154	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae	Leptosphaeria	19	20	7	0	13	22	0	0	21	15	13	0	23
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	0	0	0	0	0	153	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Nothophoma	0	0	0	0	0	0	0	0	56	0	97	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	11	14	10	0	66	3	3	11	9	10	15	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariaceae	Gelasinospora	0	0	131	0	0	17	0	0	0	4	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	0	0	151	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	0	0	0	0	0	0	134	0	17	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Australosphaerella	0	0	0	0	0	0	0	0	0	0	0	151	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chloridium	10	0	0	0	4	0	0	0	39	87	6	4	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		5	108	0	0	0	0	0	0	25	12	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	27	0	0	0	0	0	0	0	0	0	123
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Peltaster	46	0	4	23	0	62	0	3	7	0	0	4	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	18	38	17	0	19	0	0	18	9	0	17	12	0

Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	24	24	0	0	0	23	0	0	25	20	20	0	11
Ascomycota	Dothideomycetes				0	0	147	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	40	16	0	0	34	17	0	0	0	17	0	22	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Teratosphaericola	27	0	11	16	8	18	0	0	29	18	0	0	19
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola	0	0	0	0	54	0	0	60	0	0	32	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	35	0	0	0	0	86	0	0	0	0	23	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Boeremia	11	0	0	0	0	0	0	0	133	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Planistromellaceae	Ramimonilia	0	0	14	0	0	0	6	0	10	0	38	25	51
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	0	0	0	0	0	0	144	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	49	0	0	0	0	0	0	0	94	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	23	9	65	0	29	17	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	143	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		Magnibotryascoma	47	33	12	0	6	14	12	0	0	0	17	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae			0	0	128	0	0	0	0	3	0	0	6	0	4
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Neophaeothecoidea	140	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusicolla		38	26	0	0	32	44	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae		Trichoderma	26	21	42	0	9	27	0	0	0	0	0	8	7
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Gamsia		24	0	0	0	64	33	0	0	0	0	0	0	17
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Clonostachys	sp	20	35	0	0	0	61	0	0	0	0	14	7	0
Ascomycota						19	0	3	0	3	12	0	2	4	0	7	86	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae			0	57	0	0	0	78	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae		Paramyrothecium	18	24	5	0	20	32	0	0	11	17	0	6	0
Ascomycota	Dothideomycetes	Pleosporales				13	23	12	0	10	30	0	0	4	16	12	13	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		Metarhizium	0	8	7	3	0	0	0	0	38	75	0	0	0

Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriales_fam_Incertae_sedis	Dendrophoma	0	0	16	67	0	0	6	5	0	33	4	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Apiotrichum	9	0	0	0	6	7	0	0	88	9	5	0	6
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis		0	0	11	0	0	12	0	47	22	0	0	10	28
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	129	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		0	0	128	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	45	0	83	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	0	0	0	0	0	0	0	0	0	128	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	0	76	52
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	0	0	0	0	127	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	125	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	125	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	0	0	0	0	0	0	125	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	125	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	0	0	125	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Clavispora	0	0	0	0	0	8	0	0	103	0	13	0	0
Basidiomycota	Tremellomycetes	Tremellales			55	19	0	0	0	33	0	0	16	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		5	0	5	0	0	0	0	0	0	3	4	105	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Retroconis	21	11	0	0	17	31	0	0	7	0	10	11	13
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia	4	0	0	0	0	0	8	6	0	0	0	103	0
Ascomycota					0	0	0	0	28	0	0	0	0	0	93	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	0	121	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	0	0	0	0	0	0	0	0	0	0	121	0	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae	Septobasidium	0	0	0	0	0	14	0	0	0	0	6	74	25
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	119	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	0	0	118	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium	0	0	0	0	0	0	0	0	113	5	0	0	0

Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	35	83	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Paramycosphaerella	0	0	25	51	0	17	0	0	0	24	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Neosetophoma	0	6	59	0	0	4	19	22	0	0	6	0	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae			0	41	0	0	0	0	0	0	11	0	22	41	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Cephalotrichum	nanum	0	40	8	0	8	17	0	0	28	14	0	0	0
Ascomycota	Dothideomycetes					0	0	0	2	67	10	3	24	0	0	0	5	3
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	114	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Geastrumia	0	0	0	0	0	0	0	0	0	0	0	114	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Chrysozymaceae		Sampaiozyma	17	50	0	14	0	12	0	8	12	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				11	9	0	0	14	32	0	0	0	13	14	12	8
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae		Gloniopsis	0	0	0	0	0	0	0	0	0	113	0	0	0

Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	19	67	10	17
Ascomycota	Dothideomycetes	Capnodiales			59	0	0	0	0	3	5	0	0	41	0	0	4
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	15	0	83	0	0	14	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales			0	0	0	0	0	0	0	0	111	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	110	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	110	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	110	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	110	0	0
Basidiomycota	Tremellomycetes	Tremellales			5	0	0	0	3	0	0	0	91	0	0	9	0
Ascomycota	Sordariomycetes	Diaporthales	Valsaceae	Cytospora	85	0	16	0	0	0	0	0	0	0	0	0	4
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	105	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	105	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Verticillium	16	15	15	0	0	23	0	0	7	8	0	9	11

Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis		Triposporium	0	13	0	0	22	0	0	37	0	0	24	8	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae			0	0	0	0	104	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae			0	0	0	0	0	0	0	0	104	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				13	22	12	0	0	11	0	0	12	9	0	0	24
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stenella		0	0	0	0	0	103	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paraconiothyrium	0	0	0	0	0	0	0	103	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	103	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola		0	0	0	0	0	0	0	0	0	18	68	17	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	0	0	31	0	0	0	0	51	0	20	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	98	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae		Phyllosticta	0	0	0	0	0	0	101	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	100	0	0	0	0	0	0	0	0	0	0	0	0

Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae		17	3	60	0	0	0	0	0	0	10	0	0	10
Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Moellerodiscus	0	0	71	0	0	0	0	3	6	0	10	10	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		10	14	0	0	11	16	0	0	11	10	9	18	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	52	0	47	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	28	0	0	0	0	45	0	0	26
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	99	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	25	0	0	37	0	0	16	0	14	0	6	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	98	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	64	33	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	35	0	0	0	0	0	62	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	5	0	0	0	92	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cyanodermella	0	0	0	0	0	3	0	0	0	0	94	0	0

Ascomycota	Dothideomycetes				0	0	0	0	0	0	79	0	0	0	17	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	0	0	0	0	0	0	44	0	0	0	9	15	28
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	96	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	0	0	96	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	0	0	0	0	0	0	0	0	0	96	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola	0	12	0	0	0	21	0	0	29	22	0	11	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	95	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	27	0	0	0	67	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis	Ramophialophora	19	15	0	0	10	0	0	0	27	15	8	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Lepteutypa	12	5	0	9	0	11	2	29	0	0	20	6	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Catenulostroma	0	22	0	0	17	13	11	0	9	0	9	0	13
Ascomycota	Eurotiomycetes	Onygenales	Onygenaceae	Polytolypa	21	0	15	0	0	25	0	0	0	7	9	7	9

Chytridiomycota	Spizellomycetes	Spizellomycetales			0	56	35	0	0	0	0	0	0	0	0	2	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala	16	25	0	0	11	10	0	0	0	16	0	13	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Hyphopichia	0	5	0	0	0	0	0	0	86	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Paraphoma	8	7	0	0	12	8	0	0	11	17	8	13	6
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	0	0	0	0	90	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	0	0	90
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		0	0	0	0	0	0	0	0	0	0	0	0	90
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	0	0	0	0	0	0	71	0	0	0	18	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	0	0	0	0	0	0	0	0	89	0	0	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Podosphaera	0	0	0	0	0	0	8	2	20	0	51	0	7
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	87	0	0	0	0	0
Ascomycota	Sordariomycetes				77	0	0	0	0	0	0	0	9	0	0	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		5	0	0	0	22	0	18	28	0	0	13	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cladorrhinum		0	28	44	0	0	0	0	0	0	0	0	0	14
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae	Gloniopsis		0	0	0	0	86	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum		0	0	0	0	0	0	86	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Thermomyces	lanuginosus	7	0	0	2	0	11	0	0	37	4	18	6	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium		0	18	18	0	7	17	0	0	8	0	0	10	7
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae			0	0	0	0	0	66	19	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	0	0	0	0	85	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				7	2	0	0	4	0	0	0	44	23	0	0	3
Ascomycota	Sordariomycetes	Diaporthales	Lamproconiaceae			0	0	0	0	0	0	75	0	0	8	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium		0	0	0	0	0	0	0	0	0	0	83	0	0

Ascomycota	Leotiomycetes	Helotiales			4	75	0	0	3	0	0	0	0	0	0	0	0
Ascomycota					0	0	82	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Exopassalora	0	0	2	0	0	0	0	0	0	0	80	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycopsidaceae	Saccharomycopsis	0	0	0	0	0	7	0	0	61	0	14	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	82	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	82	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	0	0	0	0	81	0	0	0	0	0	0
Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia	0	0	0	0	0	0	0	0	81	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		80	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		12	15	7	0	0	14	13	0	6	0	6	0	7
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae	Gyroporus	0	0	0	0	80	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	0	0	0	54	0	0	0	0	0	0	26	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Trichosporon	0	0	0	0	0	10	0	0	66	0	4	0	0

Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	spirale	0	0	0	0	0	0	19	0	61	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	79	0	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudogymnoascus		22	17	0	0	0	17	0	0	0	0	0	0	22
Basidiomycota	Ustilaginomycetes	Ustilaginales	Ustilaginaceae	Moesziomyces		0	0	0	0	0	0	31	3	0	0	44	0	0
Ascomycota						0	0	0	0	0	0	0	0	0	0	78	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Exopassalora		0	0	0	0	0	0	0	0	0	0	0	78	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella		0	0	0	0	0	0	0	0	0	0	0	0	78
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	14	42	0	0	0	21	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	32	0	0	0	45	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium		0	0	0	0	0	0	0	0	46	31	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria		0	0	0	0	0	0	0	0	0	77	0	0	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Mrakiaceae	Tausonia		0	0	0	0	0	0	0	0	0	77	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella		8	21	15	0	18	11	0	0	3	0	0	0	0

Basidiomycota	Agaricomycetes	Corticiales				0	0	0	0	76	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		Colletotrichum	0	0	0	0	0	0	76	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gibberella	0	0	0	0	0	0	38	0	0	0	38	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	76	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae		Aureobasidium	0	0	0	0	0	0	75	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		Proliferodiscus	0	0	0	0	0	0	0	0	0	0	75	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	0	0	0	75	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	conoides	62	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		Teichospora	13	12	0	10	0	0	0	10	0	0	27	0	2
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		Proliferodiscus	4	0	0	0	65	0	0	0	3	0	0	2	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Xenocamarosporium	0	0	0	0	11	12	0	11	0	0	11	0	29
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Mariannaea	4	0	0	0	4	0	0	0	0	65	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	11	0	0	18	0	11	0	0	0	0	32	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae		6	0	7	2	0	0	6	0	3	0	42	3	3
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	72	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	0	0	0	0	0	0	0	0	0	0	72	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudogymnoascus	15	23	0	0	0	17	0	0	0	0	0	16	0
Ascomycota	Dothideomycetes	Pleosporales			9	6	48	0	0	0	8	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales			8	7	0	0	11	11	0	0	4	6	18	6	0
Ascomycota	Pezizomycetes	Pezizales	Ascodesmidaceae	Cephaliophora sp	0	14	10	0	0	8	0	0	18	7	9	0	5
Ascomycota					0	0	64	0	0	0	0	0	7	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	25	0	0	0	0	0	46	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	71	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	71	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	23	28	0	0	20	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	40	0	0	19	0	0	0	0	0	0	11	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Geopora	0	0	0	0	28	4	33	5	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	7	0	0	23	19	4	17	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	70	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	34	36	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	0	0	0	0	0	0	0	0	70	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	70	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	0	0	70	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	0	70	0
Ascomycota	Dothideomycetes	Capnodiales			0	11	3	0	0	0	0	0	0	0	55	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Aleuria	0	9	0	0	26	24	0	0	10	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales			0	2	0	0	62	0	0	0	5	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	32	0	37	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		68	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		68	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	21	0	0	47	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	68	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	68	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	68	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	0	0	68	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	0	0	0	0	67	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	0	0	0	47	20	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	0	0	67	0	0	0

Ascomycota	Sordariomycetes				0	61	0	0	0	0	0	0	0	5	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodotorula	0	8	41	0	4	0	0	9	0	0	4	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae		0	0	66	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	66	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	66	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Cercosporidium	0	0	0	0	0	0	18	0	0	0	48	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	3	0	0	0	0	0	63
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae		0	0	0	0	0	0	0	0	66	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	21	0	0	0	24	0	0	3	6	0	0	0	11
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Cryptococcus	5	16	8	0	0	9	0	0	0	20	7	0	0
Ascomycota	Leotiomycetes	Helotiales			0	7	0	0	0	0	58	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	65	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	65	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	0	65	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	0	0	0	0	65	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Retroconis	24	0	10	0	0	0	0	10	0	7	7	6	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Emericellopsis	8	0	8	0	16	0	0	0	7	0	20	0	5
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae		4	4	17	6	17	0	0	9	0	7	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	62	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	64	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales			63	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Bulleromyces	7	0	0	0	0	0	0	5	0	0	41	7	3
Ascomycota	Dothideomycetes	Capnodiales			0	62	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascodesmidaceae	Cephaliophora	0	26	0	0	0	15	0	3	11	0	7	0	0
Ascomycota	Dothideomycetes				0	0	62	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae	Erythrobasidium	0	0	11	0	0	0	0	15	0	17	0	0	19

Ascomycota	Dothideomycetes	Pleosporales	Thyridariaceae		0	0	0	0	0	5	0	0	36	21	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Monascus	0	6	0	0	16	7	0	0	0	9	7	16	0
Ascomycota					0	0	0	0	58	3	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma	0	0	0	0	0	0	0	0	61	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	0	0	0	0	0	0	0	0	0	61	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	0	0	61	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	8	53	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	23	9	17	2	0	3	0	0	0	6	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae		0	0	0	0	0	60	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	60	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	0	0	0	16	0	0	0	18	26
Ascomycota					0	0	0	0	0	0	0	0	8	52	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		16	8	12	0	0	10	0	0	3	0	10	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	21	0	0	24	0	0	14	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Gonatophragmium	0	0	59	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	5	0	6	0	26	0	0	0	22	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	59	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	39	0	20	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	0	0	0	0	0	0	0	0	0	0	0	59	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Lectera	8	16	0	0	6	19	0	9	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	58	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	58	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	58	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Valsaceae	Cytospora	22	15	0	0	0	0	0	0	20	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Crucellisporiopsis	0	57	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	43	0	0	0	0	0	0	0	0	0	14	0

Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma	0	0	0	0	0	0	57	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	57	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Lophotrichus	0	0	0	0	0	0	0	0	0	0	57	0	0
Ascomycota	Sordariomycetes				18	6	8	0	0	3	0	13	0	5	3	0	0
Ascomycota	Sordariomycetes				0	0	10	0	0	32	14	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae		0	0	4	0	0	0	0	0	0	48	0	4	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	56	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	44	0	0	0	0	11	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Lasiodiplodia	0	0	0	0	0	0	55	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	55	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Mariannaea	0	0	0	0	0	0	0	0	55	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	0	0	0	0	0	0	0	0	37	0	18	0	0

Ascomycota	Saccharomycetes	Saccharomycetales	Trichomonascaceae	Blastobotrys	19	0	4	0	0	0	0	0	6	25	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	10	0	0	0	17	27	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Phanerochaetaceae	Phanerochaete	0	2	0	0	0	0	0	6	0	0	46	0	0
Ascomycota					0	0	54	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	54	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	54	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	40	0	0	0	14	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Phaeophleospora	0	0	0	0	0	0	54	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	0	54	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	54	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Hermetothecium	4	4	0	3	0	0	0	0	0	0	0	0	42
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	53	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	0	0	0	0	0	0	0	53	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	0	0	53	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	33	0	0	0	0	0	0	0	0	19	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae		0	17	0	0	0	0	0	35	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	52	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	0	0	52	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae	Gyroporus	0	0	0	0	0	0	0	5	0	0	47	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	40	0	0	0	0	0	0	3	0	8	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	0	0	0	18	0	12	0	0	21	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	13	0	0	0	0	0	0	0	0	38
Ascomycota					0	0	0	0	51	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	51	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	0	0	0	0	0	51	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	0	46	0	0	0	5

Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	0	0	0	51	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	51	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae		Wickerhamomyces	0	0	0	0	0	0	0	0	0	0	51	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Fusculina		15	0	8	0	27	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	0	0	50	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	50	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae		Chaetothyrium	0	0	0	0	35	0	0	0	0	0	15	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	50	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae		Nigrospora	0	0	0	0	0	21	29	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae		Trichomerium	0	0	0	0	0	7	0	0	0	0	0	0	43
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae		Bullanockia	0	0	0	0	0	0	50	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	koningii	0	0	0	0	0	0	0	0	50	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	50	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia	0	0	0	0	0	0	0	0	0	0	0	50	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiotremataceae		0	11	0	0	31	0	0	0	0	7	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema	0	3	8	0	14	0	0	0	15	0	4	5	0
Basidiomycota					0	0	0	0	13	4	3	8	9	0	12	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	49	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	6	0	0	15	28	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	49	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	0	49	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	0	49	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		48	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	3	0	0	0	2	0	0	0	2	0	27	14	0
Ascomycota	Dothideomycetes				0	0	48	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Toxicocladosporium	0	0	0	0	0	48	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales			0	0	0	0	0	0	0	0	0	15	33	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	48	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	48	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	0	0	0	48
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	18	0	0	0	0	9	10	0	0	10	0	0	0
Ascomycota	Dothideomycetes				5	0	0	0	0	0	0	0	0	0	42	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Schizothecium	0	41	0	0	0	0	0	0	0	0	0	0	6
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	47	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	47	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	47	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		13	0	3	4	0	12	0	0	0	0	0	0	14

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	46	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	0	0	0	0	0	0	0	46	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	46	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae		0	0	0	0	0	0	0	0	0	2	0	0	44
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Paraboeremia	0	0	0	0	0	0	0	0	0	0	46	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	0	0	0	0	0	46	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	45	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	0	0	0	45	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	45	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	45	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	45	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Westerdykella	0	0	0	0	0	0	0	0	45	0	0	0	0

Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Saccothecium		0	0	0	0	0	0	0	0	0	0	45	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudeurotium		0	0	0	0	0	0	0	0	0	0	38	7	0
Chytridiomycota	Rhizophydiomycetes	Rhizophydiales				5	12	0	0	15	0	0	4	0	0	4	4	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae			4	28	0	0	0	9	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	44	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	truncatum	0	0	0	0	44	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	44	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	44	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola		0	0	0	0	0	0	0	0	44	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	20	0	0	24
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	10	0	0	34
Ascomycota						0	0	0	0	0	0	0	0	0	0	44	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	0	0	0	0	0	0	0	0	0	44	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	43	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pallidocercospora	0	0	0	30	0	0	0	0	0	0	0	0	13
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	15	0	0	0	14	0	0	0	14	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Simplicillium	0	0	0	4	15	0	15	0	4	0	0	5	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		0	0	0	0	0	0	43	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		0	0	0	0	0	0	43	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	0	0	0	0	0	0	0	43	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales			0	0	0	0	0	0	0	0	43	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Purpureocillium	0	0	0	0	0	0	0	0	28	15	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	0	0	0	0	0	43	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	0	0	0	0	0	0	43	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia		0	0	0	0	0	0	0	0	0	0	43	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		13	29	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium		0	42	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	13	0	0	0	2	0	2	0	0	0	25	0
Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Funneliformis		0	0	42	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Neofusicoccum		0	0	0	0	0	2	29	11	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		0	0	0	0	0	0	42	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis		0	0	0	0	0	0	0	0	42	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		0	0	0	0	0	0	0	0	0	42	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus		6	7	0	4	13	0	0	0	0	11	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	41	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	sclerotiorum	0	0	0	0	0	0	0	0	41	0	0	0	0
Basidiomycota						0	0	0	0	0	0	0	0	25	0	16	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Xenoteratosphaeria	0	0	0	0	0	0	0	0	0	41	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	0	0	0	0	0	0	0	0	0	0	41	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	40	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stenella		21	0	0	0	4	0	0	0	0	0	11	0	4
Basidiomycota	Agaricomycetes	Agaricales	Typhulaceae	Typhula		13	15	4	0	0	0	0	0	0	8	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		Neophaeomoniella	12	0	0	0	0	0	0	0	0	0	0	0	28
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		Cladosporium	0	10	0	0	0	0	21	0	0	0	9	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	3	0	0	0	10	0	0	2	15	0	10	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae		Hannaella	0	0	0	0	5	0	35	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Neophaeothecoidea	0	0	0	0	0	40	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae		Pestalotiopsis	0	0	0	0	0	3	0	0	0	0	37	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Phaeosphaeria	0	0	0	0	0	0	40	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae		Malassezia	0	0	0	0	0	0	0	7	0	0	33	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	40	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema	0	0	0	0	0	0	0	0	30	0	10	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	0	0	0	0	0	0	0	0	26	14	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	6	34	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	40	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		22	0	0	0	0	0	0	0	0	17	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Ajellomycetaceae		7	0	0	0	0	11	0	0	13	6	0	0	2
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	22	0	0	0	0	0	0	0	17	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	16	0	0	0	23	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		0	0	0	0	0	39	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria	0	0	0	0	0	0	39	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	0	0	0	0	0	0	39	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Gliomastix	0	0	0	0	0	0	0	0	39	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bionectria	0	0	0	0	0	0	0	0	39	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis	Rhodoveronaea	0	0	0	0	0	0	0	0	0	0	39	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	38	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Hermetothecium	0	10	0	0	0	3	0	0	0	0	10	0	15
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Aleuria	0	0	5	0	0	0	0	31	0	0	2	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	13	5	0	0	5	0	15	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	0	0	0	38	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascodesmidaceae	Cephaliophora	0	0	0	0	0	0	0	0	0	38	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Chordomyces	0	0	0	0	0	0	0	0	0	38	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenopenidiella	0	0	0	0	0	0	0	0	0	0	38	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	38	0	0

Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae	Gloniopsis	0	0	0	0	0	0	0	0	0	0	0	38	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	10	0	6	0	0	18	0	0	3	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	7	0	0	0	0	0	0	0	30	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	37	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	30	0	0	0	0	0	0	3	0	0	0	4
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Botryotrichum	0	20	0	0	0	0	0	0	0	0	0	0	17
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	37	0	0	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	37	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	0	37	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudeurotium	0	0	0	0	6	0	0	0	31	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	37	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	37	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Dissoconiaceae	Uwebraunia		0	0	0	0	0	0	37	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae			0	0	0	0	0	0	5	3	0	0	29	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae			0	0	0	0	0	0	0	0	10	27	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae			0	0	0	0	0	0	0	0	0	37	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Microcyclospo-rella	mali	0	0	0	0	0	0	0	0	0	0	37	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis			0	0	0	0	0	0	0	0	0	0	37	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae	Chrysofolia		36	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Sarocladium		8	9	0	0	0	0	9	0	0	0	5	0	5
Ascomycota	Saccharomycetes	Saccharomycetales	Pichiaceae	Pichia		5	0	0	0	0	0	0	0	0	0	31	0	0
Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta		0	5	0	0	20	0	0	4	0	5	0	0	2
Ascomycota	Dothideomycetes	Pleosporales	Coniothyriaceae			0	0	0	0	36	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales				0	0	0	0	0	0	36	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	36	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	36	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariaceae		Neurospora	35	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	0	35	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	19	0	0	0	0	0	0	16	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	pectinatoides	0	0	14	0	0	0	21	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	8	0	4	0	0	0	0	11	12	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gibberella	0	0	0	21	0	0	0	0	0	0	14	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	35	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Apiosporaceae			0	0	0	0	0	0	35	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		Proliferodiscus	0	0	0	0	0	0	6	0	0	0	29	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	0	0	0	0	0	0	35	0	0	0	0

Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae		0	0	0	0	0	0	0	0	26	9	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Mariannaea	0	0	0	0	0	0	0	0	0	35	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	0	0	0	35	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae		0	0	0	0	0	0	0	0	0	35	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium	0	0	0	0	0	0	0	0	0	35	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		0	0	0	0	0	0	0	0	0	0	35	0	0
Basidiomycota	Agaricomycetes	Boletales	Boletaceae	Cyanoboletus	0	0	0	0	0	0	0	0	0	0	35	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	0	35
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Madagascaromyces	34	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	13	0	0	0	0	0	0	0	0	0	0	21	0
Ascomycota	Saccharomycetes	Saccharomycetales			0	8	0	0	24	2	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	7	0	0	0	0	0	0	0	0	0	27	0
Ascomycota					0	0	34	0	0	0	0	0	0	0	0	0	0

Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	21	0	0	0	0	0	0	13	0	0	0
Ascomycota	Dothideomycetes				0	0	0	9	0	0	0	0	0	0	0	25	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Allophoma	0	0	0	0	34	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	0	0	0	0	32	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	9	25	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	34	0	0	0	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Gomphillaceae		0	0	0	0	0	3	0	0	0	3	0	0	28
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	0	34	0	0	0	0	0	0
Rozellomycota					0	0	0	0	0	0	0	34	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	34	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	17	17	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	34	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	0	0	0	0	0	0	0	0	34	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	30	4	0	0	0

Ascomycota						0	0	0	0	0	0	0	0	0	0	34	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		0	0	0	0	0	0	0	0	0	0	34	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae		Simplicillium	8	0	0	0	0	0	0	13	0	0	12	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina		4	24	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Coremiopassalora	3	0	0	0	0	0	0	0	30	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae		Hannaella	0	19	3	0	0	0	0	0	0	0	9	2	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	33	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		Magnibotryascoma	0	0	33	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	0	33	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	0	0	0	0	33	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Steccherinaceae		Steccherinum	0	0	0	0	0	0	33	0	0	0	0	0	0
Ascomycota	Sordariomycetes					0	0	0	0	0	0	24	0	4	5	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	0	0	0	0	0	0	20	0	0	0	0	13	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Curvularia	0	0	0	0	0	0	0	0	33	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	7	0	16	10	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	33	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	0	0	0	0	33	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	33	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	0	0	0	33	0
Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	Hormonema	28	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus	10	4	4	0	0	14	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	32	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Xenosonderhenia	0	32	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	32	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	32	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Tetraplosphaeriaceae		0	0	12	0	0	0	20	0	0	0	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae		Coprinellus	0	0	0	0	32	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae		Talaromyces	0	0	0	0	32	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis		Phialemoniopsis	0	0	0	0	0	26	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	32	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		Chloridium	0	0	0	0	0	0	0	4	0	28	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	0	0	32	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Neocosmospora	0	0	0	0	0	0	0	0	32	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae		Clavispora	0	0	0	0	0	0	0	0	21	0	11	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Aleuria		0	0	0	0	0	0	0	0	0	32	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	0	0	32	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		Paragibellulopsis	0	0	0	0	0	0	0	0	0	0	0	32	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida		17	3	0	0	7	0	0	0	0	0	4	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	0	18	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Lectera	0	0	31	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	0	0	0	0	31	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	31	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales	Elsinoaceae	Elsinoe	0	0	0	0	0	31	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	31	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	0	0	0	0	0	0	0	31	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	0	0	0	0	0	0	0	0	31	0	0	0	0
Ascomycota	Geoglossomycetes	Geoglossales	Geoglossaceae	Trichoglossum	0	0	0	0	0	0	0	0	31	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Dichotomopilus	0	0	0	0	0	0	0	0	24	7	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	31	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	31	0	0

