

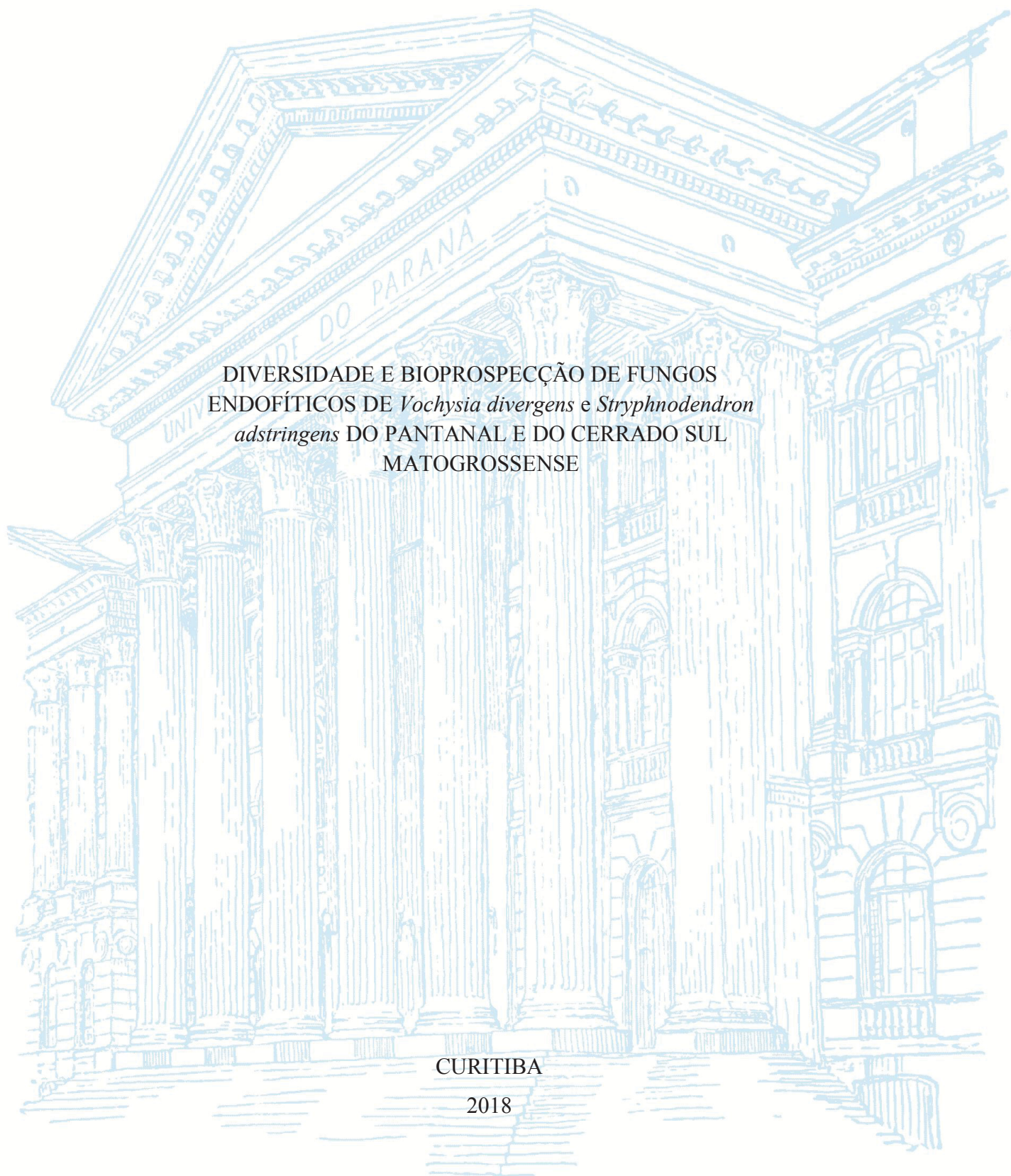
UNIVERSIDADE FEDERAL DO PARANÁ

SANDRIELE APARECIDA NORILER

DIVERSIDADE E BIOPROSPECÇÃO DE FUNGOS
ENDOFÍTICOS DE *Vochysia divergens* e *Stryphnodendron*
adstringens DO PANTANAL E DO CERRADO SUL
MATOGROSSENSE

CURITIBA

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Dissertação apresentada como requisito parcial à obtenção do grau de Mestre em Microbiologia, Parasitologia e Patologia, no curso de Pós-Graduação em Microbiologia, Parasitologia e Patologia, Setor de Ciências Biológicas, Universidade Federal do Paraná.

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TERMO DE APROVAÇÃO

**“Diversidade e Bioprospecção de Fungos Endofíticos de
Vochysia divergens e *Stryphnodendron adstrigens* do Pantanal e
do Cerrado Sul Matogrossense”**

por

Sandriele Aparecida Noriler

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de Mestre no Curso de Pós-Graduação em Microbiologia, Parasitologia
e Patologia, pela Comissão formada pelos professores:**


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**“As raízes do estudo são
amargas, porém os frutos
são doces.”
Aristóteles**

RESUMO

Os fungos endofíticos são uma das principais fontes de metabólitos secundários com vasta atividade biológica, particularmente aqueles associados a plantas medicinais. Os biomas Pantanal e Cerrado no Brasil têm alta riqueza associada, principalmente em relação à flora, e muitas das plantas encontradas nesses biomas são usadas pela comunidade local devido a suas propriedades medicinais. Portanto, catalogar a comunidade endofítica de plantas encontradas nessas regiões e explorar o potencial biotecnológico desses microrganismos é de grande importância. Os objetivos do presente trabalho foram analisar a comunidade de fungos endofíticos de duas plantas medicinais encontradas no Pantanal e Cerrado e avaliar seu potencial antimicrobiano. Um total de 1116 fungos endofíticos foram isolados das plantas *Vochysia divergens*, presente na região do Pantanal, e *Stryphnodendron adstringens* encontrada no Cerrado, em duas coletas, a primeira realizada em Janeiro e a segunda para o estudo de biodiversidade realizado em Junho de 2016. Os isolados endofíticos foram agrupados em 124 grupos com base em seus morfotipos e cada representante foi identificado por análise da região ITS (*Internal Transcribed Spacer*). As análises de diversidade foram realizadas com 1079 isolados obtidos na segunda coleta e foram utilizados: riqueza e abundância absoluta, índices de diversidade de Shannon (H'), índice de Simpson ($D-1$) e índice de uniformidade de Pielou (J). O *screening* do potencial antimicrobiano foi realizado através de cultura pareada contra fitopatógenos e *overlap* contra patógenos humanos. Para isolados que apresentaram potencial no *screening* foi realizada a produção do extrato em dois meios de cultivos, Extrato de Malte e Czapeck, e os metabólitos secundários extraídos foram avaliados novamente contra microrganismos fitopatogênicos e bactérias e levedura de importância clínica. O índice de riqueza foi alto para ambas as plantas, no entanto, a comunidade endofítica não difere entre as plantas, *Diaporthe* foi o gênero dominante em ambas as plantas. Os testes antimicrobianos revelaram o alto potencial dos isolados *Diaporthe* sp. LGMF1548 e LGMF1583 e *Neofusicoccum brasiliensis* LGMF1535, com atividade contra *Staphylococcus aureus* resistente à meticilina (MRSA), *Klebsiella pneumoniae* (KPC) e *Candida albicans*. Contra fitopatógenos o isolado *Diaporthe* sp. LGMF1631 inibiu 90% do crescimento micelial de *Phyllosticta citricarpa* e 70% de *Colletotrichum abscissum*. Esses resultados demonstram a elevada diversidade de endofíticos, filogenia e a atividade antimicrobiana de fungos endofíticos associados às plantas *V. divergens* e *S. adstringens*. Nossos dados também sugerem que essas plantas servem como hospedeiras de novas espécies e gêneros, os quais produzem compostos de interesse.

Palavras chave: Comunidades endofíticas; Antimicrobianos naturais; Biomas brasileiros; *Diaporthe*.

ABSTRACT

The endophytic fungi are a main source of interest in metabolites, particularly those associated with medicinal plants. The Pantanal region and Brazilian savannah (Cerrado) in Brazil has high richness associated and many plants used for a local community because of their medicinal properties. Therefore exploring the bioprospecting potential of endophytic microorganisms in this region is important. The goals of the present work were to analyze the community endophytic fungi in medicinal plants of Pantanal and Cerrado, and their antimicrobial potential. A total of 1116 endophytic fungi were isolated from two different medicinal plants, *Vochysia divergens* in the region of Pantanal and *Stryphnodendron adstringens*, in the Cerrado and in two collects, the first realized in January and the second for biodiversity study realized in June of 2016. These isolates were grouped in 124 clades based in their morphotypes. The ITS (Internal Transcribed Spacer) sequence was used for species identification. The analyses were realized with one isolated each group. The diversity analyses was performed with 1079 isolates obtained in the second collect, and were used: absolute richness and abundance, indices of diversity of Shannon (H') and Simpson's index ($D-1$), and Pielou's evenness index (J). Screening for antimicrobial potential was determined by dual culture against phytopathogens and overlap against human pathogens. The production of crude extract were performed in Malt Extract and Czapeck media, derived from endophytic fungal selected in the screening, was tested against pathogenic microorganisms for inhibition of micelial growth for phytopathogens and in inhibition zone for clinical pathogens. In phylogenetic analyses were obtained 28 genera, with possible new genera. The richness index was high for both plants and the most part of the isolates belonging to *Diaporthe* genus, however, the endophytic community not differ between the plants. The antimicrobial tests showed the isolates *Diaporthe* sp. LGMF1548 and LGMF1583 and *Neofusicoccum brasiliensis* LGMF1535 with the best results against methiciline-resistant *Staphylococcus aureus*, *Klebsiella pneumoniae* (KPC) and *Candida albicans*, for tests against phytopathogens the isolate *Diaporthe* sp. LGMF1631 inhibited 90% the mycelial growth of the *Phyllosticta citricarpa* and 70% of the *Colletotrichum abscissum*. These results demonstrate the biodiversity, phylogeny, and antimicrobial activity of endophytic fungi associated with the plants *V. divergens* and *S. adstringens*, and reveals the potential for discovery news taxa and compounds of interesting from the endophytes in these plants.

Keywords: Endophytic communities; Natural antimicrobials; Brazilian biomes; *Diaporthe*.

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1. INTRODUÇÃO

O aumento no número de linhagens resistentes tanto de importância clínica quanto na agricultura, aliado a dificuldade no desenvolvimento de novos medicamentos e pesticidas com amplo espectro de ação, tem despertado preocupação mundial (HWANG e GUMS, 2016). Uma medida alternativa para esse problema tem sido o desenvolvimento de novos medicamentos na área da saúde e medidas de controle biológico através da exploração de compostos naturais, principalmente por metabólitos produzidos por microrganismos diversos (STROBEL e DAISY, 2003; STROBEL, 2004). No que diz respeito à formulação de fármacos por metabólitos produzidos por microrganismos, destacam-se as penicilinas, estreptomicina, clorafenicol, polimixina, cefalosporinas, nistatina, eritromicina, vancomicina, gentamicina, lovastatina, ciclosporina, ácido fusídico, anidulafungina e caspafungina (SERRA, 2010; KUMAR et al., 2013).

O termo bioprospecção é utilizado para a aplicação biotecnológica associada ao conhecimento tradicional/popular de produtos naturais. Como por exemplo, exploração de metabólitos produzidos por microrganismos endofíticos isolados de plantas tradicionalmente conhecidas como medicinais (STROBEL e DAISY, 2003).

Endófitos são caracterizados como microrganismos que vivem no interior da planta sem causar nenhum dano aparente, auxiliando no desenvolvimento e defesa da planta contra herbivoria e patógenos (PETRINI, 1991). Vários estudos apontam que as taxas de crescimento das plantas, assim como a produção de metabólitos secundários, são dependentes de fatores propiciados pela presença de microrganismos endofíticos (SHI et al., 2014; SADEGHIAN, BONJAR e SIRCHI, 2016; SANTOYO et al., 2016).

Entre os trabalhos desenvolvidos com microrganismos endofíticos, destacam-se os isolados a partir de plantas medicinais, em função da produção de metabólitos secundários pelos endófitos poder estar associada aos compostos produzidos pela planta. Assim o caráter medicinal da planta pode estar relacionado com a sua comunidade endofítica (STROBEL et al., 2004).

Outro fator que pode influenciar diretamente na produção de metabólitos são as condições ambientais em que as plantas estão inseridas (CORREIA et al., 2017, DOS SANTOS-SOUZA e SANTOS, 2017). Alguns estudos destacam a capacidade da planta hospedeira em sobreviver em determinados ambientes devido a sua comunidade endofítica (PIETRO-SOUZA et al., 2017).

Sendo assim a composição da comunidade endofítica associada à planta hospedeira pode estar relacionada tanto ao ambiente\bioma (condições de estresse, condições climáticas, ação antropológica), quanto ao seu potencial medicinal (SINGH et al., 2017).

No Brasil, vários estudos relatam a capacidade metabólica de endófitos. Entre eles, pode-se destacar o isolamento e bioprospecção de linhagens endofíticas da planta medicinal *Vochysia divergens* Pohl, localizada na região do Pantanal (SAVI et al., 2016; HOKAMA et al., 2017; GOS et al., 2017). *V. divergens* apresenta entre suas propriedades medicinais: potencial anti-inflamatório, antimicrobiano e ação contra doenças respiratórias (BORTALANZA; FERREIRA; HESS, 2002; HESS et al., 1995).

Outra planta medicinal de importância, muito utilizada pela população do cerrado principalmente para curtição de couro, conhecida por seu poder adstringente, é o *Stryphnodendron adstringens* (Mart.) Colville. Comumente chamada de Barbatimão, *S. adstringens* é explorada também devido a propriedades medicinais da sua casca rica em taninos (ISHIDA et al., 2006). Costa et al. (2013) avaliaram a potencial antifúngico de extratos obtidos dessa planta. Carvalho et al. (2012) realizaram um estudo inicial de endófitos provenientes do Barbatimão e observaram também a atividade antibacteriana contra diversas bactérias patogênicas.

Devido à alta diversidade de espécies e as peculiaridades presentes nesses ecossistemas, os biomas do Cerrado e Pantanal foram caracterizados como áreas prioritárias de preservação pelo Ministério do Meio Ambiente, visando proteger a biodiversidade dos biomas brasileiros (MINISTÉRIO DO MEIO AMBIENTE, 2007). Nesse contexto, estudos de bioprospecção em áreas de conservação auxiliam tanto na preservação, por agregar valor à biodiversidade associada, quanto na busca de novos compostos químicos com amplo espectro de ação.

2. OBJETIVOS

2.1. OBJETIVOS GERAIS

Explorar a biodiversidade e o potencial biotecnológico de fungos endofíticos das plantas medicinais *Vochysia divergens* e *Stryphnodendron adstringens* localizadas respectivamente, nos biomas Pantanal e Cerrado.

2.2 OBJETIVOS ESPECÍFICOS

- Realizar estudo de biodiversidade da comunidade fúngica endofítica pertencentes às plantas medicinais *Vochysia divergens* e *Stryphnodendron adstringens*.
- Selecionar os endófitos com potencial de produção de compostos de interesse farmacêutico e agrícola.

3. REVISÃO BIBLIOGRÁFICA

3.1. BIOMAS DE ESTUDO

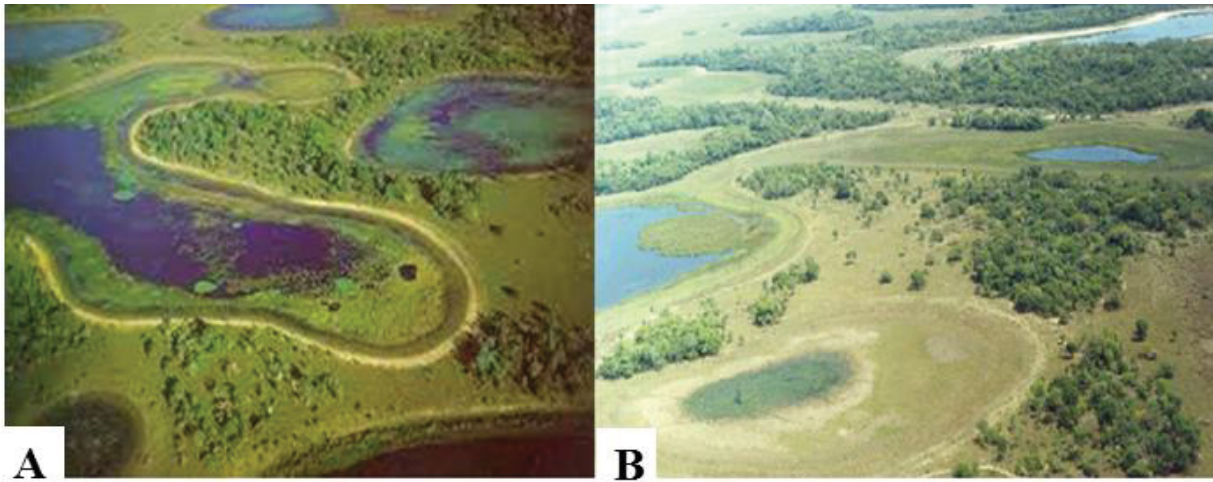
3.1.1. O Pantanal

No Brasil, o Pantanal se estende pelos estados do Mato Grosso (35%) e Mato Grosso do Sul (65%) alcançando uma parte do leste da Bolívia e do norte do Paraguai (RADAM-BRASIL, 1982). Sua localização geográfica permite uma correlação com outros biomas, como o Cerrado central, localizado ao leste, e florestas semidecíduas na região nordeste, o Chaco na porção de origem na Bolívia e no Paraguai (ADÁMOLI, 1982).

O Pantanal é uma planície sedimentar de 140.000 km², formada durante o período quaternário e banhada pelo rio do alto Paraguai. Considerado a maior área de alagamento na América do Sul (Da SILVA, 1990), o Pantanal é um ecossistema heterogêneo e que sofre de mudança sazonal abrupta pela inundação temporária em determinadas épocas do ano (JUNK; BAILEY; SPARKS, 1989). As inundações se iniciam no Norte dessa região nos meses de Setembro e Dezembro, intensificando entre Janeiro e Março e se estendem por 4 a 8 meses. O Pantanal do Rio Miranda atinge seu nível máximo de inundação em Julho, chegando até 2 m de profundidade (CARVALHO, 1986; PAIVA, 1984), e o menor nível entre Dezembro e Janeiro.

Essa região abriga cerca de 2.000 espécies de fanerógamas, entre elas encontram-se em torno de 200 espécies exóticas, leguminosas e gramíneas e 1000 que são herbáceas (POTT; POTT 2003; POTT et al., 2011). A diversidade da flora no Pantanal inclui diversas espécies de plantas medicinais utilizadas na medicina popular local (MACEDO; FERREIRA, 2005). Porém, o frágil equilíbrio nesse bioma, caracterizado por variações entre períodos de inundações e secas (Figura 1), encontra-se ameaçado por ações de desenvolvimento econômico (MINISTÉRIO DO MEIO AMBIENTE, 2007).

FIGURA 1 VISTA AÉREA DA REGIÃO DA NHECOLÂNDIA/PANTANAL DURANTE O PERÍODO DE CHEIA (A) E SECA (B).



FONTE: Embrapa Pantanal (2002).

3.1.2. O Cerrado

O Cerrado representa o segundo maior bioma da América do Sul, ocupando 22% do território brasileiro. Abriga três nascentes das maiores bacias hidrográficas da América do Sul, Amazônica/Tocantins, São Francisco e Prata (MINISTÉRIO DO MEIO AMBIENTE, 2007), e assim como o Pantanal, caracteriza-se por invernos extremamente secos e verão com períodos chuvosos (ADÁMOLI et al, 1987).

O Cerrado foi formado no quaternário, após um longo período glacial, que proporcionou a recuperação das florestas úmidas e expansão das florestas secas, possibilitando a criação de áreas campestres e mais abertas (BIGARELLA et al., 1975; SALGADO-LABOURIAU, 1994). Já no Holoceno as formações de florestas úmidas começam a sobressair nessa área (PRADO e GIBBS, 1993). A relação de presença de algumas espécies de flora características nessa região associado ao seu curso pluvial é estudado para relacionar o bioma do Cerrado com biomas adjacentes (PRADO e GIBBS, 1993).

A presença de florestas savânicas com árvores de grande porte e regiões campestres, associada a presença de importantes áreas fluviais faz com que o Cerrado tenha uma rica biodiversidade de flora e fauna (Figura 2).

FIGURA 2 REGIÃO DO CERRADO, SUDOESTE DE BRASÍLIA.

FONTE: Borges (2015).

Diversas espécies só se encontram nesse bioma (PRADO e GIBBS, 1993; OLIVEIRA FILHO e RATTER, 1995) e estima-se que existam 6.429 espécies de plantas nativas (MENDONÇA et al., 1998). Porém comparação de uma série de estudos de levantamento de diversidades de espécies associadas nessa área presume que o número de espécies pode estar subestimado. Outra problemática se encontra no nível de conservação, uma vez que várias espécies podem estar correndo risco de extinção, ainda sem serem descritas, devido a exploração indiscriminada desta região (MINISTÉRIO DO MEIO AMBIENTE, 2007). Como ação antropológica, através da extração de madeira, garimpo entre outras (COCCO et al., 2015). Além disso, a presença de espécies apenas associadas a esta região demonstra o valor do patrimônio genético associado a esta área (MINISTÉRIO DO MEIO AMBIENTE, 2007).

3.2. PLANTAS MEDICINAIS

3.2.1. *Vochysia divergens*

A planta *Vochysia divergens* Pohl pertence à família Vochysiaceae, tendo como nome popular, Cambará. É uma espécie lenhosa que pode atingir até 28 metros de altura (Figura 3). Originalmente pertencente à região amazônica, porém devido a sua capacidade de resiliência é considerada uma espécie invasora em áreas de inundação como a região pantaneira (POTT et al., 2011).

Figura 3 ÁRVORE DE *Vochysia divergens* POHL.



Fonte: Carioca-Paula, (2013).

V. divergens é considerada uma espécie monodominante da região, pela facilidade com a qual se espalhou pelo Pantanal, estende-se formando os denominados cambarazais (NUNES DA CUNHA; JUNK, 2004).

O primeiro estudo envolvendo cambarazais foi realizado por Nascimento e Nunes da Cunha (1989), que ao estudar a composição, distribuição e riqueza florística na região transpantaneira observaram a espécie *V. divergens* como dominante.

No que diz respeito às suas propriedades medicinais relatadas, Hess et al. (1995) isolaram três compostos produzidos por essa planta, β -sitosterol, ácido betulínico e ácido serício, sendo que o composto ácido serício apresentou maior atividade antimicrobiana. Além dos compostos descritos, essa planta é utilizada na medicina popular em forma de chás, produzidos através do caule, com ação contra asma. Outros trabalhos com extratos da casca dessa planta relatam a presença de ácido tormêntico com potencial medicinal (BORTOLANZA et al., 2002; WANG et al., 2016).

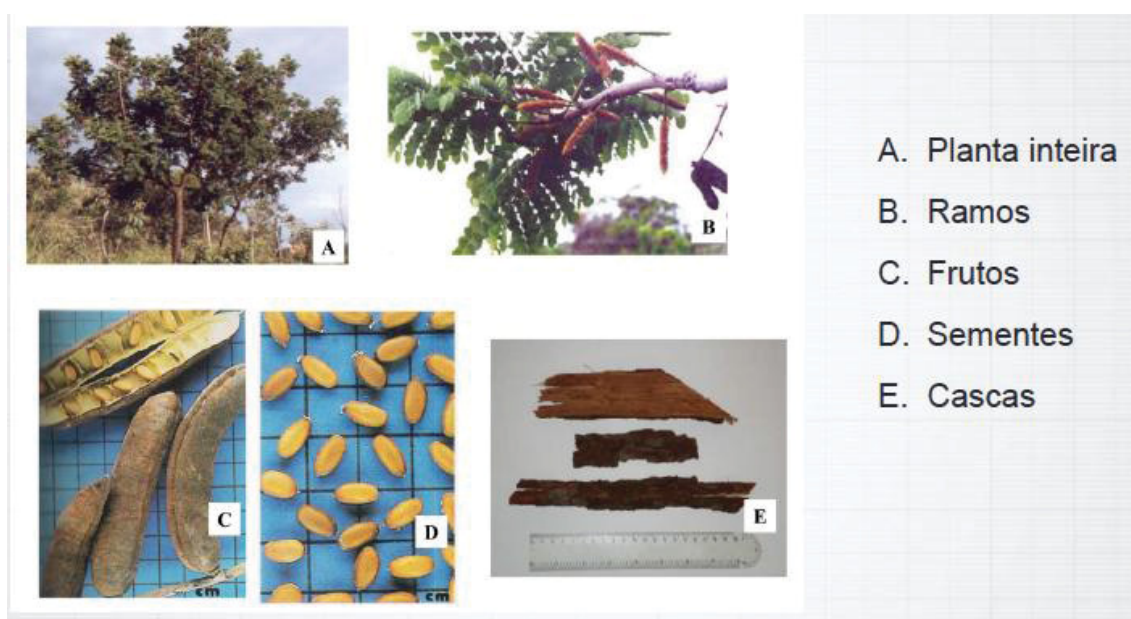
Savi et al. (2015), Hokama et al. (2017) e Gos et al. (2017) trabalharam com endófitos isolados do Cambará e observaram a produção de metabólitos secundários com ação biológica. Pimenta et al. (2017) avaliaram a produção do composto 5-metoxiflavona por endófitos em *V. divergens* relacionando a capacidade dessa planta em resistir ao estresse hídrico da região pantaneira.

Estes trabalhos são estudos preliminares da composição de endófitos dessa planta e ainda precisam ser mais explorados em relação à descrição da biodiversidade associada à *Vochysia divergens* na região do Pantanal e a prospecção de compostos de interesse.

3.2.2. *Stryphnodendron adstringens*

A planta *Stryphnodendron adstringens* (Mart.) Coville (barbatimão verdadeiro) da família Leguminosae (subfamília Mimosoideae), é nativa do Cerrado, mas se distribui por grande parte do Brasil, percorre desde a região da Amazônia até o Estado do Paraná (LIMA, 2010). É uma planta decídua, pode atingir até 10 metros, de tronco cascudo e tortuoso possui folhas compostas (Figura 4), com floração no período entre setembro-novembro e frutificação de julho-setembro (LORENZI, 1998).

Figura 4 ÁRVORE DE *Stryphnodendron adstringens* MARTH. (COVILLE).



FONTE: Lorenzi, (1998).

A ocorrência do barbatimão em épocas de seca pode estar associada a presença de raízes profundas (GOODLAND e FERRERI, 1974). Sendo assim comumente encontrada no Cerrado. O extrativismo intenso das cascas do barbatimão coloca em risco sua preservação e também pela substituição da mata nativa por campos de pastagem e lavoura (BORGES FILHO e FELFILI, 2003). O barbatimão é conhecido também na medicina popular pela composição de taninos presente em sua casca, comumente utilizados para transformar pele de animal em couro (PIO CORRÊA, 1946).

Lima et al. (1998) relatam o potencial fitoterápico do barbatimão em um dos primeiros relatos de produção de compostos de interesse clínico utilizando o extrato produzido da sua casca com ação anti-inflamatória. Outros trabalhos relatam ação dos extratos da casca e da folha dessa planta com ação contra patógenos clínicos (SILVA et

al., 2009; LUIZ et al., 2015; MOREY et al., 2016; TROLEZI et al., 2017). Souza et al. (2007) relataram além de ação bactericida também atividade anti-séptica de um sabonete líquido formulado a partir do extrato de barbatimão testado contra *Staphylococcus aureus*, *S. epidermidis* e *Escherichia coli*.

Outros estudos indicam potencial dos taninos presentes na casca do barbatimão contra leucorreia, hemorragias e sepsia de cortes e queimaduras (PANIZZA, 1997; LORENZI, 2002). Os polímeros de taninos com proantocianidina, também obtido do extrato da planta, interferiram no desenvolvimento do patógeno *Cryptococcus neoformans* (ISHIDA et al., 2009).

Os fungos endofíticos dessa planta também demonstraram que os mesmos podem ser uma fonte promissora para produção de metabólitos com ação antimicrobiana, antiparasitária contra *Leishmania amazonenses* e antitumoral (CARVALHO et al., 2012). Porém existem poucos estudos sobre a estrutura da comunidade endofítica desta planta, e os compostos bioativos de seus endófitos também foram pouco explorados.

3.3. FUNGOS ENDOFÍTICOS

O termo endófito está relacionado com microrganismos que colonizam o interior das plantas sem causar danos aparentes (Gr. Endo, dentro; phyton, planta) (CARROLL, 1988). Petrini (1991) tornou esse termo mais abrangente incluindo também microrganismos que não vivem necessariamente no interior dos tecidos, mas em certa fase de seu ciclo colonizam os tecidos. Esse termo também é relatado na literatura como sinônimo de mutualismo (MANI et al., 2015).

A presença de endófitos nas plantas auxilia no desenvolvimento e proteção de plantas. Por exemplo, Clay (1987) que verificou que o crescimento e desenvolvimento das plantas estudadas estava relacionado à presença de endofíticos, sendo que as plantas controles tinham o crescimento mais lento e menor desenvolvimento.