Ascomycota	Dothideomycetes	Pleosporales	Corynesporascaceae		Corynespora	0	0	0	0	0	0	0	0	0	0	31	0	0
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae		Gyroporus	0	0	0	0	0	0	0	0	0	0	31	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	31	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales				0	0	0	0	0	0	0	0	0	0	31	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	17	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae		Lecanicillium	0	19	0	0	0	7	0	0	4	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae		Talaromyces	0	0	30	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		Nothophoma	0	0	30	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiotremataceae	Atrocalyx		0	0	9	0	3	12	0	0	0	0	0	6	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		Didymella	0	0	0	30	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae		Trichoderma	0	0	0	0	30	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	14	0	0	0	0	0	16	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	30	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	30	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	22	8	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Amorosiaceae	Angustimassarina	0	0	0	0	0	0	0	0	8	22	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	0	30	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida	0	0	0	0	0	0	0	0	0	25	0	5	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	30	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	12	0	18
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	0	0	0	0	0	0	30	0
Ascomycota	Sordariomycetes	Sordariales			7	13	0	0	0	0	4	0	0	0	0	5	0
Ascomycota	Dothideomycetes	Capnodiales			0	27	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Stephanonectria	0	13	6	0	0	0	0	0	0	10	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Kazachstania	0	0	0	0	29	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	3	0	0	0	0	0	0	0	26
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	0	0	0	0	0	0	29	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	29	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	29	0	0	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae	Septobasidium	0	0	0	0	0	0	0	0	0	23	6	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	29	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	0	0	29
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	29
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae	Septobasidium	0	0	0	0	0	0	0	0	0	0	0	0	29
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	0	10	0	3	0	0	0	0	15	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	28	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	0	0	28	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Thyridariaceae	Roussoella	0	0	17	0	6	0	0	0	0	0	0	0	5

Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	28	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Canariomyces	0	0	0	0	24	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae	Pseudolophiostoma	0	0	0	0	15	0	0	0	0	2	0	6	5
Ascomycota	Lecanoromycetes	Ostropales	Ostropales_fam_Incertae_sedis	Mulderomyces	0	0	0	0	0	28	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		0	0	0	0	0	26	2	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		0	0	0	0	0	2	0	0	0	0	26	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	0	0	0	0	28	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Mrakiaceae	Tausonia	0	0	0	0	0	0	0	28	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	28	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Meyerozyma	0	0	0	0	0	0	0	0	28	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	28	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	0	0	0	0	0	0	0	0	28	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	0	0	0	0	0	0	0	0	28	0	0	0

Ascomycota					0	0	0	0	0	0	0	0	0	0	28	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	0	0	0	0	0	0	0	0	28	0	0
Basidiomycota	Cystobasidiomycetes	Cystobasidiomycetes_ord_Incertae_sedis	Symmetrosporaceae	Symmetrospora	0	0	0	0	0	0	0	0	0	0	20	8	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		0	0	0	0	0	0	0	0	0	0	0	28	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Subulicystidium	5	0	0	0	7	0	0	0	2	13	0	0	0
Ascomycota	Dothideomycetes	Mytilinidiales	Gloniaceae	Cenococcum	4	0	0	0	23	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	27	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Morosphaeriaceae	Acrocalymma	0	15	0	0	0	8	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Myriangiales			0	0	27	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	27	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lepiota	0	0	27	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	27	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma	0	0	0	0	27	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	27	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Neooccultibambusa	0	0	0	0	0	0	0	0	27	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	27	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	0	0	0	27	0	0
Ascomycota	Dothideomycetes	Acrospermales	Acrospermales_fam_Incertae_sedis	Paramycoleptodiscus	0	0	0	0	0	0	0	0	0	0	27	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	27	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales			0	0	26	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	26	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	0	0	18	0	0	0	8	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	26	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma	0	0	0	0	0	4	0	0	22	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	26	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	0	0	0	0	0	0	0	0	26	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	26	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	24	0	2	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	0	12	0	0	14
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	0	0	0	0	0	26	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia	0	0	0	0	0	0	0	0	0	0	26	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	26	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	0	0	0	0	0	0	0	0	0	26	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris	25	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Muscodor	5	0	0	0	0	13	0	0	0	4	0	0	3
Basidiomycota	Agaricomycetes	Russulales	Peniophoraceae	Peniophora	0	25	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Torulaceae	Dendryphion	0	0	25	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudozasmidium	0	0	0	25	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema	0	0	0	4	0	0	21	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Lophiotremataceae	Atrocalyx	0	0	0	0	25	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes				0	0	0	0	25	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales	Elsinoaceae		0	0	0	0	0	0	25	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	0	0	0	0	0	0	0	25	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	25	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis	Microcyclospora	0	0	0	0	0	0	0	0	25	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae		0	0	0	0	0	0	0	0	25	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	25	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	0	0	0	0	0	0	25	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma	0	0	0	0	0	0	0	0	25	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	25	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae		0	0	0	0	0	0	0	0	25	0	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	0	0	0	0	0	25	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Clonostachys	0	0	0	0	0	0	0	0	0	25	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	25	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Chaetothyrium	0	0	0	0	0	0	0	0	0	0	0	0	25
Ascomycota	Eurotiomycetes	Onygenales	Gymnoascaceae	Leucothecium	9	0	0	0	0	9	0	0	0	6	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	0	24	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	9	0	0	0	0	0	0	0	15	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Colletogloeum	0	0	0	24	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Striaticonidium	0	0	0	0	24	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	24	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Ramulariopsis	0	0	0	0	0	0	24	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Teratosphaericola	0	0	0	0	0	0	0	24	0	0	0	0	0

Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Clavispora		0	0	0	0	0	0	0	0	24	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae			0	0	0	0	0	0	0	0	24	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Beauveria		0	0	0	0	0	0	0	0	24	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria		0	0	0	0	0	0	0	0	24	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	24	0	0	0	0
Chytridiomycota						0	0	0	0	0	0	0	0	9	15	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	aotearoa	0	0	0	0	0	0	0	0	0	24	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia		0	0	0	0	0	0	0	0	0	24	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	24	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa		0	0	0	0	0	0	0	0	0	13	0	11	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces		0	0	0	0	0	0	0	0	0	0	24	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Allophoma		0	0	0	0	0	0	0	0	0	0	24	0	0
Basidiomycota	Agaricomycetes	Sebacinales				0	0	0	0	0	0	0	0	0	0	0	24	0

Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		0	0	0	0	0	0	0	0	0	0	0	24	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Allophoma	0	0	0	0	0	0	0	0	0	0	0	14	10
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	23	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Torulaceae	Torula	21	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Stephanonectria	8	0	0	0	0	0	0	0	15	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Dissoconiaceae	Uwebraunia	5	2	0	0	0	0	0	16	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	23	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	0	14	9	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Remotididymella	0	0	0	0	23	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	23	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	23	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	19	0	0	0	0	0	4	0	0

Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Bisifusarium	0	0	0	0	14	0	0	0	0	0	0	9	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae			0	0	0	0	2	0	0	0	0	0	0	21	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae		Pseudeurotium	0	0	0	0	0	23	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae		Punctulariopsis	0	0	0	0	0	0	23	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Phaeosphaeria	0	0	0	0	0	0	23	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Mariannaea	0	0	0	0	0	0	0	0	23	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus		0	0	0	0	0	0	0	0	23	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae	Pholiota		0	0	0	0	0	0	0	0	23	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	0	0	0	0	0	0	0	23	0	0	0
Basidiomycota						0	0	0	0	0	0	0	0	0	0	23	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae		Naganishia	0	0	0	0	0	0	0	0	0	0	23	0	0
Basidiomycota	Agaricomycetes					0	0	0	0	0	0	0	0	0	0	23	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae		Hermetothecium	0	0	0	0	0	0	0	0	0	0	0	0	23
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae		Gyroporus	0	22	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris	yamadae	0	11	0	0	0	11	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricales_fam_Incertae_sedis	Uncobasidium		0	3	0	0	2	2	0	15	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma		0	0	22	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporobolomyces		0	0	22	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	5	0	17	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Bulleromyces		0	0	3	0	5	14	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria		0	0	0	0	22	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis	Mycoarthris		0	0	0	0	22	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Beauveria		0	0	0	0	5	0	0	0	0	17	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales				0	0	0	0	0	0	0	0	22	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudeurotium		0	0	0	0	0	0	0	0	22	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	0	0	8	14	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana		0	0	0	0	0	0	0	0	0	22	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Tolypocladium	0	0	0	0	0	0	0	0	0	22	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Lasiodiplodia	0	0	0	0	0	0	0	0	0	0	22	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	0	0	0	0	0	19	0	3
Basidiomycota	Tremellomycetes				0	0	0	0	0	0	0	0	0	0	0	22	0
Ascomycota	Dothideomycetes				21	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenopenidiella	14	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Toxicocladosporium	0	12	0	3	0	0	0	0	0	0	0	6	0
Ascomycota	Dothideomycetes				0	0	21	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Teratosphaeria	0	0	0	21	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales			0	0	0	0	21	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria	0	0	0	0	21	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	21	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Hyalocladosporiella	0	0	0	0	18	0	0	0	0	0	3	0	0

Chytridiomycota	Spizellomycetes	Spizellomycetales				0	0	0	0	0	4	0	0	0	3	14	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia		0	0	0	0	0	0	18	0	0	0	3	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Glutinomyces	sp	0	0	0	0	0	0	0	21	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	6	0	0	15	0
Basidiomycota	Tremellomycetes	Trichosporonales	Tetragoniomycetaceae			0	0	0	0	0	0	0	0	0	21	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella		0	0	0	0	0	0	0	0	0	0	21	0	0
Ascomycota						0	0	0	0	0	0	0	0	0	0	21	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Lectera		0	0	0	0	0	0	0	0	0	0	21	0	0
Basidiomycota	Classiculomycetes	Classiculales	Classiculaceae	Classicula		0	0	0	0	0	0	0	0	0	0	0	0	21
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	0	0	0	0	0	0	0	21
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella		4	0	0	0	0	16	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Schizophyllum		0	20	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	20	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae			0	14	6	0	0	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis		0	4	0	0	0	0	0	0	16	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	Iodophanus	0	0	20	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariaceae	Gelasinospora	0	0	20	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Simplicillium	0	0	0	0	20	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	0	0	3	0	0	0	3	0	14	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	11	0	0	0	0	9	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	8	0	0	0	0	0	0	12
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	20	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae	Serendipita	0	0	0	0	0	0	0	2	0	0	18	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	20	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	20	0	0	0	0
Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Agaricostilbaceae	Sterigmatomyces	0	0	0	0	0	0	0	0	20	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Kodamaea	0	0	0	0	0	0	0	0	13	0	7	0	0

Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Ilyonectria	mors-panacis	0	0	0	0	0	0	0	0	10	10	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Remotididymella		0	0	0	0	0	0	0	0	0	20	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	20	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	20	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Ilyonectria		0	0	0	0	0	0	0	0	0	0	20	0	0
Ascomycota	Dothideomycetes	Acrospermales	Acrospermales_fam_Incertae_sedis	Paramycoleptodiscus		0	0	0	0	0	0	0	0	0	0	20	0	0
Basidiomycota	Exobasidiomycetes	Golubeviales	Golubeviaceae	Golubevia		0	0	0	0	0	0	0	0	0	0	20	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	0	0	20
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae			19	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium		7	0	0	0	0	8	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		6	13	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota						5	0	0	0	7	0	0	0	0	7	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	19	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	19	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Curvularia	0	14	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	19	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Peniophoraceae			0	0	19	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina		0	0	10	0	0	0	0	0	0	9	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		Toxicocladosporium	0	0	6	0	0	0	0	0	0	0	13	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Coniosporium	0	0	0	0	19	0	0	0	0	0	0	0	0
Ascomycota						0	0	0	0	19	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		Plectosphaerella	0	0	0	0	0	19	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis		Pseudoramichloridium	0	0	0	0	0	19	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Sarocladium	0	0	0	0	0	2	12	0	0	0	5	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae		Hannaella	0	0	0	0	0	0	19	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paraconiothyrium	0	0	0	0	0	0	19	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Ochroconis	0	0	0	0	0	0	15	4	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paraconiothyrium	0	0	0	0	0	0	0	19	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	19	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		Didymella	0	0	0	0	0	0	0	19	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	19	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	0	0	0	0	0	0	0	0	19	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	0	0	0	0	0	0	19	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae		Botryotinia	0	0	0	0	0	0	0	0	13	0	6	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	0	0	0	7	12	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae		Parvothecium	0	0	0	0	0	0	0	0	0	19	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	19	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	19	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	19	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	19	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	0	0	19	0	0
Basidiomycota	Cystobasidiomycetes				0	0	0	0	0	0	0	0	0	0	19	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Pseudofusicoccum	0	0	0	0	0	0	0	0	0	0	15	0	4
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		0	0	0	0	0	0	0	0	0	0	0	19	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	0	0	0	0	19	0
Ascomycota	Archaeorhizomycetes				0	0	0	0	0	0	0	0	0	0	0	19	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae	Chrysofolia	18	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	18	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodotorula	6	0	0	0	0	7	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		6	0	0	0	8	0	0	0	0	0	0	4	0

Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	18	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Apiotrichum	0	18	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	13	0	0	0	0	0	0	0	0	0	0	5
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	18	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	12	0	0	0	6	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	18	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Cylindrocladiella	0	0	0	0	18	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae	Wickerhamomyces	0	0	0	0	18	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	0	0	0	18	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	11	0	0	0	0	7	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dactylonectria	0	0	0	0	6	0	0	0	12	0	0	0	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Mrakiaceae	Mrakia	0	0	0	0	5	3	0	0	0	10	0	0	0

Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis		Radulidium	0	0	0	0	0	18	0	0	0	0	0	0	0
Ascomycota	Orbiliomycetes					0	0	0	0	0	2	0	0	0	0	0	16	0
Ascomycota	Dothideomycetes	Capnodiales	Neodevriesiaceae		Neodevriesia	0	0	0	0	0	0	18	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		0	0	0	0	0	0	0	18	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	18	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	18	0	0	0	0	0
Ascomycota	Orbiliomycetes					0	0	0	0	0	0	0	18	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae		Westerdykella	0	0	0	0	0	0	0	0	18	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	18	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae			0	0	0	0	0	0	0	0	18	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		Tolypocladium	0	0	0	0	0	0	0	0	18	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		Acrostalagmus	0	0	0	0	0	0	0	0	12	6	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	0	18	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bionectria	0	0	0	0	0	0	0	0	0	18	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	18	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	18	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporobolomyces	0	0	0	0	0	0	0	0	0	0	18	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		0	0	0	0	0	0	0	0	0	0	18	0	0
Basidiomycota	Agaricomycetes	Polyporales	Hyphodermataceae	Hypoderma	0	0	0	0	0	0	0	0	0	0	18	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	0	18
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	0	18
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	0	0	0	0	18
Ascomycota	Dothideomycetes				3	0	0	6	0	0	0	0	0	0	0	8	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	17	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	17	0	0	0	0	0	0	0	0	0	0	0

Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	0	10	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes					0	7	0	0	0	0	0	6	0	0	4	0	0
Ascomycota	Sordariomycetes	Xylariales	Coniocessiaceae		Coniocessia	0	5	0	0	4	6	0	0	0	0	0	2	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae		Saitozyma	0	2	0	0	0	0	15	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	17	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Chrysozymaceae		Sampaiozyma	0	0	17	0	0	0	0	0	0	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales				0	0	17	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Xenosonderhenia	0	0	17	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Neoceratosperma	0	0	9	0	0	0	0	0	0	8	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiotremataceae	Atrocalyx		0	0	7	0	0	0	0	10	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paracamarosporium	0	0	0	17	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae		Naganishia	0	0	0	0	17	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Gaeumannomyces	0	0	0	0	17	0	0	0	0	0	0	0	0
Chytridiomycota	Spizellomycetes	Spizellomycetales	Spizellomycetaceae	Spizellomyces	0	0	0	0	3	0	0	12	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	17	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	4	0	0	0	0	13	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11			0	0	0	0	0	3	0	0	14	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleraceae	Fonsecazyma	0	0	0	0	0	0	17	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Valsaceae	Cytospora	0	0	0	0	0	0	17	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	0	0	17	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	0	0	0	0	0	0	17	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	0	6	0	0	0	11	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	17	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	17	0	0	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Castanediella	0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metarhizium	0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales			0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		0	0	0	0	0	0	0	0	0	17	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Proliferodiscus	0	0	0	0	0	0	0	0	0	17	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Catenulostroma	0	0	0	0	0	0	0	0	0	17	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	17	0	0	0
Basidiomycota	Tremellomycetes				0	0	0	0	0	0	0	0	0	9	0	8	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	0	0	0	0	0	17	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiotremataceae	Atrocalyx	0	0	0	0	0	0	0	0	0	0	17	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	0	0	0	0	0	0	0	0	17	0	0

Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	17	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Xenopenidiella	0	0	0	0	0	0	0	0	0	0	0	17	0
Ascomycota	Orbiliomycetes					0	0	0	0	0	0	0	0	0	0	0	17	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		Epicoccum	0	0	0	0	0	0	0	0	0	0	0	17	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Geastrumia	0	0	0	0	0	0	0	0	0	0	0	17	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	0	0	0	0	0	17
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Acaulium		10	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae			0	0	16	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	16	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	16	0	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	0	0	0	16	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		Chaetomium	0	0	0	0	16	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Morosphaeriaceae	Acrocalymma	0	0	0	0	12	0	0	0	0	4	0	0	0
Ascomycota					0	0	0	0	7	0	0	4	0	0	0	5	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenopenidiella	0	0	0	0	0	16	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	16	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	0	0	7	0	0	9	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	16	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	16	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Westerdykella	0	0	0	0	0	0	0	0	16	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	16	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenaceae	Keratinophyton	0	0	0	0	0	0	0	0	14	0	2	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	16	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dialonectria	0	0	0	0	0	0	0	0	0	16	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Agaricales_fam_Incertae_sedis	Acanthocorticium	0	0	0	0	0	0	0	0	0	0	16	0	0
Ascomycota	Archaeorhizomycetes				0	0	0	0	0	0	0	0	0	0	16	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		0	0	0	0	0	0	0	0	0	0	16	0	0
Mortierellomycota					0	0	0	0	0	0	0	0	0	0	16	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	16	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	16	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	16	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae		0	0	0	0	0	0	0	0	0	0	16	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	0	0	0	0	0	0	0	0	0	0	16	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	16	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraphaeosphaeria	0	0	0	0	0	0	0	0	0	0	0	3	13
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	0	0	16
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	15	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Exophiala	0	7	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae		Striatibotrys	0	6	0	0	0	3	0	0	0	0	0	6	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		Hirsutella	0	3	0	0	0	3	0	0	4	5	0	0	0
Ascomycota	Archaeorhizomycetes					0	0	15	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Neosulcatispora	0	0	15	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		Toxicocladosporium	0	0	15	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae		Pseudofusicoccum	0	0	0	11	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	15	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Pseudodactylariales	Pseudodactylariaceae		Pseudodactylaria	0	0	0	0	15	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Phaeosphaeria	0	0	0	0	15	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris		0	0	0	0	15	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae			0	0	0	0	15	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae		Gloniopsis	0	0	0	0	15	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	15	0	0	0	0	0	0	0
Chytridiomycota	Spizellomycetes	Spizellomycetales				0	0	0	0	0	5	0	4	0	6	0	0	0
Basidiomycota						0	0	0	0	0	4	0	0	0	0	0	0	11
Ascomycota	Leotiomycetes	Rhytismatales	Rhytismataceae			0	0	0	0	0	3	0	12	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	15	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Pseudopithomyces	0	0	0	0	0	0	8	0	0	0	7	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis		Strelitziana	0	0	0	0	0	0	0	15	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae		Trichomerium	0	0	0	0	0	0	0	15	0	0	0	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae		Golovinomyces	0	0	0	0	0	0	0	5	0	0	10	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae		Scytalidium	0	0	0	0	0	0	0	2	0	4	6	3	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	15	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Clonostachys	0	0	0	0	0	0	0	0	15	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae		0	0	0	0	0	0	0	0	15	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		0	0	0	0	0	0	0	0	15	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	0	0	0	0	15	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Teichospora	0	0	0	0	0	0	0	0	15	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	15	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	7	8	0	0	0
Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Mycoleptodiscus	0	0	0	0	0	0	0	0	3	12	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	0	15	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	0	15	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	15	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Hyweljonesia	0	0	0	0	0	0	0	0	0	0	15	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Hermetothecium	0	0	0	0	0	0	0	0	0	0	15	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Auriculariaceae	Auricularia	0	0	0	0	0	0	0	0	0	0	15	0	0
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae	Gyroporus	0	0	0	0	0	0	0	0	0	0	15	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tremella	0	0	0	0	0	0	0	0	0	0	15	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	15	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	0	0	0	0	0	0	0	0	0	0	9	0	6
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Cercosporidium	0	0	0	0	0	0	0	0	0	0	0	15	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	0	0	15
Ascomycota	Dothideomycetes	Dothideales	Dothideaceae		0	0	0	0	0	0	0	0	0	0	0	0	15
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	14	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				14	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae	Septobasidium	14	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae		5	0	0	0	4	5	0	0	0	0	0	0	0

Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	5	0	0	0	0	0	0	0	0	0	0	0	9
Ascomycota	Sordariomycetes	Sordariales				0	14	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	14	0	0	0	0	0	0	0	0	0	0	0
Zoopagomycota						0	4	0	0	0	2	0	0	0	3	0	5	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae			0	0	14	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae		Scutellinia	0	0	14	0	0	0	0	0	0	0	0	0	0
Chytridiomycota	Rhizophydiomycetes	Rhizophydiales				0	0	14	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae		Hypoxylon	0	0	14	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae		Pseudofusicoccum	0	0	14	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae			0	0	0	0	14	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Coryneliales	Coryneliaceae		Hypsotheca	0	0	0	0	14	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Acaulium		0	0	0	0	14	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		Schizothecium	0	0	0	0	14	0	0	0	0	0	0	0	0

Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae		Issatchenkia	0	0	0	0	14	0	0	0	0	0	0	0	0
Basidiomycota						0	0	0	0	2	0	0	0	0	0	12	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	14	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	sp	0	0	0	0	0	0	0	14	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		Pseudolophiostoma	0	0	0	0	0	0	0	11	0	0	0	3	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11				0	0	0	0	0	0	0	0	14	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales				0	0	0	0	0	0	0	0	14	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		Hirsutella	0	0	0	0	0	0	0	0	14	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Paramycosphaerella	0	0	0	0	0	0	0	0	14	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		Didymella	0	0	0	0	0	0	0	0	14	0	0	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae		Apiotrichum	0	0	0	0	0	0	0	0	14	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Neoceratosperma	0	0	0	0	0	0	0	0	14	0	0	0	0

Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	0	0	0	0	0	0	0	0	14	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	0	0	0	0	0	0	0	0	0	14	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	14	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zymoseptoria	0	0	0	0	0	0	0	0	0	0	14	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	14	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	0	0	0	0	0	0	0	0	0	0	14	0	0
Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Clitocybula	0	0	0	0	0	0	0	0	0	0	14	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	0	0	0	0	14	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	0	0	0	0	14	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	14	0
Basidiomycota					0	0	0	0	0	0	0	0	0	0	0	14	0
Basidiomycota	Agaricomycetes	Boletales	Sclerodermataceae	Scleroderma	0	0	0	0	0	0	0	0	0	0	0	14	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	14
Ascomycota					13	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales				13	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	13	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes					13	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Xenopenidiella	13	0	0	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	3	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae		Simplicillium	0	13	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae		Trichomerium	0	13	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	13	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	13	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Trametes		0	13	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota	Rhizophydiomycetes	Rhizophydiales				0	6	0	0	0	0	0	3	0	0	4	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales				0	0	13	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae		Amphisphaeria	0	0	13	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		0	0	13	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Stagonosporopsis	0	0	0	13	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Cistella	0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Podosphaera	0	0	0	0	13	0	0	0	0	0	0	0	0
Basidiomycota					0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Botryosphaeria	0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	Selenodriella	0	0	0	0	11	0	0	0	2	0	0	0	0
Rozellomycota					0	0	0	0	9	4	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	13	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	13	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae	Wickerhamomyces	0	0	0	0	0	13	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Hyweljonesia	0	0	0	0	0	0	13	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudogymnoascus	0	0	0	0	0	0	13	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Teratoramularia	0	0	0	0	0	0	13	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	0	0	0	0	13	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	13	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	0	13	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	0	0	0	0	0	0	0	13	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	13	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	0	0	0	0	0	0	13	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Clavispora	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Morosphaeriaceae	Acrocalymma	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	0	0	0	13	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae	Eichleriella	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis	Pseudoramichloridium	0	0	0	0	0	0	0	0	13	0	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	0	0	13	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	0	13	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	0	0	0	0	0	0	0	0	0	0	13	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Simplicillium	0	0	0	0	0	0	0	0	0	0	13	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	0	0	0	0	0	0	0	0	0	13	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	0	13	0
Ascomycota	Lecanoromycetes	Caliciales	Caliciaceae		0	0	0	0	0	0	0	0	0	0	0	13	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	13	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	13	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	12	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales			12	0	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota	Chytridiomycetes	Chytridiales	Chytridiaceae	Phlyctochytrium	6	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	12	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Emericellopsis	0	12	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	12	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	12	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota					0	3	0	0	0	0	0	0	0	0	0	9	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	12	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	12	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	12	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	7	0	5	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae	Sphaerellopsis	0	0	0	0	12	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	12	0	0	0	0	0	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Humidicutis	0	0	0	0	12	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	12	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Humidicutis	0	0	0	0	12	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	12	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	12	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Phialophora	0	0	0	0	0	7	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	12	0	0	0	0	0	0
Rozellomycota					0	0	0	0	0	0	12	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Zygosporium	0	0	0	0	0	0	12	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae	Pseudolophiostoma	0	0	0	0	0	0	12	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	12	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	0	0	0	0	0	0	8	0	0	0	4	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	3	9	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		Remotididymella	0	0	0	0	0	0	0	12	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		Colletotrichum	0	0	0	0	0	0	0	12	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae			0	0	0	0	0	0	0	12	0	0	0	0	0
Kickxellomycota	GS19	GS19				0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		Retroconis	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia		0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae		Talaromyces	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Sordariomycetes	Myrmecridiales	Myrmecridiaceae		Myrmecridium	0	0	0	0	0	0	0	0	0	12	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	0	0	0	0	0	0	0	0	12	0	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae		Apiotrichum	0	0	0	0	0	0	0	0	0	12	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis	0	0	0	0	0	0	0	0	0	12	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	0	12	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Monocillium	0	0	0	0	0	0	0	0	0	12	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Toxicocladosporium	0	0	0	0	0	0	0	0	0	12	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae		0	0	0	0	0	0	0	0	0	0	12	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	Branch03			0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Parascedosporium	0	0	0	0	0	0	0	0	0	0	12	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodotorula	0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	12	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis		Strelitziana	0	0	0	0	0	0	0	0	0	0	12	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae		Vishniacozyma	0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae		Muscodor	0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	0	12	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	0	0	12	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	0	12	0
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia		0	0	0	0	0	0	0	0	0	0	0	4	8
Ascomycota	Taphrinomycetes	Taphrinales	Taphrinaceae	Taphrina		11	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	11	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Xenoteratosphaeria	11	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Tubeufiales	Tubeufiaceae		Helicosporium	11	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis		Rhodoveronaea	5	0	6	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales			4	3	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Codinaea	2	0	0	0	3	0	0	0	2	0	4	0	0
Basidiomycota	Agaricomycetes	Sebacinales			0	11	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Phaeophleospora	0	11	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Astrosporina	0	11	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	11	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Gliomastix	0	5	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Gymnoascaceae	Gymnoascus	0	3	0	0	0	4	0	0	0	4	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	11	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus	0	0	11	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		0	0	11	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	0	0	11	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	0	0	11	0	0	0	0	0	0	0	0	0	0

Basidiomycota					0	0	2	0	0	0	0	0	0	0	0	9	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	11	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	3	0	0	8	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Articulospora	0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	11	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricomycetes_ord_Incertae_sedis	Agaricomycetes_fam_Incertae_sedis	Xenasmatella	0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Meyerozyma	0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida	0	0	0	0	9	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		0	0	0	0	0	0	11	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Tolypocladium	0	0	0	0	0	0	11	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	0	0	4	2	0	0	5	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	11	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	0	0	0	0	0	0	0	11	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Madagascaromyces	0	0	0	0	0	0	0	11	0	0	0	0	0
Rozellomycota					0	0	0	0	0	0	0	11	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	11	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Oleoguttula	0	0	0	0	0	0	0	11	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	0	0	0	0	0	0	0	0	11	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales			0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	0	11	0	0	0	0
Basidiomycota	Agaricomycetes	Hymenochaetales	Schizoporaceae	Hyphodontia	0	0	0	0	0	0	0	0	11	0	0	0	0
Basidiomycota	Atractiellomycetes	Atractiellales	Hoehnelomycetaceae		0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenopenidiella	0	0	0	0	0	0	0	0	11	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma	0	0	0	0	0	0	0	0	11	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metacordyceps	0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Kodamaea	0	0	0	0	0	0	0	0	11	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Pterulaceae	Coronicium	0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	0	0	0	0	0	0	0	0	11	0	0	0
Blastocladiomycota	Blastocladiomycetes	Blastocladiales	Catenariaceae		0	0	0	0	0	0	0	0	0	11	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	0	0	11	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	11	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Cutaneotrichosporon	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cyanodermella	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	0	0	0	0	0	0	0	11	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	0	0	0	0	0	0	0	0	0	11	0	0
Chytridiomycota	Chytridiomycetes	Chytridiales	Chytridiaceae		Dendrochytrium	0	0	0	0	0	0	0	0	0	0	11	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina		0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida		0	0	0	0	0	0	0	0	0	0	11	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae		Coprinellus	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Sarocladium	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Sordariomycetes	Microascales				0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	0	11	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis		Pseudoramichloridium	0	0	0	0	0	0	0	0	0	0	0	11	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae	Exidia		0	0	0	0	0	0	0	0	0	0	0	11	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	0	11	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae			0	0	0	0	0	0	0	0	0	0	0	11	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	0	0	0	0	0	11	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	0	8	3
Ascomycota						10	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Phaeothecoidea	10	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				8	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Ramularia	7	0	0	0	0	3	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Cystobasidiales	Cystobasidiaceae	Cystobasidium	minuta	6	0	0	0	4	0	0	0	0	0	0	0	0
Chytridiomycota	Rhizophydiomycetes	Rhizophydiales				5	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	10	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes					0	10	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusicolla		0	10	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	10	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Phaeosphaeria	0	10	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Sarcosomataceae			0	10	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae			0	0	10	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Curvularia	0	0	10	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	10	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	10	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gibberella	0	0	10	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	10	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Neoceratosperma	0	0	0	10	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae			0	0	0	10	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Acrospermales	Acrospermales_fam_Incertae_sedis		Paramycoleptodiscus	0	0	0	0	10	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus		0	0	0	0	10	0	0	0	0	0	0	0	0

Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Parapyrenochaeta	0	0	0	0	0	10	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	0	0	0	10	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	10	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	0	0	0	0	0	0	10	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporobolomyces	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Apiosporaceae	Arthrinium	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Canariomyces	0	0	0	0	0	0	3	7	0	0	0	0	0

Basidiomycota	Agaricomycetes	Sebacinales				0	0	0	0	0	0	0	10	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae	Serendipita		0	0	0	0	0	0	0	10	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora		0	0	0	0	0	0	0	10	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis	Mycoarthris	corallina	0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales				0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Sordariomycetes	Annulatascales	Annulatascaceae			0	0	0	0	0	0	0	0	10	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella		0	0	0	0	0	0	0	0	10	0	0	0	0
Chytridiomycota						0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Memnoniella		0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Tolypocladium		0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Clavispora		0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae			0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae			0	0	0	0	0	0	0	0	10	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Sporormiella	dakotensis	0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	Idriella		0	0	0	0	0	0	0	0	10	0	0	0	0
Rozellomycota						0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Thelebolaceae	Ramgea		0	0	0	0	0	0	0	0	0	10	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma		0	0	0	0	0	0	0	0	0	10	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella		0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota						0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae			0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cercophora		0	0	0	0	0	0	0	0	0	0	10	0	0
Basidiomycota	Agaricomycetes	Polyporales	Phanerochaetaceae			0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cyanodermella		0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium		0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Dothideomycetes	Pleosporales	Tetraplosphaeriaceae			0	0	0	0	0	0	0	0	0	0	10	0	0

Ascomycota	Dothideomycetes	Mytilinidales	Gloniaceae		Cenococcum	0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	0	0	10	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	0	0	0	0	0	10	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae		Erythrobasidium	0	0	0	0	0	0	0	0	0	0	4	6	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis		Parapyrenochaeta	0	0	0	0	0	0	0	0	0	0	0	10	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Phaeodothis	0	0	0	0	0	0	0	0	0	0	0	10	0
Basidiomycota	Agaricomycetes	Sebacinales				0	0	0	0	0	0	0	0	0	0	0	10	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	0	0	0	0	10	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae		Papiliotrema	0	0	0	0	0	0	0	0	0	0	0	10	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	0	0	0	0	0	10	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae		Apiotrichum	0	0	0	0	0	0	0	0	0	0	0	10	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stenella		0	0	0	0	0	0	0	0	0	0	0	10	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	0	10	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	10
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	10
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Pezicula	9	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	9	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Toxicocladosporium	9	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		9	0	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota	Spizellomycetes	Spizellomycetales	Powellomycetaceae		4	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Chaetothyrium	0	9	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Ophionectria	0	9	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	3	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cercophora	0	0	9	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Geopora	0	0	9	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Microascales	Microascaceae		Canariomyces	0	0	9	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	0	9	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae			0	0	9	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae		Hannaella	0	0	4	0	0	0	0	0	0	0	0	5	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		Proliferodiscus	0	0	0	9	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Waitea		0	0	0	0	9	0	0	0	0	0	0	0	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae		Septobasidium	0	0	0	0	9	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	0	0	0	0	9	0	0	0	0	0	0	0	0
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae			0	0	0	0	9	0	0	0	0	0	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	Branch03				0	0	0	0	6	0	3	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae		Schwanniomyces	0	0	0	0	5	0	0	0	4	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Hyphopichia	burtonii	0	0	0	0	0	9	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gibberella	0	0	0	0	0	9	0	0	0	0	0	0	0

Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae		0	0	0	0	0	9	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	9	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales			0	0	0	0	0	4	0	0	5	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	9	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema	0	0	0	0	0	0	9	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	9	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Hymenopleella	0	0	0	0	0	0	9	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Clitocybula	0	0	0	0	0	0	9	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	9	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Sarocladium	0	0	0	0	0	0	9	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Nigrograna	0	0	0	0	0	0	9	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	0	0	0	0	0	0	0	9	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Sporidesmium	0	0	0	0	0	0	0	9	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	9	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	0	0	0	0	0	0	9	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Arthrocladium	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chaetosphaeria	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	0	0	0	0	0	0	0	0	9	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Monocillium	0	0	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae		0	0	0	0	0	0	0	0	0	9	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudogymnoascus	0	0	0	0	0	0	0	0	0	9	0	0	0

Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	0	0	0	9	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		Metarhizium	0	0	0	0	0	0	0	0	0	9	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae		Trichoderma	0	0	0	0	0	0	0	0	0	9	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae		Barnettozyma	0	0	0	0	0	0	0	0	0	9	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae		Synnemellisia	0	0	0	0	0	0	0	0	0	9	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Acremonium	0	0	0	0	0	0	0	0	0	9	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Aspergillus	0	0	0	0	0	0	0	0	0	0	9	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae		Eichleriella	0	0	0	0	0	0	0	0	0	0	9	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		0	0	0	0	0	0	0	0	0	0	9	0	0
Basidiomycota	Agaricomycetes	Hymenochaetales				0	0	0	0	0	0	0	0	0	0	9	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae			0	0	0	0	0	0	0	0	0	0	9	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae		Vishniacozyma	0	0	0	0	0	0	0	0	0	0	9	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	0	0	0	9	0	0

Ascomycota	Sordariomycetes	Xylariales	Apiosporaceae		Arthrinium	0	0	0	0	0	0	0	0	0	0	9	0	0
Ascomycota	Leotiomycetes	Helotiales	Myxotrichaceae		Oidiodendron	0	0	0	0	0	0	0	0	0	0	9	0	0
Basidiomycota	Atractiellomycetes	Atractiellales	Hoehnelomycetaceae		Atractiella	0	0	0	0	0	0	0	0	0	0	9	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae	Clavulina		0	0	0	0	0	0	0	0	0	0	9	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	0	0	0	9	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	0	0	9	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	0	0	0	0	0	0	0	0	0	9	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	0	0	0	0	0	0	0	0	0	9	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tremella		0	0	0	0	0	0	0	0	0	0	0	9	0
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	0	0	0	9	0
Ascomycota	Sordariomycetes	Sordariales	Sordariaceae		Gelasinospora	0	0	0	0	0	0	0	0	0	0	0	9	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	0	0	0	0	0	0	0	0	0	9	0
Chytridiomycota	Spizellomycetes	Spizellomycetales	Spizellomycetaceae		Spizellomyces	0	0	0	0	0	0	0	0	0	0	0	0	9

Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Tetracladium	0	0	0	0	0	0	0	0	0	0	0	0	9
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		8	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botryotinia	8	0	0	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	8	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				8	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			6	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			5	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Stolonocarpus	5	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida	3	0	0	0	0	0	0	0	2	3	0	0	0
Basidiomycota	Atractiellomycetes	Atractiellales	Hoehnelomycetaceae		3	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		3	0	0	3	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Pleosporales			2	0	0	0	6	0	0	0	0	0	0	0	0

Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Paracremonium	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Paramycosphaerella	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Fasciatisporaceae		Fasciatispora	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae		Ascobolus	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	6	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Paraphoma	0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		Apiosordaria	0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascodesmidaceae		Cephaliophora	0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paraphaeosphaeria	0	0	8	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Torulaceae	Torula		0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Phialoseptomonium	0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Branch06				0	0	8	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae		Tricholoma	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis		Strelitziana	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae		Stilbocrea	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	0	0	8	0	0	0	0	0	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11				0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae		Articulospora	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes					0	0	0	0	5	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae		Neopestalotiopsis	0	0	0	0	0	8	0	0	0	0	0	0	0

Basidiomycota	Tremellomycetes	Tremellales				0	0	0	0	0	8	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	8	0	0	0	0	0	0	0
Chytridiomycota						0	0	0	0	0	8	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae		Gloniopsis	0	0	0	0	0	8	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	8	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Montagnula	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paraconiothyrium	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Aspergillus	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	8	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		Ceratobasidium	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae		Issatchenkia	0	0	0	0	0	0	8	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae			0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia		0	0	0	0	0	0	4	0	0	0	0	4	0

Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Sarocladium	0	0	0	0	0	0	0	8	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	0	0	8	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		0	0	0	0	0	0	0	8	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae		Trichoderma	0	0	0	0	0	0	0	8	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Funalia		0	0	0	0	0	0	0	8	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Sordariomycetes	Coniochaetales				0	0	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Ochroconis	0	0	0	0	0	0	0	0	8	0	0	0	0
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae			0	0	0	0	0	0	0	0	8	0	0	0	0
Kickxellomycota	GS19	GS19				0	0	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Devriesia		0	0	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Eurotiomycetes					0	0	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Pseudoteratosphaeria	0	0	0	0	0	0	0	0	8	0	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Agaricales_fam_Incertae_sedis	Uncobasidium	0	0	0	0	0	0	0	0	0	8	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	0	0	0	0	0	0	8	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dactylonectria	0	0	0	0	0	0	0	0	0	8	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	8	0	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae	Erythrobasidium	0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	0	0	8	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Neofusicoccum	0	0	0	0	0	0	0	0	0	0	8	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Paracylindrocarpon	0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Arthoniomycetes	Lichenostigmatales	Phaeococcomycetaceae	Phaeococcomyces	0	0	0	0	0	0	0	0	0	0	3	0	5

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	0	8	0
Ascomycota	Sordariomycetes	Branch06			0	0	0	0	0	0	0	0	0	0	0	8	0
Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Lopharia	0	0	0	0	0	0	0	0	0	0	0	8	0
Basidiomycota	Agaricomycetes	Sebacinales			0	0	0	0	0	0	0	0	0	0	0	8	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	0	0	8	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	0	8	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	0	0	0	0	0	0	0	0	8
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae		0	0	0	0	0	0	0	0	0	0	0	0	8
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales			7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota					7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				7	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Microascales	Halosphaeriaceae		3	0	0	0	0	0	0	0	0	4	0	0	0
Zoopagomycota					0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	Microdochium	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Branch06			0	7	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota					0	7	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Fomitopsidaceae	Cinereomyces	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	5	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	0	0	7	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida	0	0	7	0	0	0	0	0	0	0	0	0	0
Ascomycota					0	0	7	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Gerronema	0	0	7	0	0	0	0	0	0	0	0	0	0

Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae	Septobasidium	0	0	7	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	7	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	7	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	0	0	7	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Mariannaea	0	0	0	7	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	7	0	0	0	0	0	0	0	0	0
Chytridiomycota					0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Chrysosporium	0	0	0	0	2	5	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	7	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	7	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Lachnella	0	0	0	0	0	7	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	0	0	0	0	0	2	0	0	5	0	0	0	0

Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	0	0	0	7	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		0	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Cryptosporiopsis	0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Rhizodermea	0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Strattonia	0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Sordariomycetes	Phomatosporales	Phomatosporaceae	Phomatospora	0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Chrysosporium	0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	7	0	0	0	0	0

Monoblepharomycota	Monoblepharidomycetes	Monoblepharidales				0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	7	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Diutina	catenulata	0	0	0	0	0	0	0	2	2	0	0	0	3
Ascomycota	Sordariomycetes	Branch06				0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cercophora		0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium		0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae			0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Arxiella		0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales				0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	0	0	0	7	0	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Gymnopilus		0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces		0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium		0	0	0	0	0	0	0	0	4	3	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	0	7	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Neophaeomoniella		0	0	0	0	0	0	0	0	0	7	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeodothis		0	0	0	0	0	0	0	0	0	7	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium		0	0	0	0	0	0	0	0	0	7	0	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Cutaneotrichosporon		0	0	0	0	0	0	0	0	0	7	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Planistromellaceae	Ramimonilia		0	0	0	0	0	0	0	0	0	7	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	buchloes	0	0	0	0	0	0	0	0	0	7	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	7	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Sclerotinia		0	0	0	0	0	0	0	0	0	4	0	0	3

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Ramularia	0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Eurotiomycetes	Onygenales			0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis	Rhodoveronaea	0	0	0	0	0	0	0	0	0	0	7	0	0
Rozellomycota					0	0	0	0	0	0	0	0	0	0	7	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia	0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Glutinomyces	0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Meliniomyces	0	0	0	0	0	0	0	0	0	0	7	0	0
Basidiomycota	Agaricomycetes	Boletales	Rhizopogonaceae	Rhizopogon	0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	0	0	0	0	0	0	0	0	7	0	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma	0	0	0	0	0	0	0	0	0	0	7	0	0
Basidiomycota	Tremellomycetes	Tremellales			0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	7	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Auriculariales_fam_Incertae_sedis	Tremellochaete	0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	7	0	0

Ascomycota	Sordariomycetes	Diaporthales	Schizoparmaceae	Coniella		0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Sordariomycetes	Sordariales				0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae		Pseudombrophila	0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris		0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Sordariomycetes					0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Nemania		0	0	0	0	0	0	0	0	0	0	7	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae		Gliomastix	0	0	0	0	0	0	0	0	0	0	0	7	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Lectera		0	0	0	0	0	0	0	0	0	0	0	7	0
Basidiomycota	Agaricomycetes	Agaricales	Pluteaceae		Chamaeota	0	0	0	0	0	0	0	0	0	0	0	7	0
Rozellomycota	Rozellomycota_cls_Incertae_sedis	Rozellomycota_ord_Incertae_sedis	Rozellomycota_fam_Incertae_sedis		Paramicrosporidium	0	0	0	0	0	0	0	0	0	0	0	7	0
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus		0	0	0	0	0	0	0	0	0	0	0	7	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		Neophaeomoniella	0	0	0	0	0	0	0	0	0	0	0	7	0

Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	0	0	0	0	0	0	0	0	0	0	0	7	0
Basidiomycota	Agaricomycetes	Polyporales			0	0	0	0	0	0	0	0	0	0	0	7	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Ilyonectria	0	0	0	0	0	0	0	0	0	0	0	7	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Cryptococcus	0	0	0	0	0	0	0	0	0	0	0	7	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis	Ramophialophora	0	0	0	0	0	0	0	0	0	0	0	0	7
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Thanatephorus	0	0	0	0	0	0	0	0	0	0	0	0	7
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales			6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes				6	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Pseudombrophila	0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Xenocylindrocladium	0	6	0	0	0	0	0	0	0	0	0	0	0

Basidiomycota	Agaricomycetes					0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	6	0	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	0	6	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus		0	6	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales				0	6	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes					0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paracamarosporium	0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pezizaceae		Iodophanus	0	4	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes					0	3	0	0	0	0	0	0	0	0	3	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		Mortierella	0	3	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Hysteriales				0	0	6	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae		Lepteutypa	0	0	6	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Pichiaceae	Pichia		0	0	6	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	6	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	0	0	0	6	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	6	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Halosphaeriaceae		0	0	0	0	6	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	0	0	0	0	6	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Kazachstania	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Cylindrocarpon	0	0	0	0	6	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae	Heterochaete shearii	0	0	0	0	6	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Phanerochaetaceae	Hyphodermella	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes				0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	0	0	6	0	0	0	0	0	0	0	0

Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		0	0	0	0	6	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	3	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium	0	0	0	0	2	0	0	4	0	0	0	0	0
Ascomycota					0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Hyweljonesia	0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Lapidomyces	0	0	0	0	0	6	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales			0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Veronaea	0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	6	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Xenocamarosporium	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Tricladiaceae	Tricladium	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	4	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	6	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	0	0	6	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	0	0	0	0	0	0	0	6	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	0	0	0	0	0	0	0	6	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		0	0	0	0	0	0	0	6	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Tolypocladium	0	0	0	0	0	0	0	6	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	6	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales			0	0	0	0	0	0	0	6	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		0	0	0	0	0	0	0	6	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Laburnicola	0	0	0	0	0	0	0	4	0	0	0	2	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Geomyces	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Melnikomyces	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	6	0	0	0	0
Rozellomycota					0	0	0	0	0	0	0	0	6	0	0	0	0
Basidiomycota					0	0	0	0	0	0	0	0	6	0	0	0	0

Ascomycota	Eurotiomycetes	Onygenales	Gymnoascaceae		Leucothecium	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes					0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Acremonium	0	0	0	0	0	0	0	0	6	0	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11				0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	0	0	0	0	0	0	0	0	6	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Steccherinaceae		Cabalodontia	0	0	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Paraconiothyrium	0	0	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Neocoleroa	0	0	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Fusicladium	0	0	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida		0	0	0	0	0	0	0	0	0	6	0	0	0
Basidiomycota	Agaricomycetes	Boletales	Sclerodermataceae		Scleroderma	0	0	0	0	0	0	0	0	0	6	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae		Talaromyces	0	0	0	0	0	0	0	0	0	6	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae	Pholiota		0	0	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		Hyaloscypha	0	0	0	0	0	0	0	0	0	6	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae		Leptosphaeria	0	0	0	0	0	0	0	0	0	3	3	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae		Vishniacozyma	0	0	0	0	0	0	0	0	0	0	6	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Clavulinaceae			0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Lecanoromycetes	Caliciales	Caliciaceae			0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Sordariomycetes	Branch06				0	0	0	0	0	0	0	0	0	0	6	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae		Sporidiobolus	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Pezicula		0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Curvularia	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	0	0	6	0	0
Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetaceae		Hymenochaete	0	0	0	0	0	0	0	0	0	0	6	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Dothideomycetes	Capnodiales	Dissoconiaceae	Ramichloridium	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeodothis	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	0	6	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Filobasidium	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Hyphopichia	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	0	0	0	0	0	0	0	6	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales			0	0	0	0	0	0	0	0	0	0	0	6	0
Basidiomycota	Geminibasidiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	0	0	0	0	0	0	0	0	0	0	0	6	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Lasiodiplodia	0	0	0	0	0	0	0	0	0	0	0	6	0

Ascomycota						0	0	0	0	0	0	0	0	0	0	0	6	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		Cladorrhinum	0	0	0	0	0	0	0	0	0	0	0	6	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae		Leptobacillium	0	0	0	0	0	0	0	0	0	0	0	6	0
Ascomycota	Dothideomycetes	Capnodiales	Neodevriesiaceae		Neodevriesia	0	0	0	0	0	0	0	0	0	0	0	6	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Zopfiella		0	0	0	0	0	0	0	0	0	0	0	6	0
Ascomycota	Lecanoromycetes	Lecanorales	Ramalinaceae			0	0	0	0	0	0	0	0	0	0	0	6	0
Basidiomycota	Agaricomycetes					0	0	0	0	0	0	0	0	0	0	0	0	6
Basidiomycota	Agaricomycetes	Agaricales	Bolbitiaceae		Conocybe	0	0	0	0	0	0	0	0	0	0	0	0	6
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	0	0	0	0	0	0	0	6
Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Ruineniaceae	Ruinenia		0	0	0	0	0	0	0	0	0	0	0	0	6
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	0	0	0	0	0	0	0	6
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		Magnibotryascoma	0	0	0	0	0	0	0	0	0	0	0	0	6
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis			5	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis		5	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Peniophoraceae	Peniophora	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metarhizium	5	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Orbiliomycetes				5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Beauveria	2	0	0	0	0	0	0	0	0	0	0	3	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	0	5	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Steccherinaceae	Nigroporus	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	5	0	0	0	0	0	0	0	0	0	0	0

Mortierellomycota	Mortierellomycetes	Mortierellales				0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae		Neocucurbitaria	0	5	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Chionosphaeraceae		Kurtzmanomyces	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Branch06				0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Hypoxylaceae		Hypomontagnella	0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Bisifusarium	0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Chlamydocillium	0	0	5	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae		Septobasidium	0	0	5	0	0	0	0	0	0	0	0	0	0
Rozellomycota						0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	5	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae			0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae		Engyodontium	0	0	5	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales				0	0	3	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleraceae		Fonsecazyma	0	0	0	5	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Inocybe		0	0	0	5	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		Toxicocladosporium	0	0	0	5	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae		Punctulariopsis	0	0	0	5	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		Thelephora	0	0	0	2	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae			0	0	0	2	0	0	0	3	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pezizaceae			0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Kondoaceae	Kondoa		0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Cystobasidiomycetes_ord_Incertae_sedis	Symmetrosporaceae		Symmetrospora	0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		Tomentella	0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Boletales	Boletaceae		Cyanoboletus	0	0	0	0	5	0	0	0	0	0	0	0	0

Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae		Helvellosebacina	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Lasionectria	0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		Tomentella	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae		Archaeorhizomyces	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae		Bionectria	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		Tolypocladium	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae		Metschnikowia	0	0	0	0	5	0	0	0	0	0	0	0	0
Mucoromycota	Umbelopsidomycetes	Umbelopsidales	Umbelopsidaceae		Umbelopsis	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae		Neoerysiphe	0	0	0	0	5	0	0	0	0	0	0	0	0
Chytridiomycota						0	0	0	0	0	5	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	5	0	0	0	0	0	0	0
Chytridiomycota						0	0	0	0	0	5	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	5	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Stemphylium	0	0	0	0	0	5	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	5	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae		Cryptosporiopsis	0	0	0	0	0	5	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	5	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes					0	0	0	0	0	5	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae		Filobasidium	0	0	0	0	0	5	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tremella		0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae			0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Lecanoromycetes					0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Penidiella	0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Schizothyriaceae		Johansonia	0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales				0	0	0	0	0	0	5	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae			0	0	0	0	0	0	5	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae			0	0	0	0	0	0	5	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina		0	0	0	0	0	0	0	5	0	0	0	0	0
Ascomycota	Dothideomycetes	Acrospermales	Acrospermales_fam_Incertae_sedis		Paramycoleptodiscus	0	0	0	0	0	0	0	5	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		0	0	0	0	0	0	0	5	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellales_fam_Incertae_sedis		Kwoniella	0	0	0	0	0	0	0	5	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	0	5	0	0	0	0	0
Glomeromycota						0	0	0	0	0	0	0	5	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis			0	0	0	0	0	0	0	5	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae		Wickerhamomyces	0	0	0	0	0	0	0	5	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Strophariaceae		Hypholoma	0	0	0	0	0	0	0	5	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Neocamarosporium	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales				0	0	0	0	0	0	0	0	5	0	0	0	0

Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae			0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Pezicula		0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae		Stachybotrys	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		Purpureocillium	0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae		Rhodotorula	0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Dothideomycetes	Acrospermales	Acrospermales_fam_Incertae_sedis		Paramycoleptodiscus	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	5	0	0	0	0
Glomeromycota	Glomeromycetes	Diversisporales				0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Virgaria		0	0	0	0	0	0	0	0	5	0	0	0	0
Glomeromycota	Glomeromycetes	Diversisporales				0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae		Clavulinopsis	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales				0	0	0	0	0	0	0	0	5	0	0	0	0

Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Nemania	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae		0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Trichomonascaceae	Trichomonascus	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Hypoxylaceae	Hypomontagnella	0	0	0	0	0	0	0	0	3	0	0	2	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	5	0	0	0

Ascomycota					0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	5	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11			0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Stilbocrea	0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Sphaerostilbella	0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae		0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Thyridariaceae	Neoroussoella	0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	0	0	5	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Gliocephalotrichum	0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	0	0	0	0	0	0	0	5	0	0	0
Basidiomycota	Agaricomycetes					0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Penicillium	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Neocoleroa	0	0	0	0	0	0	0	0	0	0	5	0	0
Chytridiomycota	Rhizophydiomycetes	Rhizophydiales	Terramycetaceae		Boothiomyces	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Pseudocercospora	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Knufia		0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia		0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Alternaria	0	0	0	0	0	0	0	0	0	0	5	0	0

Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae		0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Golovinomyces	0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiobolomycota	Basidiobolomycetes	Basidiobolales	Basidiobolaceae	Basidiobolus	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae	Cystofilobasidium	0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	5	0	0

Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Phaeosphaeria	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae		Lepteutypa	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Acremonium	0	0	0	0	0	0	0	0	0	0	0	5	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lepiota		0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Ochroconis	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	0	0	0	0	5	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae		Cystofilobasidium	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Paramycosphaerella	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae			0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria		0	0	0	0	0	0	0	0	0	0	0	5	0

Ascomycota					0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Trichothecium	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Mycophilomyces	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Ophiosphaerella	0	0	0	0	0	0	0	0	0	0	0	5	0
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae	Septobasidium	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	5	0
Zoopagomycota	Zoopagomycetes	Zoopagales	Piptocephalidaceae	Syncephalis	0	0	0	0	0	0	0	0	0	0	0	5	0
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae	Rhizophlyctis	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	5	0
Basidiomycota	Agaricomycetes	Russulales	Peniophoraceae	Peniophora	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	5
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	0	0	0	0	5

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		Neophaeothecoidea	0	0	0	0	0	0	0	0	0	0	0	0	5
Ascomycota	Dothideomycetes	Botryosphaeriales	Aplosporellaceae		Aplosporella	0	0	0	0	0	0	0	0	0	0	0	0	5
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis		Zeloasperisporium	0	0	0	0	0	0	0	0	0	0	0	0	5
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae			4	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		Hyaloscypha	4	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales				4	0	0	0	0	0	0	0	0	0	0	0	0
Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae			4	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Erysiphe		4	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae		Gliomastix	4	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria		2	0	0	2	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes					0	4	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota						0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae		Lophotrichus	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes					0	4	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Melanommataceae			0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Alternaria	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae			0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae		Stagonospora	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae		Pyrenochaeta	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Myrmecridiales	Myrmecridiaceae		Myrmecridium	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		Colletotrichum	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		Aspergillus	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Dothioraceae		Hormonema	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Xylonomycetes	GS34				0	4	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		0	2	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Coniosporium	0	2	0	0	0	0	0	0	0	2	0	0	0

Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Neofusicoccum		0	0	4	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Corticiales				0	0	4	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	4	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae			0	0	4	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma		0	0	4	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes					0	0	4	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Lyophyllaceae	Fibulochlamys	chilensis	0	0	4	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	4	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma		0	0	4	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Neocoleroa		0	0	4	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae	Flabellascoma		0	0	2	0	0	0	0	0	0	0	0	2	0
Ascomycota	Sordariomycetes	Diaporthales				0	0	0	4	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cladorrhinum		0	0	0	2	2	0	0	0	0	0	0	0	0
Mucoromycota	Mucoromycetes	Mucorales	Lichtheimiaceae	Lichtheimia		0	0	0	0	4	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Aporospora		0	0	0	0	4	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae	Serendipita		0	0	0	0	4	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae	Punctularia		0	0	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium		0	0	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Muscodor		0	0	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pyrenochaetopsidaceae	Neopyrenochaeta		0	0	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	fructigenum	0	0	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes					0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Pseudallescheria		0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria		0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae			0	0	0	0	0	4	0	0	0	0	0	0	0

Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae		Botryotinia	0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Calycina		0	0	0	0	0	4	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Cantharellales_fam_Incertae_sedis	Burgella		0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae			0	0	0	0	0	4	0	0	0	0	0	0	0
Zoopagomycota	Zoopagomycetes	Zoopagales	Piptocephalidaceae		Syncephalis	0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales				0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		Teichospora	0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae		Neocamarosporium	0	0	0	0	0	4	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae		Sporobolomyces	0	0	0	0	0	4	0	0	0	0	0	0	0
Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae		Microdominikia	0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae		Toxicocladosporium	0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae		Schizoxylon	0	0	0	0	0	4	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusicolla		0	0	0	0	0	0	4	0	0	0	0	0	0

Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusicolla		0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae		Pyrenochaetopsis	0	0	0	0	0	0	4	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Steccherinaceae		Nigroporus	0	0	0	0	0	0	4	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae			0	0	0	0	0	0	4	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae		Malassezia	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	4	0	0	0	0	0	0
Chytridiomycota	Rhizophydiomycetes	Rhizophydiales	Rhizophydiaceae		Rhizophydium	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis		Pseudorobillarda	0	0	0	0	0	0	4	0	0	0	0	0	0
Basidiomycota	Agaricomycetes					0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae			0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiotremataceae	Atrocalyx		0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		0	0	0	0	0	0	0	4	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		Phialoseptomonium	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis		Leohumicola	0	0	0	0	0	0	0	4	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		0	0	0	0	0	0	0	4	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Chrysozymaceae		Bannozyma	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	4	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae		Ganoderma	0	0	0	0	0	0	0	4	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae		Psathyrella	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae		Simplicillium	0	0	0	0	0	0	0	4	0	0	0	0	0
Rozellomycota						0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	4	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Peniophoraceae		Peniophora	0	0	0	0	0	0	0	4	0	0	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Schizophyllum	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Virgaria	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae		0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Microbotryomycetes_fam_Incertae_sedis	Colacogloea	0	0	0	0	0	0	0	0	4	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Diutina	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Halosphaeriaceae	Remispora	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Chlamydocillium	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Boletales	Sclerodermataceae	Scleroderma	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota					0	0	0	0	0	0	0	0	4	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	0	4	0	0	0	0
Rozellomycota						0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora		0	0	0	0	0	0	0	0	4	0	0	0	0
Chytridiomycota	Spizellomycetes	Spizellomycetales				0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae			0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Laboulbeniomycetes					0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	lignicola	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora		0	0	0	0	0	0	0	0	4	0	0	0	0
Kickxellomycota	GS19					0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Pseudombrophila		0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae			0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Lachnocladiaceae	Vararia		0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus		0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Pucciniomycetes	Platygloeales				0	0	0	0	0	0	0	0	4	0	0	0	0

Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	0	0	4	0	0	0	0
Zoopagomycota	Zoopagomycetes	Zoopagales	Piptocephalidaceae		Syncephalis	0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Lycoperdaceae			0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis		Pseudoramichloridium	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Biatriosporaceae		Biatriospora	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Sordariomycetes					0	0	0	0	0	0	0	0	0	4	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae			0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae		Chaetomella	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		Celerioriella	0	0	0	0	0	0	0	0	0	4	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma		0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Thelebolaceae			0	0	0	0	0	0	0	0	0	4	0	0	0

Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	0	4	0	0	0
Mucoromycota	Umbelopsidomycetes	Umbelopsidales	Umbelopsidaceae	Umbelopsis	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Gomphillaceae	Corticifraga	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Stemphylium	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Xeromyces bisporus	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Gymnostellatospora	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Canariomyces	0	0	0	0	0	0	0	0	0	0	4	0	0
Rozellomycota					0	0	0	0	0	0	0	0	0	0	4	0	0

Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Ochroconis	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis	Cadophora	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Pezizomycetes	Pezizales	Pezizaceae		0	0	0	0	0	0	0	0	0	0	4	0	0
Basidiomycota	Agaricomycetes	Auriculariales			0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Veronaeopsis	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Venturiales	Venturiaceae	Cylindrosympodium	0	0	0	0	0	0	0	0	0	0	4	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis	Pseudoramichloridium	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Sordariomycetes	Microascales			0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis	Rhodoveronaea	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	0	0	0	4	0

Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	0	0	0	4	0
Basidiomycota	Cystobasidiomycetes					0	0	0	0	0	0	0	0	0	0	0	4	0
Basidiomycota						0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes	Pleosporales	Torulaceae		Dendryphion	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Acaulium		0	0	0	0	0	0	0	0	0	0	0	4	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae		Rhodotorula	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Neocoleroa	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		Colletotrichum	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes					0	0	0	0	0	0	0	0	0	0	0	4	0
Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Ruineniaceae	Ruinenia		0	0	0	0	0	0	0	0	0	0	0	4	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	0	0	0	0	0	4	0
Chytridiomycota						0	0	0	0	0	0	0	0	0	0	0	4	0
Chytridiomycota						0	0	0	0	0	0	0	0	0	0	0	4	0

Ascomycota	Archaeorhizomycetes				0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Montagnula	0	0	0	0	0	0	0	0	0	0	0	2	2
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia	0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bionectria	0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	0	0	0	0	0	0	0	0	0	0	0	0	4
Basidiomycota	Agaricomycetes	Russulales			0	0	0	0	0	0	0	0	0	0	0	0	4
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae	Gyroporus	0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Clavispora	3	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae		Striaticonidium	3	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Geminibasidiomycetes	Geminibasidiales				3	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae			3	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				3	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Asterinales	Parmulariaceae		Parmularia	3	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota						3	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae		Komagataella	3	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		3	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes					3	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae			3	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Melanommataceae		Melanodiplodia	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria		0	3	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Pezizomycetes	Pezizales	Pezizales_fam_Incertae_sedis	Trichobolus	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae		0	3	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Piskurozymaceae	Solicoccozyma	0	3	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Stephanosporaceae		0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	3	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria	0	3	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Kondoaceae	Kondoa	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeodothis	0	3	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Thanatephorus	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	0	3	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Neoascochyta	0	3	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Schizophyllum	0	3	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Fomitopsidaceae	Skeletocutis	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Spiromastix	0	0	3	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis	Ramophialophora	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae		0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis	Arthrocatena	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	3	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Bolbitiaceae	Panaeolus	0	0	3	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	3	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	3	0	0	0	0	0	0	0	0	0	0
Chytridiomycota					0	0	3	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Botryotrichum	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae		0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	0	0	3	0	0	0	0	0	0	0	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11			0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascodesmidaceae	Cephaliophora	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Retroconis	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Lasionectria	0	0	3	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Dissoconiaceae	Uwebraunia	0	0	0	3	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Peniophoraceae	Peniophora	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Paracremonium	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	3	0	0	0	0	0	0	0	0	0
Mortierellomycota					0	0	0	0	3	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	3	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Clavispora	0	0	0	0	3	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Diatrypaceae	Monosporascus	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	3	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Fusculina	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Hirsutella	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Ochroconis	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Tetraplosphaeriaceae		0	0	0	0	0	3	0	0	0	0	0	0	0

Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Mytilinidales	Gloniaceae	Cenococcum	0	0	0	0	0	3	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodotorula	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae		0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae		0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bullanockia	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Golovinomyces	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Orbiliomycetes				0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	3	0	0	0	0	0	0

Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae		Ganoderma	0	0	0	0	0	0	3	0	0	0	0	0	0
Chytridiomycota						0	0	0	0	0	0	0	3	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae		Malassezia	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		Triangularia	0	0	0	0	0	0	0	3	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina		0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	3	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Bondarzewiaceae		Heterobasidion	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Rhinocladiella	0	0	0	0	0	0	0	3	0	0	0	0	0
Chytridiomycota	Spizellomycetes	Spizellomycetales	Spizellomycetaceae		Spizellomyces	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		Neodidymella	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		Acremonium	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Lecanoromycetes	Lecanorales	Ramalinaceae			0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	3	0	0	0	0	0
Glomeromycota						0	0	0	0	0	0	0	3	0	0	0	0	0

Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cercophora	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Pseudolachnea	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Rachicladosporium	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis		0	0	0	0	0	0	0	3	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Pezicula	0	0	0	0	0	0	0	3	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales			0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	0	0	0	0	0	3	0	0	0	0	0
Basidiomycota	Agaricomycetes	Tremellodendropsidales	Tremellodendropsidaceae	Tremellodendropsis	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Millerozyma	0	0	0	0	0	0	0	3	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Cortinariaceae	Cortinarius	0	0	0	0	0	0	0	3	0	0	0	0	0

Ascomycota					0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Polyschema	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Verticillium	0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Coniochaetales			0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	0	0	0	0	0	0	0	0	3	0	0	0	0
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae	Rhizophlyctis	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Minimelanolocus	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Dothideaceae		0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Biatriosporaceae	Biatriospora	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae		0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Cystostereaceae	Cystidiodontia	0	0	0	0	0	0	0	0	3	0	0	0	0

Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	3	0	0	0	0
Chytridiomycota						0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota	Atractiellomycetes	Atractiellales	Hoehnelomycetaceae		Atractiella	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Geopora		0	0	0	0	0	0	0	0	3	0	0	0	0
Rozellomycota						0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Cantharellales_fam_Incertae_sedis	Burgella		0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Cantharellales_fam_Incertae_sedis		Minimedusa	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae		Amphosoma	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales				0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae		Talaromyces	0	0	0	0	0	0	0	0	3	0	0	0	0

Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae			0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Cladophialophora	0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Acaulium		0	0	0	0	0	0	0	0	3	0	0	0	0
Basidiomycota						0	0	0	0	0	0	0	0	3	0	0	0	0
Glomeromycota						0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae			0	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales				0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae		Trichoderma	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Rhinocladiella	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	0	3	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae		Sporormia	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis			0	0	0	0	0	0	0	0	0	3	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Annulatascales	Annulatascaceae		0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	3	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Phialemoniopsis	0	0	0	0	0	0	0	0	0	3	0	0	0
Rozellomycota					0	0	0	0	0	0	0	0	0	3	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Podoscyphaceae	Abortiporus	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	0	3	0	0	0
Rozellomycota					0	0	0	0	0	0	0	0	0	3	0	0	0
Basidiomycota	Agaricomycetes	Agaricales			0	0	0	0	0	0	0	0	0	3	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae		Clavulinopsis	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Hypoxylaceae		Hypomontagnella	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Acaulium		0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis	Chalara		0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Nectria		0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae		Clonostachys	0	0	0	0	0	0	0	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Devriesia		0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Mollisia		0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Eurotiomycetes	Onygenales				0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		Verticillium	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		0	0	0	0	0	0	0	0	0	0	3	0	0

Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	0	0	0	0	0	0	0	0	3	0	0
Chytridiomycota					0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae		0	0	0	0	0	0	0	0	0	0	3	0	0
Chytridiomycota					0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Apiosordaria	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Eremomycetaceae	Arthrographis	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Arnium	0	0	0	0	0	0	0	0	0	0	3	0	0
Rozellomycota					0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Paraphoma	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Coniosporium	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Dendryphiella	0	0	0	0	0	0	0	0	0	0	3	0	0

Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae		0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes	Xylariales	Diatrypaceae	Eutypella	0	0	0	0	0	0	0	0	0	0	3	0	0
Basidiomycota	Agaricomycetes	Agaricomycetes_ord_Incertae_sedis	Agaricomycetes_fam_Incertae_sedis	Xenasmatella	0	0	0	0	0	0	0	0	0	0	3	0	0
Ascomycota	Sordariomycetes	Pseudodactylariales	Pseudodactylariaceae	Pseudodactylaria	0	0	0	0	0	0	0	0	0	0	3	0	0
Basidiomycota	Agaricomycetes	Boletales	Boletaceae	Hortiboletus	0	0	0	0	0	0	0	0	0	0	3	0	0
Glomeromycota					0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Apodus	0	0	0	0	0	0	0	0	0	0	0	3	0

Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Volutella	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae		0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Phomatosporales	Phomatosporaceae	Phomatospora	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Hermetothecium	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Lecanoromycetes	Lecanoromycetes_ord_Incertae_sedis	Micropeltidaceae		0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae		0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	0	0	0	3	0
Basidiomycota	Agaricomycetes	Sebacinales			0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae		0	0	0	0	0	0	0	0	0	0	0	3	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	0	0	0	0	0	0	0	3	0

Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina		0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Zasmidium	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	0	3	0
Rozellomycota						0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae		Meliniomyces	0	0	0	0	0	0	0	0	0	0	0	3	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleraceae		Fonsecazyma	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Veronaea	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Taphrinomycetes	Taphrinales	Taphrinaceae	Taphrina		0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		Exophiala	0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Daldinia		0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae		Ochroconis	0	0	0	0	0	0	0	0	0	0	0	0	3
Zoopagomycota	Zoopagomycetes	Zoopagales	Piptocephalidaceae		Syncephalis	0	0	0	0	0	0	0	0	0	0	0	0	3

Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Arthoniomycetes	Lichenostigmatales	Phaeococcomycetaceae	Phaeococcomyces	0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		0	0	0	0	0	0	0	0	0	0	0	0	3
Chytridiomycota					0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia	0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Dothideomycetes	Myriangiales			2	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Mycoacia	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cyanodermella	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota					2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Phialemoniopsis	2	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales			2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae		2	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	Peziza	flavida	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae			2	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		Tomentella	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae			2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae			2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pezizaceae	Peziza		2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae		Scutellinia	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae			0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Diplodia		0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		Leptospora	0	2	0	0	0	0	0	0	0	0	0	0	0
Zoopagomycota	Zoopagomycetes	Zoopagales	Piptocephalidaceae		Syncephalis	0	2	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Lecanoromycetes	Lecanorales				0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	2	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora		0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Branch06				0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae			0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Proliferodiscus		0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Neomassarinaceae	Neomassarina	thailandica	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis		0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stomiopeltis		0	2	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales				0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Scutellinia		0	2	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales			0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Thermomyces	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Articulospora	0	0	2	0	0	0	0	0	0	0	0	0	0
Zoopagomycota					0	0	2	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Piskurozymaceae	Solicoccozyma	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	2	0	0	0	0	0	0	0	0	0	0
Chytridiomycota	Spizellomycetes	Spizellomycetales	Powellomycetaceae		0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Asterinales	Parmulariaceae	Parmularia	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascodesmidaceae	Cephaliophora	0	0	2	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Volutella		0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	0	2	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae		Coprinopsis	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales				0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Gymnoascaceae		Leucothecium	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales				0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae			0	0	2	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		Serendipita	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		Collariella	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	2	0	0	0	0	0	0	0	0	0

Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Helvellosebacina	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		0	0	0	2	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes				0	0	0	2	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Lopharia	0	0	0	2	0	0	0	0	0	0	0	0	0
Basidiomycota					0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales	Elsinoaceae	Sphaceloma	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales			0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales			0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales			0	0	0	2	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Westerdykella	0	0	0	0	2	0	0	0	0	0	0	0	0

Basidiomycota	Agaricomycetes	Agaricales	Lyophyllaceae	Fibulochlamys	0	0	0	0	2	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	0	0	0	0	2	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	2	0	0	0	0	0	0	0	0
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae	Rhizophlyctis	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	2	0	0	0	0	0	0	0	0
Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Microdominikia	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Gomphillaceae	Corticifraga	0	0	0	0	2	0	0	0	0	0	0	0	0

Ascomycota	Lecanoromycetes	Ostropales	Odontotremataceae	Claviradulomyces	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiaceae	Capnodium	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Phomatosporales	Phomatosporaceae	Phomatospora	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		0	0	0	0	0	2	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae	Sphaerellopsis	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	2	0	0	0	0	0	0	0
Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae		0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Leucosphaerina	0	0	0	0	0	2	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	2	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Glutinomyces	0	0	0	0	0	2	0	0	0	0	0	0	0
Chytridiomycota					0	0	0	0	0	2	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Xeromyces	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	2	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tremella	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae		0	0	0	0	0	2	0	0	0	0	0	0	0
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales			0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Ulocladium	0	0	0	0	0	2	0	0	0	0	0	0	0
Chytridiomycota					0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Lophotrichus	0	0	0	0	0	0	2	0	0	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	2	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Paramyrothecium	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	2	0	0	0	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11			0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Biscogniauxia	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	2	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Arthrobotrys	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Auriscalpiaceae	Gloeodontia	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Chordomyces	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales			0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Castanediella	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae		0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae	Punctularia	0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales			0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Corticiales	Vuilleminiaceae		0	0	0	0	0	0	0	2	0	0	0	0	0

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		Diaporthe	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis		Rhodoveronaea	0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula		0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetaceae	Coltricia		0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Amanitaceae	Amanita		0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae			0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis		Liberomyces	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae			0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae			0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Arthrodermataceae		Trichophyton	0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae		Rhodotorula	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Odontotremataceae		Claviradulomyces	0	0	0	0	0	0	0	0	2	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Lecanoromycetes	Lecanoromycetes_ord_Incertae_sedis	Lecanoromycetes_fam_Incertae_sedis	Phacidiella	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Apiosporaceae	Arthrinium	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Glarea	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Melanodothis	0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales			0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Clonostachys	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Castanediella	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	2	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Crucellisporiopsis	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae		0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metarhizium	0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Mrakiaceae	Tausonia	0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Agaricomycetes	Amylocorticiales	Amylocorticiaceae	Amyloxenasma	0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	2	0	0	0	0

Ascomycota					0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Orbiliomycetes				0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Ochroconis	0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Parvothecium	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Acaulium	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Proliferodiscus	0	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Atractiellomycetes	Atractiellales	Hoehnelomycetaceae		0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales			0	0	0	0	0	0	0	0	0	2	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Rinaldiella	0	0	0	0	0	0	0	0	0	2	0	0	0
Basidiomycota					0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Bartaliniaceae		0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Mytilinidiales	Gloniaceae	Cenococcum	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Beauveria	0	0	0	0	0	0	0	0	0	2	0	0	0
Chytridiomycota					0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Knufia	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Fusidium	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	Cyanodermella	0	0	0	0	0	0	0	0	0	2	0	0	0

Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Efibulobasidium	0	0	0	0	0	0	0	0	0	2	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae		0	0	0	0	0	0	0	0	0	2	0	0	0
Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Septoglomus viscosum	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae	Gloniopsis	0	0	0	0	0	0	0	0	0	2	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma	0	0	0	0	0	0	0	0	0	2	0	0	0
Basidiomycota	Agaricomycetes	Agaricales			0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Conioscyphales	Conioscyphaceae	Conioscypha	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Scopulariopsis	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	0	0	2	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		Laburnicola	0	0	0	0	0	0	0	0	0	2	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus		0	0	0	0	0	0	0	0	0	2	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae		Trechispora	0	0	0	0	0	0	0	0	0	2	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS09				0	0	0	0	0	0	0	0	0	2	0	0	0
Basidiobolomycota	Basidiobolomycetes	Basidiobolales	Basidiobolaceae		Basidiobolus	0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	0	2	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae		Barnettozyma	0	0	0	0	0	0	0	0	0	0	2	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae		Papiliotrema	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Dothideales				0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		0	0	0	0	0	0	0	0	0	0	2	0	0

Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Mariannaea	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Phloeospora	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Thelonectria	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Leotiomycetes	Helotiales	Leotiaceae	Neobulgaria	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Lecanicillium	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascodesmidaceae	Cephaliophora	0	0	0	0	0	0	0	0	0	0	2	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae		0	0	0	0	0	0	0	0	0	0	2	0	0

Ascomycota	Leotiomycetes	Rhytismatales	Rhytismataceae		0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Scutellinia	0	0	0	0	0	0	0	0	0	0	2	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Microbotryomycetes_fam_Incertae_sedis	Colacogloea	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	2	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae		0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus	0	0	0	0	0	0	0	0	0	0	2	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae		0	0	0	0	0	0	0	0	0	0	2	0	0
Basidiomycota	Agaricomycetes	Agaricales			0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Diaporthales	Melanconidaceae	Melanconium	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	2	0	0

Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Meyerozyma	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Pseudoascochyta	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	0	0	0	0	0	0	0	0	0	2	0	0
Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Septoglomus	0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Leotiomycetes	Helotiales	Leotiaceae	Alatospora	0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Eurotiomycetes	Onygenales	Arthrodermataceae	Ctenomyces	0	0	0	0	0	0	0	0	0	0	0	2	0
Basidiomycota	Ustilaginomycetes	Ustilaginales	Ustilaginaceae	Moesziomyces	0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Dothideomycetes	Pleosporales	Thyridariaceae	Pararoussoella	0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	2	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Dothideomycetes	Dothideales	Dothioraceae	Hormonema	0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	2	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		0	0	0	0	0	0	0	0	0	0	0	2	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	0	2	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	2
Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavulinopsis	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Sordariales	Sordariaceae	Gelasinospora	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Magnaporthe	0	0	0	0	0	0	0	0	0	0	0	0	2
Zoopagomycota	Zoopagomycetes	Zoopagales	Piptocephalidaceae	Syncephalis	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Lecanoromycetes	Caliciales	Caliciaceae		0	0	0	0	0	0	0	0	0	0	0	0	2

Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae			0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae		Rhytidhysteron	0	0	0	0	0	0	0	0	0	0	0	0	2
Basidiomycota						0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		Ramularia	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Devriesia		0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae		Arthrobotrys	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes					0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Myriangiales	Elsinoaceae			0	0	0	0	0	0	0	0	0	0	0	0	2
Chytridiomycota	Spizellomycetes	Spizellomycetales	Powellomycetaceae			0	0	0	0	0	0	0	0	0	0	0	0	2

Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Lecanicillium	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	0	1	0	0	0	0	0	0

CB: *C. Brasiliense*; C: Control; N: nitrogen treatment; NP: nitrogen+phosphate treatment; P: phosphate treatment; Ca: liming.