A relação planta e endófito ainda não está totalmente clara, estudos tentam elucidar a razão pela qual a planta não seria capaz de sobreviver sem tais microrganismos (BUATONG et al., 2011). Porém o que se sabe é que estes fornecem além de proteção e metabólitos que auxiliam seu desenvolvimento, disponibilidade de sintetizar alguns nutrientes que permitem a sobrevivência da planta em ambientes de estresse (BUATONG et al., 2011; ALVIN et al., 2014; SANTOYO et al., 2016).

Freeman e Rodriguez (1993) relatam a capacidade dos endofíticos em inibir o crescimento de fitopatógenos, servindo como uma forma de proteção do hospedeiro contra microrganismos fitopatogênicos (*Fusarium* e *Colletotrichum magna* o agente causador da antracnose). Larran et al. (2016) observaram o poder antagonista de endófitos contra o agente causador da mancha amarela do trigo (*Drechslera tritici-repentis*), em testes com cultura pareada. Tais estudos apontam a importância desses microrganismos para a planta, trazendo também diversas aplicabilidades em estudos laboratoriais.

No que diz respeito à alteração do metabolismo envolvida na relação planta-endofítico, Shi et al. (2014) analisaram as bactérias endofíticas presentes na beterraba açucareira. Neste estudo os pesquisadores comprovam que as diferenças na estrutura nutricional entre os genótipos das plantas caracterizam-se pela presença de diferentes microrganismos endofíticos, que estão intrinsecamente relacionados com o desenvolvimento da planta.

Referente à distribuição dos endófitos, diversos trabalhos relatam sua presença ao redor do mundo, em ambientes diversos (LARRAN et al., 2016; SANTOYO et al., 2016). Porém o ambiente pode influenciar diretamente na estruturação da comunidade endofítica, em regiões tropicais, por exemplo, o registro desses organismos é mais diverso (HATA et al., 1998).

Arnold et al. (2000) realizaram o isolamento de 418 morfoespécies endofíticas oriundas de folhas de plantas no Panamá e verificaram que esta diversidade estava relacionada tanto a região quanto ao hospedeiro e também a heterogeneidade espacial. Correia et al. (2017) realizaram um estudo dos endófitos de plantas pertencentes ao bioma da Mata atlântica realizando a comparação da estrutura dessa comunidade relacionada ao seu hospedeiro.

No geral, esses estudos apontam a importância de entender a relação entre endofítico e hospedeiro para caracterizar um ambiente e a relação das plantas presentes nesse ambiente. Assim como no estudo de Pietro-Souza et al. (2017) em uma região do Pantanal comparando ambientes contaminados com mercúrio, onde relatou que a presença de endófitos estava relacionada à capacidade da planta em sobreviver nessa área.

A distribuição dos endófitos sua riqueza e diversidade podem ser estudadas em conjunto com seu potencial de produzir compostos bioativos (SILVA-HUGHES et al., 2015). Uma variedade de compostos com propriedades medicinais diversas são

produzidos por estes microrganismos, tais como alcaloides com ação anticancerígena, antibactericida, antiviral entre outras (DEMBITSKY, 2014). O número de compostos relatados na literatura produzidos a partir de microrganismos endofíticos demonstra que esses organismos são excelentes fontes para busca de novos compostos de interesse farmacológico e agrícola (MARTINEZ-KLIMOVA et al., 2017).

Bioprospecting and Structure of Fungal Endophyte Communities Found in the Brazilian Biomes, Pantanal, and Cerrado (accept to *Frontiers in Microbiology*)

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Abstract

Medicinal plants have been recognized as hosts of high diverse endophytic microorganisms, including fungi that produce secondary metabolites with biological activity. Two biomes in Brazil, Pantanal (wetland), and Cerrado (savannah), are known as biodiversity hotspots, and despite their importance as a reservoir for several species, knowledge about the fungal biodiversity in these biomes is very limited. Fungal endophytic communities associated with leaves and petioles of the medicinal plants *Vochysia divergens* (from Pantanal) and *Stryphnodendron adstringens* (from Cerrado) were analyzed and studied for their antimicrobial activity against human and plant pathogens. A total of 1,146 isolates of endophytic fungi were obtained from plants collected in January and June of 2016 and grouped into 124 morphotypes. One isolate of each morphotype was identified by sequencing of internal transcribed spacer (ITS) region of the rDNA gene, which revealed the presence of 24 genera, including 3 possible new genera, and 48 taxa. Differences in the endophytic community according to the biomes were observed concerning the analyzed morphotypes. However, when we analyzed the diversity of genera and richness, they were similar for both plants, with *Diaporthe*, *Phyllosticta*, and *Neofusicoccum* as dominant genera. In addition, the community composition of *V. divergens* differs according to the analyzed plant tissues (petiole and leaf). These data suggested that both, the plant species and plant tissues play a role in the composition of endophytic community. As regards the biotechnological potential, 5 isolates showed activity against the phytopathogens *Phyllosticta citricarpa*, *Colletotrichum abscissum*, and *Fusarium verticillioides*, and 8 isolates showed high activity against clinical pathogens and were selected for the production of crude extract in different culture media. Extract from cultivation of *Diaporthe* sp. LGMF1548 and LGMF1583 and *Neofusicoccum brasiliense* LGMF1535 showed activity against methicillin-resistant *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Candida albicans*. In addition, extracts of *Diaporthe* cf. *heveae* LGMF1631 inhibited 90% of the mycelial growth of the *P. citricarpa* and 70% of *C. abscissum* and may represent an alternative to be used in the biological control of these phytopathogens. Future research will focus on the chemical characterization and structural elucidation of these bioactive compounds.

Keywords: *Vochysia divergens*, *Stryphnodendron adstringens*, natural antimicrobials, medicinal plants, *Diaporthe*.

1. INTRODUCTION

In the last years, medicinal plants have gained great importance as a reservoir of new endophytic strains with biotechnological potential (Gomes et al., 2013; Köberl et al., 2013; Savi et al., 2018). The endophyte-host interaction can interfere with the plant growth, development, and defense against pathogens and insects (Murali et al., 2007; Santoyo et al., 2016). However, the endophytic community is highly variable and depends on several components, such as host species and environmental conditions (Dudeja and Giri, 2014). In this context, two Brazilian biomes are particularly prominent due to the biodiversity of the flora: the savannah (Cerrado) and the wetland (Pantanal).

The Pantanal is a wetland located in the center of South America, in the Upper Paraguay River Basin, characterized by the change between periods of flood and drought, and the flora diversity found in this biome may be the result of seasonality in this area (Junk et al., 1989). Floods can inundate 80% of the entire Pantanal, and by contrast, during the dry season, most flooded areas will be dry. The biodiversity of Pantanal constitutes a valuable natural resource, and it is recognized as one of the most important freshwater ecosystems in the world. However, the unsustainable land use in this biome has been harming this peculiar biodiversity (Alho and Silva, 2012), and effective alternatives to conservation are necessary, such as bioprospecting studies to associate an economic value to the diversity present in this area.

The Brazilian savannah (Cerrado) is a neighboring biome of Pantanal that biogeographically influences its biodiversity and hosts a huge diversity of flora (Silva and Bates, 2002). The Cerrado is classified as one of the most diverse places in the world (Myers et al., 2000), with an estimated composition of more than 6,000 vascular plant species (Oliveira-Filho and Ratter, 2002; Felfili and Fagg, 2007). The diversity composition is result of the adverse environmental conditions caused by the fire, which selects the vegetation, changing the dominant plant species (Felfili and Fagg, 2007).

As these biomes are located in unexplored transition areas and are subject to adverse climatic changes, they were declared as priority conservation areas by the Brazilian government. Studies in the Pantanal and Cerrado are usually on animal and plant biodiversity (Hyde and Soyong, 2008; Porrás-Alfaro and Bayman, 2011). A very limited number of studies in these biomes are conducted on endophytic

microorganisms, and most of them are focused on aspects of bioprospecting without community analysis (Carvalho et al., 2012; Glienke et al., 2012; Vieira et al., 2014; Savi et al., 2016; Gos et al., 2017; Hokama et al., 2017; Parpinelli et al., 2017; Sousa et al., 2017).

The environmental conditions and the composition of the plants present in the Pantanal and Cerrado represent an unrivaled variety of habitats, which can have a significant influence on the endophytic community. As there are no studies comparing the species richness and the endophytic community between these two biomes, some questions remain unclear: What is the taxonomic composition and diversity of these endophytic fungi? Is the endophytic community biome-specific? Is the diversity structured or spread among these neighboring biomes? What is the biotechnological potential of these endophytic fungi? To address these questions, we analyzed and bioprospected the fungal endophytic community from two medicinal plants: *Vochysia divergens* Pohl (Vochysiaceae) and *Stryphnodendron adstringens* (Mart.) Coville (Fabaceae), found in Pantanal and Cerrado biomes, respectively. *Vochysia divergens* is considered as monodominant remaining during dry and flood season in the Pantanal (Junk et al., 2006) and *S. adstringens* is a native Cerrado species widely used in traditional medicine for its biological properties. These plants were selected according to the biome specificity, the medicinal properties and the lack of endophytic community studies

2. MATERIAL AND METHODS

2.1. Plant Material

The leaves and petioles of *S. adstringens* and *V. divergens* were collected in January and June 2016 from two Brazilian biomes, Cerrado (Savanna) and Pantanal. The collection of leaves and petioles of *V. divergens* was carried out in Pantanal of Miranda River (19°32'36.9"S 57°02'21.8"W), along of MS184 Road in Corumbá, Mato Grosso do Sul State, Brazil (Figure 1; were performed using R 3.4.4 R Core Team, 2017, source IBGE, 2004). The *S. adstringens* leaves and petioles were collected in Cerrado along the BR262 road (20°18'10.8"S 56°15'44.3"W) in Miranda, Mato Grosso do Sul State, Brazil (Figure 1). The samples of the

S. adstringens were collected from 10 plants in January and 23 in June, and the

samples of *V. divergens* were collected from 8 plants in January and 24 in June. For both species, 10 leaves and 10 petioles were collected for each individual plant. The plant tissues were stored at 4°C and isolation was performed within 72 h.

The January collection was used as a preliminary test for the epiphytic elimination protocol. The isolated endophytes of this collection were used only for bioprospecting and phylogenetic studies and were not included in the community analysis. With the optimized epiphytic elimination protocol, a second collection was performed in June, and the isolates obtained were used for endophytic community evaluation, phylogeny, and bioprospecting studies.

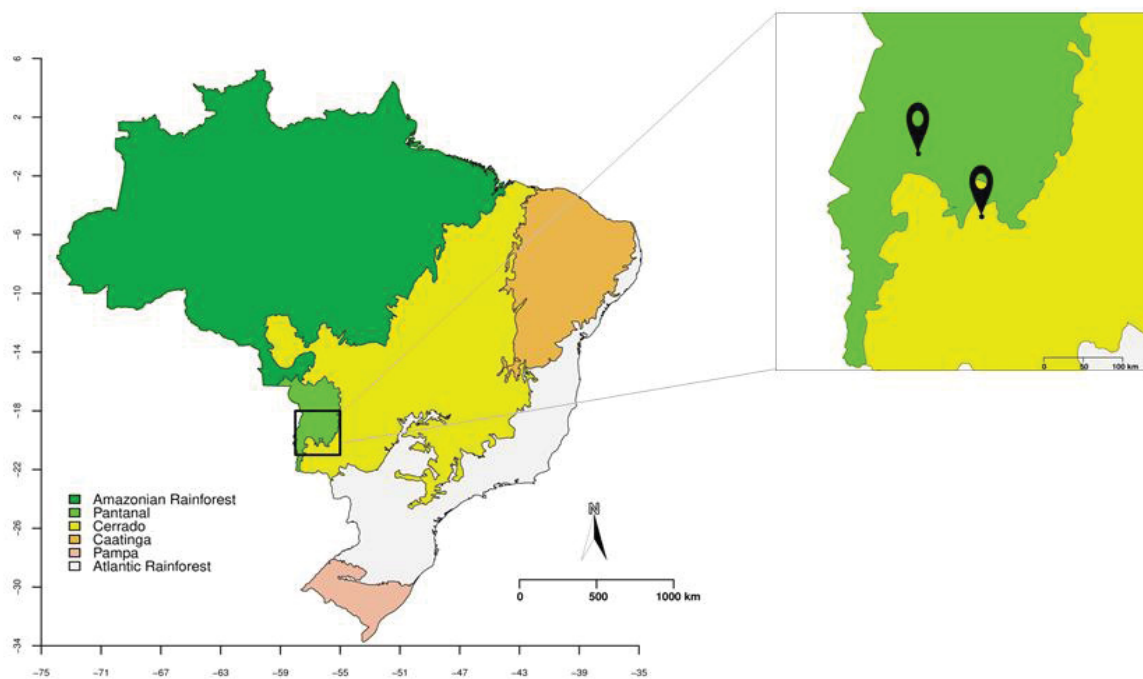


FIGURE 1. Brazil map showing the Pantanal (in green) and Cerrado (in yellow) biomes. In the magnified box are represented the collecting points of leaves and petioles of *Vochysia divergens* (Pantanal) and *Stryphnodendron adstringens* (Cerrado).

2.2. Isolation and morphotyping

The leaves and petioles, without lesions, from healthy plants, were used for endophytic fungi isolation using the 6 steps protocol described by Petrini (1986), with modifications: the leaves and petioles were submerged in autoclaved water for 1 min, immersion in 70% ethanol (v/v) for 1, 3 min in sodium hypochlorite 3% (v/v), 30 s in

70% ethanol (v/v), and then washed in sterilized distilled water for 1 min. After surface sterilization, the samples were fragmented into 5 pieces of 8 x 8 mm and aseptically transferred to plates containing potato dextrose agar (PDA), pH 5.8. The plates were incubated at 28°C for 30 days, and the endophytic growth was checked daily, the emerging mycelia were transferred to a new plate and stored at 4°C on PDA for further identification.

The isolation frequency (IF) of endophytes was calculated as the number of fragments from which one or more endophytic fungi were isolated, divided by the total number of fragments analyzed (Petrini et al., 1982). The isolates were assigned to morphotypes based on growth rate, colony color, hypha aspects, presence/absence and morphology of spores. One isolate from each morphotype was randomly selected for molecular identification and bioprospecting. For each isolate, a pure culture was obtained through single spore culture approach, according to Gilchrist-Saavedra et al. (2006). The isolates were deposited in the Laboratório de Genética de Microrganismos (LabGeM) culture collection, at the Federal University of Paraná, Brazil (<http://www.labgem.ufpr.br/>).

2.3. Isolates identification

Isolates were cultivated on PDA for 3 days at 28°C, and genomic DNA extraction was performed according to Raeder and Broda (1985). Primers V9G (de Hoog and Gerrits van den Ende, 1998) and ITS4 (White et al., 1990) were used to amplify the internal transcribed spacer region (ITS) of the nuclear ribosomal RNA gene. PCR reaction was performed using Top Taq Master Mix (QIAGEN), purified with the Exo1 and FastAP enzymes (ThermoFisher Scientific, USA) and sequenced using the BigDye Terminator Cycle Sequencing Kit v 3.1 kit (Applied Biosystems, Foster City, CA, USA). DNA sequences were obtained on an ABI Prism 3500 sequencer (Applied Biosystems, Foster City, CA, USA). Chromatograms were inspected using MEGA 7 software (Kumar et al., 2015) and BioEdit 7.0.5.3 (Hall, 1999) and compared to sequences available in the NCBI / GenBank database (National Center for Biotechnology Information - <Http://www.ncbi.nlm.nih.gov/BLAST/>) using the tool Blast, and comparing with the types strains found in MycoBank database (<http://www.mycobank.org/>).

The phylogenetic analyses were performed using sequences from the available

type strains of each genus identified in addition to the sequences generated in this study. Alignments of DNA sequences were performed using the Mafft (Kato and Toh, 2008; <https://mafft.cbrc.jp/alignment/server/>) and manually corrected when necessary in MEGA version 7 (Tamura et al., 2013). Phylogeny based on Bayesian inference was performed in MrBayes version 3.2.1 (Ronquist et al., 2011), using two parallel runs with one cold and three heated chains each, using the number of generations needed to reach split frequencies of

≤ 0.01 and a sampling frequency set to every 100 generations. The posterior probability values were calculated after discarding the first 25% of the generated trees as burn-in. Resulting trees were plotted in FigTree v.1.4.2 (<http://tree.bio.ed.ac.uk/software/figtree/>). The substitution model was selected for each genus using the MEGA software. All sequences obtained were deposited in GenBank, access codes listed in Table S1.

2.4. Analysis of Endophytic Fungi Community

Analyses of the endophytic community were performed at genera and morphotypes levels, comparing fungal community in both plants, and between leaves and petioles tissues. To analyze the data a matrix of abundance was used, and plants with no endophyte recovered were removed from the analysis, as well as, those rare taxa that accomplished <5 percent of total abundance for genera and for morphotypes. The diversity index, total abundance, and richness were calculated based on the identified morphotypes and genera, without exclusions.

The community structure was assessed using Shannon-Weaver (H') diversity index (Shannon and Weaver, 1949), Simpson (1-D) index (Simpson, 1949), and Pielou (J) evenness (Pielou, 1975). Absolute abundance (N) and richness (S) also were estimated. Data were compared using two-way ANOVA for medians (Wilcox, 2012) once the data is non-parametric and no transformation normalized it. We also performed a non-metric multidimensional scaling (nMDS) analysis followed by analysis of similarity (ANOSIM) (Clarke, 1993), Permutational multivariate analysis of variance (PERMANOVA) (Anderson, 2001) using Bray-Curtis distance matrix and Indicator Value (IndVal) analysis (Dufrene and Legendre, 1997) to better elucidate taxa distribution and structures amongst plants. The indicator species are defined as the most characteristic species of each group, found mainly in a single group and present in most of the samples belonging to such group.

All the analyses and graphics were performed using R 3.4.4 (R Core Team, 2017) and packages *vegan* (Oksanen et al., 2018), *labdsv* (Roberts, 2016), *WRS2* (Mair et al., 2017) and *ggplot2* (Wickham, 2009). The sampling effort and richness based on both taxonomic levels were evaluated using rarefaction curves (Sanders, 1968).

2.5. Biological Activities of Endophytic Fungi

2.5.1. Antifungal Activity

The antifungal potential of the endophytic isolates was initially assessed by dual culture method (Badalyan et al., 2002) against the phytopathogens *Colletotrichum abscissum* (CA142), *Phyllosticta citricarpa* (LGMF06), and *Fusarium verticillioides* (LGMF1762). These pathogens were selected because of their importance in citrus (*C. abscissum* and *P. citricarpa*) and maize (*Fusarium verticillioides*) crops (Kotzé, 1981; Leslie and Summerell, 2006; Lima et al., 2011). The endophytic and pathogenic strains were previously cultured on PDA medium pH 5.8, for 7–21 days. One disc (6 mm) from the endophyte and one from phytopathogen were inoculated in opposite sides of the petri dish and incubated at 28°C for 10 days for *F. verticillioides*, 14 days for *C. abscissum* and 21 days for *P. citricarpa*. As negative control, only the phytopathogen was inoculated. The experiments were performed in triplicate.

The percentage of inhibition was calculated according to Quiroga et al. (2001), comparing the growth diameter of phytopathogen on pairing plates to control plates. The antifungal activity was classified as low (50–59%), moderate (60–69%), and high ($\geq 70\%$) according to the percentage of inhibition.

2.5.2. Antibacterial Activity

The antibacterial activity against clinical pathogens was evaluated using overlap method according to Mapperson et al. (2014) against methicillin-sensitive *Staphylococcus aureus* (MSSA) (ATCC 27213), methicillin-resistant *S. aureus* (MRSA) (ATCC 33591), *Klebsiella pneumoniae* producer of the enzyme KPC (*K. pneumoniae* carbapenemase) (BACHC-KPC), *Acinetobacter baumannii* (BACHAC-ABA), and *Pseudomonas aeruginosa* (ATCC 27853). All the pathogens were selected on the basis of their importance in human diseases and antibiotic resistance (CDC, 2013). The

bacteria were cultivated for 12 h at 37°C, and diluted according to the McFarland standard 0.5 scales. One 6 mm disk of each endophyte was inoculated into the center of the PDA plate and incubated at 28°C until the endophyte reaches more than 2 cm in diameter. The bacteria were then streaked with a cotton swab on the boards of these plates and incubated at 36°C for 24 h. The experiments were performed in duplicate, and saline (0.85%) was used as negative control. The analysis was based on the spectrum of action of endophytes: the number of pathogens inhibited; and intensity of inhibition classified as no activity (-), low (+), moderate (++), and high (+++) activity. The endophytes with higher activity and a large spectrum of action were selected for extract production.

2.6. Biological Activities from Extracts of Endophytic Fungi

2.6.1. Extracts Production

The endophytes selected in the biological activity assays were used for the preparation of extracts after fermentation in two liquid media, Malt extract (ME) (Schulz et al., 1995) and Czapeck yeast extract (CY) (Wiseman, 1975). The isolates were previously cultivated for 7 days on PDA, pH 5.8 at 28°C. Four mycelial discs (6 mm) were then added to 250 mL (500 mL Erlenmeyer flasks) of ME medium (Schulz et al., 1995) or CY medium (Wiseman, 1975), and incubated under agitation for 10 days (180 rpm, 28°C). The cultures were filtered-off on Whatmann filter and the water fraction was extracted with EtOAc (3 × 100 mL). The combined organics were evaporated in vacuo at 45°C and diluted in methanol at 10 mg/mL.

2.6.2. Activity of Extracts Against Phytopathogens

The extracts produced by the endophytes were evaluated against phytopathogens *P. citricarpa*, *C. abscissum*, and *F. verticillioides*. One hundred microliter of each extract were spread over the surface of PDA medium (48 × 12 mm plates), using the Drigalski spatula, and one mycelial disc of each phytopathogen was inoculated in the center of the plates. As the positive control, the fungicide Derosal (1.0 mg/mL) was used for *P. citricarpa* and *F. verticillioides* and the fungicide Carbendazim (0.1 mg/mL) was used for *C. abscissum*. Methanol was used as the negative control. Plates were incubated in

BOD at 28°C for 7 days for *F. verticillioides*, 10 days for *C. abscissum*, and 21 days for *P. citricarpa*. The growth inhibition was assessed comparing the diameter of the colony in the presence of treatment and controls (Savi, 2011). This experiment was performed in triplicate and the data were submitted to analysis of parametric variance (ANOVA) in GraphPad Prims v. 6.01.

2.6.3. Activity of Extracts Against the Clinical Pathogen

The antimicrobial activity of extracts produced by the endophytes was evaluated using the pathogens *S. aureus* (MSSA) (ATCC 27213) and methicillin-resistant *S. aureus* (MRSA) (ATCC 33591), *P. aeruginosa* (ATCC 27853), *A. baumannii* (BACHAC-ABA), *K. pneumoniae* (KPC) (BACHC-KPC), *Stenotrophomonas maltophilia* (BACHC-SMA), *Enterobacter cloacae* a producer of the enzyme VIM (Verona integron-encoded metallo- β -lactamase) (BACHC-VIM), and *Candida albicans* (ATCC 10231). The pathogens were inoculated previously on 7 mL of LB broth and incubated at 37°C, 180 rpm for 10 h. The culture was inoculated on TSB (Tryptone Soy Broth TM Medium) plate with a cotton swab and on these plates were placed discs impregnated with each 10 μ L of extract. The plates were incubated at 37°C for 24 h. As controls, one disc with a standard antibiotic with activity against each of the bacteria and pure methanol were used (CLSI, 2015; Savi et al., 2015). The antibacterial activity was evaluated by the measure of the inhibitory zone.

3. RESULTS

3.1. Isolation, Morphotyping, and Phylogenetic Analyses of Endophytic Fungi from *V. divergens* and *S. adstringens*

A high number (1,146) of cultivable endophytic fungal was recovered from *V. divergens* and *S. adstringens* in collections performed in January and June 2016. Based on the morphological analysis the isolates were grouped into 124 morphotypes, 116 of them were isolated from both plants, seven were isolated exclusively from *V. divergens*, and one was isolated exclusively from *S. adstringens*. Regarding tissue specificity, five morphotypes were recovered exclusively from leaf tissues (morphotypes 29, 31, 111, and 114 were recovered exclusively from *V. divergens* and morphotype 106 was isolated exclusively from *S. adstringens*) and three morphotypes were recovered only

from petiole (morphotypes 78 and 80 from *V. divergens* and morphotype 54 from *S. adstringens*) (Table S1).

The morphotypes were identified at genus and species level based on Bayesian phylogeny analysis using sequence of ITS region (Supplementary material: Figures S2–S27; Figure 2), and grouped at phylum, class and family level following the classification present at Mycobank and CABI databases (mycobank.org and speciesfungorum.org). The majority of the isolates belong to Phylum Ascomycota (95.6% of isolates from *S. adstringens* and 96.7% from *V. divergens*) within two classes: Dothiomycetes and Sordariomycetes. The dominant class in the phylum Ascomycota was Sordariomycetes corresponding to 61% of the isolates obtained from *S. adstringens* and 63% from *V. divergens*. The dominant orders in Sordariomycetes class were Diaporthales (representing 46.6% of isolates from *S. adstringens* and 43.4% from *V. divergens*), Xylariales (10.9% from *S. adstringens* and 9.8% from *V. divergens*), and Glomerellales (2% from *S. adstringens* and 4% from *V. divergens*) (Table 1). The remaining morphotypes belong to the Phylum Basidiomycota, representing 0.7% of isolates from *S. adstringens* and 0.9% from *V. divergens*, within Agaricomycetes class. Seven morphotypes were identified at the family level because they did not cluster with any type species of Xylariaceae family, and possibly belong to three new genera in this family (Table 1; Figure 2).

In addition, we also identified 48 taxa (Table S1), from these, 16 isolates did not cluster with any type strain of *Diaporthe* (Figure S11), *Epicoccum* (Figure S14), *Fusarium* (Figure S16), *Hypoxylon* (Figure S17), *Pestalotiopsis* (Figure S23), *Phyllosticta* (Figure S25), *Pseudofusicoccum* (Figure S26), *Rousoella* (Figure S27), and *Phaeophleospora* genera in the phylogeny analysis and may represent new species into these genera, however multilocus and morphological analyses are required for species description. Nine morphotypes (~3%) did not grow in different culture media after few replications (morphotypes 8, 42, 72, 94, 95, 96, and 99), probably due to the growth-dependence of host tissues, and were characterized only at Kingdom level (fungi).

3.2. Community Analysis of Endophytic Fungi from *V. divergens* and *S. adstringens*

In June 2016, we isolated 777 (IF: 72%) and 339 (IF: 49%) endophytic fungi from *V. divergens* and *S. adstringens*, respectively (Table S1). Concerning of

777 isolates from *V. divergens*, 367 (IF: 72%) were isolated from leaves and 410 (IF: 77%) were isolated from petioles. For the isolates obtained from *S. adstringens* 174 (IF: 45%) were obtained from leaves and 165 (IF: 43%) were obtained from petioles (Tables S1, S2).

The analyses of genera composition showed that Diaporthe was the dominant genus in both plants *V. divergens* (51.8% of isolates from petioles and 51.4% from leaves) and *S. adstringens* (49.3% of isolates from petioles and 49.7% from leaves). The second most frequent genus was *Phyllosticta* (5.1 and 19.1% of isolates from petioles and leaves of *V. divergens* and 6.8 and 11.8% from petioles and leaves of *S. adstringens*) followed by *Neofusicoccum* (5.5 and 2.2% from petioles and leaves of *V. divergens* and 6.8 and 7.7% from petioles and leaves of *S. adstringens*). The morphological characteristics from the dominant groups are illustrated in the Figure S1. The genera *Alternaria*, *Coniochaeta*, *Neopestalotiopsis*, and *Paraphaeosphaeria* (obtained from leaves and petioles), *Daldinia* and *Efibula* (isolated only from petioles), and *Roussoella* (from leaves) were recovered exclusively from *V. divergens* and *Acrocalymma* were isolated exclusively from leaves of *S. adstringens* (Figure 3).

Community structuring analyses based on genera showed no difference between plant species or plant tissues sampled (Table 2, Figure S28) as seen in PERMANOVA ($p > 0.05$) and nMDS (Figure 4, Tables S3, S4). On the other hand, the analysis of morphotypes composition (a lower taxonomic identification when compared to genera) presented higher abundance and richness for endophytic isolated from *V. divergens* (Table 2; Figures S28–S30) than from *S. adstringens*, and differences in community composition regarding to *V. divergens* plant tissues as shown by PERMANOVA ($p < 0.05$) and nMDS—ANOSIM (Figure 4B). No significance was observed in the diversity indexes (H' , 1-D, J) for genera and morphotypes analyze in *V. divergens* and *S. adstringens* (Table 2).