Suplementary table 6. Taxonomic attribution of fungal ITS sequences obtained from *Ouratea hexasperma* in different treatments of addition of nutrients to the soil

Phylum	Class	Order	Family	Genus	Species	OH1078C	OH1536CA	OH1827NP	OH1943N	OH2208C	OH2226C	OH243P	OH2611N	OH2725P	OH2891CA	OH610NP	OH618NP	OH800N	OH874CA
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis		149	3847	1949	8198	553	338	62462	2078	56184	3806	1572	3222	1266	55308
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora		173	953	1125	571	100	85	33985	762	35100	759	103230	1428	660	782
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia		24706	137	135	8041	39077	10939	83	565	83	138	961	21974	105	115
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris		49	4366	227	125	42	0	104	231	128	74724	171	169	169	182
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis		122	394	424	59245	1173	323	491	3477	570	358	8650	760	1367	863
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	neriicola	0	436	529	17877	564	0	8776	339	8955	391	27743	627	272	419
Ascomycota	Sordariomycetes	Diaporthales				8098	93	16414	526	20980	448	1763	278	1534	759	63	97	92	2064
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta		28	234	25223	556	0	0	4164	391	6783	2904	158	3784	5601	256
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta		311	206	22902	170	178	8	1556	174	1865	0	173	539	18887	330

Ascomycota	Dothideomycetes	Pleosporales				0	45241	175	115	27	97	101	172	187	170	175	192	241	218
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium		233	800	52	41	621	0	51	50	85	58	72	33518	64	65
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae			182	2468	4352	36	63	436	2035	102	819	5607	3263	3790	2765	2779
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		141	5338	4718	116	66	3889	155	234	189	0	461	2751	7017	3421
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium		71	0	0	10	40	28368	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				639	98	86	84	0	0	71	23132	79	70	91	98	73	97
Ascomycota	Leotiomycetes	Helotiales	Pezizellaceae	Porodiplodia	livistonae	7508	0	0	394	13814	260	0	206	0	4	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	135	252	92	0	0	92	154	102	127	164	155	19533	159
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria		0	17945	370	143	0	0	204	290	183	253	190	259	194	268
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium		0	100	95	33	0	0	64	144	68	72	98	65	18148	75
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium		0	397	154	88	0	0	114	143	117	154	116	15842	97	142
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium		1360	383	475	530	521	3104	103	1020	99	193	114	6460	1144	290
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella		744	2095	1333	381	817	4295	222	653	268	1403	744	517	858	351
Ascomycota	Dothideomycetes	Asterinales	Parmulariaceae	Parmularia		578	2227	26	4	328	1262	0	0	0	6201	9	17	9	2276
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		469	5068	1083	60	147	984	244	169	406	1903	671	373	448	726
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		236	285	4004	258	52	138	145	2671	173	0	172	252	149	3112
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma		9493	0	21	8	77	216	0	324	5	13	8	0	115	4
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria		472	385	4870	719	246	411	395	844	332	281	175	429	203	356
Basidiomycota	Tremellomycetes	Tremellales	Bulleraceae	Fonsecazyma		0	17	0	335	6807	1094	88	0	60	83	25	1522	0	14

Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	112	44	48	124	105	38	78	4880	93	65	3667	56	0	462
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	610	724	282	169	865	1905	404	202	287	34	44	4028	39	103
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria	0	60	8990	36	0	0	0	80	26	37	24	44	43	68
Ascomycota	Leotiomycetes	Helotiales			0	8187	82	37	0	0	53	64	49	60	43	65	68	85
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosulcatispora	0	64	86	41	11	17	101	120	134	214	261	746	49	5898
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	7266	0	0	0	70	0	48	0	0	95	73	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Neofusicoccum	0	29	46	21	0	0	25	57	39	65	29	43	40	6594
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	77	1791	232	232	32	539	100	424	106	112	98	207	2624	198
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Ochroconis	0	13	37	14	0	0	17	12	10	34	16	12	13	6353
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae	Gloniopsis	0	175	35	19	0	0	21	16	24	16	25	6034	14	25
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	249	82	395	210	93	212	123	2994	97	0	80	127	49	1658
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	158	18	47	0	64	5936	0	118	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	197	2558	563	23	125	36	43	43	47	706	40	165	884	797
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	1537	12	0	112	3938	82	0	197	14	17	7	0	8	0
Ascomycota	Dothideomycetes	Capnodiales	Schizothyriaceae	Johansonia	424	16	798	12	106	2344	10	1444	13	13	311	29	5	20
Ascomycota	Dothideomycetes	Pleosporales			1137	73	0	487	478	2348	0	883	5	35	9	5	40	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bullanockia	0	58	97	67	0	0	75	66	55	68	59	81	48	4592
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	136	1452	34	0	63	31	74	44	2879	108	46	68	226
Ascomycota	Eurotiomycetes	Phaeomoniellales			7	105	36	4094	118	0	28	43	30	25	24	68	20	35
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	0	0	0	0	0	0	1205	0	1878	109	0	0	1404	0

Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**	**Chaetosphaeriaceae**		**18**	**30**	**34**	**62**	**13**	**59**	**30**	**0**	**33**	**38**	**34**	**4035**	**38**	**58**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Aspergillus**	**35**	**22**	**181**	**21**	**21**	**415**	**988**	**26**	**1295**	**50**	**155**	**124**	**19**	**1008**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Phyllostictaceae**	**Phyllosticta**	**0**	**0**	**0**	**43**	**0**	**0**	**73**	**0**	**95**	**0**	**0**	**1797**	**2298**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Alternaria**	**340**	**288**	**539**	**142**	**235**	**1349**	**28**	**181**	**10**	**224**	**96**	**210**	**120**	**84**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Hypocreales_fam_Incertae_sedis**	**Sarocladium**	**0**	**19**	**3252**	**11**	**0**	**0**	**20**	**25**	**21**	**23**	**22**	**21**	**21**	**19**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**85**	**343**	**215**	**12**	**42**	**234**	**23**	**37**	**19**	**780**	**584**	**270**	**422**	**86**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**			**728**	**0**	**0**	**58**	**1059**	**528**	**67**	**225**	**40**	**58**	**0**	**89**	**0**	**109**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleraceae**	**Fonsecazyma**	**2824**	**0**	**0**	**0**	**0**	**0**	**0**	**114**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zasmidium**	**78**	**55**	**110**	**121**	**0**	**82**	**71**	**1103**	**67**	**61**	**0**	**49**	**0**	**1134**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Phyllostictaceae**	**Phyllosticta**	**0**	**0**	**2001**	**0**	**0**	**0**	**79**	**0**	**99**	**0**	**0**	**0**	**726**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Rhynchogastremataceae**	**Papiliotrema**	**853**	**2**	**0**	**92**	**1661**	**77**	**0**	**58**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**326**	**0**	**0**	**128**	**177**	**694**	**0**	**321**	**0**	**126**	**0**	**629**	**0**	**331**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Didymella**	**350**	**0**	**0**	**0**	**104**	**470**	**0**	**48**	**0**	**0**	**0**	**28**	**1687**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2646**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Madagascaromyces**	**303**	**20**	**58**	**0**	**123**	**583**	**202**	**0**	**0**	**0**	**0**	**1315**	**0**	**9**
Ascomycota	**Sordariomycetes**				**3**	**35**	**235**	**1337**	**57**	**0**	**211**	**18**	**148**	**290**	**18**	**59**	**0**	**30**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Meruliaceae**	**Phlebia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**18**	**14**	**0**	**16**	**0**	**2353**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Phaeophleospora**	**306**	**7**	**242**	**42**	**111**	**912**	**8**	**112**	**0**	**23**	**166**	**220**	**78**	**60**
Ascomycota	**Dothideomycetes**	**Dothideales**	**Aureobasidiaceae**	**Aureobasidium**	**393**	**0**	**0**	**1471**	**333**	**12**	**0**	**52**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Xenosonderhenia**	**155**	**49**	**11**	**3**	**84**	**289**	**0**	**0**	**0**	**1637**	**0**	**0**	**0**	**25**

Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**			**0**	**15**	**20**	**76**	**67**	**1047**	**0**	**0**	**0**	**248**	**0**	**727**	**10**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Madagascaromyces**	**214**	**0**	**0**	**0**	**134**	**385**	**0**	**0**	**0**	**16**	**0**	**1279**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Botryosphaeriaceae**	**Lasiodiplodia**	**26**	**0**	**0**	**0**	**13**	**1971**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**887**	**0**	**0**	**63**	**926**	**43**	**0**	**60**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zasmidium**	**204**	**0**	**0**	**0**	**74**	**0**	**0**	**1016**	**0**	**71**	**0**	**79**	**0**	**488**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1917**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**41**	**0**	**0**	**0**	**18**	**0**	**13**	**0**	**41**	**1791**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Phialoseptomonium**	**173**	**1253**	**0**	**0**	**120**	**291**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**	**Chaetosphaeriaceae**	**Dictyochaeta**	**734**	**0**	**0**	**40**	**826**	**169**	**0**	**50**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota					**355**	**0**	**0**	**63**	**1287**	**59**	**0**	**31**	**0**	**0**	**0**	**20**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**50**	**73**	**84**	**0**	**22**	**54**	**0**	**35**	**0**	**0**	**33**	**0**	**1426**	**17**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**1533**	**0**	**17**	**0**	**17**	**52**	**0**	**44**	**0**	**0**	**0**	**0**	**40**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriaceae**	**Ceramothyrium**	**65**	**11**	**19**	**7**	**0**	**0**	**9**	**1480**	**7**	**20**	**8**	**11**	**10**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Neodidymella**	**347**	**20**	**0**	**130**	**102**	**573**	**0**	**278**	**0**	**27**	**0**	**0**	**24**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**	**Colletotrichum**	**0**	**0**	**33**	**1308**	**45**	**0**	**0**	**45**	**35**	**0**	**25**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Phyllostictaceae**	**Phyllosticta**	**0**	**0**	**538**	**0**	**0**	**0**	**81**	**27**	**133**	**0**	**31**	**0**	**667**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Madagascaromyces**	**159**	**0**	**0**	**0**	**89**	**283**	**0**	**14**	**0**	**0**	**0**	**915**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**		**0**	**106**	**645**	**349**	**34**	**0**	**32**	**74**	**24**	**21**	**76**	**40**	**22**	**27**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**1319**	**0**	**0**	**55**	**0**	**0**	**25**	**0**	**0**	**29**	**0**	**16**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Phyllostictaceae**	**Phyllosticta**	**0**	**0**	**0**	**0**	**0**	**0**	**579**	**0**	**834**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**	**Hyaloscyphaceae**	**Proliferodiscus**	**0**	**0**	**20**	**14**	**0**	**0**	**642**	**0**	**621**	**0**	**0**	**20**	**12**	**0**

Ascomycota	**Sordariomycetes**	**Glomerellales**	**Plectosphaerellaceae**	**Plectosphaerella**	**91**	**42**	**514**	**15**	**0**	**48**	**210**	**51**	**177**	**27**	**14**	**23**	**0**	**37**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**55**	**0**	**23**	**17**	**0**	**85**	**0**	**1013**	**7**	**0**	**9**	**18**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**21**	**14**	**43**	**41**	**33**	**43**	**22**	**11**	**22**	**44**	**7**	**30**	**0**	**884**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**	**Chaetosphaeriales_fam_Incertae_sedis**	**Dendrophoma**	**40**	**15**	**15**	**58**	**24**	**73**	**27**	**12**	**46**	**282**	**393**	**177**	**16**	**29**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**	**Colletotrichum**	**64**	**75**	**39**	**31**	**178**	**32**	**29**	**24**	**33**	**92**	**24**	**28**	**18**	**509**
Ascomycota	**Sordariomycetes**	**Trichosphaeriales**	**Trichosphaeriaceae**	**Nigrospora**	**263**	**195**	**27**	**52**	**190**	**58**	**0**	**183**	**0**	**71**	**15**	**31**	**0**	**89**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**15**	**34**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**213**	**894**	**0**	**17**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zasmidium**	**0**	**42**	**60**	**0**	**0**	**0**	**0**	**0**	**0**	**38**	**0**	**0**	**25**	**1000**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**		**0**	**11**	**17**	**19**	**0**	**0**	**491**	**30**	**525**	**17**	**10**	**11**	**16**	**13**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Pseudoteratosphaeria**	**0**	**0**	**1144**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Asterinales**	**Parmulariaceae**	**Parmularia**	**319**	**0**	**0**	**0**	**215**	**583**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Gibberella**	**78**	**50**	**123**	**32**	**124**	**227**	**33**	**0**	**0**	**132**	**32**	**120**	**130**	**37**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1067**	**13**	**0**	**0**	**35**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Meruliaceae**	**Phlebia**	**0**	**62**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1015**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Pseudoteratosphaeria**	**0**	**62**	**0**	**135**	**13**	**79**	**77**	**150**	**53**	**0**	**0**	**33**	**343**	**99**
Basidiomycota	**Malasseziomycetes**	**Malasseziales**	**Malasseziaceae**	**Malassezia**	**712**	**0**	**119**	**0**	**101**	**43**	**5**	**32**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Phyllostictaceae**	**Phyllosticta**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1012**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**138**	**0**	**0**	**0**	**138**	**0**	**0**	**0**	**610**	**0**	**0**	**0**	**120**
Ascomycota	**Eurotiomycetes**	**Onygenales**	**Onygenales_fam_Incertae_sedis**	**Zeloasperisporium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**980**	**0**	**0**

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	206	0	0	0	0	0	0	0	167	0	0	602	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Septoria	96	82	86	71	47	121	18	243	10	74	56	18	21	26
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Proliferodiscus	5	0	0	0	0	256	92	0	117	405	0	56	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	35	0	0	0	16	34	0	728	0	0	0	23	92	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		37	30	26	66	9	137	114	208	102	40	54	20	26	54
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Neofusicoccum	0	41	46	0	0	0	0	0	0	85	0	0	0	734
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	695	31	18	0	0	0	25	0	112	0	0	9	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Nigrograna	0	12	12	13	0	10	10	23	8	11	0	11	0	760
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		0	0	0	6	0	0	0	0	0	0	0	857	5	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	200	0	0	90	93	320	0	161	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	70	0	17	0	0	0	0	735	0	0	14	13	0	10
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	76	258	30	0	16	173	0	120	18	41	43	37	37
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Proliferodiscus	0	12	633	7	0	0	8	10	0	10	11	126	9	6
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	75	0	0	0	0	0	0	671	0	0	0	0	0	75
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	810	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			31	0	0	0	0	0	12	761	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tremella	11	0	4	47	0	0	443	82	191	10	5	0	10	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	800	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			67	9	8	3	0	0	0	646	14	0	7	16	8	5
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia	0	0	0	0	0	0	0	0	0	0	0	0	0	782

Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		12	0	0	0	0	763	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	156	66	0	16	466	0	0	51	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			35	0	261	0	25	177	26	36	15	0	29	110	20	8
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	101	83	9	0	56	208	0	0	12	0	11	102	0	155
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		147	0	0	0	69	193	0	0	0	0	0	326	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	0	0	0	0	0	0	290	0	409	17	18	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	0	80	38	35	12	28	0	0	21	21	31	337	14	98
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	0	11	0	0	0	0	0	4	0	0	0	0	700	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	52	0	181	0	99	0	76	0	0	0	307
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Exopassalora	44	0	0	0	0	0	2	629	7	6	0	11	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	36	0	0	128	9	56	0	326	0	0	77	0	0	44
Ascomycota	Dothideomycetes				164	0	0	18	472	12	0	8	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	32	0	7	17	97	0	18	84	0	387	0	11	5	6
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papilio- frias trema	554	0	5	0	0	41	0	53	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	606	0	47
Ascomycota					0	2	599	3	0	0	0	6	2	9	0	4	7	12
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	4	0	0	26	0	0	0	0	0	611	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	103	0	0	0	0	0	0	0	0	0	0	507
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	602
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Catenulostroma	13	0	16	31	0	61	9	117	25	221	11	33	19	39

Ascomycota	Sordariomycetes	Diaporthales	Valsaceae	Cytospora		0	0	0	0	0	593	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora		0	0	110	0	0	207	0	129	0	42	58	0	0	38
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium		87	20	14	15	180	231	0	25	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Xenocamarosporium		123	0	0	9	400	22	0	0	0	0	0	16	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella		131	4	0	43	35	262	0	84	0	6	0	0	4	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	0	0	0	40	0	0	0	0	0	0	0	527
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		0	0	0	0	0	17	65	432	49	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	483	0	0	0	0	0	0	0	0	75	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Fusculina		0	4	517	0	0	0	0	0	0	23	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum		0	139	0	0	38	0	28	0	0	26	0	0	0	307
Ascomycota	Dothideomycetes	Capnodiales				27	0	0	0	0	0	0	510	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium		0	0	326	9	0	0	0	18	0	0	14	155	0	10
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium		0	389	8	0	0	0	0	0	0	8	0	121	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		35	0	0	20	0	0	0	250	0	0	0	0	0	220
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae			206	0	116	0	103	85	0	14	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellales_fam_Incertae_sedis	Kwoniella		58	0	0	15	445	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Hyweljonesia		0	18	16	0	0	0	12	7	7	11	6	427	5	9
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	pectinatoides	329	0	35	0	47	93	0	6	0	0	0	0	0	0

Ascomycota	**Dothideomycetes**	**Pleosporales**			**137**	**0**	**0**	**0**	**0**	**279**	**0**	**91**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota					**0**	**7**	**12**	**9**	**0**	**0**	**5**	**0**	**5**	**7**	**0**	**10**	**8**	**428**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Trimorphomycetaceae**	**Saitozyma**	**127**	**10**	**0**	**41**	**36**	**181**	**0**	**79**	**0**	**0**	**0**	**0**	**11**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**		**291**	**0**	**0**	**17**	**109**	**26**	**0**	**41**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**38**	**0**	**22**	**0**	**0**	**0**	**0**	**138**	**61**	**0**	**0**	**225**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Trimorphomycetaceae**	**Saitozyma**	**0**	**84**	**19**	**13**	**20**	**51**	**7**	**19**	**0**	**19**	**3**	**0**	**235**	**13**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriaceae**	**Chaetothyrium**	**13**	**0**	**0**	**3**	**0**	**0**	**0**	**453**	**2**	**2**	**0**	**0**	**0**	**5**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Paraconiothyrium**	**0**	**0**	**0**	**0**	**0**	**478**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Bipolaris**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**477**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**	**0**	**0**	**0**	**0**	**0**	**0**	**36**	**287**	**27**	**0**	**0**	**0**	**117**	**0**
Ascomycota	**Sordariomycetes**	**Trichosphaeriales**	**Trichosphaeriaceae**	**Nigrospora**	**97**	**0**	**0**	**57**	**44**	**176**	**0**	**91**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Paramycosphaerella**	**49**	**43**	**49**	**0**	**0**	**161**	**16**	**19**	**0**	**47**	**0**	**26**	**30**	**18**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**			**38**	**0**	**5**	**0**	**0**	**0**	**2**	**405**	**0**	**0**	**3**	**0**	**0**	**2**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**20**	**0**	**0**	**0**	**0**	**421**
Basidiomycota	**Ustilaginomycetes**	**Ustilaginales**	**Ustilaginaceae**	**Moesziomyces**	**114**	**0**	**0**	**55**	**65**	**117**	**0**	**85**	**0**	**4**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**52**	**57**	**64**	**0**	**0**	**109**	**0**	**0**	**0**	**0**	**0**	**91**	**0**	**66**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Ophiocordycipitaceae**	**Tolypocladium**	**8**	**0**	**0**	**0**	**6**	**420**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**378**	**0**	**0**	**0**	**11**	**0**	**22**	**0**	**15**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**			**246**	**0**	**0**	**5**	**162**	**0**	**0**	**10**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**419**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Geopora	202	0	0	0	52	160	0	4	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Waitea	399	0	0	0	0	0	0	15	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	38	0	0	12	254	55	0	0	0	10	0	0	0	43
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	0	0	4	380	5	0	0	0	9	0	0	0	0	7
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Neophaeomoniella	0	0	0	0	0	0	246	0	143	0	0	0	0	16
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	0	0	0	0	405	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		33	0	85	0	13	218	0	0	0	0	48	5	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	83	0	0	38	40	106	0	78	52	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	69	4	3	27	31	150	6	93	10	0	2	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	0	0	52	33	0	0	0	0	0	0	0	50	260	0
Ascomycota	Dothideomycetes				19	0	0	0	0	0	0	369	0	0	0	0	0	4
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	0	0	0	0	0	0	0	386	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales			0	0	0	0	0	0	0	0	0	0	14	0	55	317
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	0	0	71	0	0	275	0	0	0	0	38	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	60	0	0	0	0	48	0	0	0	0	0	0	20	255
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	12	0	100	0	36	104	0	0	0	70	61	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Pseudodinemasporium	158	0	74	0	147	0	0	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Chrysozymaceae	Sampaiozyma	22	143	92	0	0	88	2	0	0	0	8	0	19	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	7	7	0	0	0	7	0	7	320	0	11	8	6

Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	342	17	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	121	0	0	0	235	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			18	0	12	6	0	0	7	313	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Phaeophleospora	85	0	0	0	45	174	0	0	0	0	0	51	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	34	12	46	0	11	144	10	6	6	37	0	23	9	16
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		29	0	0	0	0	0	0	317	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	34	0	82	0	0	102	0	83	0	0	27	0	0	18
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	0	36	7	24	89	24	11	12	18	17	0	71	0	37
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	36	43	12	30	44	0	27	17	48	0	29	43	11
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	5	0	0	0	0	0	0	0	0	0	0	331
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	19	0	312
Ascomycota	Dothideomycetes				0	4	6	4	0	0	44	6	29	6	4	222	5	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	0	0	0	0	0	0	130	0	200	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium	43	17	0	64	125	0	16	22	0	27	13	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	105	49	0	0	155	0	0	15	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		0	7	0	0	0	0	0	0	0	0	0	0	317	0
Basidiomycota	Wallemiomycetes	Wallemiales	Wallemiaceae	Wallemia	49	22	14	15	17	140	0	32	0	9	0	5	16	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	0	14	0	20	230	0	0	0	0	0	0	54	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	291	0	0	0	22	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium	77	0	16	0	158	0	0	0	0	56	0	0	0	0

Ascomycota					**0**	**0**	**6**	**0**	**0**	**0**	**4**	**0**	**0**	**9**	**0**	**11**	**0**	**270**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**		**0**	**6**	**83**	**3**	**0**	**0**	**6**	**4**	**3**	**8**	**2**	**172**	**0**	**10**
Ascomycota	**Dothideomycetes**	**Dothideales**	**Aureobasidiaceae**	**Aureobasidium**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**288**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**49**	**0**	**0**	**37**	**34**	**125**	**0**	**48**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Onygenales**	**Onygenales_fam_Incertae_sedis**	**Zeloasperisporium**	**32**	**90**	**0**	**0**	**88**	**0**	**81**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**			**28**	**0**	**0**	**0**	**0**	**0**	**0**	**257**	**6**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**281**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Epicoccum**	**44**	**0**	**0**	**12**	**32**	**135**	**0**	**31**	**0**	**0**	**26**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**30**	**0**	**0**	**43**	**0**	**0**	**0**	**44**	**0**	**0**	**0**	**163**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Dissoconiaceae**	**Uwebraunia**	**57**	**0**	**0**	**39**	**37**	**85**	**0**	**58**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**	**0**	**0**	**0**	**0**	**274**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Dissoconiaceae**	**Uwebraunia**	**82**	**0**	**0**	**51**	**0**	**80**	**0**	**50**	**0**	**0**	**0**	**0**	**8**	**0**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Phyllostictaceae**	**Phyllosticta**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**271**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Periconiaceae**	**Periconia**	**11**	**0**	**0**	**0**	**0**	**27**	**54**	**135**	**39**	**0**	**0**	**0**	**4**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**17**	**17**	**0**	**0**	**72**	**0**	**0**	**0**	**164**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Trichosphaeriales**	**Trichosphaeriaceae**	**Nigrospora**	**51**	**0**	**0**	**57**	**0**	**93**	**0**	**48**	**0**	**0**	**0**	**0**	**19**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**36**	**0**	**16**	**0**	**0**	**0**	**0**	**216**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Xenosonderhenia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**267**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**267**	**0**	**0**
Mortierellomycota	**Mortierellomycetes**	**Mortierellales**	**Mortierellaceae**	**Mortierella**	**0**	**0**	**0**	**16**	**0**	**0**	**11**	**24**	**0**	**13**	**0**	**0**	**202**	**0**

Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	0	126	0	0	0	0	46	0	92	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	24	32	0	0	15	60	0	11	0	0	0	82	0	39
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	21	0	6	0	0	10	8	171	2	0	0	23	18	4
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Coniothyrina	11	11	63	56	6	72	4	9	0	4	6	0	2	18
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	7	16	0	0	0	75	7	0	0	13	0	99	0	44
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	231	0	0	0	11	0	0	17	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	9	0	0	0	0	0	0	0	0	0	240	9	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	2	5	0	0	8	0	8	0	5	0	0	228
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudogymnoascus	125	42	0	5	26	31	0	10	0	0	5	6	0	4
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	15	0	0	0	0	13	53	135	33	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			9	0	0	0	0	0	0	239	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			7	0	0	2	0	0	4	229	0	0	3	3	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Filobasidium	213	0	0	0	0	16	0	9	0	5	0	0	3	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Phialoseptomonium	88	0	0	0	0	158	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			18	0	0	0	0	0	0	227	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium	0	219	0	0	0	0	10	0	0	0	0	0	0	16
Ascomycota	Ascomycota_cls_Incertae_sedis	Ascomycota_ord_Incertae_sedis	Ascomycota_fam_Incertae_sedis	Hormodochis	0	0	0	0	0	0	0	0	0	0	0	0	0	241
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Blumeria	212	0	0	0	0	17	0	10	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	132	15	43	0	0	15	0	7	0	20	2	5	0	0

Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea		20	0	0	0	0	0	0	129	0	0	0	89	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	82	0	16	90	0	0	0	0	49	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	37	0	0	108	0	71	0	0	0	20	0	0
Ascomycota						0	0	0	0	0	0	15	19	0	202	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta		0	0	142	0	0	0	0	0	0	0	0	0	93	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			4	0	0	13	0	0	0	19	0	190	0	0	7	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	233	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Togniniales	Togniniaceae	Phaeoacremonium		0	0	0	0	0	0	0	0	8	0	0	0	0	223
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Lophotrichus		32	41	31	3	10	37	3	21	0	13	10	21	6	0
Ascomycota	Dothideomycetes	Capnodiales				51	0	0	0	0	0	0	176	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema		61	9	0	14	26	80	0	32	0	0	0	0	0	4
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae			14	0	0	0	0	0	0	205	0	0	0	3	0	4
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	conoides	0	216	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana		42	0	0	0	45	54	14	44	10	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae			0	0	0	0	0	0	0	0	0	0	0	0	209	0
Ascomycota	Dothideomycetes	Pleosporales				0	208	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum		0	0	16	0	0	0	0	72	0	17	0	79	22	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	0	0	0	206	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Muscodor		57	6	14	0	20	0	0	9	0	44	6	0	0	45
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma		115	0	14	4	22	31	0	12	0	0	0	2	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	0	0	0	0	200
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Waitea	183	0	0	0	0	16	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes				59	0	15	14	28	36	0	0	0	13	0	22	12	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	59	0	27	112	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	12	0	32	0	12	42	0	0	0	0	0	82	0	17
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	43	0	0	0	154	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	197	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	11	0	0	0	13	99	0	0	0	0	0	0	72	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	0	0	0	0	0	19	0	0	0	0	0	174	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Dinemasporium	0	0	0	0	0	0	0	189	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria	48	0	0	19	23	65	0	32	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	187	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	157	0	0	0	0	29	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	0	0	0	0	0	0	61	0	123	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	0	182
Ascomycota	Sordariomycetes				0	0	0	0	0	159	0	0	0	0	0	10	12	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		0	0	42	40	27	39	0	0	0	0	24	0	0	7
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	0	176
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	53	0	0	96	0	0	0	0	16	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	107	0	58	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		0	12	7	0	0	98	0	10	30	0	0	0	7	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	112	0	36	0	0	0	0	15
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Neophaeomoniella	0	29	10	41	2	56	0	6	0	0	10	0	6	0
Ascomycota	Dothideomycetes	Capnodiales	Dissoconiaceae	Uwebraunia	0	102	0	0	0	36	0	17	4	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	155	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	27	23	0	0	43	0	0	0	0	26	0	0	35
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	50	0	0	78	0	0	0	0	26	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Dinemasporium	0	0	0	0	0	0	0	154	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	153	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	42	0	0	29	0	50	0	31	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	151	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	0	0	0	0	0	0	0	0	151	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Canariomyces	120	0	0	0	18	0	0	0	0	0	0	9	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae		12	3	0	0	0	0	0	132	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Neophaeothecoidea	0	113	0	0	0	0	0	0	0	10	9	14	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	146	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	146	0	0	0	0	0	0
Ascomycota					23	0	0	0	0	0	0	111	0	0	0	7	0	4
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	46	0	0	0	0	96	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Cyphellophoraceae	Cyphellophora	0	136	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae	Aureobasidium	50	0	0	0	90	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		0	2	0	0	0	136	0	0	0	0	0	0	0	2
Basidiomycota	Tremellomycetes	Tremellales	Bulleraceae	Fonsecazyma	0	0	140	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales	Elsinoaceae		0	4	6	0	0	80	0	10	5	8	9	6	6	5
Basidiomycota	Agaricomycetes	Corticiales	Punctulariaceae	Punctulariopsis	0	0	0	2	0	0	0	0	0	0	0	0	0	136
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	70	13	0	0	0	0	10	0	0	0	11	0	33
Ascomycota	Eurotiomycetes	Eurotiales			55	0	9	0	0	34	0	10	0	15	0	0	0	13
Ascomycota	Sordariomycetes	Sordariales			101	0	0	0	19	0	0	10	0	0	0	0	0	4
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		22	0	0	0	0	0	0	88	0	0	0	24	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	3	0	0	0	0	131	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Catenulostroma	0	0	4	0	0	7	0	0	0	103	0	4	0	15
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	0	0	0	132	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Exopassalora	17	0	0	0	0	0	0	112	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	0	131	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Waitea	130	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	126	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	0	4	0	0	0	0	10	0	0	0	114	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae	Aurantiosacculus	0	0	0	0	0	0	0	125	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	127	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Filobasidium	44	15	16	0	9	18	2	7	0	0	0	11	3	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		27	0	0	0	0	40	0	0	0	58	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	19	12	0	11	28	4	3	0	25	4	14	0	4

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	42	0	0	73	0	0	0	0	0	0	9	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	0	0	0	0	0	0	0	0	0	124	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	122	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			9	0	5	0	0	0	0	96	0	4	0	6	0	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	0	6	0	0	0	83	0	7	0	6	12	6	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	120	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		53	0	0	7	28	0	0	29	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris yamadae	37	0	0	0	0	0	0	0	0	80	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	3	0	0	0	0	0	0	0	27	0	0	87	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	19	8	0	63	0	24	0	0	3	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	0	0	0	0	0	75	0	0	0	0	0	42
Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae		0	97	3	0	0	0	0	5	0	5	4	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	3	0	0	0	0	0	0	0	0	0	0	111
Ascomycota	Dothideomycetes	Capnodiales	Dissoconiaceae	Uwebraunia	0	15	0	0	39	56	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Phaeophleospora	0	0	29	0	0	81	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Teichospora	8	0	0	0	0	0	0	0	0	0	0	93	8	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	108	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	86	0	0	22	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	108	0

Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zasmidium**	**0**	**0**	**0**	**26**	**0**	**0**	**0**	**80**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**	**5**	**7**	**6**	**5**	**73**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Cucurbitariaceae**	**Pyrenochaetopsis**	**0**	**51**	**23**	**0**	**0**	**0**	**0**	**16**	**4**	**0**	**0**	**0**	**6**	**5**
Ascomycota	**Eurotiomycetes**	**Onygenales**	**Onygenales_fam_Incertae_sedis**	**Zeloasperisporium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**105**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Ramularia**	**84**	**0**	**0**	**0**	**0**	**7**	**0**	**13**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Epicoccum**	**0**	**20**	**38**	**0**	**0**	**46**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Stenella**	**0**	**0**	**4**	**0**	**0**	**0**	**8**	**19**	**0**	**0**	**7**	**0**	**0**	**66**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**	**4**	**74**	**4**	**10**	**0**	**7**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Teratoramularia**	**20**	**0**	**0**	**6**	**11**	**46**	**0**	**20**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Rhynchogastremataceae**	**Papiliotrema**	**19**	**0**	**0**	**9**	**14**	**47**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Neoascochyta**	**89**	**0**	**0**	**0**	**0**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Phaeomoniellales**	**Phaeomoniellaceae**		**0**	**4**	**0**	**74**	**6**	**0**	**5**	**0**	**8**	**0**	**2**	**0**	**2**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**	**Colletotrichum**	**0**	**0**	**0**	**5**	**0**	**65**	**0**	**8**	**0**	**0**	**9**	**0**	**0**	**14**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**0**	**0**	**29**	**0**	**0**	**42**	**0**	**7**	**0**	**10**	**0**	**0**	**12**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**100**
Ascomycota	**Sordariomycetes**	**Trichosphaeriales**	**Trichosphaeriaceae**	**Nigrospora**	**59**	**0**	**0**	**0**	**40**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**51**	**0**	**0**	**0**	**35**	**2**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Epicoccum**	**42**	**0**	**0**	**28**	**0**	**29**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricostilbomycetes**	**Agaricostilbales**	**Chionosphaeraceae**	**Kurtzmanomyces**	**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**93**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**99**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	0	0	0	0	0	0	0	0	0	13	0	86	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	36	0	0	0	61	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	96	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	60	0	0	14	0	0	0	0	0	22	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	0	0	0	0	0	0	0	0	96	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia	0	0	0	0	0	0	0	0	0	0	0	96	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Neofusicoccum	0	0	0	0	0	0	0	0	0	0	0	0	0	96
Ascomycota	Saccharomycetes	Saccharomycetales			0	0	22	0	0	15	5	2	0	0	0	51	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia	56	0	0	0	0	38	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae		0	0	0	0	3	0	0	0	2	84	0	0	0	5
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	93	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Simplicillium	0	7	15	4	0	38	6	3	0	0	0	11	0	9
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	75	0	0	16	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	90	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	16	0	0	0	0	0	0	67	0	0	0	0	3	4
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	4	4	6	0	0	0	0	76	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	83	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	89	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	32	0	0	57	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	26	63	0	0	0	0	0	0	0	0

Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Didymella**	**23**	**0**	**16**	**0**	**8**	**32**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**			**11**	**15**	**0**	**0**	**14**	**24**	**8**	**0**	**0**	**0**	**0**	**16**	**0**	**0**
Ascomycota					**0**	**0**	**87**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**0**	**0**	**0**	**0**	**80**	**0**	**0**	**7**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Hypocreales_fam_Incertae_sedis**	**Sarocladium**	**22**	**0**	**0**	**11**	**4**	**27**	**0**	**16**	**0**	**3**	**0**	**0**	**3**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**21**	**21**	**0**	**0**	**12**	**0**	**0**	**0**	**27**	**0**	**5**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Phaeomoniellales**	**Phaeomoniellaceae**	**Xenocylindrosporium**	**0**	**0**	**0**	**0**	**0**	**24**	**0**	**0**	**21**	**0**	**0**	**26**	**15**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**20**	**0**	**0**	**0**	**0**	**0**	**0**	**65**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**46**	**9**	**3**	**0**	**5**	**0**	**12**	**0**	**0**	**0**	**10**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Pseudoteratosphaeria**	**0**	**0**	**8**	**30**	**0**	**0**	**11**	**12**	**24**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Gibberella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**40**	**0**	**33**	**0**	**0**	**0**	**12**
Ascomycota	**Archaeorhizomycetes**	**Archaeorhizomycetales**	**Archaeorhizomycetaceae**	**Archaeorhizomyces**	**0**	**6**	**16**	**4**	**2**	**15**	**0**	**0**	**0**	**4**	**4**	**29**	**4**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Neocosmospora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**11**	**0**	**73**	**0**
Mortierellomycota	**Mortierellomycetes**	**Mortierellales**	**Mortierellaceae**	**Mortierella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**84**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**83**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**0**	**0**	**0**	**0**	**11**	**0**	**72**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Neocosmospora**	**37**	**0**	**26**	**0**	**0**	**0**	**0**	**0**	**0**	**19**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Stagonosporopsis**	**26**	**0**	**0**	**0**	**0**	**0**	**0**	**56**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Phaeomoniellales**	**Phaeomoniellaceae**		**0**	**2**	**0**	**3**	**0**	**0**	**21**	**2**	**19**	**0**	**0**	**15**	**20**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**82**

Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	81	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	3	0	0	0	7	2	0	0	0	64	0	5
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	0	0	81	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	15	0	65
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	39	0	0	0	9	0	0	0	0	0	0	31	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris	0	32	0	0	0	13	0	0	0	34	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	0	0	6	0	0	16	0	0	2	5	0	3	0	47
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia	78	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae		78	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	78	0	0	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Chrysozymaceae	Sampaiozyma	0	0	0	0	26	0	0	0	6	11	0	35	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	0	0	0	0	0	0	0	0	0	78	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Parapyrenochaeta	0	0	0	0	0	0	36	0	25	0	0	16	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Filobasidium	76	0	0	0	0	0	0	0	0	0	0	0	0	0
Olpidiomycota	Olpidiomycetes	Olpidiales	Olpidiaceae	Olpidium	2	42	12	0	0	10	0	6	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	76	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	76	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	0	0	0	0	0	0	76

Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Ochroconis	0	0	0	0	0	0	0	0	0	0	0	0	0	76
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosulcatispora	0	31	0	0	0	0	0	0	0	44	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	75	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	0	0	0	7	0	68
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	0	0	6	0	0	38	0	0	0	0	0	24	6	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	74	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	0	74
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	0	0	0	0	0	74
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	73	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	0	3	0	3	0	60	0	4	0	0	3	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae		0	0	0	0	0	0	0	8	0	0	0	0	0	65
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola grisea	0	0	0	0	0	56	0	0	0	0	0	0	16	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodotorula	11	0	0	0	0	5	0	0	0	0	0	55	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Erysiphe	0	0	71	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Favolus	0	0	0	0	71	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium cairnsense	0	0	0	0	0	71	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Cylindrocarpon	0	0	0	0	0	0	0	0	0	8	0	5	50	8
Ascomycota	Dothideomycetes	Botryosphaeriales	Phyllostictaceae	Phyllosticta	0	0	70	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	35	0	0	7	0	27	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	12	0	0	57	0	0	0	0	0	0	0	0

Ascomycota					0	0	0	69	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis	Triposporium	24	0	0	0	39	5	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Planistromellaceae	Ramimonilia	0	12	0	0	0	0	0	0	2	0	0	54	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	11	2	4	25	8	2	0	2	9	0	0	0	5
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Phialophora	0	0	0	0	0	0	0	0	0	65	3	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	66	0	0	0	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	17	0	0	0	0	49	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	0	0	66	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	66	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Phialemoniopsis	0	0	0	0	0	0	0	7	0	0	4	0	0	55
Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Mycoleptodiscus	0	0	0	0	0	0	0	0	0	0	0	0	66	0
Ascomycota	Dothideomycetes	Myriangiales			0	0	0	0	0	0	0	0	0	0	14	51	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	55	9	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma sp	56	0	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusicolla	0	0	7	0	0	0	0	0	6	0	0	0	0	50
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	0	0	0	0	0	0	63	0	0
Basidiomycota	Tremellomycetes	Holtermanniales	Holtermanniales_fam_Incertae_sedis	Holtermanniella	52	0	0	0	0	5	0	5	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Gnomoniaceae		0	17	0	0	8	19	0	0	0	6	0	0	0	12
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	5	0	0	0	36	6	0	6	4	0	0	0	5

Basidiomycota	Tremellomycetes	Tremellales	Tremellales_fam_Incertae_sedis	Kwoniella	0	0	0	0	62	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	0	0	0	0	0	0	0	62	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	62	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	22	0	0	0	0	0	0	0	0	19	0	0	9	11
Ascomycota	Sordariomycetes	Sordariales	Sordariaceae	Neurospora	0	0	10	0	3	34	0	0	0	14	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Liberomyces	21	0	0	3	24	0	0	3	0	0	0	9	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	60	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	0	30	0	0	0	0	0	0	0	30	0
Basidiomycota	Exobasidiomycetes	Exobasidiales			0	0	0	0	0	0	0	60	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	0	60
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	0	0	0	0	0	0	0	60
Ascomycota	Eurotiomycetes	Eurotiales			0	0	0	0	0	0	0	0	0	0	0	0	0	60
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	22	0	0	0	0	19	0	18	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Ochroconis	0	0	0	0	0	0	0	0	0	0	0	0	0	59
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Apiotrichum	0	6	3	4	0	0	0	8	0	0	3	0	28	6
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe sackstonii	0	0	22	0	0	36	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	0	0	14	0	44	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Muyocopronaceae	Muyocopron	8	0	0	0	49	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	31	0	0	0	26	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	57	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	9	0	48	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	56	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	0	0	0	0	0	0	0	56	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	0	0	0	0	56	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Geopora	55	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Lepteutypa	3	0	0	0	0	52	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	8	0	17	0	0	0	0	0	0	12	0	0	18
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae		0	0	34	0	0	21	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	0	0	8	47	0	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	54	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	46	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	4	2	0	43	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Branch06			0	0	3	0	0	0	0	0	0	0	3	0	48	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Daldinia	0	0	0	0	10	36	0	0	0	0	0	8	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Boeremia	53	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	15	0	0	0	5	20	0	8	0	5	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	12	0	0	0	0	15	0	26	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		12	0	0	6	5	20	0	10	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		7	0	0	6	19	0	0	21	0	0	0	0	0	0

Ascomycota	**Sordariomycetes**	**Hypocreales**	**Cordycipitaceae**	**Simplicillium**	**0**	**5**	**3**	**0**	**5**	**23**	**2**	**0**	**0**	**6**	**0**	**0**	**0**	**9**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Nothophoma**	**0**	**0**	**53**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**53**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**53**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Kalmusia**	**52**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Microdochiaceae**	**Selenodriella**	**0**	**3**	**5**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**6**	**0**	**27**	**8**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**		**0**	**0**	**0**	**0**	**9**	**39**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Amphisphaeriaceae**	**Amphisphaeria**	**0**	**0**	**0**	**0**	**0**	**52**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Hypocreaceae**	**Trichoderma**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**49**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**52**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**52**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**52**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**		**51**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Amphisphaeriaceae**	**Lepteutypa**	**0**	**13**	**4**	**3**	**0**	**0**	**3**	**0**	**0**	**26**	**0**	**0**	**0**	**2**
Ascomycota	**Eurotiomycetes**	**Phaeomoniellales**	**Phaeomoniellaceae**	**Xenocylindrosporium**	**0**	**0**	**0**	**0**	**51**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**	**Phaeosphaeria**	**0**	**0**	**0**	**0**	**0**	**32**	**0**	**19**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**	**Triangularia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**48**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**50**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Penidiella**	**0**	**0**	**0**	**0**	**0**	**50**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Bionectriaceae**	**Gliomastix**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**46**	**0**

Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	50	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	0	0	0	0	0	0	0	0	0	0	0	0	50	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	0	50
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	49	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	49	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	13	0	12	0	0	0	24	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	49	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Conioscyphales	Conioscyphaceae	Conioscypha	0	0	0	0	0	0	0	0	3	0	0	46	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	0	0	0	0	0	0	0	49	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris	0	0	0	0	0	0	0	0	0	0	0	49	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	48	0	0	0	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	12	0	0	0	0	0	0	0	0	0	0	36	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	0	33	0	0	0	0	0	0	0	0	0	0	14	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	20	0	0	27	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	11	0	0	0	0	0	6	0	0	30	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	43	0	0	0	4	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	0	38	0	9	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	0	0	0	0	47	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	0	47
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporobolomyces	38	0	0	0	0	0	0	8	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae	Gloniopsis	0	46	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	32	0	0	0	0	14	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeodothis	0	0	0	0	0	0	0	46	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	7	0	0	0	0	39	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	46	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			38	0	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Lapidomyces	35	0	0	0	0	0	0	10	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	15	0	0	0	0	19	0	11	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	45	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	11	0	0	25	0	0	0	0	9	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	45	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pallidocercospora	0	0	0	0	0	26	0	0	0	0	0	19	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	45	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Meyerozyma	7	0	0	2	5	0	0	3	0	0	0	16	6	5
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	22	0	0	0	0	0	22	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Australosphaerella	0	0	0	0	0	25	0	0	0	0	0	19	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Hirsutella	41	0	0	0	0	2	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus	0	43	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota					0	0	0	4	10	2	10	0	13	0	0	0	4	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	0	2	9	16	0	0	0	0	8	5	3	0

Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	43	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellales_fam_Incertae_sedis	Kwoniella	0	0	0	0	43	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia	0	0	0	0	0	43	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	43	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	43	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma	17	0	0	0	0	25	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes				6	0	0	0	0	0	2	34	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria	0	0	42	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	42	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	42	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae		0	0	0	0	0	0	0	42	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	0	0	42	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Exopassalora	4	0	0	0	0	0	0	37	0	0	0	0	0	0
Ascomycota	Sordariomycetes				3	9	17	0	8	0	0	0	0	0	0	0	0	4
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae	Cystofilobasidium	0	3	0	0	0	0	0	0	0	0	0	0	38	0
Ascomycota	Sordariomycetes	Togniniales	Togniniaceae	Phaeoacremonium	0	0	41	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	41	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosetophoma	0	0	3	7	13	18	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		0	0	0	0	0	41	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Myxospora	0	0	0	0	0	0	0	16	0	0	0	5	3	17

Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zasmidium**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**41**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**	**Humicola**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**41**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**		**40**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Alternaria**		**40**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Diatrypaceae**	**Peroneutypa**		**33**	**0**	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Saccharomycetaceae**	**Issatchenkia**	**orientalis**	**17**	**5**	**0**	**0**	**0**	**4**	**0**	**6**	**0**	**0**	**0**	**0**	**8**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**		**0**	**0**	**0**	**0**	**0**	**40**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Myriangiales**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**31**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**40**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**40**
Ascomycota	**Sordariomycetes**					**39**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**		**39**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**		**39**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**	**Chaetosphaeriaceae**			**36**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**			**0**	**39**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**			**0**	**39**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Corticiales**	**Punctulariaceae**	**Punctulariopsis**		**0**	**32**	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Penidiella**		**0**	**0**	**0**	**35**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**			**0**	**0**	**0**	**0**	**39**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	16	23	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	0	0	0	39	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	0	0	0	0	39	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	39	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Ochroconis	0	0	0	0	0	0	0	0	0	0	0	39	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	0	0	0	0	0	39
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Thozetella	38	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	38	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	38	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	20	0	0	0	0	0	0	0	0	18	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	5	0	0	0	0	0	3	30	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	0	0	0	0	0	38	0	0
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus	0	0	0	0	0	0	0	0	0	0	0	0	38	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	37	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			37	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales			0	37	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	0	37	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Dothideomycetes_fam_Incertae_sedis	Radulidium	0	0	0	0	0	30	0	0	0	0	0	0	0	7
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis	0	0	0	0	0	0	0	37	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris	0	0	0	0	0	0	0	0	37	0	0	0	0	0

Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma		36	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium		36	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			36	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae			29	0	0	0	4	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma		29	0	0	0	0	0	0	7	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Saitozyma		17	0	0	0	0	0	0	0	0	0	0	19	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia		0	0	36	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	36	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces		0	0	17	0	0	0	0	0	0	0	0	10	0	9
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Neophaeomoniella		0	0	0	0	0	36	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	0	0	0	0	0	0	36	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Cylindrocarpon		0	0	0	0	0	0	0	0	0	0	0	0	36	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium		0	0	0	0	0	0	0	0	0	0	0	0	0	36
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola		21	0	0	0	0	0	0	0	0	0	0	0	0	14
Ascomycota	Dothideomycetes	Capnodiales	Capnodiales_fam_Incertae_sedis	Pseudoramichloridium		0	0	0	7	28	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Ilyonectria	morspanacis	0	0	0	0	0	0	0	0	5	0	0	0	20	10
Basidiomycota	Agaricomycetes	Agaricales	Pleurotaceae	Hohenbuehelia		0	0	0	0	0	0	0	0	0	0	0	35	0	0
Ascomycota	Sordariomycetes					4	0	0	0	5	0	0	0	0	0	0	25	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		0	0	0	0	0	34	0	0	0	0	0	0	0	0

Ascomycota	**Eurotiomycetes**	**Onygenales**	**Onygenales_fam_Incertae_sedis**	**Zeloasperisporium**	**0**	**0**	**0**	**0**	**0**	**34**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**	**Phaeodothis**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**34**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**27**	**3**	**0**	**0**	**4**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Clavicipitaceae**	**Metacordyceps**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**34**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Pseudoteratosphaeria**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**34**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Ramularia**	**33**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**33**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Curvularia**	**9**	**0**	**4**	**0**	**0**	**16**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Pichiaceae**	**Pichia**	**0**	**0**	**20**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**13**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Pallidocercospora**	**0**	**0**	**0**	**16**	**0**	**0**	**0**	**17**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Muscodor**	**0**	**0**	**0**	**0**	**33**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**		**0**	**0**	**0**	**0**	**0**	**33**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**			**0**	**0**	**0**	**0**	**0**	**33**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Penicillifer**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**33**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Ilyonectria**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**33**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Penicillium**	**28**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Russulales**			**0**	**0**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**30**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Dothideomycetes_ord_Incertae_sedis**	**Dothideomycetes_fam_Incertae_sedis**	**Radulidium**	**0**	**0**	**0**	**0**	**0**	**32**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Tremellaceae**	**Cryptococcus**	**31**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	**Leotiomycetes**	**Erysiphales**	**Erysiphaceae**	**Blumeria**	**31**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Tremellales_fam_Incertae_sedis**	**Kwoniella**	**31**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**31**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**25**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Paraphaeosphaeria**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**25**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Onygenales**	**Onygenales_fam_Incertae_sedis**	**Zeloasperisporium**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**26**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Phanerochaetaceae**		**0**	**0**	**29**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Amphisphaeriaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**31**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**30**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**30**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Cystofilobasidiales**	**Cystofilobasidiaceae**	**Cystofilobasidium**	**30**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**0**	**23**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Tremellaceae**	**Bulleromyces**	**0**	**16**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**5**	**0**	**7**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**		**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**15**
Ascomycota	**Eurotiomycetes**	**Onygenales**	**Onygenales_fam_Incertae_sedis**	**Zeloasperisporium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**30**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Trichomeriaceae**	**Brycekendrickomyces**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**30**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Onygenales**	**Onygenales_fam_Incertae_sedis**	**Zeloasperisporium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**30**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**30**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**30**	**0**	**0**	**0**	**0**

Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	0	0	5	0	0	0	25
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae	Gyroporus	0	0	0	0	0	0	0	0	0	0	0	30	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	0	0	0	0	0	0	0	0	0	0	30	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	29	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	29	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	29	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Neoascochyta	29	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Mycoacia	26	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Coniothyriaceae		15	0	0	0	6	8	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia	4	0	0	0	0	6	0	17	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Emericellopsis	0	0	21	0	0	0	0	0	0	4	0	4	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	14	0	9	0	0	0	0	0	0	0	0	6
Ascomycota	Eurotiomycetes	Phaeomoniellales			0	0	0	29	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Parateratosphaeria	0	0	0	7	22	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema	0	0	0	0	29	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	0	0	0	0	0	29	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	29	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae		0	0	0	0	0	0	0	0	0	29	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales			0	0	0	0	0	0	0	0	0	29	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia	28	0	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium		23	0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Sordariomycetes					0	28	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae			0	26	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Hypocreales				0	0	19	0	9	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	8	0	0	0	0	0	0	20	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellales_fam_Incertae_sedis	Kwoniella		0	0	0	0	28	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella		0	0	0	0	0	28	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	longibrachiatum	0	0	0	0	0	0	0	0	0	0	0	28	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae			0	0	0	0	0	0	0	0	0	0	0	24	4	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium		0	0	0	0	0	0	0	0	0	0	0	7	0	21
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus		0	0	0	0	0	0	0	0	0	0	0	0	28	0
Ascomycota	Dothideomycetes	Pleosporales				27	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Ramularia		27	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma		27	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma		27	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma		27	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes					25	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				5	0	0	0	0	0	0	22	0	0	0	0	0	0