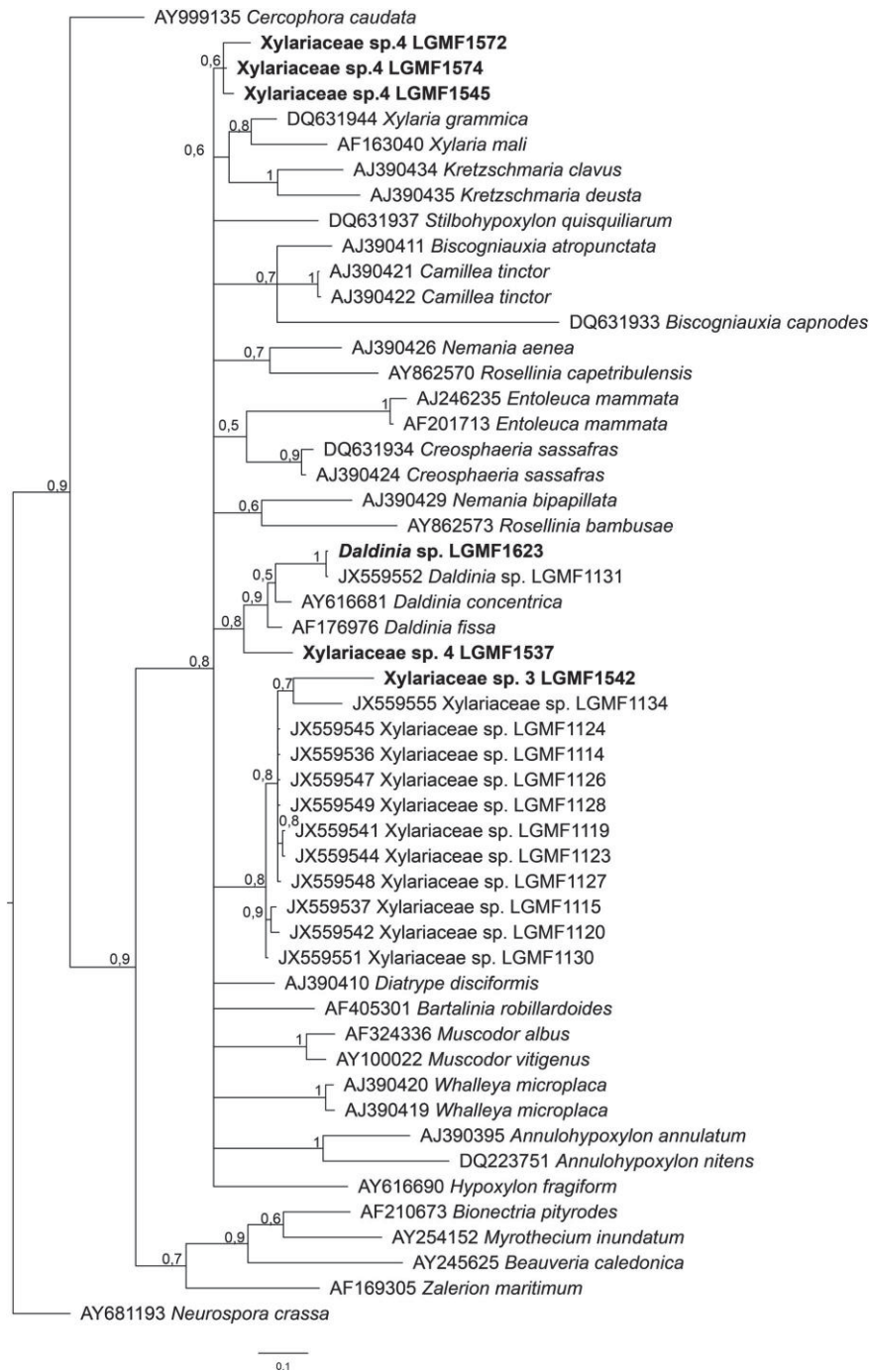


FIGURE 2. Bayesian phylogenetic tree based on ITS partial sequence of LGMF1572, LGMF1574, LGMF1545, LGMF1613, LGMF1537, and LGMF1542 (bold) sequence of genera of Xylariaceae family. The data matrix had 52 taxa and 416 characters. The tree was rooted to: *Neurospora crassa* (AY681193). Scale bar shows 0.1 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

TABLE 1 | Taxonomic classification of endophytic fungi isolated from *Stryphnodendron adstringens* and *Vochysia divergens*.

Taxa						
Class	Order	Family	Genera	Species	Morphotype	
Dothideomycetes (36% Sa; 33% Vd)	Pleosporales	Lophiostomataceae	<i>Acrocalyma</i>	<i>Acrocalymma medigans</i>	106	
		Didymellaceae		<i>Didymella</i>	<i>Didymella</i> sp.	32, 16
				<i>Epicoccum</i>	<i>Epicoccum</i> sp.1	43, 98,
					<i>Epicoccum</i> sp.2	61, 100
					<i>Epicoccum</i> sp.	45, 97,
		Corynesporascaceae	<i>Corynespora</i>	<i>Corynespora cambrensis</i>	20	
		Pleosporaceae	<i>Alternaria</i>	<i>Alternaria alternata</i>	33	
			<i>Curvularia</i>	<i>Curvularia</i> sp.	1	
		Didymosphaeriaceae	<i>Paraphaeosphaeria</i>	<i>Paraphaeosphaeria</i> spp.	110, 111	
		Thyridariaceae	<i>Roussoella</i>	<i>Roussoella</i> sp.1	114	
	Capnodiales	Mycosphaerellaceae	<i>Phaeophleospora</i>	<i>Phaeophleospora</i> sp.1,	82	
				<i>Phaeophleospora</i> sp.2	109, 118	
	Botryosphaeriales	Phyllostictaceae		<i>Phyllosticta</i> sp.1	107, 108,	
				<i>Phyllosticta</i> sp.	116	
		Botryosphaeriaceae		<i>Pseudofusicoccum</i>	<i>Pseudofusicoccum</i> sp.1	3
				<i>Pseudofusicoccum stromaticcum</i>	119	
		<i>Neofusicoccum</i>	<i>Neofusicoccum brasiliense</i>	7, 67		
		<i>Lasiodiplodia</i>	<i>Lasiodiplodia</i> spp.	123, 40, 5		
Sordariomycetes (61% Sa; 63% Vd)	Xylariales	Diatrypaceae	Diatrypaceae sp.	Diatrypaceae sp.	24	
		Xylariaceae		Xylariaceae sp.3,	18	
				Xylariaceae sp.4,	25, 64, 66	
				Xylariaceae sp.5	9	
		Hypoxyloaceae		<i>Daldinia</i>	<i>Daldinia</i> sp.1	31
				<i>Hypoxylon</i>	<i>Hypoxylon</i> sp.1	6
	Glomerellales	Apiosporaceae	<i>Nigrospora</i>	<i>Nigrospora hainanensis</i>	28, 89	
		Glomerellaceae	<i>Colletotrichum</i>	<i>Colletotrichum</i> spp.	62, 71, 90, 117, 47, 76, 84, 86,	
	<i>Colletotrichum siamense</i>			22, 36, 74, 93, 104		
	Sordariales	Coniochaetaceae	<i>Coniochaeta</i>	<i>Coniochaeta nepalica</i>	68	
	Diaporthales	Diaporthaceae		<i>Diaporthe</i>	<i>Diaporthe</i> spp.	29, 37, 58, 69, 80, 113, 4, 46, 10, 83, 103, 112, 120, 121, 49, 52, 65, 2, 124, 11, 39
				<i>Diaporthe</i> sp.1	122, 101, 102	
				<i>Diaporthe</i> sp.2	12, 13, 14	
				<i>Diaporthe</i> sp.3	30, 15, 19	
				<i>Diaporthe</i> sp.4	21, 81	
				<i>Diaporthe</i> cf. <i>heveae</i> 1	56, 60, 91, 92, 63, 70, 54	
				<i>Diaporthe ocoteae</i>	55	
				<i>Diaporthe schini</i>	17, 120	
<i>Fusarium</i> sp.1				26, 38		
<i>Fusarium</i> sp.2				27, 44		
<i>Fusarium pseudocircinatum</i>				47		
<i>Fusarium</i> spp.				23, 48, 57, 51, 53,		
Hypocreales	Nectriaceae		<i>Fusarium</i>	<i>Fusarium</i> sp.1	26, 38	
				<i>Fusarium</i> sp.2	27, 44	
				<i>Fusarium pseudocircinatum</i>	47	
			<i>Fusarium</i> spp.	23, 48, 57, 51, 53,		

	Amphisphaeriales	Pestalotiopsidaceae	<i>Pestalotiopsis</i>	<i>Pestalotiopsis</i> sp.1	59, 85, 87, 88, 115
			<i>Neopestalotiopsis</i>	<i>Pestalotiopsis</i> spp.	34, 75, 77, 35
				<i>Neopestalotiopsis</i> sp.	50
Agaricomycetes (0.7% Sa; 0.9% Vd)	Polyporales	Meruliaceae	<i>Bjerkandera</i>	<i>Bjerkandera</i> sp.	41, 72, 73
		Phanerochaetaceae	<i>Efibula</i>	<i>Efibula</i> sp.	78

Vd, *Vochysia divergens*; *Sa*, *Stryphnodendron adstringens*.

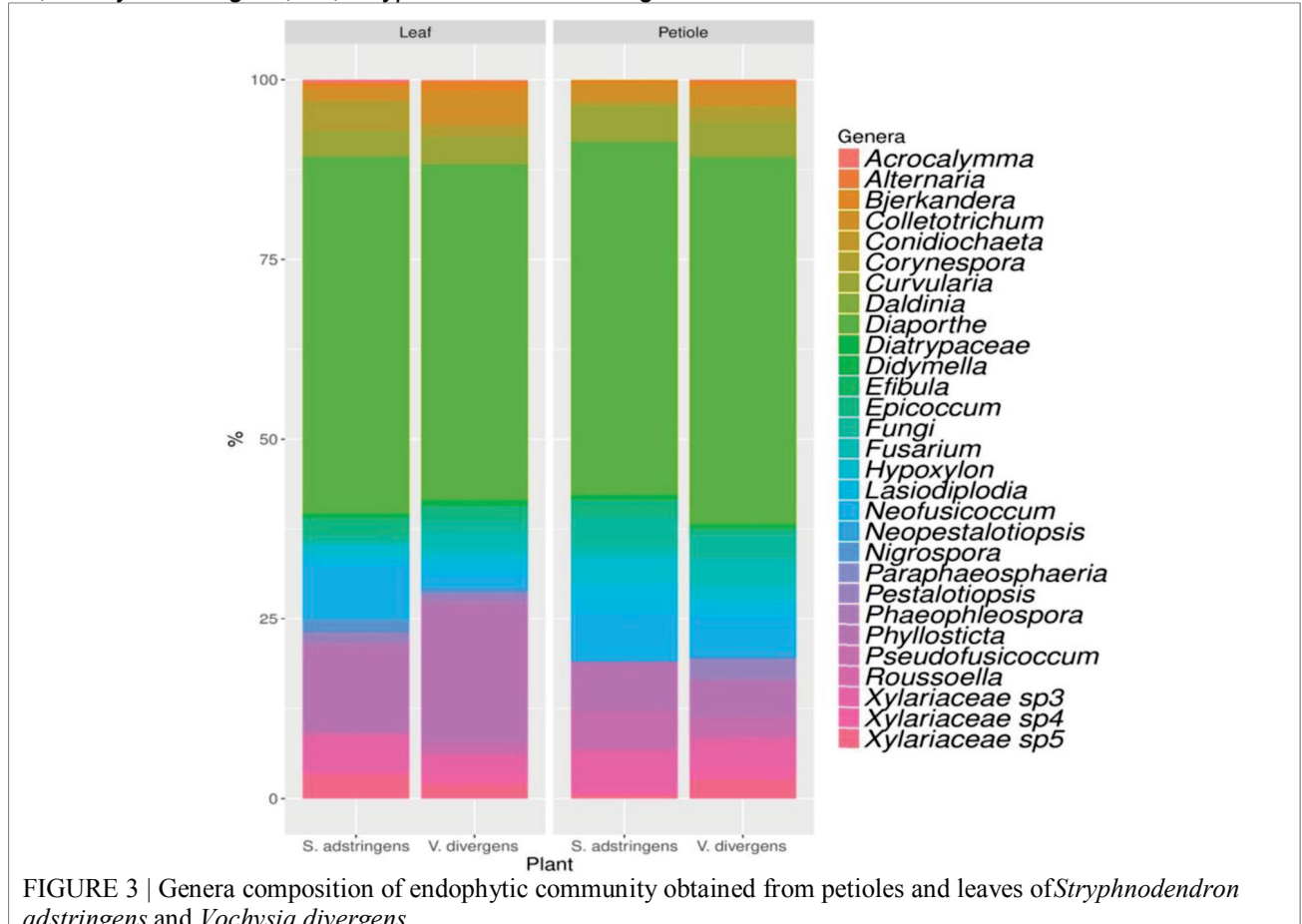
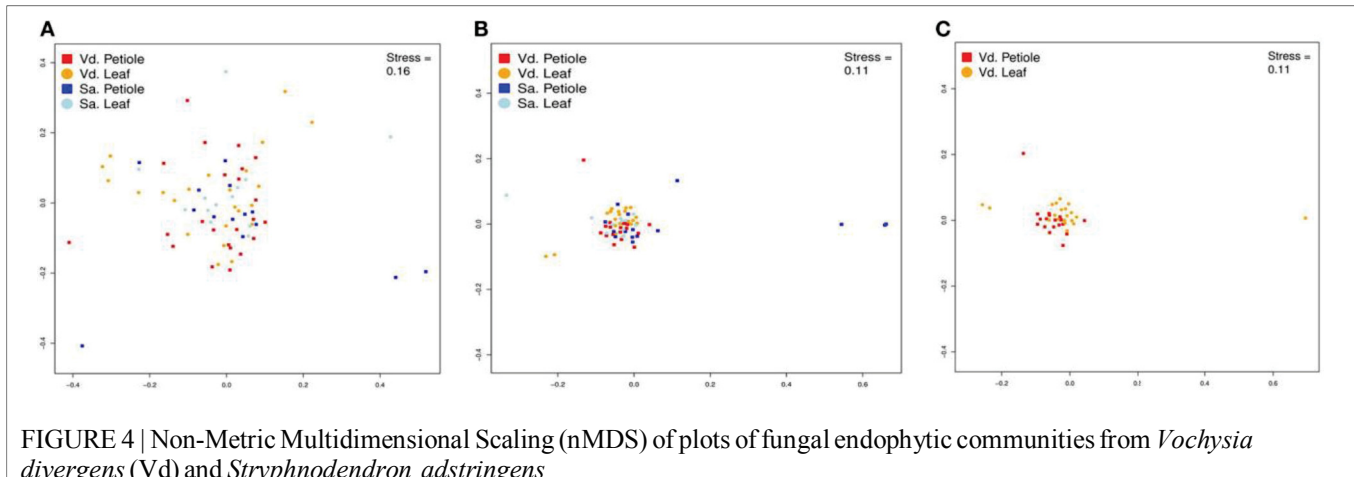


TABLE 2 | Diversity index and descriptive data for morphotypes and genus analyzed.

Plant (1-D)	Tissues J	Abundance	Richness H	Simpson		
DIVERSITY INDEX PER MORPHOTYPE						
<i>V. divergens</i>	Petiole	22.56 ± 11.91*	14.28 ± 6.35*	3.41 ± 1.02	0.85 ± 0.22	1.37 ± 0.04
	Leaf	17.85 ± 11.51*	10.60 ± 6.30*	2.79 ± 1.25	0.75 ± 0.28	1.33 ± 0.11
<i>S. adstringens</i>	Petiole	9.80 ± 5.57	7.13 ± 4.10	2.33 ± 1.23	0.69 ± 0.31	1.38 ± 0.05
	Leaf	13.33 ± 5.60	8.33 ± 3.26	2.66 ± 0.96	0.76 ± 0.25	1.34 ± 0.11
DIVERSITY INDEX PER GENUS						
<i>V. divergens</i>	Petiole	17.52 ± 11.99	6.35 ± 3.68	1.85 ± 0.88	0.59 ± 0.22	1.12 ± 0.22
	Leaf	13.29 ± 11.24	5.13 ± 3.17	1.64 ± 0.76	0.56 ± 0.21	1.17 ± 0.17
<i>S. adstringens</i>	Petiole	10.80 ± 6.79	4.47 ± 2.50	1.51 ± 0.90	0.51 ± 0.28	1.18 ± 0.14
	Leaf	11.27 ± 7.40	4.27 ± 2.55	1.34 ± 0.99	0.44 ± 0.31	1.10 ± 0.17

H' , Shannon-Weaver; J, Pielou evenness; *Significate differences between plants.



3.3. Biological Activity

3.3.1. Screening of Antimicrobial of Endophytic

Of the 124 morphotypes, 117 isolates were used in the screening for antimicrobial analysis using dual culture, since 7 morphotypes did not grow under the culture conditions used in the present study.

In the screening of antifungal activity among the 117 isolates evaluated *Diaporthe* sp. LGMF1530, *Diaporthe* cf. *heveae* LGMF1631, *Colletotrichum siamense* LGMF1604, *Fusarium* sp. LGMF1630, and *Epicoccum* sp. LGMF1641 inhibited more than 60% the mycelial growth of *P. citricarpa* and *C. abscissum* in the dual culture assay (Figure 5A) and were selected for the extract production. None of the isolates was able to inhibit the fungus *F. verticillioides* (Table S6).

The endophytes were also screened for their antimicrobial activity against clinical pathogens based on the spectrum and intensity of action. The isolates *Phaeophleospora* sp.2 LGMF1513, *Epicoccum* sp.1 LGMF1598, and *Epicoccum* sp.2 LGMF1600 showed high activity (+++) against *S. aureus* (MSSA and MRSA). The isolates *Diaporthe* sp. LGMF1548 and LGMF1614, *Diaporthe* cf. *heveae* LGMF1631, *Fusarium* sp. LGMF1630, and *Hypoxylon* sp.1 LGMF1613 showed broad spectrum with moderate (++) to high (+++) activity against *S. aureus* (MSSA and MRSA), *P. aeruginosa* and *A. baumannii*. The isolates *Neofusicoccum brasiliense* LGMF1535 and *Diaporthe* sp. LGMF1583 showed moderate (++) to high (+++) activity against *S. aureus* (MSSA and MRSA), *P. aeruginosa*, *A. baumannii*, and *K. Pneumoniae* (KPC)

(Table 3; Table S7). The above-mentioned isolates were selected for secondary metabolites production in different culture media.

3.3.2. Antifungal Activity of Extracts Produced by the Selected Endophytes Against Phytopathogens

Eleven endophytic fungi were cultured in two different media, and seven of them produced extracts that inhibited the mycelial growth of *P. citricarpa* (Figure 5B), especially the extracts from strain *Diaporthe cf. heveae* LGMF1631 cultured in ME (IG: 88%) and CY (IG:50%) media, and extracts of *Diaporthe sp.* LGMF1530 (IG:42%) and *Epicoccum sp.1* LGMF1598 (IG:45%). Extracts from four isolates inhibited the mycelial growth of *C. abscissum* (Figure 5B), highlighting the extracts from *Diaporthe cf. heveae* LGMF1631 produced in ME medium (Inhibition growth—IG: 72%) and in CY medium (IG: 59%) and the extract from *Epicoccum sp.2* LGMF1600 in ME medium (IG: 40%). In the other hand, the extracts from *Diaporthe cf. heveae* LGMF1631 (IG: 50%) and *Hypoxylon sp.1* LGMF1613 (IG: 45%) showed moderate activity against *F. verticillioides* (Figure 5B).

3.3.3. Antimicrobial Activity of extracts Produced by the Selected Endophytes Against Clinical Pathogens

All extracts inhibited the growth of at least one clinical pathogen and the best results were obtained with extracts produced in ME medium (Table S8). The extracts from *Diaporthe sp.* LGMF1548 caused the highest inhibition zone against four clinical pathogens: *S. aureus* (MSSA) (23 mm), *S. maltophilia* (16 mm), *K. pneumoniae* (KPC) (18 mm), and *E. cloacae* (18 mm). Extract produced by *Epicoccum sp.1* LGMF1598 showed equivalent inhibition zone against *S. maltophilia* (16 mm), and, curiously, it was the only extract that showed high activity against *A. baumannii* (15 mm) (Table 3; Table S8). The extract produced by *N. brasiliense* LGM1535 presented the largest inhibition zone (23 mm) against Methicillin-resistant *S. aureus* (MRSA) growth.

The second best result (17 mm) against MRSA was observed in the treatment with the extract of the isolate *Diaporthe sp.* LGMF1583, that also showed the highest inhibition zone against *C. albicans* (19 mm) and *P. aeruginosa* (17 mm). Table 3 showed only the highest inhibition values against each pathogen, the complete data is in the Table S8.

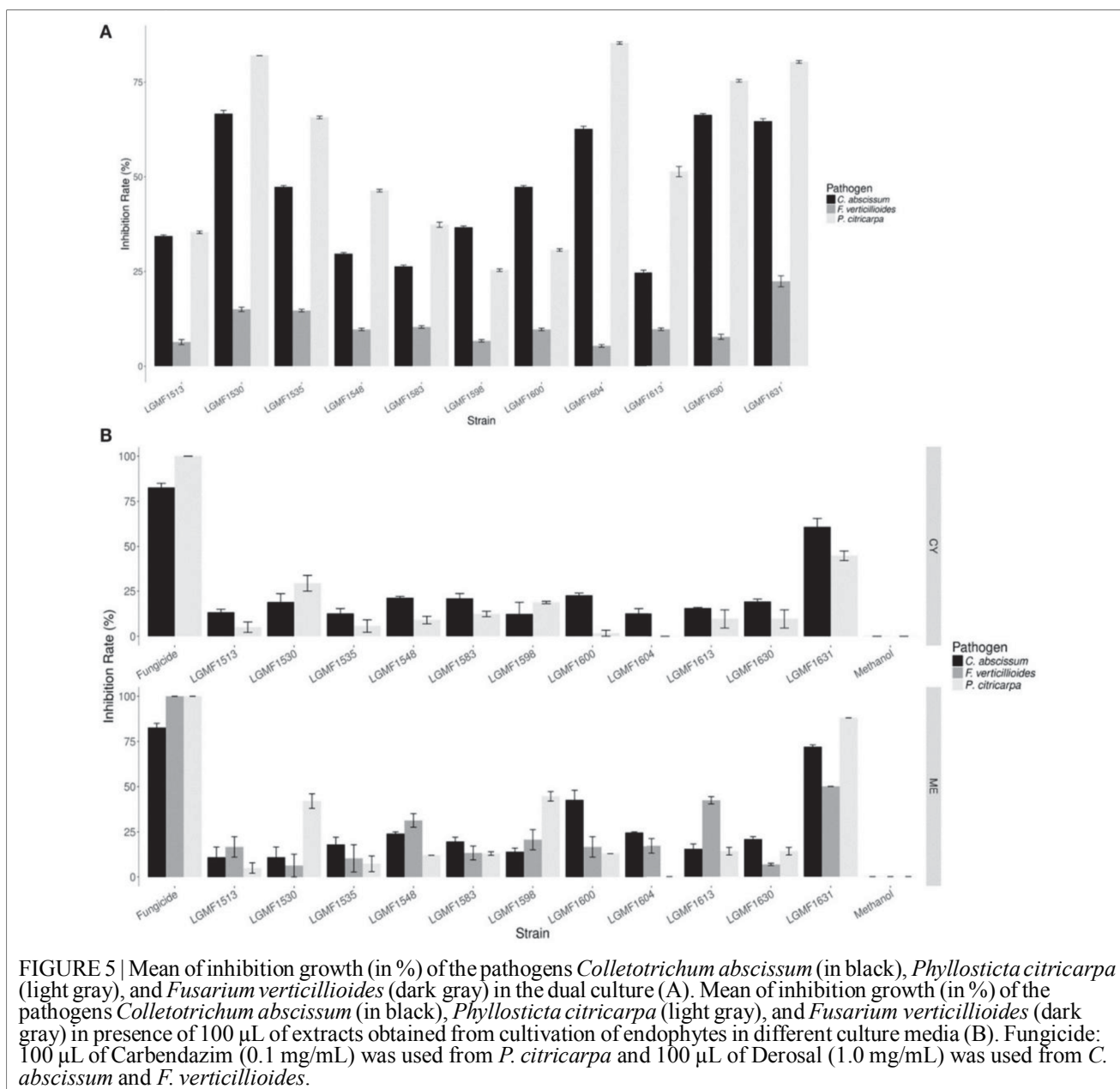


TABLE 3 | Selected results of antimicrobial activity of the extracts produced by endophytic fungi in malt extract medium against clinical pathogens.

Taxon	Endophytic Strain	Number of pathogens inhibited in Screening	Pathogens ¹							
			MRSA	MSSA	<i>S. maltophilia</i>	KPC	<i>E. cloacae</i>	<i>A. baumannii</i>	<i>P. aeruginosa</i>	<i>C. albicans</i>
<i>Colletotrichum siamense</i>	LGMF1604	<u>2/5</u>	<u>15 ± 2</u>	9.5 ± 0.7	11 ± 0.7	10 ± 1.4	10 ± 0	0	9.5 ± 0.7	10 ± 2
	LGMF1530	<u>2/5</u>	<u>15 ± 2</u>	10 ± 1.4	11 ± 0.7	11 ± 0	14 ± 1.7	0	10 ± 0.7	12 ± 0
<i>Diaporthe</i> sp.	LGMF1548	4/5	14 ± 1.4	<u>23 ± 0.7</u>	<u>17 ± 3.5</u>	<u>18 ± 0</u>	<u>19 ± 1.4</u>	0	<u>16 ± 0.7</u>	9.5 ± 0.7
	LGMF1583	<u>5/5</u>	<u>17 ± 2</u>	<u>23 ± 2.8</u>	14 ± 1.4	14 ± 0.7	14 ± 0.7	0	<u>16 ± 0</u>	<u>19 ± 1.4</u>
<i>Diaporthe</i> cf <i>hevea</i>	LGMF1631	5/5	10 ± 0	11 ± 1.4	12 ± 0.7	11 ± 1.4	<u>16 ± 2.8</u>	0	0	13 ± 0.7
	LGMF1598	3/5	11 ± 0.7	11 ± 0.7	<u>16 ± 0.7</u>	14 ± 1.4	11 ± 1.4	0	9 ± 0	11 ± 0.7
<i>Epicoccum</i> sp.1	LGMF1600	3/5	9.5 ± 0.7	9.7 ± 0.7	<u>15 ± 1.4</u>	9.5 ± 0.7	10 ± 0	<u>15 ± 0.7</u>	10 ± 0	11 ± 1.4
	LGMF1535	<u>5/5</u>	<u>23 ± 2</u>	<u>20 ± 0</u>	14 ± 0.7	<u>16 ± 0.7</u>	<u>16 ± 1.4</u>	0	<u>17 ± 0.7</u>	14 ± 0
<i>Neofusicoccum brasiliense</i>		<u>5/5</u>								
		<u>4/5</u>								
		<u>2/5</u>								

Notes: *The antibacterial screening refer to the number of clinical pathogens inhibited/the number of pathogens evaluated, the full data is in supplementary information Table S6. MRSA, Methicillin-resistant *Staphylococcus aureus*; MSSA, methicillin-sensitive *S. aureus*; *S. maltophilia*, *Stenotrophomonas maltophilia*; KPC, *Klebsiella pneumoniae* producer of KPC; *E. cloacae* VIM, *Enterobacter cloacae* producer of VIM; *A. baumannii*, *Acinetobacter baumannii*; *P. aeruginosa*, *Pseudomonas aeruginosa*; *C. albicans*, *Candida albicans*. All the highest inhibition zone for each pathogen are underlined. The best result for each pathogen is in bold. 0, No inhibition zone.

4. DISCUSSION

In order to verify if the peculiar environmental conditions found in Pantanal and Cerrado can influence the endophytic community in these biomes, we evaluated the diversity and composition of endophytic fungi in two resilient and dominant plants found in these regions, *V. divergens* of the Pantanal and *S. adstringens* of the Cerrado. Our data revealed that *V. divergens* and *S. adstringens* are hosts of high diversity of endophytic fungi, belonging to 23 known genera, and three possible new genera in the Xylariaceae family. The number of isolates (genera and morphotypes) found in our study is larger than previous reports (Carvalho et al., 2012; Hokama et al., 2017), which may be a result of the number of evaluated plants or the region where the collections were carried out. Hokama et al. (2017) studied the endophytes of *V. divergens* found in another region of the Pantanal, denominated Rio Negro. The authors also obtained isolates of genera *Colletotrichum*, *Diaporthe*, and *Phyllosticta* and strains belonging to possible new genera of the family Xylariaceae. However, in the present work we report for the first time the genera *Acrocalymma*, *Alternaria*, *Bjerkandera*, *Coniochaeta*, *Corynespora*, *Curvularia*, *Didymella*, *Efibula*, *Epicoccum*, *Fusarium*, *Hypoxyton*, *Lasiodiplodia*, *Neopestalotiopsis*, *Paraphaeosphaeria*, *Phaeophleospora*, and *Rousoella* as endophytes of *V. divergens* (Table S1; Figures S1–S3, S6–S8, S11–S13, S15–S17, S19, S21, S23, S26). With the results obtained in this work, we are increasing knowledge about the endophytic community of these important medicinal plants.

Considering the limitations of the ITS sequences to identify some isolates at the species level, we analyzed the endophytic community using two matrix data, based on the classification of genera and morphotypes. As expected, the lower taxonomic level (morphotype) resulted in a higher resolution in the community structure. Therefore, correct identification at lower levels is of great importance for the assessment of community structure (Singh et al., 2017). The variation of the composition of the morphotypes among the analyzed hosts, *V. divergens* and *S. adstringens*, may be associated with the analyzed plant or even the environmental conditions. Pantanal plants can be severely damaged by flooding, however, *V. divergens* is highly adapted and only a short leaf falls period is reported (Da cunha Nunes et al., 2000). In this context, the endophytic community of the leaves of *V. divergens* do not change seasonally, providing a longer interaction between the endophytic community and the plant, both of which are adapted to the environmental conditions. In contrast, the leaves of plants

found in the Cerrado can be destroyed by flames or damaged by the hot air flow (Silvério et al., 2015; Dodonov et al., 2017), which results in a shorter interaction time between the community and the plant. In addition, the region of analysis in the Cerrado is severely affected by anthropological action. Certainly, these characteristics impact the endophytic community in these biomes and may play a role in the differences observed for the composition of the morphotypes between *V. divergens* and *S. adstringens*. The community also differs among the tissues from *V. divergens* analyzed, not easily visible in the results of nMDS, but confirmed by ANOSIM (Figure 4; Tables S4, S5). The main difference in the community structure comes from a higher abundance and richness of endophytes in petioles, which may be result of a specialized endophytic microbiota (Persoh, 2015; Correia et al., 2017).

Diaporthe was the dominant genus in both plants (Figure 3; Table S1). This genus has also been described as dominant in *S. adstringens* by Carvalho et al. (2012) and is widely distributed in different plants of several biomes, such as the Pantanal (Hokama et al., 2017; Pietro-Souza et al., 2017), Mangrove forest (de Souza Sebastianes et al., 2013), Atlantic Rainforest (Correia et al., 2017), Cerrado and Caatinga (Ferreira et al., 2012; Lisboa et al., 2013). The ability of *Diaporthe* species to colonize different plants may result from the produced metabolites that bypass the plants defenses, or even by acting on host development and defense against plant pathogens (Nicoletti and Fiorentino, 2015; Santos et al., 2016; Tahir et al., 2017). Associated with the high frequency of isolation, we also found new species of *Diaporthe*, named as *Diaporthe* sp.1 (clade 1), *Diaporthe* sp. 2 (clade 2), (Figure S11). Gomes et al. (2013) also reported a large number of *Diaporthe* isolates as new species, suggesting medicinal plants in Brazil as a repository for this genus. The description of new species of *Diaporthe* is carried out based on the polyphasic approach, and will be carried out in a future study.

In order to associate economic value with biodiversity, bioprospecting studies have reported the biotechnological potential of endophytes against a large number of pathogens (Schulz et al., 2002; Gathage et al., 2016; Larran et al., 2016; Li et al., 2016; Hokama et al., 2017; Parpinelli et al., 2017). In this context, we investigated the antimicrobial potential of the endophytes of *V. divergens* and *S. adstringens*. Extracts produced by *Diaporthe* cf. *heveae* LGMF1631 inhibited almost 90% the mycelial growth of *P. citricarpa* the causal agent of Citrus Black Spot (CBS), a disease that affects fruits and leaves of several citrus hosts (Kotzé, 1996). The control of CBS in Brazil is based on fungicides applications, such as Derosal, and on cultural management

(Kotzé, 1996; Baldassari et al., 2006). However in fruits destined to the production of juice for export, the application of the fungicide Derosal is restricted (EPA, 2012; Fundecitrus, 2015). *Diaporthe* cf. *heveae* LGMF1631 also caused excellent inhibition (72%) of the mycelial growth of *C. abscissum*, the epidemiological agent of Post-bloom Fruit Drop (PFD) (Pinho et al., 2015; Silva et al., 2016). In favorable climatic conditions, frequent rainy days during the bloom period, PFD can drastically reduce citrus production, reaching approximately 80% (Lima et al., 2011). Thus, the use of secondary metabolites produced by *Diaporthe* endophytic strains, in a biological control scenario, may be an alternative to reduce the use of fungicides in the control of citrus diseases such as CBS and PFD (Santos et al., 2016; Tonial et al., 2017).

The antimicrobial tests also revealed a high potential of endophytes to produce active secondary metabolites with broad spectrum against clinical pathogens, especially those produced by *N. brasiliense* LGMF1535, *Diaporthe* sp. LGMF1548 and LGMF1583 (Table 3). Significant results were obtained against MRSA (a gram-positive) and KPC (a gram-negative), two bacteria with resistance to β -lactam antibiotics, cephalosporins, monobactams, and carbapenems, respectively (Queenan and Bush, 2007). There is an urgency in finding new compounds to contain the global pandemic involving resistance to gram-positive pathogens to several antibiotics (including MRSA as the main species), and which is currently one of the greatest threats to human health. In patients with bloodstream infection, for example, the range of antibiotic resistance can reach up to 82% (CDC, 2013; Ventola, 2015; World Health Organization, 2018).

The species belonging to the genera *Diaporthe* and *Neopestalotiopsis* are described as producing a large number of compounds with activity against several clinical pathogens, such as *Escherichia coli*, *S. aureus*, *Enterococcus hirae*, *Micrococcus luteus*, and *Salmonella typhi* (Specian et al., 2012). Thus, the exploration of metabolites produced by endophytes belonging to these genera and obtained from unexplored environments may represent a source for new compounds (Monciardini et al., 2014), and the extracts of the strains *N. brasiliense* LGMF1535, *Diaporthe* sp. LGMF1548 and LGMF1583 will be further explored in the chemical characterization.

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Alternaria alternantherae (KC584179). Scale bar shows 0.003 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S4- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1627, LGMF1578 and LGMF1579 (bold) identified as *Bjerkandera* sp. and sequences of all accepted species from *Bjerkandera*. The tree was rooted to *Phanerochaete chrysosporiu* (HQ188436). Scale bar shows 0.03 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S5- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1559, LGMF1580 LGMF1586, LGMF1621, LGMF1625, LGMF1636, LGMF1595 and LGMF1604 (bold) identified as *Colletotrichum gloeosporioides* sensu lato and sequences of all species of *Colletotrichum gloeosporioides* species complex. The data matrix had 60 taxa and 407 characters. The tree was rooted to *Colletotrichum boninense* (JX010292). Scale bar shows 0.03 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S6- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1571, LGMF1577, LGMF1592, and LGMF1522 (bold) identified as *Colletotrichum boninense* sensu lato and sequences of all accepted species from *Colletotrichum boninense* species complex. The data matrix had 26 taxa and 312 characters. The tree was rooted to *Colletotrichum gloeosporioides* (JQ005152). Scale bar shows 0.002 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S7- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1575 (bold) identified as *Coniochaeta nepalica*. The data matrix had 30 taxa and 488 characters. The tree was rooted to *Phialemonium obovatum* (HE610365). Scale bar shows 0.04 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S8- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1619 (bold) identified as *Corynespora cambrensis* and sequences of all accepted species from *Corynespora* genus. The data matrix had 11 taxa and 409 characters. The tree was rooted to *Cylothyriella rubronotata* (KX650544). Scale bar shows 0.04 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S9- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1533 (bold) identified as *Curvularia* sp. and sequences of all accepted species from *Curvularia* genus. The data matrix had 47 taxa and 491 characters. The tree was rooted to *Setosphaeria turcica* (HF934950). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S10- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1623 (bold) identified as *Daldinia* sp. and sequences of all accepted species from *Daldinia* genus. The data matrix had 69 taxa and 522 characters. The tree was rooted to *Hypoxylon fragiforme* (AY616690). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S11- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1610, LGMF1612, LGMF1614, 1538, LGMF1539, LGMF1540, LGMF1615, LGMF1616, LGMF1541, LGMF1618, LGMF1620, LGMF1548, 1549, LGMF1554, LGMF1629, LGMF 1561, LGMF1563, LGMF1631, LGMF1632, LGMF 1565, LGMF1567, LGMF 1569, LGMF 1633, LGMF1573, LGMF1576, LGMF1635, LGMF1583, LGMF1639, LGMF1593, LGMF1594, LGMF1601, LGMF1602, LGMF1508, LGMF1517, LGMF1606, LGMF1525, LGMF1526, LGMF1530, LGMF1531, LGMF1532, and LGMF1526 (bold) sequences of all accepted species from *Diaporthe* genus. The data

matrix had 383 taxa and 537 characters. The tree was rooted to *Diaporthella corylina* (KC343004). Scale bar shows 0.04 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S12- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1617 (bold) identified as *Didymella* sp. and sequences of all accepted species from *Didymella*. The data matrix had 60 taxa and 497 characters. The tree was rooted to *Epicoccum nigrum* (FJ426996). Scale bar shows 0.003 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 51

Figure S13- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1581 (bold) identified as *Efibula* sp. and sequences of all accepted species from *Efibula* genus. The data matrix had 8 taxa and 615 characters. The tree was rooted to *Ceraceomyces serpens* (KP135030). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain R: representative strain. 52

Figure S14- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1603, LGMF1628, LGMF1641, LGMF1598 and LGMF1557 (bold) identified as *Epicoccum* sp. and sequences of all accepted species from *Epicoccum* genus The data matrix had 35 taxa and 455 characters. The tree was rooted to *Didymella americana* (FJ426974). Scale bar shows 0.002 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 53

Figure S15- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1544 (bold) identified as *Diatrypaceae* sp. and sequences of all accepted genera from *Diatrypaceae* family The data matrix had 110 taxa and 641 characters. The tree was rooted to *Whalleya microplaca* (AJ4390420). Scale bar shows 0.002 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 54

Figure S16- Bayesian phylogenetic tree based on EF partial sequence of LGMF1546, LGMF1553, LGMF1590, LGMF1547 and LGMF1558 (bold) identified as *Fusarium* sp. and sequences of all accepted species from *Fusarium* genus The data matrix had 97 taxa and 680 characters. The tree was rooted to *Fusarium oxysporum* (NRRL22902). Scale bar shows 0.008 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 55

Figure S17- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1613 (bold) identified as *Hypoxylon* sp. and sequences of all accepted species from *Hypoxylon* genus The data matrix had 35 taxa and 369 characters. The tree was rooted to *Nemania serpens* (FN428829). Scale bar shows 0.04 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 56

Figure S18- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1609, LGMF1555 and LGMF1534 (bold) identified as of *Lasiodiplodia* sp. and sequences of all accepted species from *Lasiodiplodia* genus The data matrix had 34 taxa and 401 characters. The tree was rooted to *Spencermartinsia viticola* (AY905554). Scale bar shows 0.004 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 57

Figure S19- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1535 and LGMF1634 (bold) identified as *Neofusicoccum brasiliense* and *Neofusicoccum* sp. The data matrix had 30 taxa and 505 characters. The tree was rooted to *Botryosphaeria dothidea* (AY259092). Scale bar shows 0.005 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 58

Figure S20- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1562 59

(bold) identified as *Neopestalotiopsis* sp. and sequences of all accepted species from *Neopestalotiopsis* genus. The data matrix had 59 taxa and 480 characters. The tree was rooted to *Pestalotiopsis trachicarpicola* (JQ845947). Scale bar shows 0.005 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

Figure S21- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1622 and LGMF1591 (bold) identified as *Nigrospora hainanensis* and sequences of all accepted species from *Nigrospora* genus. The data matrix had 27 taxa and 500 characters. The tree was rooted to *Arthrinium malaysianum* (KX986096). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 60

Figure S22- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1515 and LGMF1516 (bold) identified as *Paraphaeophaeria* sp. and sequences of all accepted species from *Paraphaeophaeria* genus. The data matrix had 19 taxa and 488 characters. The tree was rooted to *Paraconiothyrium archidendri* (JX496049). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 61

Figure S23- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1519, LGMF1552, LGMF1551, LGMF1637 and LGMF1638 (bold) identified as *Pestalotiopsis* sp. and sequences of all accepted species from *Pestalotiopsis* genus. The data matrix had 84 taxa and 376 characters. The tree was rooted to *Neopestalotiopsis saprophytica* (KY082708). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 62

Figure S24- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1584, LGMF1513 and LGMF1524 (bold) identified as *Phaeophleospora* sp. and sequences of all accepted species from *Phaeophleospora* genus. The data matrix had 27 taxa and 496 characters. The tree was rooted to *Pseudoramichloridium henryi* (KF901535). Scale bar shows 0.08 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 63

Figure S25- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1584, LGMF1513 and LGMF1524 (bold) identified as *Phyllosticta* sp. and sequences of all accepted species from *Phyllosticta* genus. The data matrix had 69 taxa and 358 characters. The tree was rooted to *Phyllosticta mimosopisicola*. Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 64

Figure S26- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1611 and LGMF1608 (bold) identified as *Pseudofusicoccum stromaticcum* and *Pseudofusicoccum* sp. and sequences of all accepted species from *Pseudofusicoccum* genus. The data matrix had 11 taxa and 519 characters. The tree was rooted to *Endomelanconiopsis microspore* (KF766165). Scale bar shows 0.008 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 65

Figure S27- Bayesian phylogenetic tree based on ITS partial sequence of LGMF1518 (bold) identified as *Roussoella* sp. and sequences of all accepted species from *Roussoella* genus. The data matrix had 23 taxa and 388 characters. The tree was rooted to *Neoroussoella bambusae* (KJ474827). Scale bar shows 0.06 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain. 66

Figure S28- Boxplot graphic showing median, quartiles and outliers for diversity indexes, abundance and richness A) in Morphotype and B) in Genera. Note: Vd for *Vochysia divergens* and Sa for *Stryphnodendron adstringens*. 67

Figure S29-Rarefaction curve of richness and abundance per morphotype of endophytic fungi associated with *Vochysia divergens* (blue), *Stryphnodendron adstringens* (green) and both (grey). 68

Figure S30-Rarefaction curve of richness and abundance per genus of endophytic fungi associated with *Vochysia divergens* (blue), *Stryphnodendron adstringens* (green) and both (grey). 69

Table S2. Endophytic fungi isolated from medicinal plants *Stryphnodendron adstringens* (Sa) and *Iochysia divergens* (Vd): Identification and number of isolates obtained for each morphotype, source (leave and/or petiole), plant species, selected strain code, Genbank accession number of ITS sequence and phylogeny analysis

Identification	Macromorphological characteristics	Morphotypes	Number of isolates	Source	Plant	Strain	ITS Genbank	Supplementary material
<i>Acrocalymma medicaginis</i>	Mycelium powdery, slow growing, colony colour: grey, from above, black and red, from reverse, moderate growing.	106	1	Lf	Sa	LGMF1605	MG976365	Figure S2
<i>Alternaria section alternata</i>	Aerial mycelium, colony colour: gray reddish brown, from above, gray reverse, moderate growing.	33	4	Lf / Pt	Vd	LGMF1550	MG976387	Figure S3
<i>Bjerkandera</i> sp.	Mycelium fluffy, colony colour : white from above and from reverse, moderate growing.	72	3	Lf / Pt	Vd / Sa	LGMF1578	MG976388	Figure S4
<i>Bjerkandera</i> sp.	Mycelium fluffy, colony colour: white, from above, and black from reverse, moderate growing.	73	4	Lf / Pt	Vd / Sa	LGMF1579	MG976430	Figure S4
<i>Bjerkandera</i> sp.	Mycelium fluffy, colony colour: white, from above, and gray, from reverse, moderate growing.	41	1	Pt	Vd / Sa	LGMF1627	MG976343	Figure S34
<i>Colletotrichum</i>	Mycelium fluffy, colony colour: white, from above,	74	1	Lf	Vd /	LGMF1636	MG976384	Figure S5

<i>siamense</i>	and creamy yellow from reverse, fast-growing.						Sa		
<i>Colletotrichum gloeosporioides</i> sensu lato	Mycelium fluffy, colony colour: white to orange-colored, from above and reverse, fast-growing.	47	4	Lf/Pt	Vd/Sa	LGMF1559	MG976380	Figure S5	
<i>Colletotrichum siamense</i>	Dense mycelium, colony colour: whitish to gray, from above, and orange, from reverse, fast-growing.	36	5	Lf/Pt	Vd/Sa	LGMF1625	MG976438	Figure S5	
<i>Colletotrichum siamense</i>	Dense mycelium, colony colour: whitish to yellow, from above and creamy yellow from reverse, fast-growing.	22	7	Lf/Pt	Vd/Sa	LGMF1621	MG976428	Figure S5	
<i>Colletotrichum gloeosporioides</i> sensu lato	Mycelium irregular, colony colour: white to yellow-colored reddish, from above and reverse, fast-growing.	76	1	Pt	Vd/Sa	LGMF1580	MG976393	Figure S5	
<i>Colletotrichum gloeosporioides</i> sensu lato	Mycelium irregular, colony colour: white to orangish colored, from above and reverse, fast-growing.	84	4	Lf/Pt	Vd/Sa	LGMF1586	MG976395	Figure S5	
<i>Colletotrichum gloeosporioides</i> sensu lato	Mycelium irregular, colony colour: flat and white to grayish colored, from above and reverse, fast-growing.	86	4	Lf/Pt	Vd/Sa	LGMF1588	MG976398	Figure S5	
<i>Colletotrichum siamense</i>	Mycelium fluffy, colony colour: white to yellow-colored, from above, and yellow from reverse, fast-growing.	104	1	Lf	Vd/Sa	LGMF1604	MG976424	Figure S5	
<i>Colletotrichum siamense</i>	Dense mycelium, colony colour: whitish to gray, from above, and yellow, from reverse, fast-growing.	93	1	Lf	Vd/Sa	LGMF1595	MG976407	Figure S5	

<i>Colletotrichum boninense</i> sensu lato	Dense mycelium, colony colour: light grey, from above, and dark yellow, from reverse, fast-growing.	90	1	Lf	Vd / Sa	LGMF1592	MG976401	Figure S6
<i>Colletotrichum boninense</i> sensu lato	Dense mycelium, colony colour: cream, from above and light grey from reverse, fast-growing.	71	1	Pt	Vd / Sa	LGMF1577	MG976389	Figure S6
<i>boninense</i> sensu lato	Dense mycelium, colony colour: white to yellow, from above and light grey, from reverse, fast-growing.	62	5	Lf / Pt	Vd / Sa	LGMF1571	MG976386	Figure S6
<i>Colletotrichum boninense</i> sensu lato	Dense mycelium, colony colour: whitish-orange, from above and white, from reverse, fast-growing.	117	1	Lf	Vd / Sa	LGMF1522	MG976371	Figure S6
<i>Coniochaeta nepalica</i>	Aerial mycelium, colony colour: white, from above and cream to reddish, from reverse, slow-growing.	68	3	Lf / Pt	Vd	LGMF1575	MG976422	Figure S7
<i>Corynespora cambrensis</i>	Fluffy mycelium, colony colour: dark blackish brown, from above and reverse, moderate-growing.	20	22	Lf / Pt	Vd / Sa	LGMF1619	MG976352	Figure S8
<i>Curvularia</i> sp.	Fluffy mycelium, colony colour: blackish brown, from above and dark, from reverse, fast-growing.	1	45	Lf / Pt	Vd / Sa	LGMF1533	MG976426	Figure S9
<i>Daldinia</i> sp.1	Dense mycelium, colony colour: grey with reddish in patches, from above, and brownish, from reverse, moderate-growing.	31	2	Pt	Vd	LGMF1623	MG976413	Figure S10
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white from above and black to yellow from reverse, fast-growing.	2	29	Lf / Pt	Vd / Sa	LGMF1610	MG976330	Figure S11

<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white with greenish in patches from above and white to dark green from reverse, fast-growing.	103	2	Lf	Vd / Sa	LGMF1508	MG976338	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white with yellow in patches from above and cream to brown from reverse, fast-growing.	112	3	Lf	Vd / Sa	LGMF1517	MG976349	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white with yellow in patches from above and cream to brown from reverse, fast-growing	121	1	Lf	Vd / Sa	LGMF1530	MG976350	Figure S11
<i>Diaporthe</i> sp.	Powdery mycelium, colony colour: light grey with dark grey in patches from above and dark grey from reverse, fast-growing	122	1	Lf	Vd / Sa	LGMF1531	MG976351	Figure S11
<i>Diaporthe</i> sp.	Mycelium powdery, colony colour: light grey from above and white from reverse, fast-growing.	124	1	Lf	Vd / Sa	LGMF1532	MG976356	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white from above and cream to light yellow from reverse, fast-growing.	11	15	Lf/Pt	Vd / Sa	LGMF1538	MG976357	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white from above and white with black from reverse, fast-growing.	12	31	Lf/Pt	Vd / Sa	LGMF1539	MG976358	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: grey to grey greenish, from above and dark from reverse, fast-growing.	13	19	Lf/Pt	Vd / Sa	LGMF1540	MG976359	Figure S11
<i>Diaporthe schini</i>	Aerial mycelium, colony colour: white from above and white to cream from reverse, fast-growing.	17	112	Lf/Pt	Vd / Sa	LGMF1541	MG976363	Figure S11

<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white from above and cream to brown from reverse, fast-growing.	29	1	Lf	Vd	LGMF1548	MG976364	Figure S11
<i>Diaporthe</i> sp.2	Aerial mycelium, colony colour: white to brown from above and dark brown from reverse, fast-growing.	30	1	Lf	Vd / Sa	LGMF1549	MG976368	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: cream white from above and white to reddish from reverse, fast-growing.	39	2	Pt	Vd / Sa	LGMF1554	MG976372	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: cream white from above and light grey from reverse, fast-growing.	49	5	Lf / Pt	Vd / Sa	LGMF1561	MG976374	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white to reddish from above and white, fast-growing.	52	5	Lf / Pt	Vd / Sa	LGMF1563	MG976375	Figure S11
<i>Diaporthe</i> cf. <i>heveae</i> 1	Aerial mycelium, colony colour: cream white from above and cream from reverse, fast-growing.	56	6	Lf / Pt	Vd / Sa	LGMF1565	MG976377	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white from above and dark grey from reverse, fast-growing.	58	6	Lf / Pt	Vd / Sa	LGMF1567	MG976378	Figure S11
<i>Diaporthe</i> cf. <i>heveae</i> 1	Aerial mycelium, colony colour: white to light grey from above and dark grey from reverse, fast-growing.	60	2	Pt	Vd / Sa	LGMF1569	MG976382	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white to light grey from above and dark grey to black from reverse, fast-growing.	65	2	Pt	Vd / Sa	LGMF1573	MG976385	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white to yellow from above and white from reverse, fast-growing.	69	4	Pt	Vd / Sa	LGMF1576	MG976391	Figure S11

<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: dark brown with white patches from above and cream to dark brown from reverse, fast-growing.	80	1	Pt	Vd	LGMF1583	MG976347	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: cream to brown from above and cream to brown from reverse, fast-growing.	83	1	Lf	Vd / Sa	LGMF1585	MG976399	Figure S11
<i>Diaporthe</i> cf. <i>heveae</i> 1	Aerial mycelium, colony colour: white from above and white to grey from reverse, fast-growing.	91	2	Pt	Vd / Sa	LGMF1593	MG976400	Figure S11
<i>Diaporthe</i> cf. <i>heveae</i> 1	Aerial mycelium, colony colour: light grey from above and white from reverse, fast-growing.	92	1	Lf	Vd / Sa	LGMF1594	MG976404	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: light pink from above and white from reverse, fast-growing.	101	1	Lf	Vd / Sa	LGMF1601	MG976405	Figure S11
<i>Diaporthe</i> sp.	Aerial mycelium, colony colour: white to orange from above and white from reverse, fast-growing.	102	1	Lf	Vd / Sa	LGMF1602	MG976409	Figure S11
<i>Diaporthe</i> sp.	Mycelium cottony, colony colour: white from above and white from reverse, fast-growing.	113	3	Lf	Vd / Sa	LGMF1606	LGMF1612	Figure S11
<i>Diaporthe</i> sp.	Mycelium cottony, colony colour: black from above and grey to black from reverse, fast-growing.	4	16	Lf / Pt	Vd / Sa	LGMF1612	LGMF1614	Figure S11
<i>Diaporthe</i> sp.	Mycelium cottony, colony colour: white from above and white to brown from reverse, fast-growing.	10	11	Lf / Pt	Vd / Sa	LGMF1614	LGMF1615	Figure S11
<i>Diaporthe</i> sp.	Mycelium cottony, colony colour: white to black from above and brown from reverse, fast-growing.	14	14	Lf / Pt	Vd / Sa	LGMF1615	MG976419	Figure S11

<i>Diaporthe</i> sp.2	Aerial mycelium, colony colour: white from above and cream to brown from reverse, fast-growing.	15	33	Lf/Pt	Vd / Sa	LGMF1616	MG976421	Figure S11
<i>Diaporthe</i> sp.2	Mycelium cottony, colony colour: white from above and white with black from reverse, fast-growing.	19	73	Lf/Pt	Vd / Sa	LGMF1618	MG976423	Figure S11
<i>Diaporthe</i> sp.1	Mycelium cottony, colony colour: white to grey from above and grey yellowish from reverse, fast-growing.	21	31	Lf/Pt	Vd / Sa	LGMF1620	MG976429	Figure S11
<i>Diaporthe</i> sp.	Pulvinate mycelium, colony colour: white to yellow from above and reverse, fast-growing.	37	3	Lf/Pt	Vd / Sa	LGMF1626	MG976432	Figure S11
<i>Diaporthe</i> sp.	Mycelium cottony, colony colour: white to grey from above and grey greyish white from reverse, fast-growing.	46	4	Lf/Pt	Vd / Sa	LGMF1629	MG976433	Figure S11
<i>Diaporthe</i> cf. <i>heveae</i> 1	Mycelium cottony, colony colour: white to cream from above and cream to brown from reverse, fast-growing.	54	2	Pt	Sa	LGMF1631	MG976434	Figure S11
<i>Diaporthe ocoteae</i>	Pulvinate mycelium, colony colour: white to yellow from above and dark brown reverse, fast-growing.	55	4	Lf/Pt	Vd / Sa	LGMF1632	MG976435	Figure S11
<i>Diaporthe</i> cf. <i>heveae</i> 1	Mycelium cottony, colony colour: white to grey from above and cream to brown from reverse, fast-growing.	63	5	Pt	Vd / Sa	LGMF1633	MG976437	Figure S11
<i>Diaporthe</i> cf. <i>heveae</i> 1	Mycelium cottony, colony colour: white to grey from above and grey to brown from reverse, fast-growing.	70	2	Lf/Pt	Vd / Sa	LGMF1635	MG976441	Figure S11
<i>Diaporthe</i> sp.1	Mycelium cottony, colony colour: white from above and brown to reddish from reverse, fast-growing.	81	51	Lf/Pt	Vd / Sa	LGMF1639	MG976346	Figure S11

<i>Diaporthe schini</i>	Aerial mycelium, colony colour: cream from above and cream to brown from reverse, fast-growing.	120	1	Lf	Vd / Sa	LGMF1525	MG976361	Figure S11
Diatrypaceae sp.	Aerial mycelium, colony colour: light pink from above and black from reverse, fast-growing.	24	3	Lf/Pt	Vd / Sa	LGMF1544	MG976420	Figure S15
<i>Didymella</i> sp.	Aerial mycelium, colony colour: white from above and brown from reverse, fast-growing.	16	32	Lf/Pt	Vd / Sa	LGMF1617	MG976427	Figure S12
<i>Didymella</i> sp.	Aerial mycelium, colony colour: dark grey from above and black from reverse, fast-growing.	32	4	Lf/Pt	Vd / Sa	LGMF1624	MG976390	Figure S12
<i>Efibula</i> sp.	Mycelium cottony, colony colour: white to grey from above and dark grey from reverse, fast-growing.	78	1	Pt	Vd	LGMF1581	MG976370	Figure S13
<i>Epicoccum</i> sp.1	Mycelium cottony, colony colour: white to reddish from above and grey from reverse, fast-growing.	43	3	Lf/Pt	Vd / Sa	LGMF1557	MG976379	Figure S14
<i>Epicoccum</i> sp.2	Mycelium cottony, colony colour: white to orange from above and dark grey to yellow from reverse, fast-growing.	61	5	Lf/Pt	Vd / Sa	LGMF1570	MG976402	Figure S14
<i>Epicoccum</i> sp.1	Mycelium cottony, colony colour: light pink to orange from above and dark red from reverse, fast-growing.	98	8	Lf	Vd / Sa	LGMF1598	MG976403	Figure S14
<i>Epicoccum</i> sp.2	Mycelium cottony, colony colour: white to grey to from above and dark red with black patches from reverse, fast-growing.	100	1	Lf	Vd / Sa	LGMF1600	MG976431	Figure S14
<i>Epicoccum</i> sp.	Mycelium cottony, colony colour: light pink to grey from above and grey with red patches from reverse,	45	4	Lf	Vd /	LGMF1628	MG976442	Figure S14

	fast-growing.									
<i>Epicoccum</i> sp.	Mycelium cottony, colony colour: grey to yellow from above and red to orange from reverse, fast-growing.	97	2	Pt	Vd / Sa	LGMF1641	MG976365	Figure S14		
Fungi	Aerial mycelium, colony colour: white to brown from above and white from reverse, low-growing.	8	19	Lf / Pt	Vd / Sa	LGMF1536	-	-		
Fungi	Aerial mycelium, white to brown from above and purple from reverse, low-growing.	42	1	Pt	Vd / Sa	LGMF1556	-	-		
Fungi	Aerial mycelium, colony colour: white and light rose, from above, and rose to violet, from reverse, low-growing	79	1	Pt	Vd / Sa	LGMF1582	-	-		
Fungi	Aerial mycelium colony colour: pink to white, from above, and grey, from reverse, low-growing.	94	3	Lf	Vd / Sa	LGMF1596	-	-		
Fungi	Aerial mycelium colony colour: white to purple, from above and cream, from reverse, low-growing.	95	3	Lf	Vd / Sa	LGMF1597	-	-		
Fungi	Aerial mycelium colony colour: white to cream, from above, and cream with black patches, from reverse, moderate-growing.	99	1	Pt	Vd / Sa	LGMF1599	-	-		
Fungi	Fluffy mycelium, colony colour: yellow from above and cream to reverse, moderate-growing.	96	1	Pt	Vd / Sa	LGMF1640	-	-		
<i>Fusarium</i> sp.	Mycelium cottony, colony colour: light pink from above and dark pink from reverse, fast-growing	23	9	Lf / Pt	Vd / Sa	LGMF1543	-	Figure S16		