Basidiomycota	Pucciniomycetes	Septobasidiales	Septobasidiaceae	Septobasidium	0	27	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Geminibasidiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	0	3	0	0	0	0	0	0	0	0	0	0	24	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Crucellisporiopsis	0	0	0	0	0	16	0	0	6	5	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	27	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Exopassalora	0	0	0	0	0	0	0	27	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	0	0	27	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Epicoccum	0	0	0	0	0	0	0	27	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium	0	0	0	0	0	0	0	0	0	0	0	0	27	0
Ascomycota	Dothideomycetes	Capnodiales			26	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema	0	5	0	0	14	0	0	0	0	3	0	0	4	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola	0	0	26	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Schizophyllum	0	0	9	0	0	0	0	0	0	0	0	17	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	0	0	0	0	0	26	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	26	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	0	0	0	26	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	0	0	0	0	0	26	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		0	0	0	0	0	0	26	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	0	0	0	0	0	0	0	26	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	24	0	0	0	2	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	0	0	0	0	0	0	0	0	26

Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**			**25**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Trichocomaceae**	**Talaromyces**		**3**	**0**	**0**	**0**	**0**	**22**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Botryosphaeriales**	**Phyllostictaceae**	**Phyllosticta**		**0**	**25**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Massarinaceae**	**Helminthosporium**		**0**	**17**	**8**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**		**0**	**5**	**0**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**15**	**0**
Basidiomycota	**Agaricomycetes**	**Auriculariales**				**0**	**0**	**0**	**0**	**25**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Microbotryomycetes**	**Sporidiobolales**	**Sporidiobolaceae**	**Rhodotorula**		**0**	**0**	**0**	**0**	**17**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**8**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Curvularia**	**buchloes**	**0**	**0**	**0**	**0**	**0**	**20**	**0**	**0**	**0**	**0**	**0**	**5**	**0**	**0**
Ascomycota	**Lecanoromycetes**	**Ostropales**	**Stictidaceae**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**25**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Sporocadaceae**	**Hymenopleella**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**25**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**		**24**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**	**Ceratobasidium**		**24**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Malasseziomycetes**	**Malasseziales**	**Malasseziaceae**	**Malassezia**		**24**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Thelephorales**	**Thelephoraceae**			**0**	**0**	**24**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Trichocomaceae**	**Talaromyces**		**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Saccharomycetaceae**	**Issatchenkia**		**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**13**	**0**	**0**
Ascomycota	**Dothideomycetes**					**0**	**0**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**	**13**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Xenopenidiella**		**0**	**0**	**0**	**0**	**0**	**24**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Microbotryomycetes**	**Sporidiobolales**	**Sporidiobolaceae**	**Sporobolomyces**		**0**	**0**	**0**	**0**	**0**	**24**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Monascus	0	0	0	0	0	24	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	0	0	0	0	0	13	0	0	0	0	0	11	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	14	0	10	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	0	0	0	0	0	0	0	0	24	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	0	0	0	15	0	0	0	9
Zoopagomycota	Zoopagomycetes	Zoopagales	Piptocephalidaceae	Syncephalis	0	0	0	0	0	0	0	0	0	0	0	24	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodotorula	0	0	0	0	0	0	0	0	0	0	0	17	0	7
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Ramularia	23	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Devriesia	23	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Devriesia	21	0	0	0	0	0	0	2	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		19	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	14	9	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			2	4	7	0	0	0	0	0	0	0	0	2	8	0
Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Schizophyllum	0	23	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	23	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	23	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	23	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	23	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	23	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	0	0	0	0	0	0	0	5	18	0	0

Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	0	0	0	0	0	0	23	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	0	0	0	0	23	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Dioszegia	15	0	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Tetracladium	9	0	0	0	0	13	0	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Cystobasidiomycetes_ord_Incertae_sedis	Symmetrosporaceae	Symmetrospora	0	22	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	14	0	0	0	0	0	0	0	0	0	0	0	8
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae	Erythrobasidium	0	7	0	0	0	0	0	15	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	0	22	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	0	22	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		0	0	0	0	0	0	0	7	0	0	0	0	0	15
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	0	0	0	0	0	0	0	22	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	0	0	0	0	0	0	0	0	0	0	0	22	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	0	22
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	21	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		21	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Myrmecridiales	Myrmecridiaceae	Myrmecridium	4	0	12	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes				0	21	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola	0	21	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Togniniales	Togniniaceae	Phaeoacremonium	0	0	21	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales			0	0	21	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Monascus	0	0	6	0	2	0	0	2	0	0	0	0	3	8
Ascomycota	Dothideomycetes	Pleosporales	Lophiostomataceae		0	0	0	21	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Cuniculitremaceae	Kockovaella	0	0	0	0	18	3	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	0	0	0	0	9	0	0	0	0	8	0	0	4	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudeurotium	0	0	0	0	5	9	0	0	0	7	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Bulleromyces	0	0	0	0	3	18	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	21	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Pseudoteratosphaeria	0	0	0	0	0	0	0	0	0	21	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Paramyrothecium	0	0	0	0	0	0	0	0	0	0	21	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	0	21	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	21	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	20	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Russulaceae	Russula	20	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	15	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	20	0	0	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	7	0	0	0	0	0	0	0	0	0	0	13	0
Basidiomycota	Agaricomycetes	Russulales	Stereaceae	Acanthophysium	0	0	20	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota					0	0	14	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	2	0	0	0	18	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Thanatephorus	0	0	0	0	18	0	2	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Dothideomycetes_ord_Incertae_sedis	Eremomycetaceae	Arthrographis		0	0	0	0	0	20	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria		0	0	0	0	0	13	0	5	0	0	0	0	2	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Stemphylium		0	0	0	0	0	6	0	0	0	14	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Pestalotiopsis		0	0	0	0	0	0	0	15	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Daldinia		0	0	0	0	0	0	0	0	0	20	0	0	0	0
Basidiomycota	Agaricomycetes	Tremellodendropsidales				0	0	0	0	0	0	0	0	0	0	0	0	20	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium		19	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium		19	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae			19	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Ustilaginomycetes	Ustilaginales	Ustilaginaceae	Moesziomyces	antarcticus	12	0	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Dothideomycetes					0	0	19	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	19	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella		0	0	19	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Sarocladium		0	0	13	0	6	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales				0	0	0	11	0	0	0	0	0	8	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium		0	0	0	0	19	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium		0	0	0	0	19	0	0	0	0	0	0	0	0	0

Ascomycota	**Sordariomycetes**	**Trichosphaeriales**	**Trichosphaeriaceae**	**Nigrospora**		**0**	**0**	**0**	**0**	**19**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Cucurbitariaceae**	**Pyrenochaetopsis**		**0**	**0**	**0**	**0**	**0**	**19**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Dictyosporiaceae**	**Pseudocoleophoma**		**0**	**0**	**0**	**0**	**0**	**19**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Psathyrellaceae**	**Coprinellus**		**0**	**0**	**0**	**0**	**0**	**19**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**				**0**	**0**	**0**	**0**	**0**	**0**	**5**	**0**	**8**	**0**	**0**	**6**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**19**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zasmidium**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**19**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleraceae**	**Fonsecazyma**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**19**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Microdochiaceae**	**Idriella**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**19**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Clavulinaceae**	**Clavulina**		**0**	**18**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**flabelliforme**	**0**	**18**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**				**0**	**0**	**9**	**0**	**0**	**0**	**4**	**0**	**3**	**0**	**2**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Volutella**		**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Trimorphomycetaceae**	**Saitozyma**		**0**	**0**	**0**	**0**	**8**	**0**	**0**	**10**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Epicoccum**		**0**	**0**	**0**	**0**	**0**	**18**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Boletales**	**Gyroporaceae**	**Gyroporus**		**0**	**0**	**0**	**0**	**0**	**18**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Chytridiomycota	**Rhizophydiomycetes**	**Rhizophydiales**	**Alphamycetaceae**	**Betamyces**		**0**	**0**	**0**	**0**	**0**	**18**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Trichocomaceae**	**Talaromyces**		**0**	**0**	**0**	**0**	**0**	**18**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Myriangiales**	**Elsinoaceae**	**Elsinoe**		**0**	**0**	**0**	**0**	**0**	**10**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**5**

Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Geastrumia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**18**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Sporormiaceae**	**Preussia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**18**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Kalmusia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**18**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Clavicipitaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**18**	**0**
Rozellomycota	**Rozellomycotina_cls_Incertae_sedis**	**GS11**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**18**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Melanommataceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**18**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Didymella**	**17**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**17**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**17**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**			**14**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**13**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Sporormiaceae**	**Preussia**	**2**	**0**	**0**	**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Pezizomycotina_cls_Incertae_sedis**	**Pezizomycotina_ord_Incertae_sedis**	**Pezizomycotina_fam_Incertae_sedis**	**Kramasamuha**	**0**	**8**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**			**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**
Ascomycota	**Orbiliomycetes**	**Orbiliales**			**0**	**0**	**17**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Herpotrichiellaceae**	**Exophiala**	**0**	**0**	**10**	**0**	**7**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Monascus**	**0**	**0**	**0**	**0**	**0**	**17**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Eurotiomycetes	Onygenales	Gymnoascaceae	Leucothecium	0	0	0	0	0	17	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Steccherinaceae	Nigroporus	0	0	0	0	0	17	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Botryotrichum	0	0	0	0	0	17	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	0	17	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	17	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Humicola	0	0	0	0	0	17	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae	Serendipita	0	0	0	0	0	13	0	0	0	0	0	0	4	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Hermetothecium	0	0	0	0	0	0	0	17	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	17	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	0	0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Phialophora	0	0	0	0	0	0	0	0	0	17	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	17	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	0	0	0	0	0	0	17	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	0	17	0	0
Basidiomycota	Agaricomycetes	Polyporales	Fomitopsidaceae	Cinereomyces	0	0	0	0	0	0	0	0	0	0	0	17	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia	0	0	0	0	0	0	0	0	0	0	0	17	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae		0	0	0	0	0	0	0	0	0	0	0	0	17	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dactylonectria	0	0	0	0	0	0	0	0	0	0	0	0	17	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Gamsia	0	0	0	0	0	0	0	0	0	0	0	0	17	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	0	0	0	0	0	0	0	0	0	0	0	17

Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**	**Waitea**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Pallidocercospora**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Kalmusia**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Cordycipitaceae**	**Simplicillium**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Herpotrichiellaceae**	**Exophiala**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Rozellomycota					**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Dioszegia sp**	**12**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Hymenochaetales**	**Hymenochaetaceae**	**Hymenochaete**	**10**	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriaceae**	**Hermetothecium**	**2**	**0**	**2**	**0**	**0**	**0**	**0**	**12**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**				**0**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**		**0**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**11**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Ganodermataceae**	**Perenniporia**	**0**	**0**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Plectosphaerellaceae**	**Plectosphaerella**	**0**	**0**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Rozellomycota					**0**	**0**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Monoblepharomycota	**Monoblepharidomycetes**	**Monoblepharidales**			**0**	**0**	**12**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Cuniculitremaceae**	**Fellomyces**	**0**	**0**	**0**	**0**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Lapidomyces**	**0**	**0**	**0**	**0**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**5**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Thelephorales**	**Thelephoraceae**		**0**	**0**	**0**	**0**	**0**	**16**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Rozellomycota	Rozellomycotina_cls_Incertae_sedis	Branch03			0	0	0	0	0	14	0	0	0	0	0	2	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenopenidiella	0	0	0	0	0	0	9	0	7	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Xenoteratosphaeria	0	0	0	0	0	0	0	16	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	0	0	0	16	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	10	0	0	0	0	6	0
Ascomycota	Sordariomycetes	Diaporthales	Melanconidaceae	Melanconium	0	0	0	0	0	0	0	0	0	16	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	0	0	0	0	0	0	0	16	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	0	16	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Codinaea	0	0	0	0	0	0	0	0	0	0	0	0	16	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		0	0	0	0	0	0	0	0	0	0	0	0	12	4
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	0	0	0	16
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	15	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia	15	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		15	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			15	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	Arxiella	11	0	0	0	0	2	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium	10	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	11	0	0	0	0	0	0	0	0	4	0	0	0

Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**9**	**0**	**0**	**0**	**0**	**3**	**3**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**		**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Trechisporales**	**Hydnodontaceae**	**Trechispora**	**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Dactylonectria**	**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**0**	**0**	**9**	**0**	**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Lophiotremataceae**	**Atrocalyx**	**0**	**0**	**4**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Xylaria**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**3**	**0**	**6**
Mortierellomycota	**Mortierellomycetes**	**Mortierellales**	**Mortierellaceae**	**Mortierella**	**0**	**0**	**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Hannaella**	**0**	**0**	**0**	**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**10**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**
Ascomycota	**Eurotiomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**15**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Neoceratosperma**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**15**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Russulales**	**Russulaceae**	**Russula**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**15**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**15**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Mariannaea**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**5**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**	**Waitea**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**	**Acrophialophora**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Neocosmospora**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Herpotrichiellaceae**		**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**		**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Microbotryomycetes**	**Sporidiobolales**	**Sporidiobolaceae**	**Sporobolomyces**	**12**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Cystobasidiomycetes**	**Cystobasidiales**	**Cystobasidiaceae**	**Occultifur**	**10**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zymoseptoria**	**10**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**			**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**3**	**0**	**0**	**0**	**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Polyporaceae**	**Trametes**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Saccharomycetales_fam_Incertae_sedis**	**Candida**	**0**	**0**	**10**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Parapenidiella**	**0**	**0**	**7**	**0**	**0**	**7**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Plectosphaerellaceae**	**Lectera**	**0**	**0**	**6**	**0**	**0**	**8**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**	**0**	**12**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Penicillium**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**		**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Fasciatisporaceae**	**Fasciatispora**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Mortierellomycota	**Mortierellomycetes**	**Mortierellales**	**Mortierellaceae**	**Mortierella**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Bipolaris**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**		**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Xenoteratosphaeria**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Tubeufiales**	**Tubeufiaceae**		**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Lecanoromycetes**	**Ostropales**	**Stictidaceae**	**Cyanodermella**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**3**	**2**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Myriangiales**	**Elsinoaceae**	**Elsinoe**	**0**	**0**	**0**	**0**	**0**	**8**	**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Cucurbitariaceae**	**Pyrenochaetopsis**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**10**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Neoascochyta**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Sporocadaceae**	**Neopestalotiopsis**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Amphisphaeriaceae**	**Amphisphaeria**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Russulales**	**Peniophoraceae**	**Peniophora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Teichosporaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Phanerochaetaceae**	**Phlebiopsis**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**	**0**
Ascomycota	**Dothideomycetes**	**Venturiales**	**Sympoventuriaceae**	**Ochroconis**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**14**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Leptosphaeriaceae**	**Acicuseptoria**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Cystobasidiomycetes**	**Cystobasidiomycetes_ord_Incertae_sedis**	**Symmetrosporaceae**	**Symmetrospora**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**	**Phaeosphaeria**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Trichosporonales**	**Trichosporonaceae**	**Apiotrichum**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Laburnicola	0	0	13	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	0	0	13	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	4	0	0	0	0	0	0	9	0	0	0	0
Ascomycota	Sordariomycetes	Microascales			0	0	4	0	0	0	0	0	0	0	0	0	0	9
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	13	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	13	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Ilyonectria	0	0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Penicillifer	0	0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		0	0	0	0	0	13	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales			0	0	0	0	0	13	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Trichothecium	0	0	0	0	0	9	0	0	0	0	4	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	13	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	13	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Allophoma	0	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	0	0	0	0	0	0	13	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	13	0	0	0

Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida	0	0	0	0	0	0	0	0	0	0	0	13	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	0	0	0	0	0	0	0	13	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	0	0	0	0	0	0	0	0	13	0	0
Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma	0	0	0	0	0	0	0	0	0	0	0	0	13	0
Basidiomycota	Microbotryomycetes	Leucosporidiales	Leucosporidiaceae	Leucosporidium scottii	0	0	0	0	0	0	0	0	0	0	0	0	13	0
Basidiomycota	Geminibasidiomycetes	Geminibasidiales	Geminibasidiaceae	Geminibasidium	0	0	0	0	0	0	0	0	0	0	0	0	13	0
Ascomycota	Eurotiomycetes	Phaeomoniellales			0	0	0	0	0	0	0	0	0	0	0	0	0	13
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Proliferodiscus	0	0	0	0	0	0	0	0	0	0	0	0	0	13
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Volutella	12	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		12	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae	Cystofilobasidium	12	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosetophoma	12	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium	12	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes				12	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales			0	12	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Neoceratosperma	0	12	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Steccherinaceae	Nigroporus	0	12	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricales_fam_Incertae_sedis	Acanthocorticium	0	8	0	0	0	0	0	4	0	0	0	0	0	0
Rozellomycota					0	0	12	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	Microdochium	0	0	12	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	3	0	0	0	0	0	0	0	0	0	9	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Naganishia	0	0	0	0	3	0	0	0	0	0	0	9	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraphaeosphaeria	0	0	0	0	0	12	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	12	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosetophoma	0	0	0	0	0	0	0	12	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	12	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	12	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Phialophora	0	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Bipolaris	0	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Neophaeomoniella	0	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Paraboeremia	0	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		0	0	0	0	0	0	0	0	0	12	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Geopora	0	0	0	0	0	0	0	0	0	0	0	12	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	0	0	0	0	3	9	0
Basidiomycota	Agaricomycetes	Agaricales			0	0	0	0	0	0	0	0	0	0	0	0	12	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	0	0	0	12	0
Basidiomycota	Tremellomycetes	Trichosporonales	Tetragoniomycetaceae		0	0	0	0	0	0	0	0	0	0	0	0	12	0

Ascomycota	**Sordariomycetes**	**Hypocreales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**12**	**0**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**12**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Hypocreaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**12**	**0**
Ascomycota	**Sordariomycetes**	**Trichosphaeriales**	**Trichosphaeriaceae**	**Nigrospora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**12**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**12**
Basidiomycota	**Tremellomycetes**	**Filobasidiales**	**Filobasidiaceae**	**Filobasidium**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**			**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota					**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Neocosmospora**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**	**Chaetosphaeriaceae**		**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Polyporaceae**	**Funalia**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Cystobasidiomycetes**	**Cystobasidiales**	**Cystobasidiaceae**	**Occultifur**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**	**Setophoma**	**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Lamproconiaceae**		**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Sebacinales**	**Serendipitaceae**		**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
Basidiomycota	**Ustilaginomycetes**	**Ustilaginales**	**Ustilaginaceae**	**Pseudozyma**	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Trechisporales**			**0**	**0**	**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Hannaella**	**0**	**0**	**0**	**0**	**11**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Rachicladosporium	0	0	0	0	4	7	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae		0	0	0	0	0	11	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Clitocybula	0	0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae		0	0	0	0	0	11	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	11	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Penidiella	0	0	0	0	0	0	0	11	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	0	0	0	11	0	0	0	0	0
Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta	0	0	0	0	0	0	0	0	11	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Toxicocladosporium	0	0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	11	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Paracremonium	0	0	0	0	0	0	0	0	0	0	0	11	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		0	0	0	0	0	0	0	0	0	0	0	11	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Diplodia	10	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	10	0	0	0	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	10	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	5	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Helminthosporium	0	10	0	0	0	0	0	0	0	0	0	0	0	0

Basidiomycota	Cystobasidiomycetes				0	10	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Meyerozyma	0	10	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Favolus	0	10	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metarhizium	0	2	0	0	0	0	0	0	0	2	0	0	3	3
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Thielavia	0	0	10	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota					0	0	10	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	10	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudeurotium	0	0	5	0	0	0	0	0	0	0	0	0	0	5
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	3	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Stenella	0	0	0	10	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	0	0	0	3	7	0	0	0	0	0	0	0	0	0
Basidiomycota	Exobasidiomycetes	Golubeviales	Golubeviaceae	Golubevia	0	0	0	0	4	6	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Hysteriales	Hysteriaceae	Gloniopsis	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae	Wickerhamomyces	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Paraboeremia	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Zopfiella	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales			0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae		0	0	0	0	0	10	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae	Bannoa	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Liberomyces	0	0	0	0	0	10	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Schizothyriaceae	Johansonia	0	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Zasmidium	0	0	0	0	0	0	0	10	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	0	10	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	0	0	0	10	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	0	0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	10	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Metapochonia	0	0	0	0	0	0	0	0	0	10	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	0	0	0	3	0	0	0	7
Ascomycota	Sordariomycetes	Chaetosphaeriales			0	0	0	0	0	0	0	0	0	0	0	10	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae		0	0	0	0	0	0	0	0	0	0	0	10	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia	0	0	0	0	0	0	0	0	0	0	0	10	0	0

Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**	**Ceratobasidium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**
Ascomycota	**Archaeorhizomycetes**	**Archaeorhizomycetales**	**Archaeorhizomycetaceae**	**Archaeorhizomyces**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Devriesia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**
Ascomycota	**Dothideomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**
Ascomycota	**Leotiomycetes**	**Helotiales**	**Myxotrichaceae**	**Oidiodendron**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Sporormiaceae**	**Preussia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**10**
Ascomycota	**Leotiomycetes**	**Helotiales**	**Pezizellaceae**	**Porodiplodia**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**6**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Hannaella**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**		**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Trimorphomycetaceae**	**Saitozyma**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Devriesia**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Pseudoteratosphaeria**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Polyporaceae**	**Funalia**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Penicillium**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**	**Cladorrhinum**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Anthostomella**	**0**	**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**

Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis			0	0	5	0	0	0	0	0	0	2	0	0	0	2
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces		0	0	0	3	0	6	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia		0	0	0	0	9	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Hansfordia		0	0	0	0	9	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae			0	0	0	0	9	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	2	7	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema		0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Geosmithia		0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	intermedia	0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Gliomastix		0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma		0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia		0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae			0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae			0	0	0	0	0	9	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Erysiphales	Erysiphaceae	Podosphaera		0	0	0	0	0	5	0	0	0	4	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	9	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Montagnula		0	0	0	0	0	0	0	9	0	0	0	0	0	0

Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Zasmidium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Cryphonectriaceae**	**Mastigosporella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Plectosphaerellaceae**	**Verticillium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Plectosphaerellaceae**	**Paragibellulopsis**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Periconiaceae**	**Periconia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**
Ascomycota	**Archaeorhizomycetes**	**Archaeorhizomycetales**	**Archaeorhizomycetaceae**	**Archaeorhizomyces**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Neoascochyta**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Hypocreales_fam_Incertae_sedis**	**Sporidesmium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**	**Phaeosphaeria**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Penidiella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**
Basidiomycota	**Agaricomycetes**	**Sebacinales**	**Sebacinaceae**	**Sebacina**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**
Ascomycota	**Leotiomycetes**	**Helotiales**	**Helotiaceae**	**Tetracladium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**9**
Basidiomycota	**Cystobasidiomycetes**	**Cystobasidiomycetes_ord_Incertae_sedis**	**Symmetrosporaceae**	**Symmetrospora**	**8**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Asterinales**	**Parmulariaceae**	**Parmularia**	**8**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**	**Setophoma**	**8**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Coniochaetales**	**Coniochaetaceae**	**Coniochaeta**	**8**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**	**Diaporthe**	**3**	**0**	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Basidiomycota	Agaricomycetes	Polyporales	Polyporaceae	Fomitella	0	8	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Teichosporaceae	Magnibotryascoma	0	8	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Paecilomyces	0	5	0	0	0	0	0	0	0	3	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia	0	0	8	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Cystofilobasidiales	Mrakiaceae	Tausonia	0	0	8	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia	0	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriaceae	Nigrospora	0	0	8	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	4	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	3	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Pseudopithomyces	0	0	3	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia	0	0	0	8	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus	0	0	0	0	8	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	8	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Myriangiales			0	0	0	0	8	0	0	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae	Erythrobasidium	0	0	0	0	8	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	8	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	Pseudofusicoccum	0	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusicolla	0	0	0	0	0	8	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Westerdykella		0	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Curvularia		0	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium		0	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Paracremonium	binnewijzendii	0	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Pseudoascochyta		0	0	0	0	0	8	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Apiosporaceae			0	0	0	0	0	6	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae			0	0	0	0	0	4	0	0	0	4	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales				0	0	0	0	0	0	5	0	3	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Apiosporaceae	Arthrinium	hydei	0	0	0	0	0	0	0	8	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales				0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Schizothyriaceae	Johansonia		0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium		0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales				0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Apiosporaceae	Arthrinium		0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Xenosonderhenia		0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	8	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	0	3	0	0	0	0	5
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe		0	0	0	0	0	0	0	0	0	8	0	0	0	0

Ascomycota	Eurotiomycetes	Phaeomoniellales			0	0	0	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales			0	0	0	0	0	0	0	0	0	8	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		0	0	0	0	0	0	0	0	0	0	8	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Halorosellinia	0	0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Phaffomycetaceae	Cyberlindnera	0	0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Muscodor	0	0	0	0	0	0	0	0	0	0	0	8	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae	Amphisphaeria	0	0	0	0	0	0	0	0	0	0	0	0	8	0
Basidiomycota	Tremellomycetes	Tremellales			0	0	0	0	0	0	0	0	0	0	0	0	8	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dactylonectria	0	0	0	0	0	0	0	0	0	0	0	0	8	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	0	0	0	0	0	0	0	0	0	0	0	0	8	0
Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae		0	0	0	0	0	0	0	0	0	0	0	0	8	0
Basidiomycota	Tremellomycetes	Tremellales	Rhynchogastremataceae	Papiliotrema	0	0	0	0	0	0	0	0	0	0	0	0	8	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	0	0	0	0	8	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	0	0	0	0	0	0	0	0	0	0	0	0	0	8
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Knufia	0	0	0	0	0	0	0	0	0	0	0	0	0	8
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia	0	0	0	0	0	0	0	0	0	0	0	0	0	8
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Stemphylium	0	0	0	0	0	0	0	0	0	0	0	0	0	8
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	7	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae		7	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Mollisia	5	0	0	0	0	0	0	2	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Xylariales	Xylariaceae		0	7	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	0	7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	0	7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota					0	7	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Lecanoromycetes				0	7	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricostilbomycetes	Agaricostilbales	Agaricostilbaceae	Sterigmatomyces	0	7	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales			0	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Coniothyriaceae		0	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae		0	0	7	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	0	0	7	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Exobasidiomycetes	Golubeviales	Golubeviaceae	Golubevia	0	0	7	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	7	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium	0	0	0	4	0	0	0	3	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	7	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	7	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae		0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	7	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	japonicus	0	0	0	0	0	7	0	0	0	0	0	0	0	0
Basidiomycota						0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Sporormiaceae	Preussia		0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycotina_cls_Incertae_sedis	Pezizomycotina_ord_Incertae_sedis	Pezizomycotina_fam_Incertae_sedis	Kramasamuha		0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Daldinia		0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Muscodor		0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	7	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Penicillifer		0	0	0	0	0	7	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Cutaneotrichosporon		0	0	0	0	0	4	3	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Diatrypaceae	Peroneutypa		0	0	0	0	0	4	0	3	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	7	0	0	0	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia		0	0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria		0	0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma		0	0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales				0	0	0	0	0	0	0	0	0	7	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales				0	0	0	0	0	0	0	0	0	7	0	0	0	0

Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Herpotrichiellaceae**	**Cladophialophora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Curvularia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Plectosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**	**0**	**0**	**2**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Lophiotremataceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**3**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**	**Schizothecium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Branch06**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Penicillium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Thelonectria**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Saccharomycetales_fam_Incertae_sedis**	**Candida**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Saccharomycetaceae**	**Kazachstania**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**
Olpidiomycota	**Olpidiomycetes**	**Olpidiales**	**Olpidiaceae**	**Olpidium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Kalmusia**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Chytridiomycota					**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Phallales**	**Phallaceae**	**Phallus**	**0**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Basidiomycota	Agaricomycetes	Sebacinales				0	6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Tubeufiales	Tubeufiaceae			0	6	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Boletales	Gyroporaceae	Gyroporus		0	6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycotina_cls_Incertae_sedis	Pezizomycotina_ord_Incertae_sedis	Pezizomycotina_fam_Incertae_sedis	Kramasamuha		0	6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma		0	6	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetaceae	Fuscoporia		0	6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Valsaceae	Cytospora		0	6	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota						0	4	0	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium		0	4	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes					0	0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes					0	0	6	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae			0	0	6	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Tremella		0	0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Periconiaceae	Periconia		0	0	6	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Amphisphaeriaceae			0	0	2	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Diutina	catenulata	0	0	2	0	0	4	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	0	0	6	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis			0	0	0	6	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Corynesporascaceae	Corynespora		0	0	0	3	0	0	0	0	0	0	0	0	0	3

Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Simplicillium	0	0	0	0	6	0	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	0	0	0	0	6	0	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	0	0	0	0	6	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	0	0	0	0	6	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	6	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Helminthosphaeriaceae	Spadicoides	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	6	0	0	0	0	0	0	0	0
Basidiomycota					0	0	0	0	0	6	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gliocephalotrichum	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Ilyonectria	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Planistromellaceae	Ramimonilia	0	0	0	0	0	6	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Neodevriesiaceae	Neodevriesia	0	0	0	0	0	4	0	0	0	2	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Phlebia	0	0	0	0	0	0	6	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	0	0	0	0	0	2	0	0	0	0	4	0	0

Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Parapyrenochaeta	0	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	0	0	0	0	0	0	6	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales			0	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	6	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae		0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Drechslera	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Lyophyllaceae	Fibulochlamys	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinellus	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Apiosordaria	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae		0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Trichocladium	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae	Erythrobasidium	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Diatrypaceae	Peroneutypa	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	0	0	0	6	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales			0	0	0	0	0	0	0	0	0	0	0	6	0	0
Ascomycota	Leotiomycetes	Helotiales	Leotiaceae	Miniancora	0	0	0	0	0	0	0	0	0	0	0	6	0	0

Basidiomycota	**Pucciniomycetes**	**Septobasidiales**	**Septobasidiaceae**	**Septobasidium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Hannaella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**	**Humicola**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**	**0**
Ascomycota	**Archaeorhizomycetes**	**GS31**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Hymenochaetales**	**Hymenochaetaceae**	**Fuscoporia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**	**Helotiales_fam_Incertae_sedis**	**Chalara**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**
Ascomycota	**Sordariomycetes**	**Branch06**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**
Basidiomycota	**Agaricomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**	**Curvularia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**
Olpidiomycota	**Olpidiomycetes**	**Olpidiales**	**Olpidiaceae**	**Olpidium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Penicillium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**
Ascomycota	**Sordariomycetes**	**Xylariales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**
Ascomycota	**Sordariomycetes**	**Microascales**	**Microascaceae**	**Pseudallescheria**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Tremellaceae**	**Tremella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**
Ascomycota	**Dothideomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6**
Ascomycota	**Sordariomycetes**	**Branch06**			**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Pezizomycetes**	**Pezizales**	**Ascobolaceae**	**Ascobolus**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**		**5**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	5	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				5	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Penicillifer	5	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			5	0	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Ustilaginomycetes	Ustilaginales	Ustilaginaceae	Moesziomyces	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota	Rhizophydiomycetes	Rhizophydiales	Halomycetaceae	Paranamyces	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Acremonium	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Drechslera	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Brycekendrickomyces	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		0	5	0	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota	Chytridiomycetes				0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae		0	5	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Phialophora	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Minutisphaerales	Minutisphaeraceae	Minutisphaera	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae	Serendipita	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Setophoma	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes				0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales			0	5	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Zygosporium	0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota					0	5	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Kodamaea	0	3	0	0	0	0	0	0	0	2	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodosporidiobolus	0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Neodidymella	0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota					0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Simplicillium	0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Volutella	0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae		0	0	5	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Paraphoma	0	0	5	0	0	0	0	0	0	0	0	0	0	0
Rozellomycota					0	0	5	0	0	0	0	0	0	0	0	0	0	0
Chytridiomycota					0	0	3	0	0	0	0	0	0	0	0	2	0	0
Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta	0	0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	5	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Anthostomella	0	0	0	5	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Naganishia	0	0	0	5	0	0	0	0	0	0	0	0	0	0

Ascomycota	Sordariomycetes				0	0	0	5	0	0	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	5	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Ramularia	0	0	0	0	5	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	5	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	5	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Melanodothis	0	0	0	0	3	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Wojnowiciella	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Tricladiaceae	Mycofalcella	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Leptospora	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales			0	0	0	0	0	5	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae		0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes				0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Bionectria	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Leptospora	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis	Emericellopsis	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodosporidiobolus	0	0	0	0	0	5	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales			0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Sordariales_fam_Incertae_sedis	Rhodoveronaea	0	0	0	0	0	3	0	0	0	0	2	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Trichomeriaceae	Trichomerium	0	0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Spegazzinia	0	0	0	0	0	0	0	5	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Filobasidium	0	0	0	0	0	0	0	5	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora	0	0	0	0	0	0	0	5	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	5	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales			0	0	0	0	0	0	0	3	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Alfaria	0	0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Rhodotorula	0	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Pseudodinemasporium	0	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudogymnoascus	0	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Phialomyces	0	0	0	0	0	0	0	0	0	5	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Hyaloscypha	0	0	0	0	0	0	0	0	0	5	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Xeromphalina	0	0	0	0	0	0	0	0	0	0	5	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Verticillium	0	0	0	0	0	0	0	0	0	0	2	0	3	0

Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta	0	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae		0	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Stachybotrys	0	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Diaporthales	Valsaceae	Cytospora	0	0	0	0	0	0	0	0	0	0	0	5	0	0
Basidiomycota	Agaricomycetes	Boletales	Boletaceae	Cyanoboletus	0	0	0	0	0	0	0	0	0	0	0	5	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Basidiomycota	Agaricomycetes	Polyporales	Fomitopsidaceae	Skeletocutis	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		0	0	0	0	0	0	0	0	0	0	0	0	5	0
Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae		0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium solani	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Botryotrichum	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	0	5
Ascomycota	Eurotiomycetes	Coryneliales	Coryneliaceae	Corynelia	0	0	0	0	0	0	0	0	0	0	0	0	0	5
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	0	5

Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporales_fam_Incertae_sedis**	**Thyrostroma**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Stachybotryaceae**	**Xepicula**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**
Ascomycota	**Dothideomycetes**	**Dothideales**	**Aureobasidiaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**5**
Ascomycota	**Dothideomycetes**	**Asterinales**	**Parmulariaceae**	**Parmularia**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Dothideales**	**Aureobasidiaceae**	**Aureobasidium**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**			**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**	**Hyaloscyphaceae**	**Hyaloscypha**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriaceae**		**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Mariannaea**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**				**2**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Hannaella**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Erysiphales**	**Erysiphaceae**	**Erysiphe**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Apiosporaceae**		**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Phomatosporales**	**Phomatosporaceae**	**Phomatospora**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Saccharomycetales_fam_Incertae_sedis**	**Candida**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Lecanoromycetes	Ostropales	Ostropales_fam_Incertae_sedis	Mulderomyces	0	4	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	4	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	0	4	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		0	4	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	4	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Glomerellaceae	Colletotrichum	0	4	0	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Naganishia	0	2	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Scytalidium	0	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Microascus	0	0	4	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	4	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	0	4	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales			0	0	0	4	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	4	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Dioszegia	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	4	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	4	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Rhytismatales	Rhytismataceae		0	0	0	0	4	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Vishniacozyma	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	4	0	0	0	0	0	0	0	0

Ascomycota	**Archaeorhizomycetes**	**Archaeorhizomycetales**	**Archaeorhizomycetaceae**	**Archaeorhizomyces**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**		**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Archaeorhizomycetes**	**GS31**			**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**		**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Microascales**	**Microascaceae**	**Canariomyces**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Microbotryomycetes**	**Sporidiobolales**	**Sporidiobolaceae**	**Rhodotorula**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Phaeophleospora**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Pleosporaceae**		**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Microbotryomycetes**	**Sporidiobolales**	**Sporidiobolaceae**	**Rhodosporidiobolus**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**			**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Chytridiomycota					**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Myriangiales**	**Elsinoaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Stenella**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Schizoparmaceae**	**Coniella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**0**	**0**	**0**

Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	Trechispora		0	0	0	0	0	0	0	4	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes					0	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales				0	0	0	0	0	0	0	4	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae			0	0	0	0	0	0	0	0	4	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Erythrobasidiales	Erythrobasidiaceae	Erythrobasidium		0	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	Idriella		0	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae			0	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales				0	0	0	0	0	0	0	0	4	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Meyerozyma		0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota						0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Xenosonderhenia		0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria		0	0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales				0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium		0	0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus		0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Eurotiomycetes					0	0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	pagnoccae	0	0	0	0	0	0	0	0	0	4	0	0	0	0

Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Plectosphaerella	0	0	0	0	0	0	0	0	0	4	0	0	0	0
Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella	0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Tubeufiales	Tubeufiaceae		0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida	0	0	0	0	0	0	0	0	0	4	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Dissoconiaceae	Uwebraunia	0	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		0	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium	0	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	0	0	0	4	0	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Sordariomycetes	Myrmecridiales	Myrmecridiaceae	Myrmecridium	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Chytridiomycota					0	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Basidiomycota	Tremellomycetes	Tremellales			0	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Orbiliomycetes	Orbiliales	Orbiliaceae	Orbilia	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chloridium	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Rozellomycota	Rozellomycota_cls_Incertae_sedis	Rozellomycota_ord_Incertae_sedis	Rozellomycota_fam_Incertae_sedis	Paramicrosporidium	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Basidiomycota	Agaricomycetes	Agaricales	Inocybaceae	Astrosporina	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Geopora	0	0	0	0	0	0	0	0	0	0	0	0	4	0

Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Kazachstania	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	GS11			0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Sporoschisma	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Sphaerostilbella	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Dothideomycetes	Venturiales	Sympoventuriaceae	Veronaeopsis	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Basidiomycota	Agaricomycetes	Agaricales	Schizophyllaceae	Schizophyllum	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Basidiomycota	Cystobasidiomycetes	Cystobasidiomycetes_ord_Incertae_sedis	Symmetrosporaceae	Symmetrospora	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis	Microbotryomycetes_fam_Incertae_sedis	Colacogloea	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Basidiomycota	Cystobasidiomycetes	Cystobasidiales	Cystobasidiaceae	Occultifur	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Zopfiella	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Basidiomycota	Tremellomycetes	Tremellales	Bulleribasidiaceae	Hannaella	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	0	0	0	0	0	0	0	0	4

Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**	**Colletotrichum**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Bionectriaceae**	**Clonostachys**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**	**Chaetomium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Dothideomycetes**	**Asterinales**	**Parmulariaceae**	**Parmularia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Eurotiomycetes**	**Phaeomoniellales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Psathyrellaceae**	**Coprinellus**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Glomerellaceae**	**Colletotrichum**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Exutisphaerella**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Ustilaginomycetes**	**Ustilaginales**	**Ustilaginaceae**	**Macalpinomyces**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Cladosporiaceae**	**Cladosporium**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota					**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Asterinales**	**Parmulariaceae**	**Parmularia**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**		**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Glomeromycota	**Glomeromycetes**	**Glomerales**	**Glomeraceae**	**Rhizophagus**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**	**Madagascaromyces**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**			**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**		**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**			**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Ceratobasidiaceae**		**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**	**Arnium**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Cyphellophoraceae**	**Cyphellophora**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Botryobasidiaceae**		**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Agaricaceae**	**Agaricus**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**			**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Lecanoromycetes**	**Ostropales**	**Gomphillaceae**	**Corticifraga**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Dipodascaceae**		**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Hypocreales_fam_Incertae_sedis**	**Acremonium**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Vishniacozyma**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Rozellomycota					**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**	**Tricladiaceae**	**Mycofalcella**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Rozellomycota					**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**			**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Glomerellales**	**Reticulascaceae**	**Blastophorum**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Cortinariaceae**	**Cortinarius**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Volutella**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Basidiomycota	Tremellomycetes	Tremellales	Cuniculitremaceae	Kockovaella	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Calvolachnella	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae		0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Mollisia	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Glomerellales			0	0	0	3	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetales_fam_Incertae_sedis	Skvortzovia	0	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Dimorphiseta	0	0	0	3	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botryotinia	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Dipodascaceae	Dipodascus	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	3	0	0	0	0	0	0	0	0	0
Basidiomycota	Cystobasidiomycetes	Cystobasidiomycetes_ord_Incertae_sedis	Symmetrosporaceae	Symmetrospora	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiales_fam_Incertae_sedis	Leohumicola	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		0	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Coniothyriaceae	Coniothyrium	0	0	0	0	3	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales			0	0	0	0	3	0	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycodaceae	Hanseniaspora	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paracamarosporium	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Veronaea	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Apiosordaria	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Asterinales	Parmulariaceae	Parmularia	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	Ascobolus	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	Hydropisphaera	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Clitopilus	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	3	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Neodidymella	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	0	0	0	0	0	0	3	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Geastrumia	0	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Valsaceae	Cytospora	0	0	0	0	0	0	3	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes				0	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	3	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	3	0	0	0	0	0	0	0
Basidiomycota					0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	0	0	0	0	0	0	0	3	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus	0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae		0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriales_fam_Incertae_sedis	Strelitziana	0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Pseudocercospora	0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	3	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Sebacinales	Serendipitaceae		0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Hyaloscyphaceae	Rodwayella	0	0	0	0	0	0	0	3	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		0	0	0	0	0	0	0	0	3	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	0	0	0	0	0	0	0	0	3	0	0	0	0	0

Ascomycota	**Dothideomycetes**	**Capnodiales**	**Teratosphaeriaceae**	**Xenopenidiella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Mortierellomycota	**Mortierellomycetes**	**Mortierellales**	**Mortierellaceae**	**Mortierella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Clavicipitaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**	**Chaetosphaeriaceae**	**Thozetella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Thelebolales**	**Thelebolaceae**	**Ramgea**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Sporocadaceae**	**Pestalotiopsis**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Archaeorhizomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**	**Cladorrhinum**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Clavicipitaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Aspergillaceae**	**Penicillium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Microdochiaceae**	**Microdochium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Thelephorales**	**Thelephoraceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Eurotiales**	**Trichocomaceae**	**Talaromyces**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Asterinales**	**Parmulariaceae**	**Parmularia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Schizophyllaceae**	**Schizophyllum**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**0**

Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriales_fam_Incertae_sedis**	**Strelitziana**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**	**Cladorrhinum**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Cucurbitariaceae**	**Pyrenochaeta**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Neodevriesiaceae**	**Neodevriesia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Basidiomycota	**Cystobasidiomycetes**	**Cystobasidiomycetes_ord_Incertae_sedis**	**Symmetrosporaceae**	**Symmetrospora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Dipodascaceae**	**Dipodascus**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Mortierellomycota	**Mortierellomycetes**	**Mortierellales**	**Mortierellaceae**	**Mortierella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Cordycipitaceae**	**Beauveria**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Sordariomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Clavicipitaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Bionectriaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Pluteaceae**	**Pluteus**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**
Basidiomycota	**Agaricomycetes**	**Boletales**	**Boletaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Sporormiaceae**	**Preussia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**0**

Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	Paragibellulopsis	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Atractium	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Basidiomycota	Agaricomycetes	Hymenochaetales	Hymenochaetales_fam_Incertae_sedis	Skvortzovia	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Paraconiothyrium	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Archaeorhizomycetes				0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Dothideomycetes	Capnodiales	Capnodiaceae	Leptoxyphium	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreales_fam_Incertae_sedis		0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Stephanonectria	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Aleuria	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Leucoagaricus	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Cladorrhinum	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Dothideomycetes	Mytilinidiales	Gloniaceae	Cenococcum	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Eurotiomycetes	Onygenales	Onygenaceae	Arachnotheca	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Phialomyces	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Ascomycota	Eurotiomycetes	Chaetothyriales			0	0	0	0	0	0	0	0	0	0	0	0	0	3

Ascomycota	**Pezizomycetes**	**Pezizales**	**Pezizales_fam_Incertae_sedis**	**Trichobolus**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Basidiomycota	**Wallemiomycetes**	**Wallemiales**	**Wallemiaceae**	**Wallemia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Bionectriaceae**	**Gliomastix**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Basidiomycota	**Cystobasidiomycetes**	**Erythrobasidiales**	**Erythrobasidiaceae**	**Erythrobasidium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Chaetomiaceae**	**Corynascus**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Hypoxylon**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**
Ascomycota	**Leotiomycetes**	**Thelebolales**	**Pseudeurotiaceae**	**Gymnostellatospora**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**				**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Malasseziomycetes**	**Malasseziales**	**Malasseziaceae**	**Malassezia**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Hypocreales_fam_Incertae_sedis**	**Acremonium**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Xylariaceae**	**Xylaria**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**			**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Chytridiomycota					**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Spegazzinia**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**				**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Trichomeriaceae**	**Trichomerium**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Ascomycota	Sordariomycetes	Diaporthales				2	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Pezizellaceae	Porodiplodia		2	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Thermomyces	lanuginosus	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Dothideales	Aureobasidiaceae			0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales				0	2	0	0	0	0	0	0	0	0	0	0	0	0
Rozellomycota						0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Paramycosphaerella		0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae			0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales				0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Tubeufiales	Tubeufiaceae			0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria		0	2	0	0	0	0	0	0	0	0	0	0	0	0
Rozellomycota	Rozellomycotina_cls_Incertae_sedis	Branch03				0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae			0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Articulospora		0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetales_fam_Incertae_sedis	Candida		0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Montagnula		0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala		0	0	2	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosulcatispora	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Cryphonectriaceae		0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae	Xenocylindrosporium	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes				0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota					0	0	2	0	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Microbotryomycetes	Microbotryomycetes_ord_Incertae_sedis			0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Pezizomycetes	Pezizales	Pyronemataceae	Sphaerosporella	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Euteratosphaeria	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Rozellomycota					0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Veronaea	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Hypoxylon	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Cantharellales	Botryobasidiaceae		0	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae	Capnobotryella	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales			0	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Chaetomellaceae	Pilidium	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Ascomycota	Lecanoromycetes	Ostropales			0	0	0	0	2	0	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Hymenochaetales	Rickenellaceae	Sidera	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Sordariales			0	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Articulospora	0	0	0	0	2	0	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Onygenales	Onygenales_fam_Incertae_sedis	Zeloasperisporium	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Polyporales	Podoscyphaceae	Rickiopora	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales			0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Verrucocladosporium	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Acrospermales	Acrospermales_fam_Incertae_sedis	Leptodiscella	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Mortierellomycota	Mortierellomycetes	Mortierellales	Mortierellaceae	Mortierella	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales			0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales			0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Boliniales	Boliniales_fam_Incertae_sedis		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Strickeria	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Wojnowiciella	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Basidiomycota	Agaricomycetes	Auriculariales			0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Calosphaeriales	Calosphaeriaceae	Jattaea	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	2	0	0	0	0	0	0	0	0

Ascomycota	Eurotiomycetes	Chaetothyriales	Cyphellophoraceae	Cyphellophora	fusarioides	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Basidiomycota	Exobasidiomycetes	Exobasidiales				0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Saccharomycetes	Saccharomycetales	Trichomonascaceae	Blastobotrys		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Asterinales	Parmulariaceae	Parmularia		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Ophiocordyceps		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae			0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Leptospora		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Teratosphaeriaceae			0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales				0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Neosulcatispora		0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae	Neopestalotiopsis		0	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Pezicula		0	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Corynesporascaceae	Corynespora		0	0	0	0	0	0	2	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales				0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariales_fam_Incertae_sedis	Hansfordia		0	0	0	0	0	0	0	2	0	0	0	0	0	0
Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Naganishia		0	0	0	0	0	0	0	2	0	0	0	0	0	0

Ascomycota	Sordariomycetes	Xylariales			0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Diaporthales	Diaporthaceae	Diaporthe	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Botryosphaeriales	Aplosporellaceae	Aplosporella	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Microascales	Halosphaeriaceae		0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota					0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botryotinia	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Ceramothyrium	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Basidiomycota	Ustilaginomycetes	Ustilaginales	Ustilaginaceae	Pseudozyma	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Xylariales	Xylariaceae	Xylaria	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Parapyrenochaeta	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Basidiomycota	Agaricomycetes	Russulales	Peniophoraceae	Peniophora	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Archaeorhizomycetes				0	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae	Coniochaeta	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Stachybotryaceae	Stachybotrys	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Dothideomycetes	Asterinales	Parmulariaceae	Parmularia	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Ascomycota	Sordariomycetes	Microascales			0	0	0	0	0	0	0	0	0	2	0	0	0	0

Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Herpotrichiellaceae**	**Rhinocladiella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**	**Mycosphaerellaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Ganodermataceae**	**Ganoderma**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Ascomycota					**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Chaetosphaeriales**	**Chaetosphaeriaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Ascomycota	**Saccharomycetes**	**Saccharomycetales**	**Pichiaceae**	**Pichia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Kickxellomycota	**Kickxellomycetes**	**Kickxellales**	**Kickxellaceae**	**Ramicandelaber**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Asterinales**	**Parmulariaceae**	**Parmularia**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Phaeosphaeriaceae**	**Neosulcatispora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**0**
Basidiomycota	**Tremellomycetes**	**Tremellales**	**Bulleribasidiaceae**	**Hannaella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Polyporales**	**Fomitopsidaceae**	**Skeletocutis**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ascomycota	**Pezizomycetes**	**Pezizales**	**Pezizaceae**	**Peziza flavida**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Russulales**	**Peniophoraceae**	**Peniophora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Sporormiaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Branch06**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Capnodiales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Microascales**	**Microascaceae**	**Canariomyces**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Sordariales**	**Lasiosphaeriaceae**	**Schizothecium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Apiosporaceae**	**Arthrinium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Cryphonectriaceae**	**Mastigosporella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**

Ascomycota	**Sordariomycetes**	**Hypocreales**	**Bionectriaceae**	**Gliomastix**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Ophiocordycipitaceae**	**Tolypocladium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Ascomycota	**Leotiomycetes**	**Helotiales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Cantharellales**	**Botryobasidiaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Chytridiomycota	**Spizellomycetes**	**Spizellomycetales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**	**0**
Ascomycota	**Dothideomycetes**				**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**			**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Dothideomycetes**	**Minutisphaerales**	**Minutisphaeraceae**	**Minutisphaera**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Lecanoromycetes**	**Ostropales**	**Gomphillaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Melanommataceae**	**Pleotrichocladium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Agaricales_fam_Incertae_sedis**	**Acanthocorticium**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Sordariomycetes**	**Diaporthales**	**Diaporthaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymosphaeriaceae**	**Cylindroaseptospora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Basidiomycota	**Agaricomycetes**	**Agaricales**	**Agaricaceae**	**Leucoagaricus**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Sordariomycetes**	**Hypocreales**	**Ophiocordycipitaceae**	**Hirsutella**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Basidiomycota	**Agaricomycetes**	**Sebacinales**	**Sebacinaceae**	**Sebacina**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Eurotiomycetes**	**Chaetothyriales**	**Chaetothyriaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**
Ascomycota	**Sordariomycetes**	**Phomatosporales**	**Phomatosporaceae**	**Phomatospora**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**0**

Ascomycota	Sordariomycetes				0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Microascales	Microascaceae	Cephalotrichum	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Saccharomycetes	Saccharomycetales	Metschnikowiaceae	Clavispora	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Leotiomycetes	Helotiales	Dermateaceae	Pezicula	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Eurotiomycetes	Phaeomoniellales	Phaeomoniellaceae		0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Veronaea	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Leotiomycetes	Thelebolales	Pseudeurotiaceae	Pseudogymnoascus	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Orbiliomycetes	Orbiliales			0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Hypocreales			0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes				0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota					0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Dothideomycetes	Capnodiales			0	0	0	0	0	0	0	0	0	0	0	0	0	2
Basidiomycota	Agaricomycetes	Auriculariales	Exidiaceae	Exidia	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Ascomycota	Sordariomycetes	Chaetosphaeriales			1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Phialoseptomonium	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Leotiomycetes	Helotiales	Pezizellaceae	Porodiplodia	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae	Cladosporium	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Kalmusia	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae		1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	Madagascaromyces	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Ascomycota	**Sordariomycetes**	**Hypocreales**	**Nectriaceae**	**Neocosmospora**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Dothideomycetes**	**Pleosporales**	**Didymellaceae**	**Similiphoma**	**0**	**0**	**0**	**0**	**0**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Basidiomycota	**Agaricomycetes**	**Thelephorales**	**Thelephoraceae**	**Tomentella**	**0**	**0**	**0**	**0**	**0**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Ascomycota	**Sordariomycetes**	**Xylariales**	**Sporocadaceae**		**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**0**	**0**	**0**	**0**	**0**	**0**

OH: *O. hexasperma*; C: control; N: nitrogen treatment; NP: nitrogen+phosphate treatment; P: phosphate treatment; Ca: liming.