<i>Fusarium</i> sp.1	26	2	Pt	Vd / Sa	LGMF1546	MH105813	Figure S16
<i>Fusarium</i> sp.2	27	1	Lf	Vd / Sa	LGMF1547	MH105814	Figure S16
<i>Fusarium</i> sp.1	38	1	Pt	Vd / Sa	LGMF1553	MH105815	Figure S16
<i>Fusarium</i> sp.2	44	1	Lf	Vd / Sa	LGMF1558	MH105816	Figure S16
<i>Fusarium</i> sp.	88	3	Lf / Pt	Vd / Sa	LGMF1590	MH105817	Figure S16
<i>Fusarium</i> sp.	53	1	Pt	Vd / Sa	LGMF1564	MH144142	Figure S16
<i>Fusarium</i> sp.	57	2	Lf / Pt	Vd / Sa	LGMF1566	MG976376	-
<i>Fusarium</i> sp.	59	3	Lf / Pt	Vd / Sa	LGMF1568	MH144143	-
<i>Fusarium</i> sp.	85	3	Lf	Vd / Sa	LGMF1587	MG976394	-
<i>Fusarium</i> sp.	87	1	Pt	Vd / Sa	LGMF1589	MH144144	-

<i>Fusarium</i> sp.	Mycelium cottony, dark violet from above and dark violet from reverse, fast-growing.	48	1	Pt	Vd / Sa	LGMF1560	MG976396	-
<i>Fusarium</i> sp.	Mycelium cottony, colony colour: dark red from above and dark red from reverse, fast-growing.	51	3	Pt	Vd / Sa	LGMF1630	MH144145	-
<i>Hypoxylon</i> sp.1	Mycelium cottony, colony colour: white, from above and white with green dark, from reverse, fast-growing.	6	23	Lf / Pt	Vd / Sa	LGMF1613	MG976416	Figure S17
<i>Lasiodiplodia</i> sp.	Mycelium powdery, colony colour: light rose, from above and white with black patches, from reverse, moderate-growing.	123	1	Lf	Vd / Sa	LGMF1609	MG976412	Figure S18
<i>Lasiodiplodia</i> sp.	Mycelium powdery, colony colour: brown, from above and from reverse, moderate-growing	5	22	Lf / Pt	Vd / Sa	LGMF1534	MG976353	Figure S18
<i>Lasiodiplodia</i> sp.	Mycelium powdery colony colour: cream, from above and dark brown, from reverse, moderate-growing.	40	2	Lf / Pt	Vd / Sa	LGMF1555	MG976369	Figure S18
<i>Neofusicoccum brasiliense</i>	Aerial mycelium, colony colour: white to brown, from above and white with black, from reverse, fast-growing.	7	50	Lf / Pt	Vd / Sa	LGMF1535	MG976354	Figure S19
<i>Neofusicoccum brasiliense</i>	Aerial mycelium, colony colour: white, from above and black, from reverse, fast-growing.	67	6	Lf / Pt	Vd / Sa	LGMF1634	MG976436	Figure S19
<i>Neopestalotiopsis</i> sp.	Aerial mycelium, colony colour: dark, from above and from reverse, fast-growing	50	3	Lf / Pt	Vd	LGMF1562	MG976373	Figure S20
<i>Nigrospora</i>	Aerial mycelium colony colour: white with black patches, from above and white, from reverse,	89	2	Lf	Vd /	LGMF1591	MG976397	Figure S21

<i>hainanensis</i>	moderate-growing.					Sa		
<i>Nigrospora hainanensis</i>	Aerial mycelium colony colour: black, from above and grey, from reverse, moderate-growing	28	2	Lf	Vd / Sa	LGMF1622	MG976425	Figure S21
<i>Paraphaeosphaeria</i> sp.	Dense mycelium, colony colour: green to greyish, from above and dark, from reverse, low-growing.	110	1	Pt	Vd / Sa	LGMF1515	MG976336	Figure S22
<i>Paraphaeosphaeria</i> sp.	Powdery mycelium, colony colour: dark green, from above and dark green, from reverse, moderate-growing.	111	1	Lf	Vd	LGMF1516	MG976337	Figure S22
<i>Pestalotiopsis</i> sp.	Aerial mycelium colony colour: grayish to white, from above, and dark from reverse, moderate-growing.	34	4	Pt	Vd / Sa	LGMF1551	MG976366	Figure S23
<i>Pestalotiopsis</i> sp.	Aerial mycelium colony colour: grayish to white, from above and grey, from reverse, fast-growing.	35	3	Lf / Pt	Vd / Sa	LGMF1552	MG976367	Figure S23
<i>Pestalotiopsis</i> sp.	Aerial mycelium colony colour: grayish to white, from above and dark grey with black patches, from reverse, fast-growing.	75	1	Lf	Vd / Sa	LGMF1637	MG976439	Figure S23
<i>Pestalotiopsis</i> sp.	Aerial mycelium colony colour: grayish to white, from above and white with black patches, from reverse, fast-growing.	77	1	Lf	Vd / Sa	LGMF1638	MG976440	Figure S23
<i>Pestalotiopsis</i> sp.1	Dense mycelium colony colour: greenish to grey, from above and black, from reverse, moderate-growing.	115	3	Lf	Vd / Sa	LGMF1519	MG976340	Figure S23
<i>Phaeophleospora</i> sp.1	Mycelium cottony, colony colour: white to redish, from above and red, from reverse, fast-growing.	82	2	Lf	Vd / Sa	LGMF1584	MG976392	Figure S24

<i>Phaeophleiospora</i> sp.2	Mycelium cottony, colony colour: white, from above and white with bright red, from reverse fast-growing.	109	2	Lf	Vd / Sa	LGMF1513	MG976335	Figure S24
<i>Phaeophleiospora</i> sp.2	Mycelium powdery colony colour: dark with white patches, from above and dark, from reverse, fast-growing.	118	1	Pt	Vd / Sa	LGMF1524	MG976345	Figure S24
<i>Phyllosticta</i> sp.1	Mycelium powdery, colony colour: light grey, from above and dark from reverse, moderate-growing.	107	1	Lf	Vd / Sa	LGMF1511	MG976333	Figure S25
<i>Phyllosticta</i> sp.1	Mycelium powdery, colony colour: grey to green, from above and dark, from reverse, moderate-growing.	108	1	Lf	Vd / Sa	LGMF1512	MG976334	Figure S25
<i>Phyllosticta</i> sp.	Mycelium powdery, colony colour: black, from above and dark, from reverse, moderate-growing.	116	123	Lf/Pt	Vd / Sa	LGMF1521	MG976342	Figure S25
Pleomassariaceae sp.	Mycelium powdery, colony colour: white to grey, from above and black with yellow, from reverse, fast-growing.	105	1	Lf	Vd / Sa	LGMF1509	MG976331	-
<i>Pseudofusicoccum</i> sp.1	Mycelium cottony, colony colour: light grey, from above and white with grey, from reverse, fast-growing.	3	22	Lf/Pt	Vd / Sa	LGMF1611	MG976414	Figure S25
<i>Pseudofusicoccum</i> <i>stromaticum</i>	Aerial mycelium colony colour: white, from above and white with yellow patches, from reverse, fast-growing.	119	3	Lf	Vd / Sa	LGMF1608	MG976411	Figure S26
<i>Roussioella</i> sp.	Powdery mycelium, colony colour: white with green, from above and dark, from reverse, moderate-growing.	114	2	Lf	Vd	LGMF1518	MG976339	Figure S27
Xylariaceae sp.3	Aerial mycelium white, from above and white to grey,	18	44	Lf/Pt	Vd /	LGMF1542*	MG976360	Figure 2

	from reverse, fast-growing								
Xylariaceae sp.4	Aerial mycelium colony colour: light rose, from above and white to from reverse, fast-growing.	25	3	Lf/Pt	Vd / Sa	LGMF1545*	MG976362	Figure 2	
Xylariaceae sp.4	Aerial mycelium colony colour: white to grey, from above and, from reverse, fast-growing.	64	2	Pt	Vd / Sa	LGMF1572*	MG976381	Figure 2	
Xylariaceae sp.4	Aerial mycelium colony colour: grey, from above and dark, from reverse, fast-growing.	66	6	Lf/Pt	Vd / Sa	LGMF1574*	MG976383	Figure 2	
Xylariaceae sp.5	Aerial mycelium colony colour: white, from above and yellowish, from reverse, fast-growing.	9	29	Lf/Pt	Vd / Sa	LGMF1537*	MG976355	Figure 2	

Table S2-Indicator Species Values table for morphotypes. Highlighted values indicate significant representatives of a group. (Continue)

Morphotype	<i>S. adstringens</i> Leaf	<i>S. adstringens</i> Petiole	<i>V. divergens</i> Leaf	<i>V. divergens</i> Petiole	P
1	0.08	0.06	0.07	0.22	0.20
2	0.02	0.08	0.07	0.11	0.82
3	0.02	0.04	0.06	0.11	0.65
4	0.00	0.04	0.22	0.01	0.04
5	0.02	0.05	0.07	0.10	0.79
6	0.01	0.10	0.01	0.23	0.05
7	0.15	0.09	0.03	0.25	0.13
8	0.01	0.10	0.02	0.17	0.20
9	0.20	0.00	0.06	0.19	0.24
10	0.06	0.09	0.00	0.04	0.51
11	0.05	0.02	0.05	0.07	0.92
12	0.03	0.01	0.11	0.19	0.19
13	0.11	0.00	0.04	0.14	0.31
14	0.07	0.02	0.15	0.01	0.25
15	0.18	0.04	0.03	0.16	0.37
16	0.06	0.01	0.08	0.32	0.02
17	0.16	0.05	0.12	0.35	0.03
18	0.18	0.05	0.07	0.20	0.43
19	0.19	0.09	0.12	0.19	0.77
20	0.09	0.00	0.05	0.08	0.81
21	0.06	0.05	0.07	0.20	0.21
22	0.00	0.05	0.01	0.05	0.72
23	0.00	0.03	0.02	0.15	0.13
24	0.00	0.03	0.01	0.02	1.00
25	0.00	0.00	0.06	0.02	0.45
26	0.00	0.00	0.00	0.06	0.70
27	0.00	0.00	0.05	0.00	1.00
28	0.17	0.00	0.00	0.00	0.03
29	0.00	0.00	0.05	0.00	1.00
30	0.00	0.00	0.05	0.00	1.00
31	0.00	0.00	0.00	0.11	0.17
32	0.03	0.00	0.04	0.01	0.86
33	0.00	0.00	0.05	0.06	0.53
34	0.00	0.00	0.00	0.11	0.18
35	0.00	0.00	0.02	0.04	0.67
36	0.00	0.00	0.09	0.05	0.33
37	0.00	0.01	0.00	0.09	0.25
38	0.00	0.00	0.00	0.06	0.71
39	0.00	0.00	0.00	0.11	0.16
40	0.00	0.00	0.02	0.03	1.00
41	0.00	0.00	0.00	0.06	0.69
42	0.00	0.00	0.00	0.06	0.68
43	0.00	0.00	0.03	0.02	0.94
44	0.00	0.00	0.05	0.00	1.00
45	0.00	0.00	0.05	0.00	1.00
46	0.00	0.04	0.02	0.00	0.69
47	0.02	0.01	0.03	0.03	1.00
48	0.00	0.00	0.02	0.04	0.66
49	0.00	0.00	0.02	0.04	0.67
50	0.00	0.00	0.02	0.08	0.35
51	0.03	0.00	0.01	0.03	0.86
52	0.00	0.02	0.01	0.07	0.45
53	0.00	0.00	0.00	0.06	0.70
54	0.00	0.13	0.00	0.00	0.09
55	0.00	0.02	0.05	0.01	0.78

56	0.00	0.00	0.02	0.11	0.16
57	0.00	0.00	0.02	0.03	1.00
58	0.00	0.00	0.05	0.06	0.57
59	0.00	0.00	0.06	0.02	0.47
60	0.00	0.04	0.00	0.03	0.84
61	0.02	0.00	0.02	0.04	0.80
62	0.00	0.00	0.07	0.02	0.41
63	0.00	0.13	0.00	0.04	0.13
64	0.00	0.00	0.00	0.11	0.14
65	0.00	0.00	0.00	0.11	0.18
66	0.00	0.01	0.02	0.08	0.40
67	0.00	0.00	0.00	0.28	0.01
68	0.00	0.00	0.06	0.02	0.46
69	0.00	0.00	0.05	0.03	0.70
70	0.00	0.00	0.02	0.03	1.00
71	0.00	0.00	0.00	0.06	0.69
72	0.13	0.00	0.01	0.00	0.11
73	0.00	0.00	0.04	0.02	0.87
74	0.08	0.00	0.00	0.00	0.20
75	0.08	0.00	0.00	0.00	0.18
76	0.00	0.00	0.00	0.06	0.68
77	0.08	0.00	0.00	0.00	0.19
78	0.00	0.00	0.00	0.06	0.70
79	0.00	0.00	0.00	0.06	0.67
80	0.00	0.00	0.00	0.06	0.73
81	0.07	0.02	0.21	0.16	0.26
82	0.00	0.00	0.05	0.00	1.00
83	0.00	0.00	0.05	0.00	1.00
84	0.00	0.04	0.02	0.00	0.71
85	0.00	0.00	0.15	0.00	0.06
86	0.00	0.00	0.06	0.02	0.49
87	0.00	0.00	0.00	0.06	0.69
88	0.00	0.00	0.00	0.06	0.70
89	0.00	0.00	0.05	0.00	1.00
90	0.00	0.00	0.05	0.00	1.00
91	0.00	0.04	0.00	0.03	0.81
92	0.00	0.00	0.05	0.00	1.00
93	0.00	0.00	0.05	0.00	1.00
94	0.00	0.03	0.06	0.00	0.59
95	0.00	0.00	0.05	0.00	1.00
96	0.00	0.07	0.00	0.00	0.42
97	0.00	0.04	0.00	0.03	0.82
98	0.00	0.14	0.01	0.01	0.11
99	0.00	0.00	0.00	0.06	0.73
100	0.00	0.00	0.05	0.00	1.00
101	0.00	0.00	0.05	0.00	1.00
102	0.00	0.00	0.05	0.00	1.00
103	0.13	0.03	0.41	0.07	0.01

Table S3-Permanova results for morphotypes.

	DF	Sum of Sq.	Mean of Sq.	F	R2	p
Plant	1	0.44	0.44	1.38	0.02	0.12
Tissues	1	0.61	0.61	1.89	0.03	0.02

Note: Highlighted values indicate significant differences inside a group. Number of permutations: 1000.

DF=Degrees of freedom; Sq=squares; p= probability value.

Table S4-ANOSIMs results per morphotype comparing plants and tissues.

Petiole x Leaf (Vd and Sa)	Petiole x Leaf (Vd only)
Dissimilarity: bray	Dissimilarity: bray
ANOSIM statistic R: 0.04677	ANOSIM statistic R: 0.1111
Significance: 0.014	Significance: 0.002
Permutation: free	Permutation: free
Number of permutations: 999	Number of permutations: 999
Upper quantiles of permutations (null model):	Upper quantiles of permutations (null model):
90% 95% 97.5% 99%	90% 95% 97.5% 99%
0.0225 0.0302 0.0401 0.0518	0.0373 0.0525 0.0623 0.0766
Dissimilarity ranks between and within classes:	Dissimilarity ranks between and within classes:
0% 25% 50% 75% 100% N	0% 25% 50% 75% 100% N
Between 1 550.5 1081.50 1808.5 1808.5 1056	Between 2 196.000 394.25 540.25 635 360
Leaf 5 433.0 929.50 1490.0 1808.5 496	Leaf 1 184.375 348.00 635.00 635 190
Petiole 5 527.5 1073.75 1808.5 1808.5 528	Petiole 5 137.000 275.50 425.50 635 153

Note: Highlighted values indicate significant differences between morphogroups. Vd for *V. divergens* and Sa for *S. adstringens*.

Table S5-Screening of antimicrobial activity of the endophytic fungi against phytopathogens.
(Continue)

Identification	Strain	Inhibition Rate (%)		
		<i>P. citricarpa</i>	<i>C. abscissum</i>	<i>F. verticillioides</i>
<i>Curvularia</i> sp.	LGMF1533	20	10	8
<i>Diaporthe</i> sp.	LGMF1610	45	10	5
<i>Pseudofusicoccum</i> sp.	LGMF1611	35	39	7
<i>Diaporthe</i> sp.	LGMF1612	33	15	9
<i>Lasiodiplodia</i> sp.	LGMF1534	35	46	0
<i>Hypoxyton</i> sp.	LGMF1613	50	24	10
<i>Neofusicoccum brasiliense</i>	LGMF1535	66	47	15
Xylariaceae sp. 5	LGMF1537	47	35	10
<i>Diaporthe</i> sp.	LGMF1614	70	36	8
<i>Diaporthe</i> sp.	LGMF1538	44	25	8
<i>Diaporthe</i> sp.	LGMF1539	48	35	10
<i>Diaporthe</i> sp.	LGMF1540	51	35	4
<i>Diaporthe</i> sp.	LGMF1615	48	30	6
<i>Diaporthe</i> sp.	LGMF1616	47	40	9
<i>Didymella</i> sp.	LGMF1617	33	30	10
<i>Diaporthe schini</i>	LGMF1541	45	25	8
Xylariaceae sp.3	LGMF1542	49	30	10
<i>Diaporthe</i> sp.	LGMF1618	37	35	8
<i>Corynespora cambrensis</i>	LGMF1619	38	22	7
<i>Diaporthe</i> sp.	LGMF1620	41	30	9
<i>Colletotrichum</i> sp.	LGMF1621	49	22	7
<i>Fusarium</i> sp.	LGMF1543	50	38	15
Diatrypaceae sp.	LGMF1544	36	13	8
Xylariaceae sp.4	LGMF1545	48	39	10
<i>Fusarium</i> sp.	LGMF1546	51	44	10
<i>Fusarium</i> sp.	LGMF1547	49	38	12
<i>Nigrospora</i> sp.	LGMF1622	49	31	8
<i>Diaporthe</i> sp.	LGMF1548	46	30	10
<i>Diaporthe</i> sp.	LGMF1549	35	30	9
<i>Daldinia</i> sp.	LGMF1623	33	14	9
<i>Didymella</i> sp.	LGMF1624	54	33	7
<i>Alternaria alternata</i>	LGMF1550	38	22	5
<i>Pestalotiopsis</i> sp.	LGMF1551	36	16	8
<i>Pestalotiopsis</i> sp.	LGMF1552	51	22	7
<i>Colletotrichum siamense</i>	LGMF1625	48	34	3
<i>Diaporthe</i> sp.	LGMF1626	19	14	6
<i>Fusarium</i> sp.	LGMF1553	49	38	9
<i>Diaporthe</i> sp.	LGMF1554	47	41	8
<i>Lasiodiplodia</i> sp.	LGMF1555	20	13	7
<i>Bjerkandera</i> sp.	LGMF1627	33	18	0
<i>Epicoccum</i> sp.	LGMF1557	39	36	9
<i>Fusarium</i> sp.	LGMF1558	49	22	7

<i>Epicoccum</i> sp.	LGMF1628	44	39	9
<i>Diaporthe</i> sp.	LGMF1629	47	38	10
<i>Colletotrichum gloeosporioides</i>	LGMF1559	50	41	8
<i>Fusarium</i> sp.	LGMF1560	50	42	8
<i>Diaporthe</i> sp.	LGMF1561	49	37	9
<i>Neopestalotiopsis</i> sp.	LGMF1562	25	50	7
<i>Fusarium</i> sp.	LGMF1630	75	66	7
<i>Diaporthe</i> sp.	LGMF1563	45	36	8
<i>Fusarium</i> sp.	LGMF1564	51	36	9
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1631	80	64	22
<i>Diaporthe</i> sp.	LGMF1632	33	25	7
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1565	25	14	7
<i>Fusarium</i> sp.	LGMF1566	50	38	9
<i>Diaporthe</i> sp.	LGMF1567	39	23	7
<i>Fusarium</i> sp.	LGMF1568	47	31	9
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1569	37	29	10
<i>Epicoccum</i> sp.	LGMF1570	38	29	10
<i>Colletotrichum</i> sp.	LGMF1571	48	33	15
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1633	33	19	12
Xylariaceae sp.4	LGMF1572	36	24	12
<i>Diaporthe</i> sp.	LGMF1573	38	28	9
Xylariaceae sp.4	LGMF1574	36	23	17
<i>Neofusicoccum brasiliense</i>	LGMF1634	45	34	9
<i>Conidiochaeta nepalica</i>	LGMF1575	33	19	0
<i>Diaporthe</i> sp.	LGMF1576	39	24	14
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1635	44	32	6
<i>Colletotrichum</i> sp.	LGMF1577	47	33	6
<i>Bjerkandera</i> sp.	LGMF1578	38	19	0
<i>Bjerkandera</i> sp.	LGMF1579	38	21	0
<i>Colletotrichum siamense</i>	LGMF1636	44	34	0
<i>Pestalotiopsis</i> sp.	LGMF1637	45	33	0
<i>Colletotrichum gloeosporioides</i>	LGMF1580	48	35	0
<i>Pestalotiopsis</i> sp.	LGMF1638	36	22	8
<i>Efibula</i> sp.	LGMF1581	33	18	9
<i>Diaporthe</i> sp.	LGMF1583	38	26	10
<i>Diaporthe</i> sp.	LGMF1639	41	26	9
<i>Phaeophleospora</i> sp.	LGMF1584	40	28	14
<i>Diaporthe</i> sp.	LGMF1585	39	27	10
<i>Colletotrichum gloeosporioides</i>	LGMF1586	35	30	6
<i>Fusarium</i> sp.	LGMF1587	48	35	9
<i>Colletotrichum gloeosporioides</i>	LGMF1588	44	32	6
<i>Fusarium</i> sp.	LGMF1589	55	19	9
<i>Fusarium</i> sp.	LGMF1590	46	22	9
<i>Nigrospora hainanensis</i>	LGMF1591	36	33	12
<i>Colletotrichum boninense</i>	LGMF1592	38	45	3
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1593	32	23	5

<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1594	47	27	0
<i>Colletotrichum siamense</i>	LGMF1595	31	22	0
<i>Epicoccum</i> sp.	LGMF1641	78	60	15
<i>Epicoccum</i> sp.	LGMF1598	25	37	7
<i>Epicoccum</i> sp.	LGMF1600	31	47	6
<i>Diaporthe</i> sp.	LGMF1601	48	44	14
<i>Diaporthe</i> sp.	LGMF1602	50	37	12
<i>Diaporthe</i> sp.	LGMF1508	85	31	2
<i>Colletotrichum siamense</i>	LGMF1604	85	62	5
Pleomassariaceae sp.	LGMF1509	21	29	7
<i>Acrocalymma</i> sp.	LGMF1605	32	29	6
<i>Phyllosticta</i> sp.	LGMF1511	22	19	3
<i>Phyllosticta</i> sp.	LGMF1512	69	30	6
<i>Phaeophleospora</i> sp.	LGMF1513	35	35	7
<i>Paraphaeosphaeria</i> sp.	LGMF1515	76	22	7
<i>Paraphaeosphaeria</i> sp.	LGMF1516	26	36	7
<i>Diaporthe</i> sp.	LGMF1517	54	40	6,7
<i>Diaporthe</i> sp.	LGMF1606	60	41	6,3
<i>Roussoella</i> sp.	LGMF1518	18	31	8
<i>Pestalotiopsis</i> sp.	LGMF1519	20	64	13
<i>Phyllosticta</i> sp.	LGMF1521	24	32	7,5
<i>Colletotrichum boninense</i>	LGMF1522	24	50	7,5
<i>Phaeophleospora</i> sp.	LGMF1524	25	61	17
<i>Pseudofusicoccum stromaticum</i>	LGMF1608	26	31	6
<i>Diaporthe schini</i>	LGMF1525	10	24	6
<i>Diaporthe</i> sp.	LGMF1530	82	67	15
<i>Diaporthe</i> sp.	LGMF1531	43	43	17
<i>Lasiodiplodia</i> sp.	LGMF1609	26	26	9
<i>Diaporthe</i> sp.	LGMF1532	48	42	10

Table S6-Screening of antimicrobial activity of the endophytic fungi against clinical pathogens.

Identification	Strain	Spectrum of Action
<i>Curvularia</i> sp.	LGMF1533	MSSA (+); MRSA (+); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1610	MSSA (+); MRSA (+); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (-); KPC (-)
<i>Pseudofusicoccum</i> sp.	LGMF1611	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1612	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Lasiodiplodia</i> sp.	LGMF1534	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Hypoxylon</i> sp.	LGMF1613	KPC (-)
<i>Neofusicoccum brasiliense</i>	LGMF1535	MSSA(+++); MRSA(+++); <i>P. aeruginosa</i> (+++); <i>A. baumannii</i> (+++); KPC(++)
Xylariaceae sp.5	LGMF1537	MSSA (+++); MRSA (+); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe</i> sp.	LGMF1614	MSSA (+++); MRSA (+++); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe</i> sp.	LGMF1538	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)

<i>Diaporthe</i> sp.	LGFMF1539	MSSA (+++); MRSA (+); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1540	MSSA (+++); MRSA (+); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1615	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1616	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Didymella</i> sp.	LGFMF1617	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe schini</i>	LGFMF1541	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (-); KPC (-)
Xylariaceae sp.3	LGFMF1542	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1618	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (++) ; <i>A. baumannii</i> (+); KPC (-)
<i>Corynespora cambrensis</i>	LGFMF1619	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1620	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum siamense</i>	LGFMF1621	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (+); KPC (-)
<i>Fusarium</i> sp.	LGFMF1543	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
Diatrypaceae sp.	LGFMF1544	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
Xylariaceae sp.4	LGFMF1545	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Fusarium</i> sp.	LGFMF1546	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGFMF1547	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (-)
<i>Nigrospora</i> sp.	LGFMF1622	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1548	MSSA(+++); MRSA (+++); <i>P. aeruginosa</i> (+++); <i>A. baumannii</i> (++) ; KPC (-)
<i>Diaporthe</i> sp.	LGFMF1549	MSSA (++) ; MRSA (+); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (-); KPC (-)
<i>Daldinia</i> sp.	LGFMF1623	MSSA (++) ; MRSA (+); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Didymella</i> sp.	LGFMF1624	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Alternaria</i> sp.	LGFMF1550	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Pestalotiopsis</i> sp.	LGFMF1551	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Pestalotiopsis</i> sp.	LGFMF1552	MSSA (++) ; MRSA (+); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum siamense</i>	LGFMF1625	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1626	MSSA (++) ; MRSA (+); <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGFMF1553	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1554	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Lasiodiplodia</i> sp.	LGFMF1555	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Bjerkandera</i> sp.	LGFMF1627	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Epicoccum</i> sp.	LGFMF1557	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (++) ; <i>A. baumannii</i> (+); KPC (-)
<i>Fusarium</i> sp.	LGFMF1558	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Epicoccum</i> sp.	LGFMF1628	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1629	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum</i> sp.	LGFMF1559	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGFMF1560	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGFMF1561	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Neopestalotiopsis</i> sp.	LGFMF1562	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)

<i>Fusarium</i> sp.	LGMF1630	MSSA (+++); MRSA (++) ; <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (+)
<i>Diaporthe</i> sp.	LGMF1563	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGMF1564	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1631	MSSA (+++); MRSA (++) ; <i>P. aeruginosa</i> (+); <i>A. baumannii</i> (+); KPC (+)
<i>Diaporthe</i> sp.	LGMF1632	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1565	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGMF1566	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (++) ; <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1567	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGMF1568	MSSA (++) ; MRSA (+); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1569	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Epicoccum</i>	LGMF1570	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum</i>	LGMF1571	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1633	MSSA (++) ; MRSA (+); <i>P. aeruginosa</i> (++) ; <i>A. baumannii</i> (+); KPC (-)
Xylariaceae sp.3	LGMF1572	MSSA (++) ; MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (+); KPC (-)
<i>Diaporthe</i> sp.	LGMF1573	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
Xylariaceae sp.4	LGMF1574	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Neofusicoccum brasiliense</i>	LGMF1634	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Conidiochaeta nepalica</i>	LGMF1575	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1576	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1635	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum boninense</i>	LGMF1577	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Bjerkandera</i> sp.	LGMF1578	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Bjerkandera</i> sp.	LGMF1579	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum siamense</i>	LGMF1636	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Pestalotiopsis</i> sp.	LGMF1637	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum gloeosporioides</i>	LGMF1580	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Pestalotiopsis</i> sp.	LGMF1638	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Efibula</i> sp.	LGMF1581	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1583	MSSA (+++); MRSA (+++); <i>P. aeruginosa</i> (+++); <i>A. baumannii</i> (+++); KPC (++)
<i>Diaporthe</i> sp.	LGMF1639	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Phaeophleospora</i> sp.	LGMF1584	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1585	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum gloeosporioides</i>	LGMF1586	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGMF1587	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum gloeosporioides</i>	LGMF1588	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGMF1589	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Fusarium</i> sp.	LGMF1590	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Nigrospora hainanensis</i>	LGMF1591	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum boninense</i>	LGMF1592	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1593	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)

<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1594	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum siamense</i>	LGMF1595	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Epicoccum</i> sp.	LGMF1641	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Epicoccum</i> sp.	LGMF1598	MSSA (+++); MRSA (+++); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Epicoccum</i> sp.	LGMF1600	MSSA (+++); MRSA (+++); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1601	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1602	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1508	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum siamense</i>	LGMF1604	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
Pleomassariaceae sp.	LGMF1509	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Acrocalymma medicaginis</i>	LGMF1605	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Phyllosticta</i> sp.	LGMF1511	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Phyllosticta</i> sp.	LGMF1512	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Phaeophleospora</i> sp.	LGMF1513	MSSA (+++); MRSA (+++); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Paraphaeosphaeria</i> sp.	LGMF1515	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Paraphaeosphaeria</i> sp.	LGMF1516	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1517	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1606	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Roussoella</i> sp.	LGMF1518	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Pestalotiopsis</i> sp.	LGMF1519	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Phyllosticta</i> sp.	LGMF1521	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Colletotrichum boninense</i>	LGMF1522	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Phaeophleospora</i> sp.	LGMF1524	MSSA (+); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Pseudofusicoccum stromaticum</i>	LGMF1608	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe schini</i>	LGMF1525	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1530	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1531	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Lasiodiplodia</i> sp.	LGMF1609	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)
<i>Diaporthe</i> sp.	LGMF1532	MSSA (-); MRSA (-); <i>P. aeruginosa</i> (-); <i>A. baumannii</i> (-); KPC (-)

Note: MSSA= *Staphylococcus aureus* methicillin-sensitive; MRSA= *Staphylococcus aureus* methicillin-resistant; *P. aeruginosa*= *Pseudomonas aeruginosa*; *A. baumannii*= *Acinetobacter baumannii*; KPC= *Klebsiella pneumoniae* Carbapenemase. no activity (-), low (+), moderate (++) and high (+++) activity.

Table S7-Extract yield performed in 250 mL in two culture media: ME (Malte extract) and CY (Czapeck).

Morphotype	Identification	Isolate	Extract yield (mg)	
			ME	CY
6	<i>Hypoxylon</i> sp. <i>Neofusicoccum</i>	LGMF1613	97	11
7	<i>brasiliense</i>	LGMF1535	20	2
29	<i>Diaporthe</i> sp.	LGMF1548	41	8
51	<i>Fusarium</i> sp.	LGMF1630	11	6
54	<i>Diaporthe</i> cf. <i>heveae</i>	LGMF1631	42	15
80	<i>Diaporthe</i> sp.	LGMF1583	110	31
98	<i>Epicoccum</i> sp.	LGMF1598	21	4

100	<i>Epicoccum</i> sp	LGMF1600	11	6
	<i>Colletotrichum</i>			
104	<i>siamense</i>	LGMF1604	100	40
109	<i>Phaeophleospora</i> sp	LGMF1513	18	14
121	<i>Diaporthe</i> sp.	LGMF1530	33	4

Table S8-Inhibition zone of the crud extracts produced by endophytic fungi against clinical pathogens.

Strain/Genera	Antimicrobial activity (inhibition zone in mm)															
	MRSA		MSSA		S. maltophilia		KPC		E. cloacae		A. baumannii		P. aeruginosa		C. albicans	
	ME	CY	ME	CY	ME	CY	ME	CY	ME	CY	ME	CY	ME	CY	ME	CY
<i>Colletotrichum</i>																
LGMF1604	15 ± 2	9.5 ± 0.7	9.5 ± 0.7	0	0.7	13 ± 1.4	10 ± 1.4	10.5 ± 0.7	10 ± 0	0	0	0	9.5 ± 0.7	11 ± 0.7	10 ± 2	10 ± 0
<i>Diaporthe</i>																
LGMF1530	15 ± 2	0	10 ± 1.4	11.5 ± 2.1	0.7	13 ± 1.4	11 ± 0	13 ± 0	14 ± 1.7	11.5 ± 0.7	0	9.5 ± 0.7	10 ± 0.7	10 ± 0	12 ± 0	13 ± 0
<i>Diaporthe</i>																
LGMF1548	± 1.4	15 ± 0	23 ± 0.7	11.5 ± 2.1	3.5	12 ± 1.4	18 ± 0	14 ± 1.4	19 ± 1.4	11.5 ± 2	0	0	16 ± 0.7	10 ± 0	9.5 ± 0.7	9.5 ± 0.7
<i>Diaporthe</i>																
LGMF1583	17 ± 2	10 ± 0	23 ± 2.8	10 ± 0	1.4	13 ± 1.4	14 ± 0.7	11.5 ± 0.7	14 ± 0.7	14 ± 0.7	0	0	16 ± 0	9,0 ± 0	1.4	14 ± 1.4
<i>Diaporthe</i>																
LGMF1631	10 ± 0	0	11 ± 1.4	0	0.7	0	11 ± 1.4	0	16 ± 2.8	0	0	0	0	0	0.7	0
<i>Epicoccum</i>																
LGMF1598	± 0.7	9 ± 0	11 ± 0.7	0	0.7	11.5 ± 0.7	14 ± 1.4	11.5 ± 0.7	11 ± 1.4	14 ± 1.4	0	0	9 ± 0	0	11 ± 0.7	9.5 ± 0.7
<i>Epicoccum</i>																
LGMF1600	± 0.7	9.5 ± 0.7	9.7 ± 0.7	9.5 ± 0.7	1.4	10.5 ± 0.7	9.5 ± 0.7	9.5 ± 0.7	10 ± 0	11.5 ± 2	15 ± 0.7	10.5 ± 0.7	10 ± 0	0	1.4	10.5 ± 0.7
<i>Fusarium</i>																
LGMF1630	10 ± 0	15 ± 0	9.0 ± 0	11.5 ± 2.1	10 ± 0	13 ± 1.4	15 ± 0	13 ± 0	1,2,5 ± 0,07	13.5 ± 2	0	0	0,5 ± 0,7	12.5 ± 0.7	0	13 ± 1.4
<i>Hypoxylon</i>																
LGMF1613	11 ± 2	0	10 ± 0	0	13 ± 2	0	12,5 ± 0.7	0	13 ± 1.4	0	0	0	0	0	0	0
<i>Neofusicoccum</i>																
LGMF1535	23 ± 2 ²	0	20 ± 0	16 ± 0.7	0.7	11.5 ± 2	16 ± 0.7	11 ± 1.4	16 ± 1.4	12.5 ± 0.7	0	0	17 ± 0.7	11 ± 1.4	14 ± 0	15 ± 0
<i>Phaeophleospora</i>																
LGMF1513	11 ± 1.4	1.1 ± 0.14	11.5 ± 2.1	11 ± 0	15 ± 1.4	15 ± 1.4	12.5 ± 0.7	9.5 ± 0.7	14 ± 0.7	12 ± 0.7	11.5 ± 0.7	0	11.5 ± 0.7	0	13 ± 1.4	12 ± 0
Antibiotic	25 ± 0				20 ± 0	20 ± 0	20 ± 0	20 ± 0	20 ± 0	20 ± 0	30 ± 0	25 ± 0	25 ± 0	20 ± 0	20 ± 0	20 ± 0

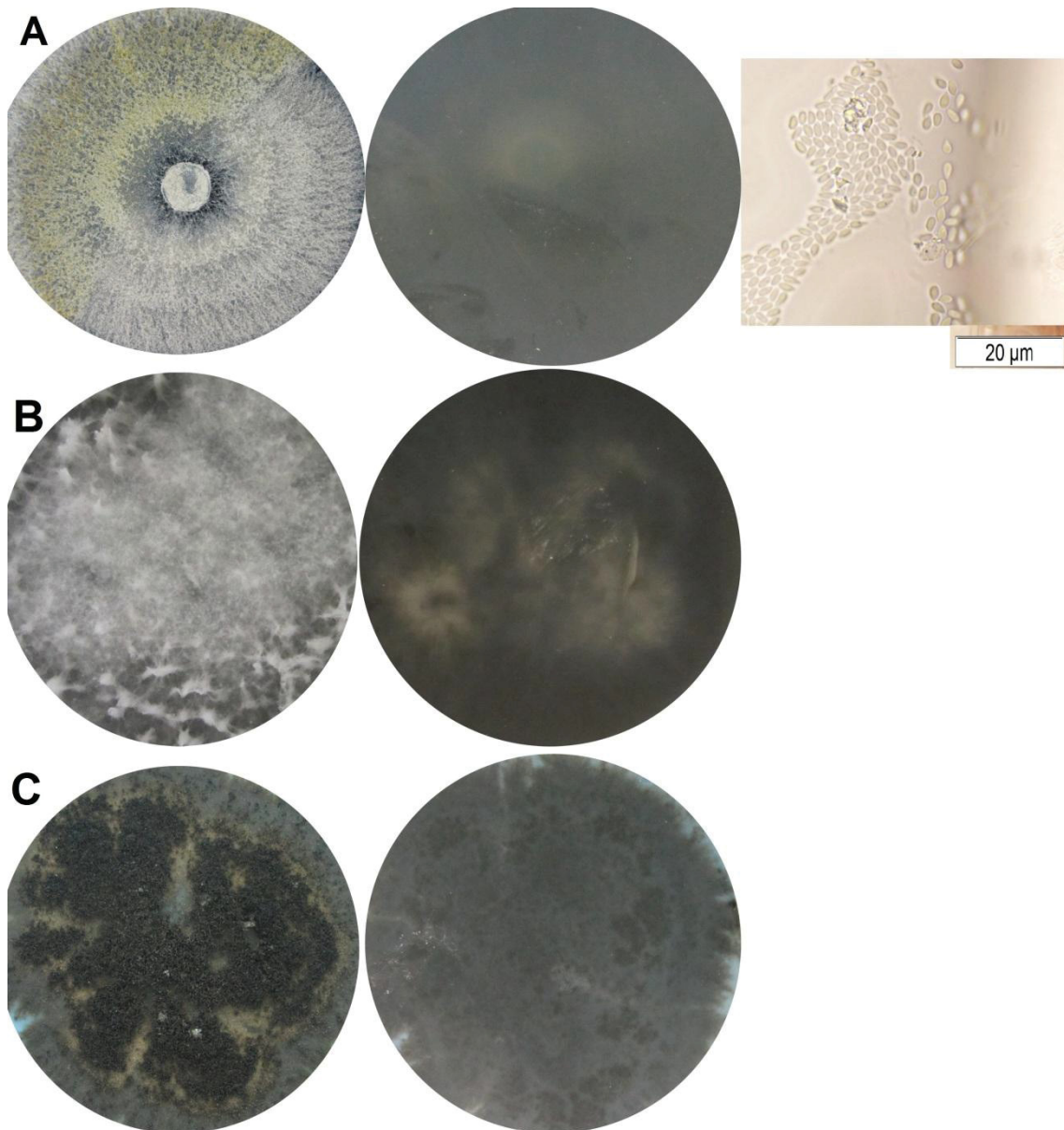


Figure S5-Morphological aspect of the dominant endophytic fungi found in this study. For details on the source (plant species), see Table 1. A: *Diaporthe schini* (morphotype 17), B: *Neofusicoccum brasiliense* (morphotype 7), C: *Phyllosticta* sp. (morphotype 116).

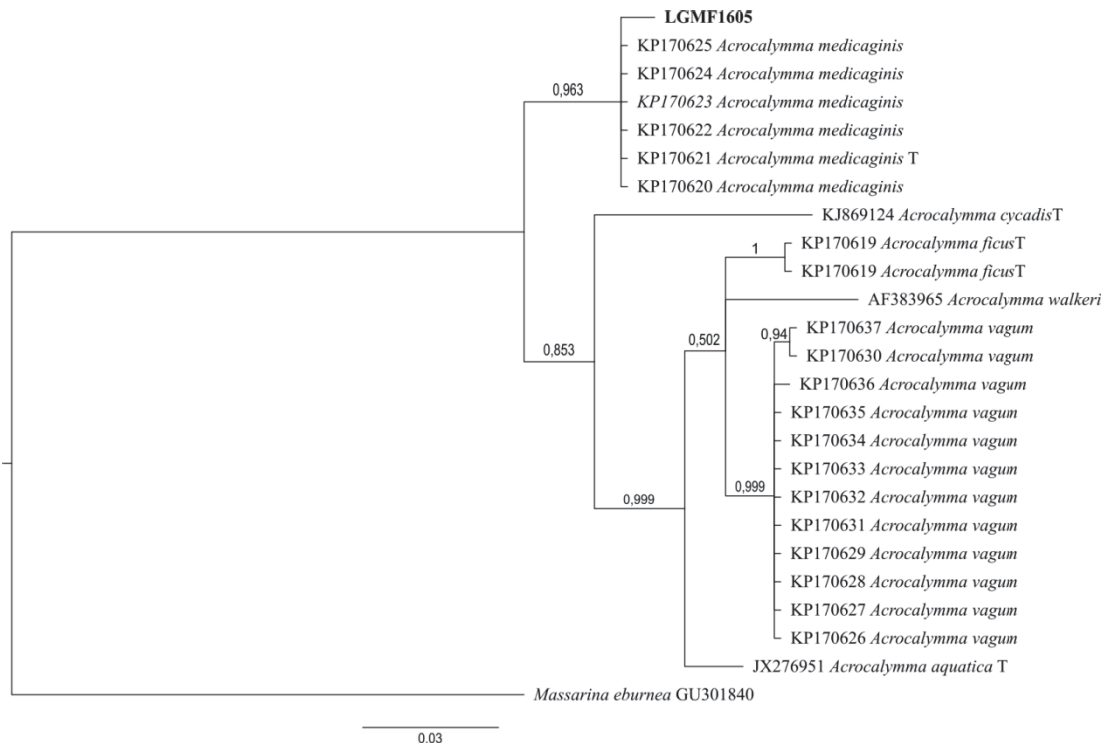


Figure S2-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1605 (bold) identified as *Acrocalymma medicaginis* and sequences of all accepted species from *Acrocalymma* genus. The data matrix had 25 taxa and 465 characters. The tree was rooted to *Massarina eburnea* (AF383959). Scale bar shows 0.03 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

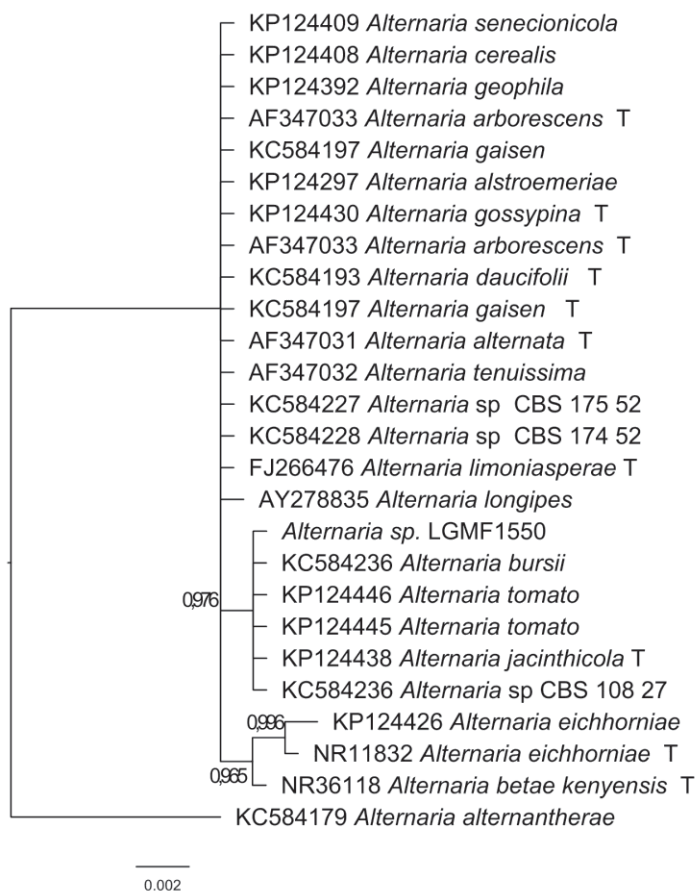


Figure S3-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1550 (bold) identified as *Alternaria* sp., and sequence of all species allocated in *Alternaria* sect. *Alternaria*. The data matrix had 12

taxa and 500 characters. The tree was rooted to *Alternaria alternantherae* (KC584179). Scale bar shows 0.003 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

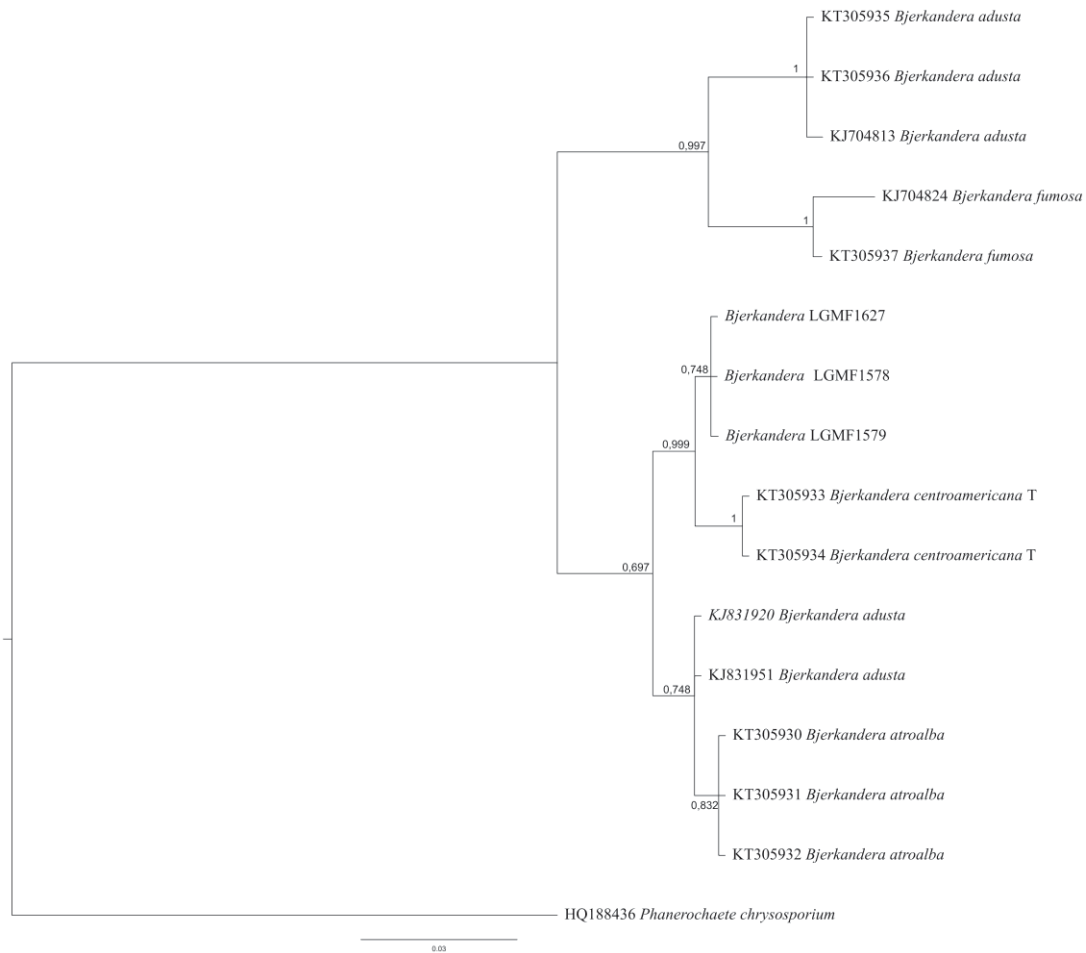


Figure S4—Bayesian phylogenetic tree based on ITS partial sequence of LGMF1627, LGMF1578 and LGMF1579 (**bold**) identified as *Bjerkandera* sp. and sequences of all accepted species from *Bjerkandera*. The tree was rooted to *Phanerochaete chrysosporium* (HQ188436). Scale bar shows 0.03 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

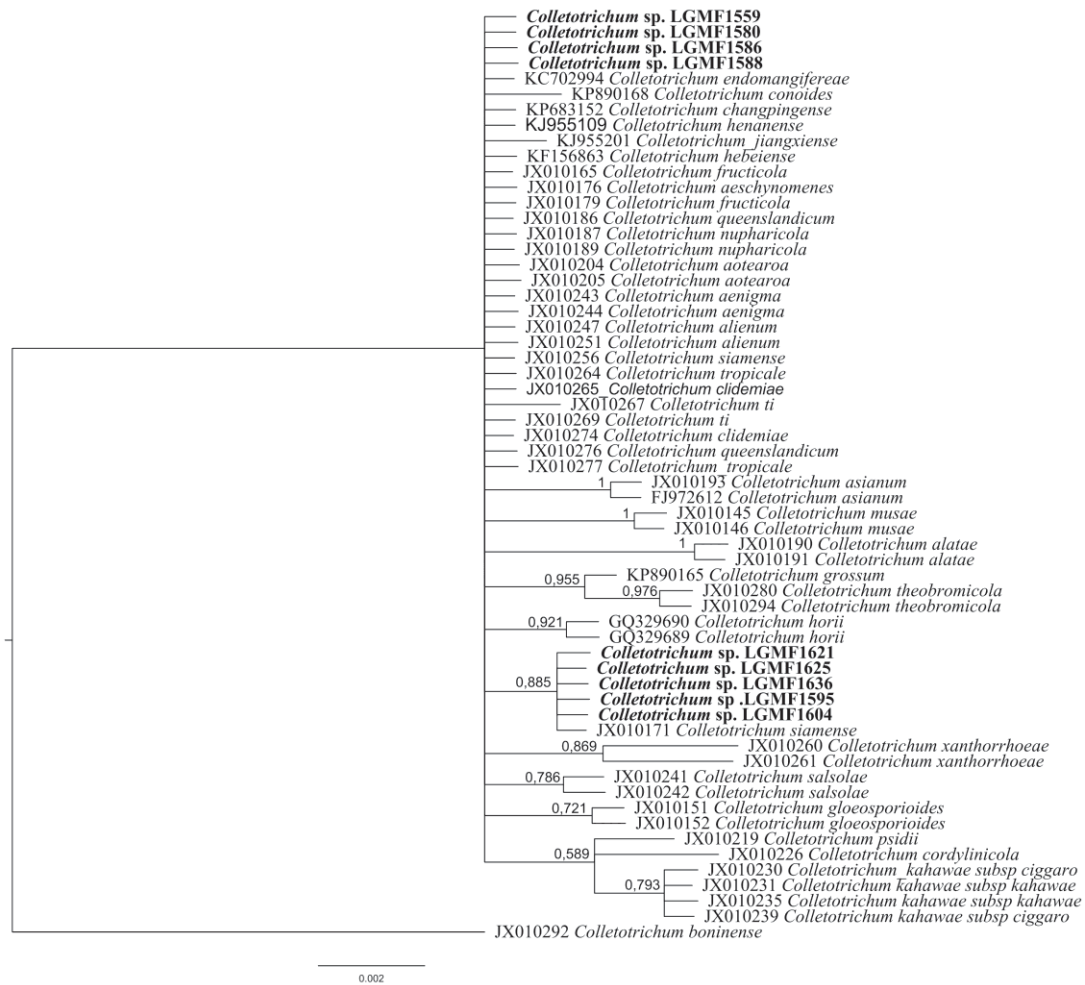


Figure S5-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1559, LGMF1580, LGMF1586, LGMF1621, LGMF1625, LGMF1636, LGMF1595 and LGMF1604 (bold) identified as *Colletotrichum gloeosporioides* sensu lato and sequences of all species of *Colletotrichum gloeosporioides* species complex. The data matrix had 60 taxa and 407 characters. The tree was rooted to *Colletotrichum boninense* (JX010292). Scale bar shows 0.03 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

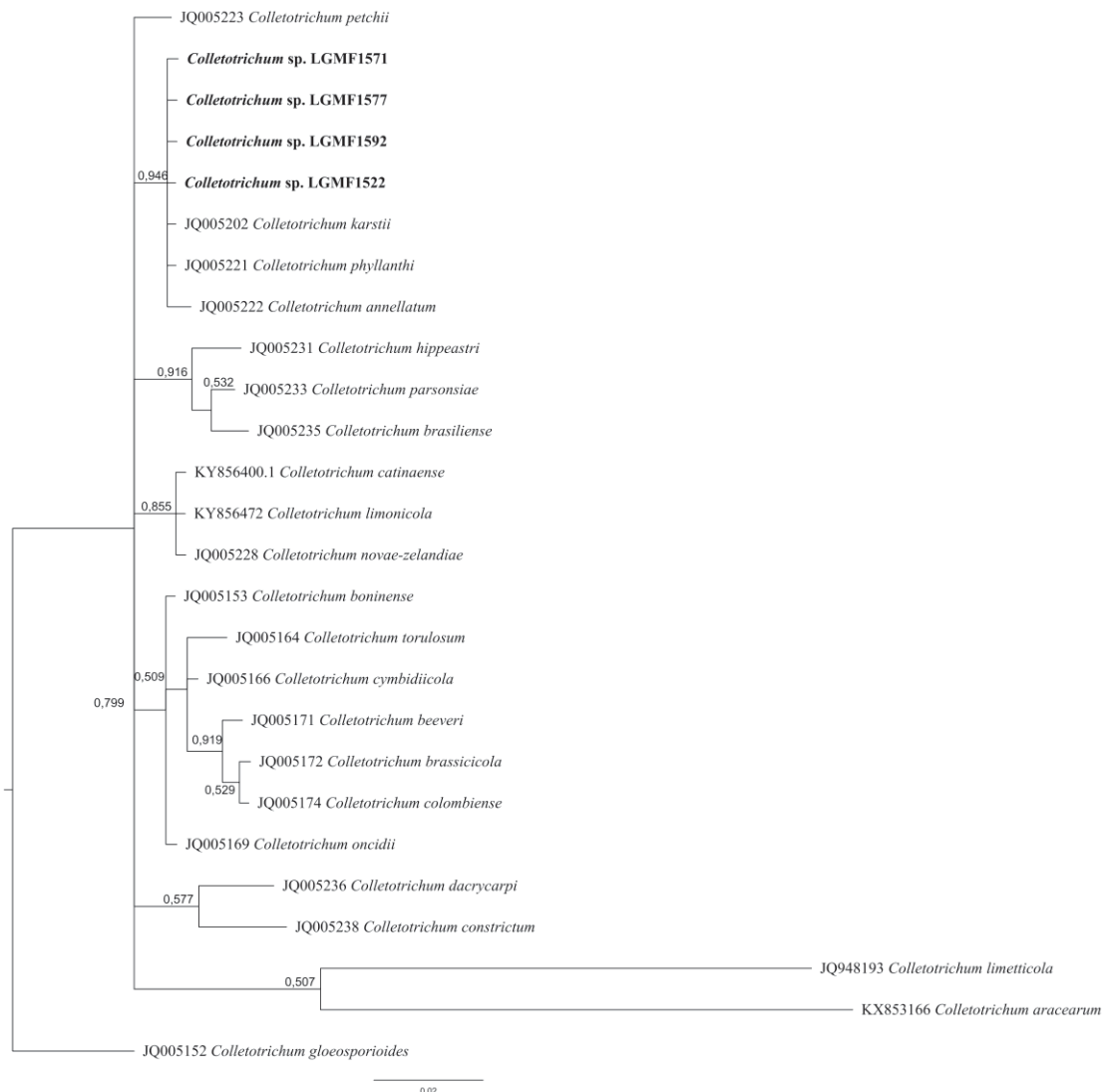


Figure S6-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1571, LGMF1577, LGMF1592, and LGMF1522 (bold) identified as *Colletotrichum boninense* sensu lato and sequences of all accepted species from *Colletotrichum boninense* species complex. The data matrix had 26 taxa and 312 characters. The tree was rooted to *Colletotrichum gloeosporioides* (JQ005152). Scale bar shows 0.002 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

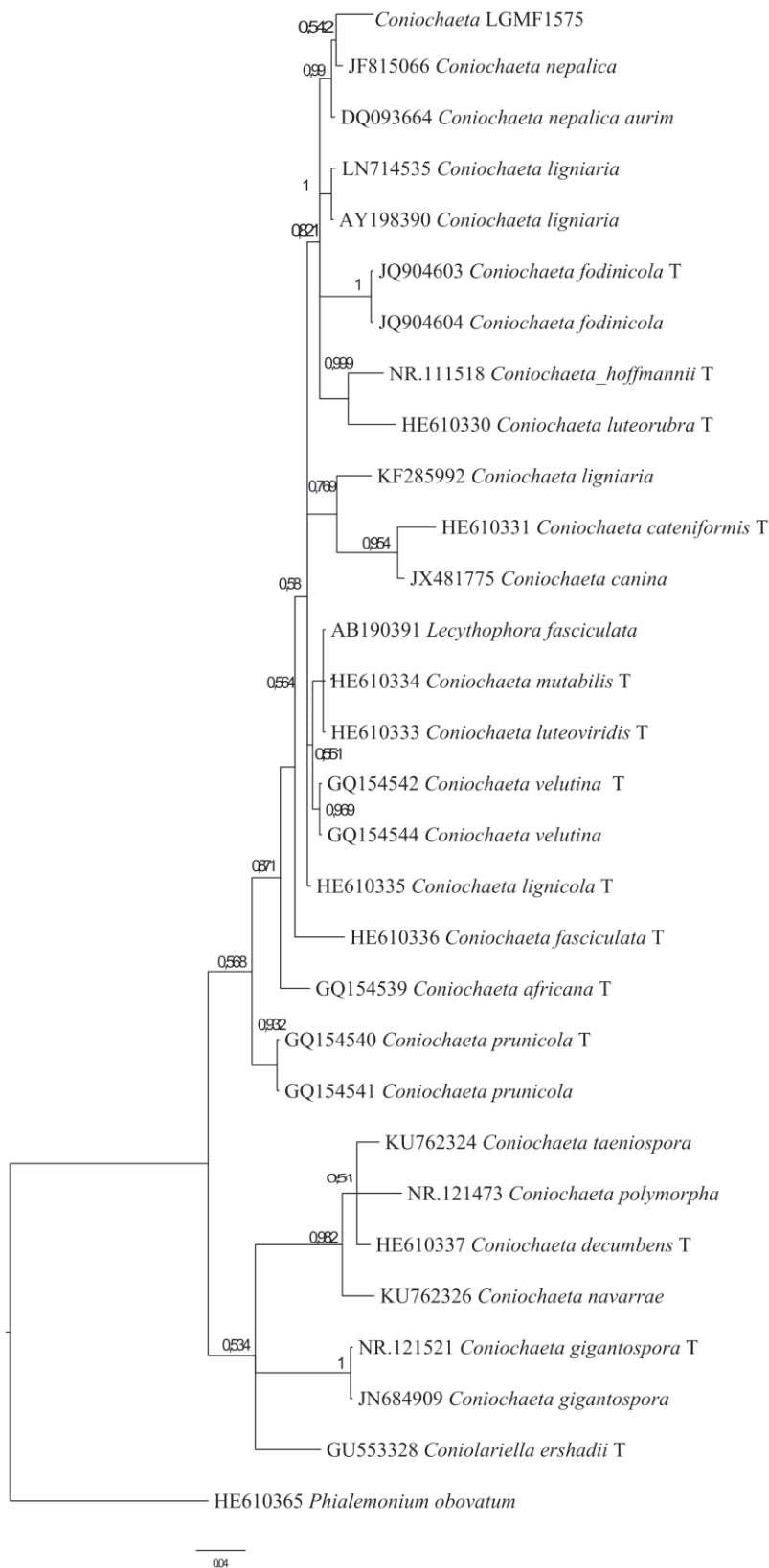


Figure S7-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1575 (bold) identified as *Coniochaeta* sp. and sequences of all accepted species from *Coniochaeta* genus. The data matrix had 30 taxa and 488 characters. The tree was rooted to *Phialemonium obovatum* (HE610365). Scale bar shows 0.004 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

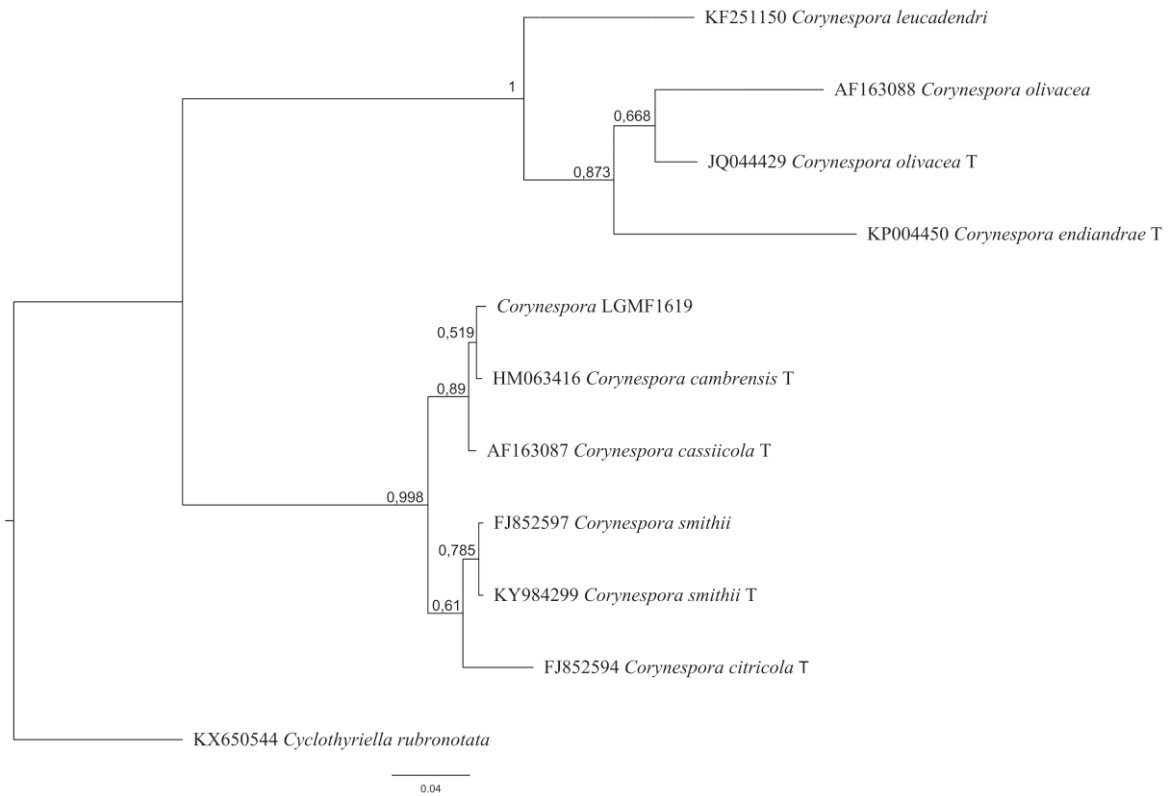


Figure S8-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1619 (bold) identified as *Corynespora cambrensis* and sequences of all accepted species from *Corynespora* genus. The data matrix had 11 taxa and 409 characters. The tree was rooted to *Cyclothyriella rubronotata* (KX650544). Scale bar shows 0.04 changes and Bayesian posterior probability values are indicated at the nodes T: type strain.

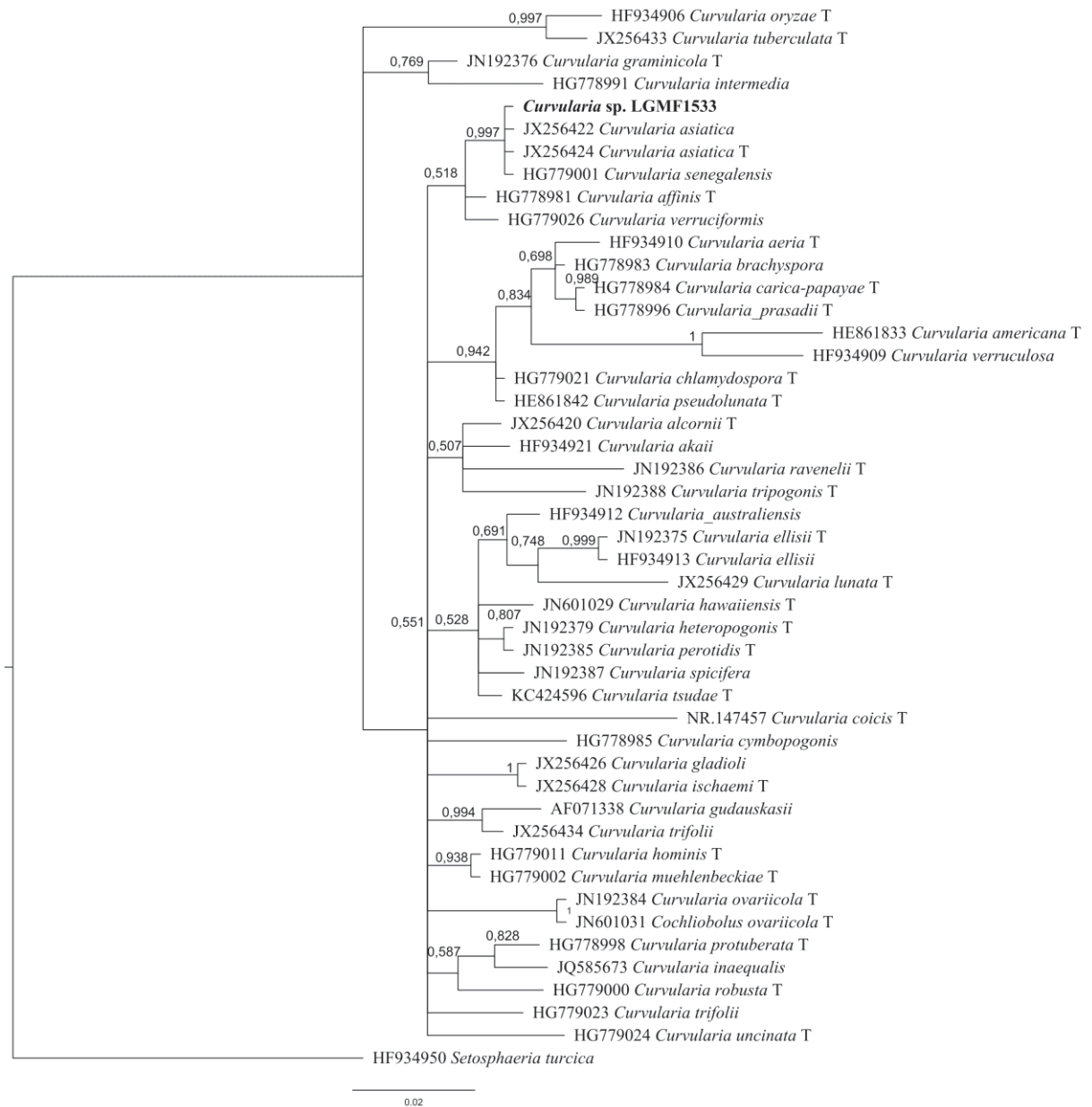


Figure S9-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1533 (bold) identified as *Curvularia* sp. and sequences of all accepted species from *Curvularia* genus. The data matrix had 47 taxa and 491 characters. The tree was rooted to *Setosphaeria turcica* (HF934950). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

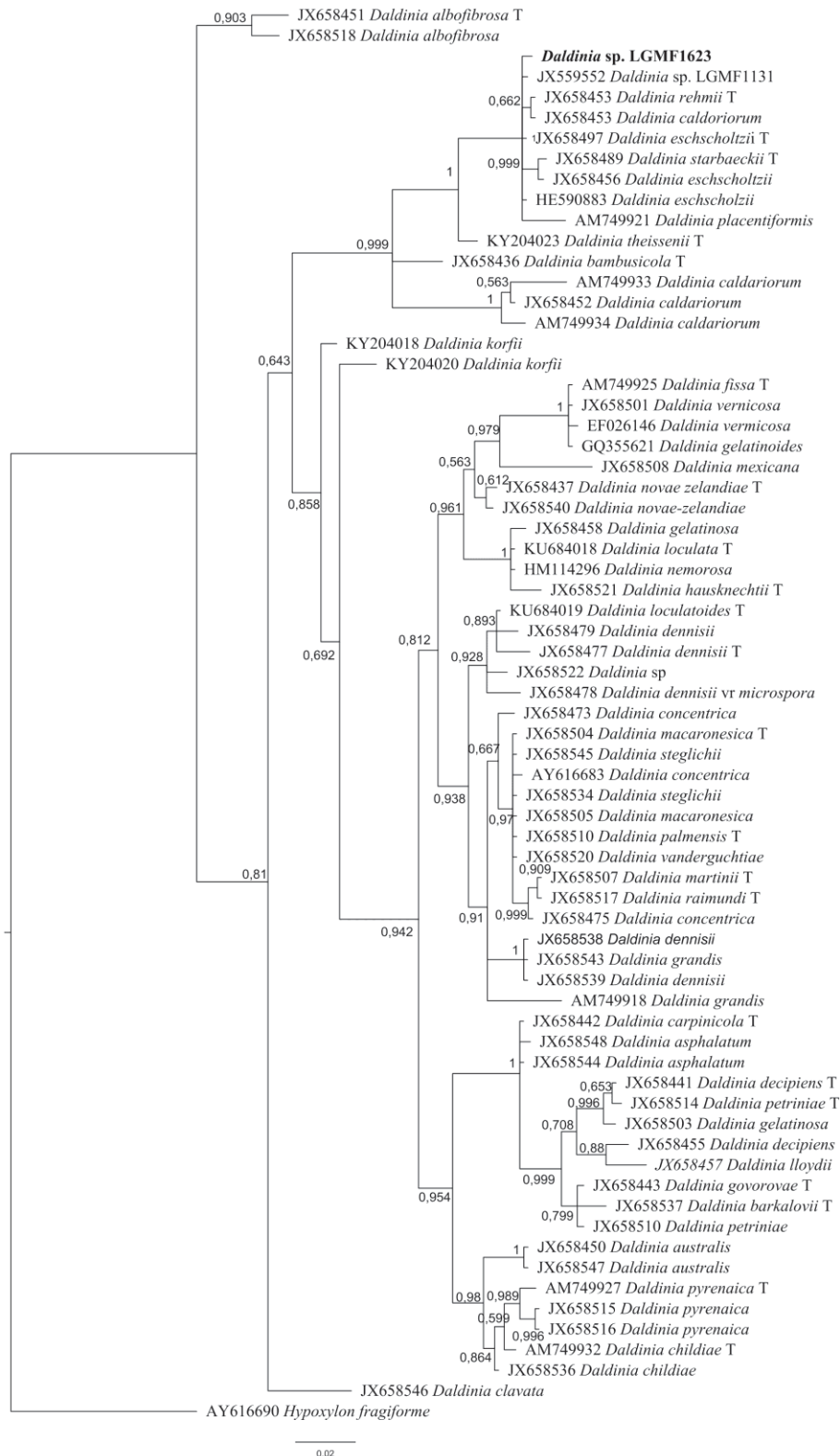
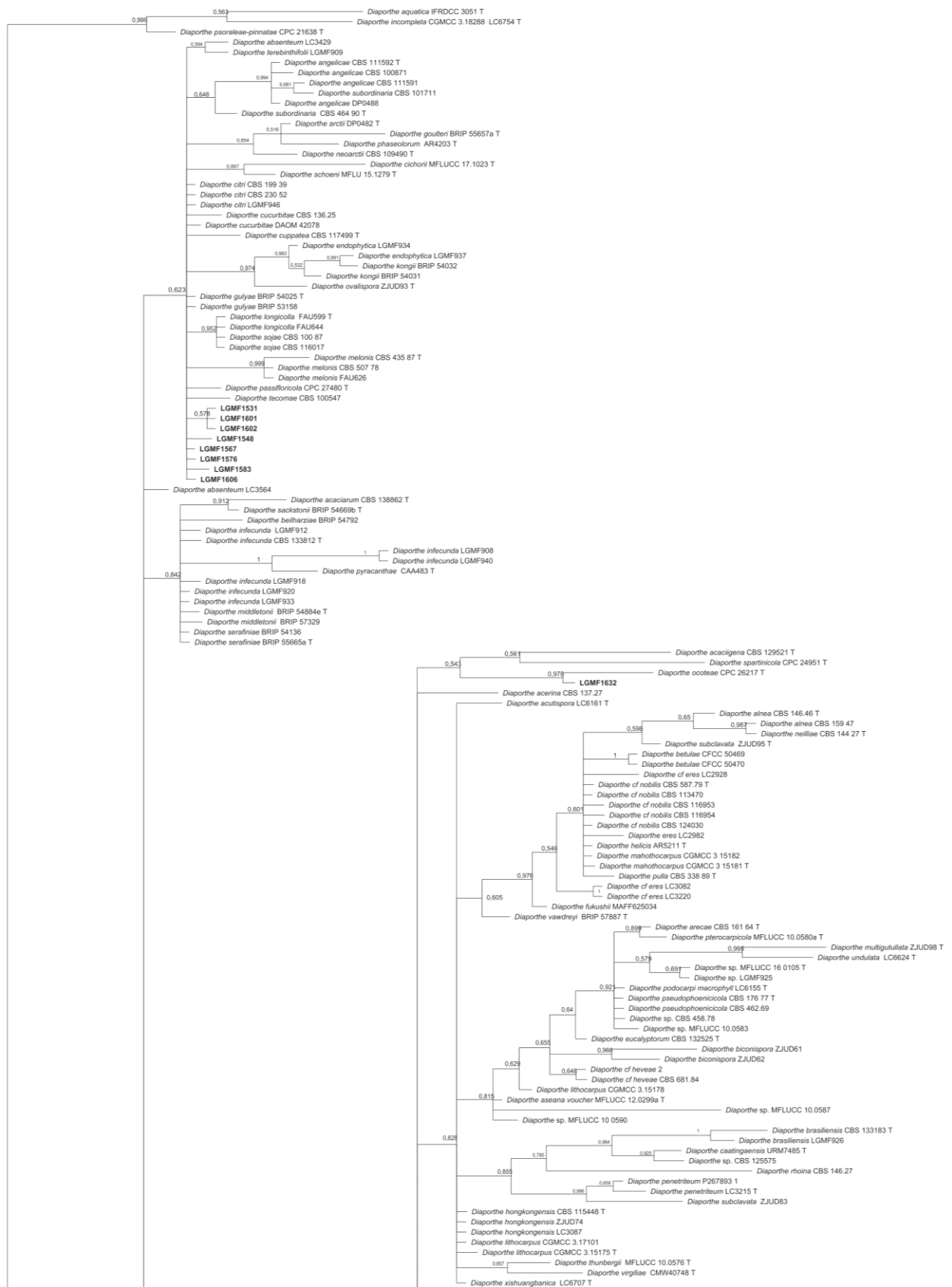
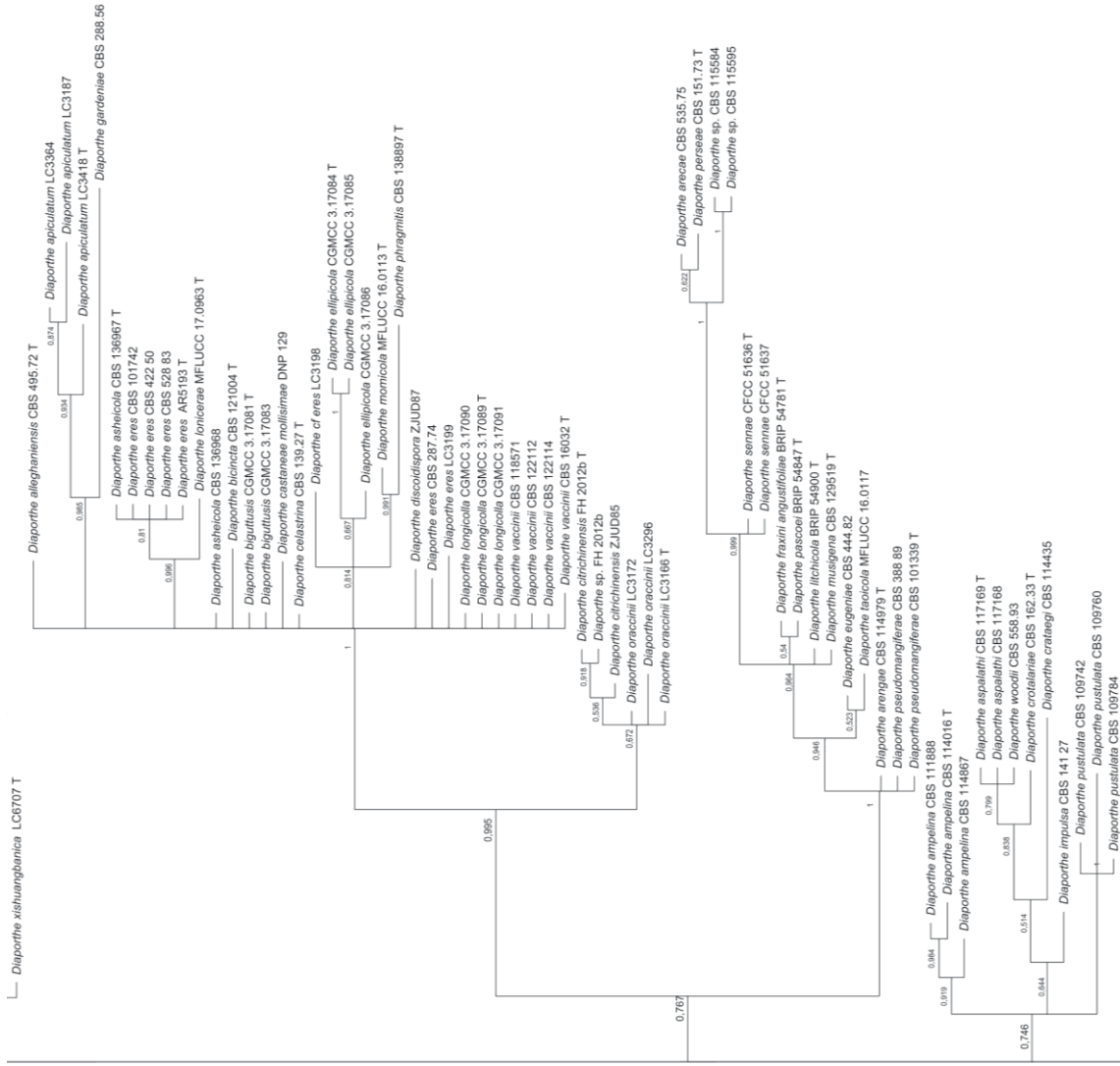
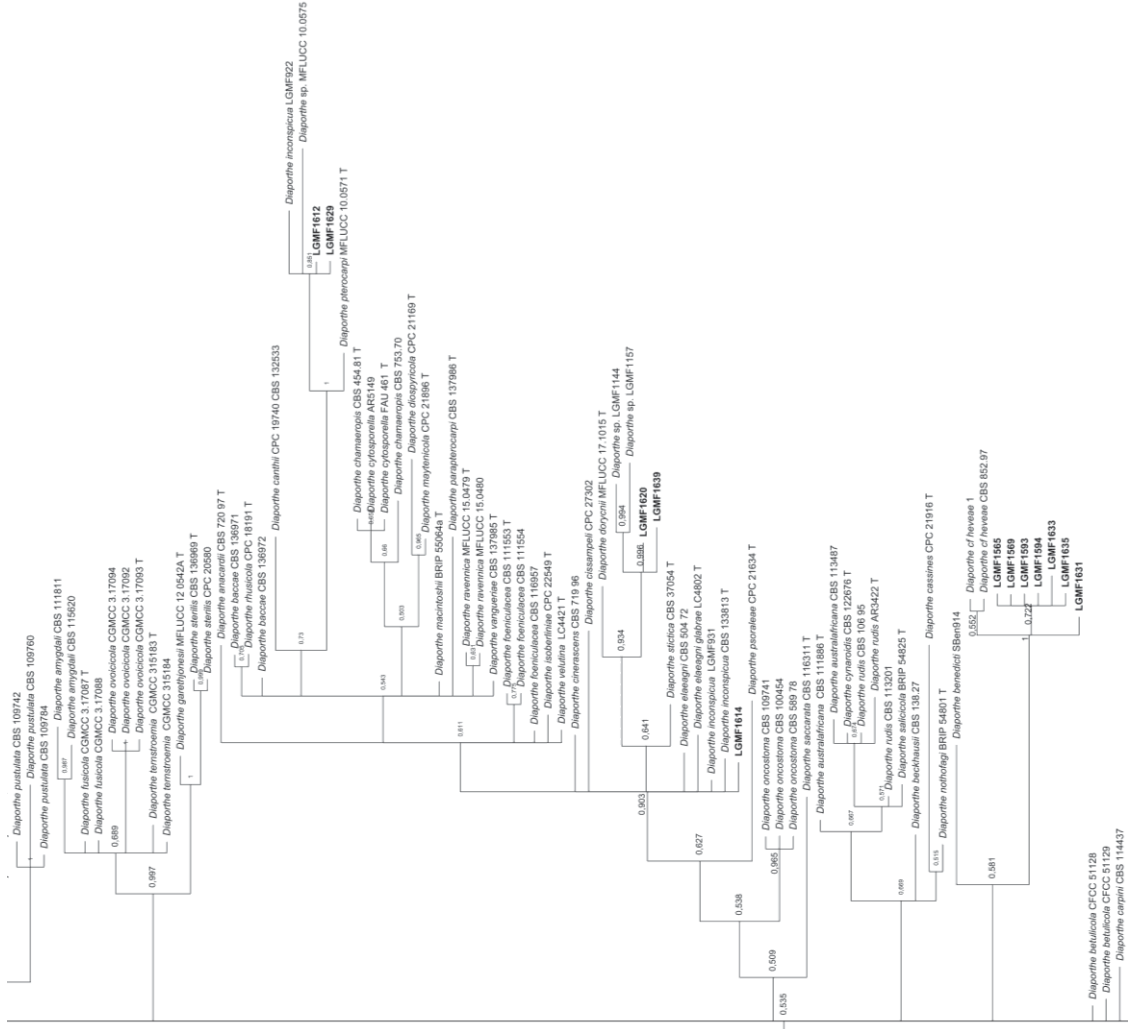


Figure S10-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1623 (bold) identified as *Daldinia* sp. and sequences of all accepted species from *Daldinia* genus. The data matrix had 69 taxa and 522 characters. The tree was rooted to *Hypoxylon fragiforme* (AY616690). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain







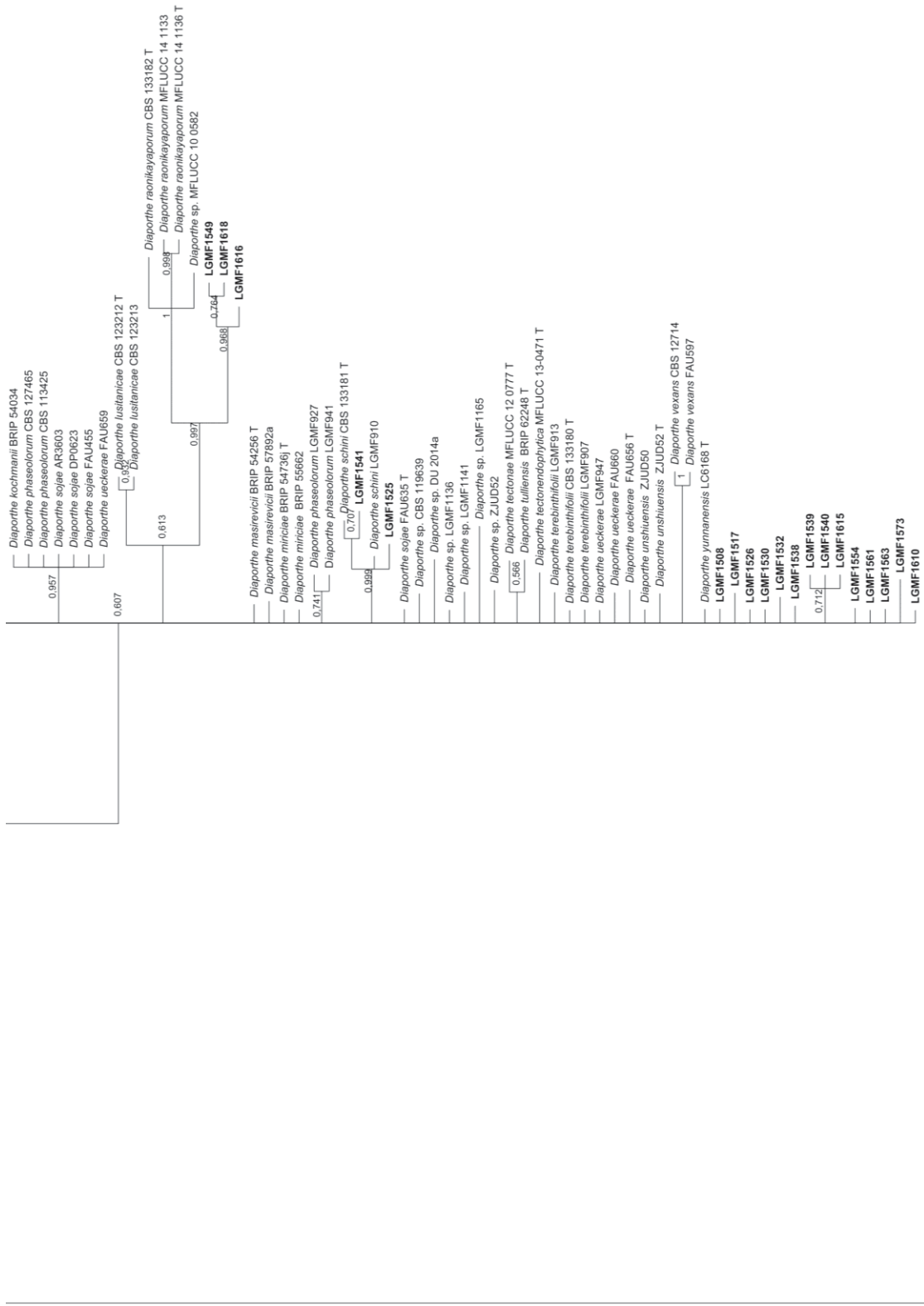


Figure S11-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1610, LGMF1612, LGMF1614, 1538, LGMF1539, LGMF1540, LGMF1615, LGMF1616, LGMF1541, LGMF1618, LGMF1620, LGMF1548, 1549, LGMF1554, LGMF1629, LGMF 1561, LGMF1563, LGMF1631, LGMF1632, LGMF 1565, LGMF1567, LGMF 1569, LGMF 1633, LGMF1573, LGMF1576, LGMF1635, LGMF1583, LGMF1639, LGMF1593, LGMF1594, LGMF1601, LGMF1602, LGMF1508, LGMF1517, LGMF1606, LGMF1525, LGMF1526, LGMF1530, LGMF1531, LGMF1532, and LGMF1526 (bold) sequences of all accepted species from *Diaporthe* genus. The data matrix had 383 taxa and 537 characters. The tree was rooted to *Diaporthe corylina* (KC343004). T: type strain.

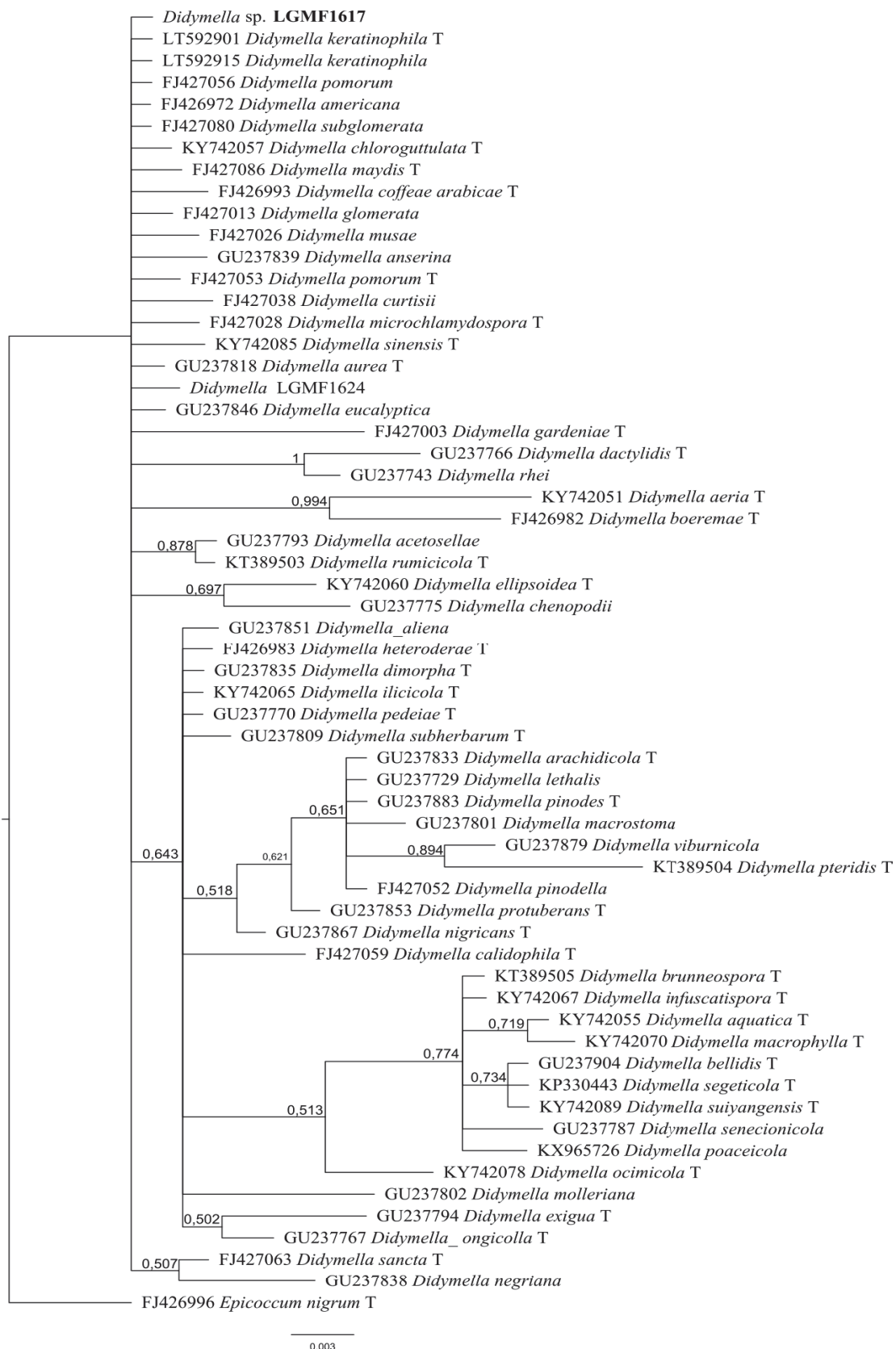


Figure S12-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1617 (bold) identified as *Didymella* sp. and sequences of all accepted species from *Didymella*. The data matrix had 60 taxa and 497 characters. The tree was rooted to *Epicoccum nigrum* (FJ426996). Scale bar shows 0.003 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

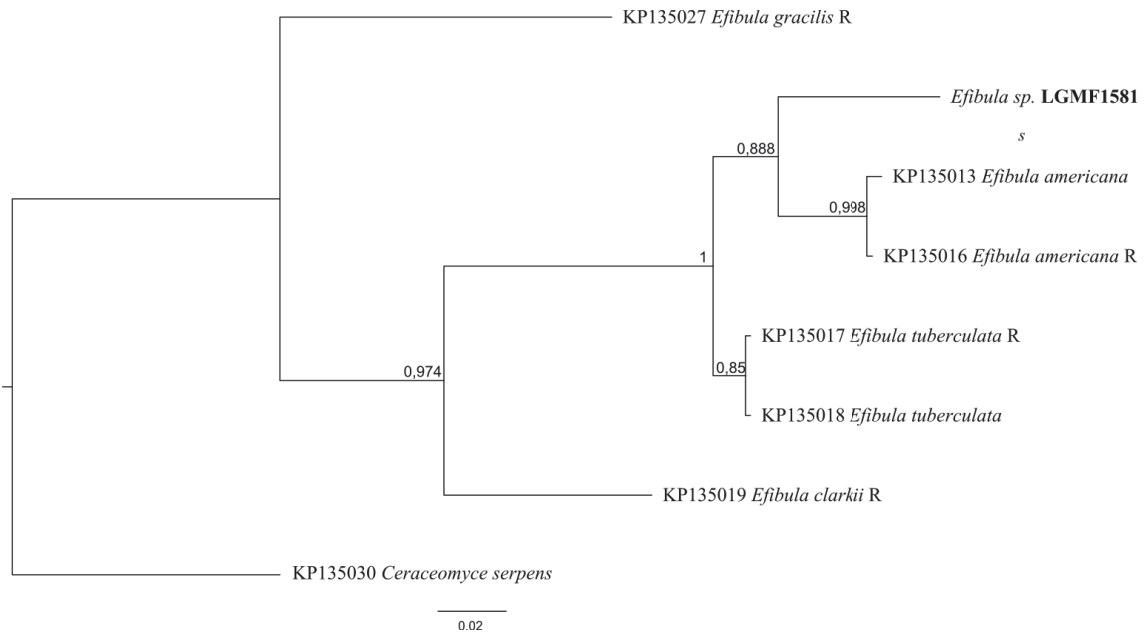


Figure S13-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1581 (bold) identified as *Efibula* sp. and sequences of all accepted species from *Efibula* genus. The data matrix had 8 taxa and 615 characters. The tree was rooted to *Ceraceomyces serpens* (KP135030). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain; R: representative strain.

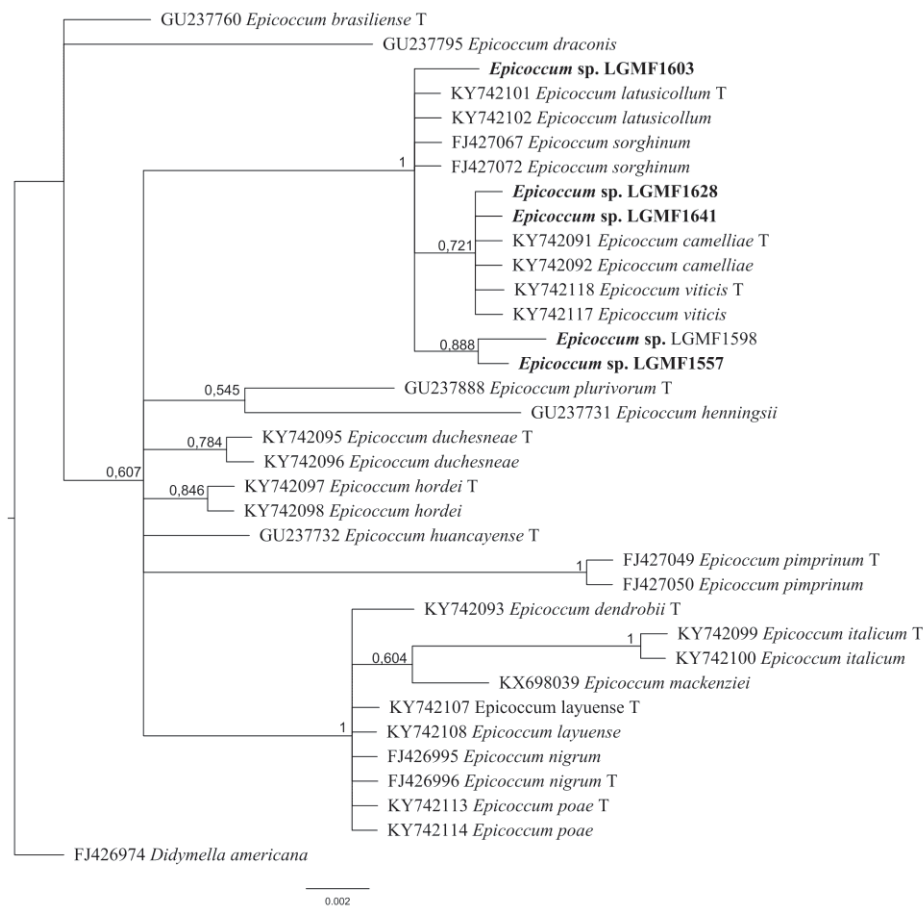


Figure S14-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1603, LGMF1628, LGMF1641, LGMF1598 and LGMF1557 (bold) identified as *Epicoccum* sp. and sequences of all accepted species from *Epicoccum* genus. The data matrix had 35 taxa and 455 characters. The tree was rooted to *Didymella americana* (FJ426974). Scale bar shows 0.002 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

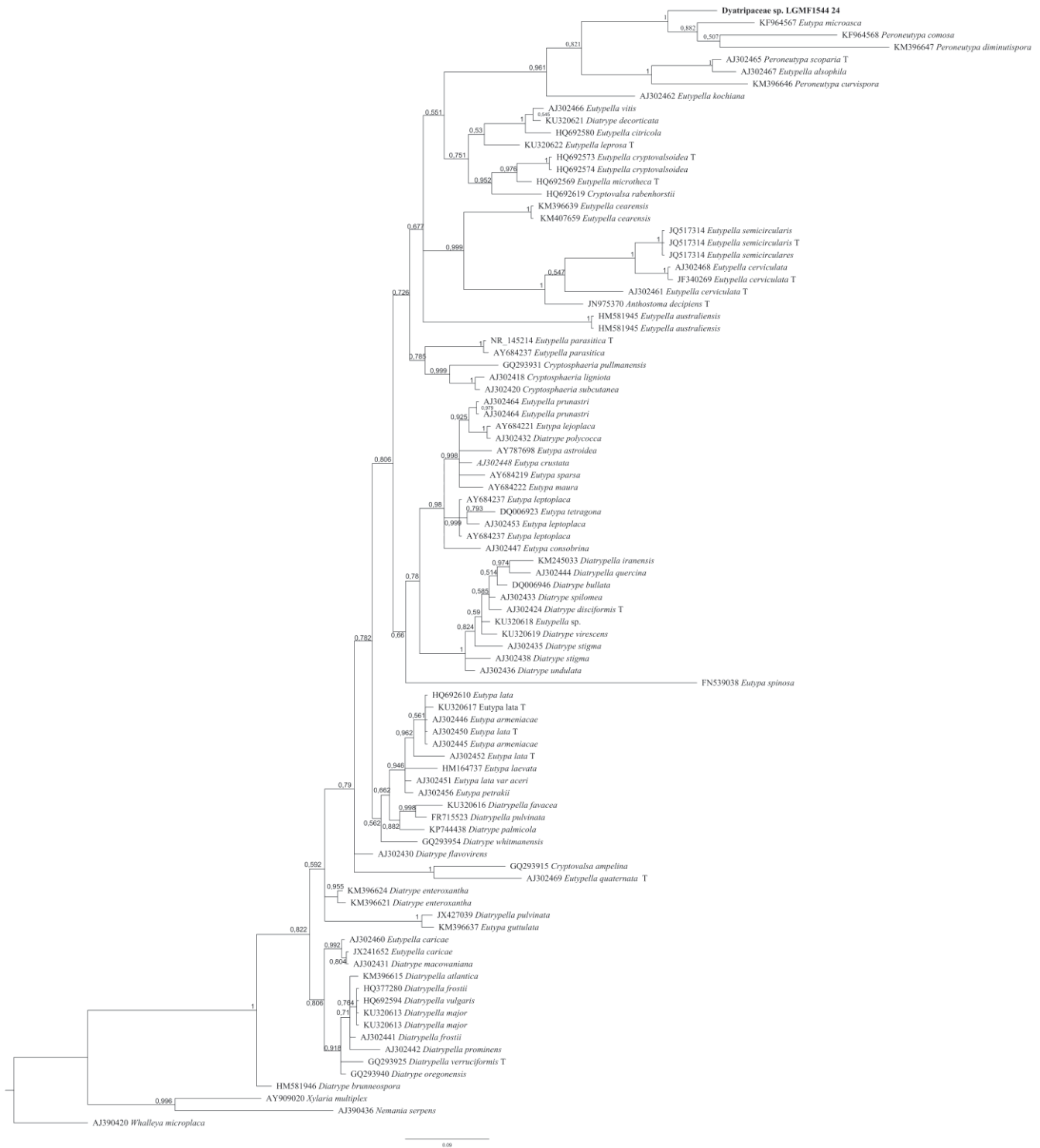


Figure S15-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1544 (bold) identified as *Diatrypaeae* sp. and sequences of all accepted genera from *Diatrypaeae* family. The data matrix had 110 taxa and 641 characters. The tree was rooted to *Whalleya microplaca* (AJ390420). Scale bar shows 0.002 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.



Figure S16-Bayesian phylogenetic tree based on EF partial sequence of LGMF1546, LGMF1553, LGMF1590, LGMF1547 and LGMF1558 (bold) identified as *Fusarium* sp. and sequences of all accepted species from *Fusarium* genus. The data matrix had 97 taxa and 680 characters. The tree was rooted to *Fusarium oxysporum* (NRRL22902). Scale bar shows 0.008 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

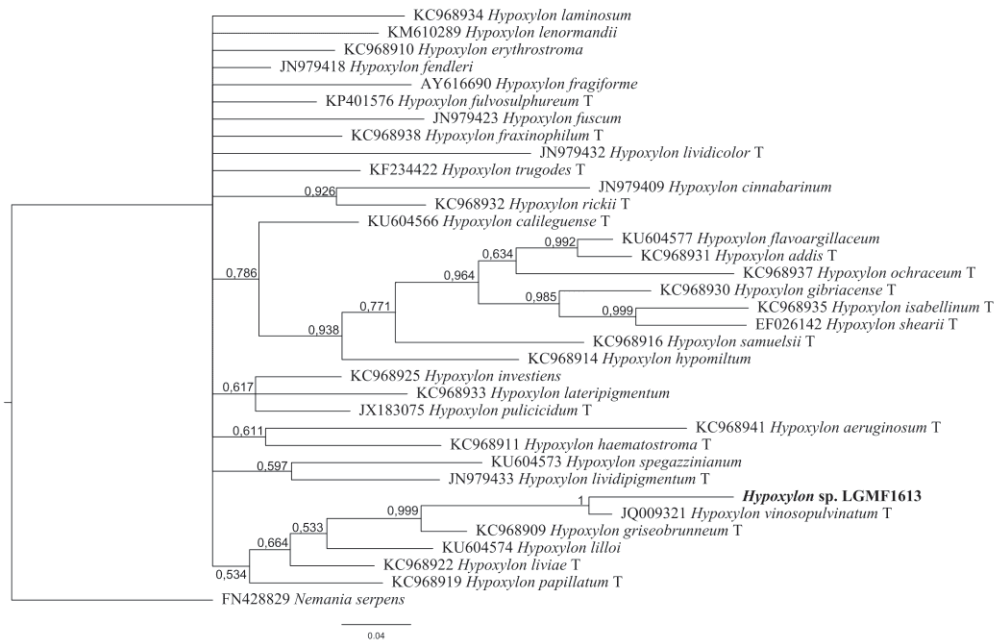


Figure S17-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1613 (bold) identified as *Hypoxylon* sp. and sequences of all accepted species from *Hypoxylon* genus. The data matrix had 35 taxa and 369 characters. The tree was rooted to *Nemaniam serpens* (FN428829). Scale bar shows 0.04 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

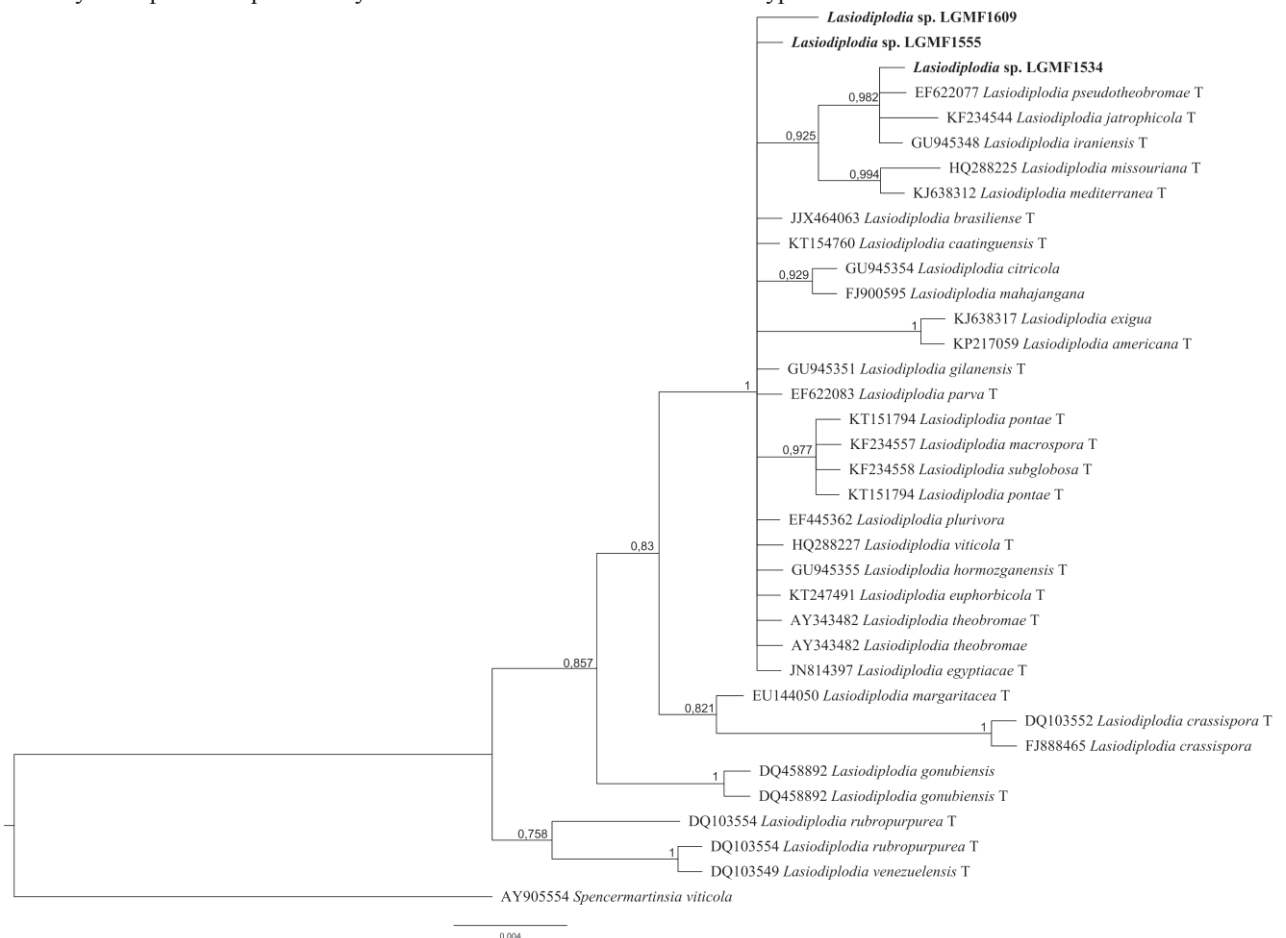


Figure S18-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1609, LGMF1555 and LGMF1534 (bold) identified as of *Lasiodiplodia* sp. and sequences of all accepted species from *Lasiodiplodia* genus. The data matrix had 34 taxa and 401 characters. The tree was rooted to

Spencermartinsia viticola (AY905554). Scale bar shows 0.004 changes and Bayesian posterior probability values are indicated at the nodes T: type strain.

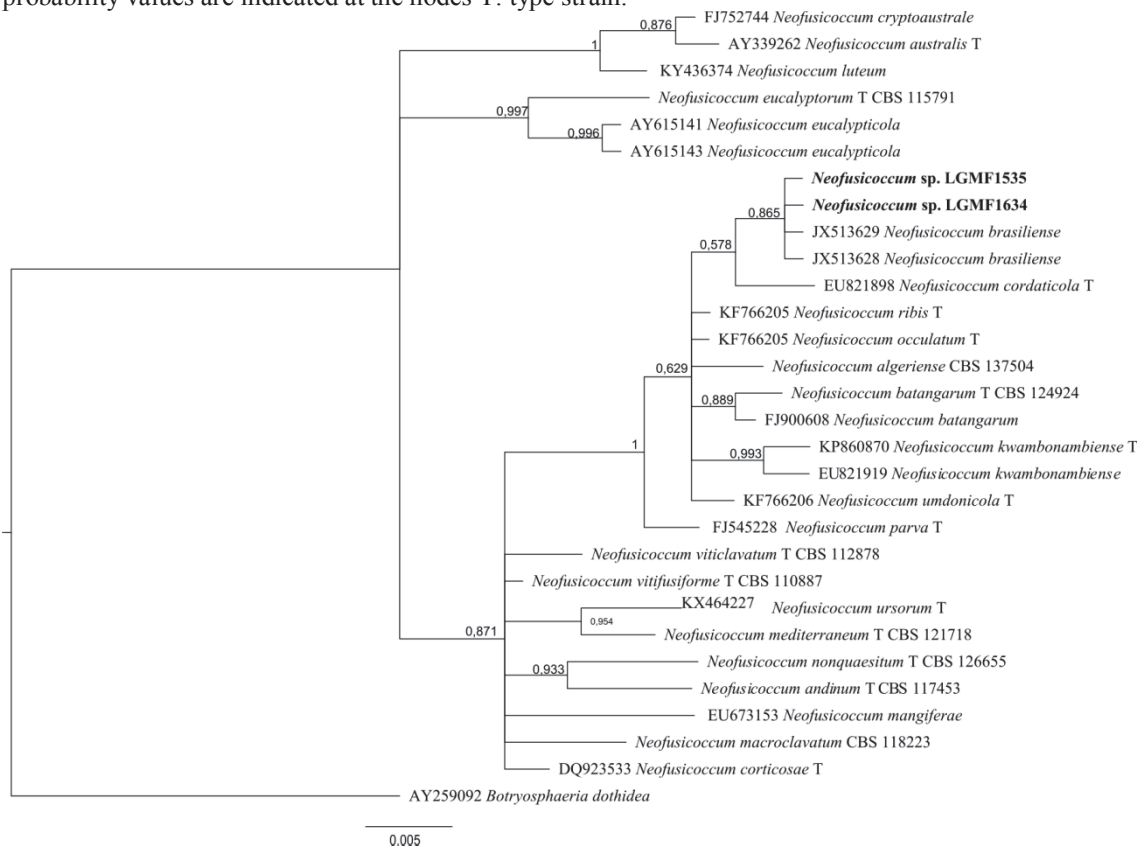


Figure S19-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1535 and LGMF1634 (bold) identified as *Neofusicoccum brasiliense* and *Neofusicoccum* sp. The data matrix had 30 taxa and 505 characters. The tree was rooted to *Botryosphaeria dothidea* (AY259092). Scale bar shows 0.005 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

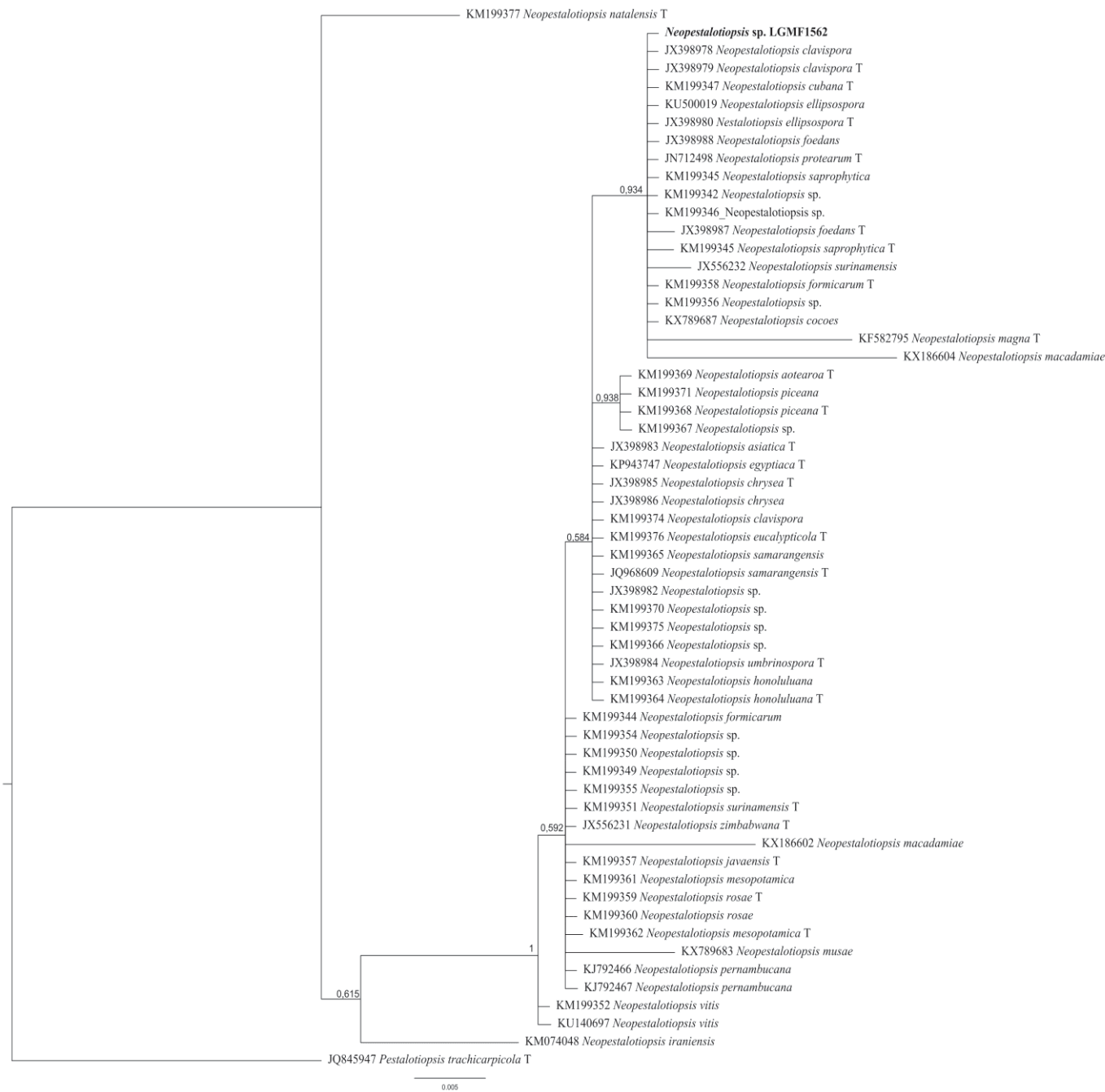


Figure S20-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1562 (bold) identified as *Neopestalotiopsis* sp. and sequences of all accepted species from *Neopestalotiopsis* genus. The data matrix had 59 taxa and 480 characters. The tree was rooted to *Pestalotiopsis trachicarpicola* (JQ845947). T: type strain.

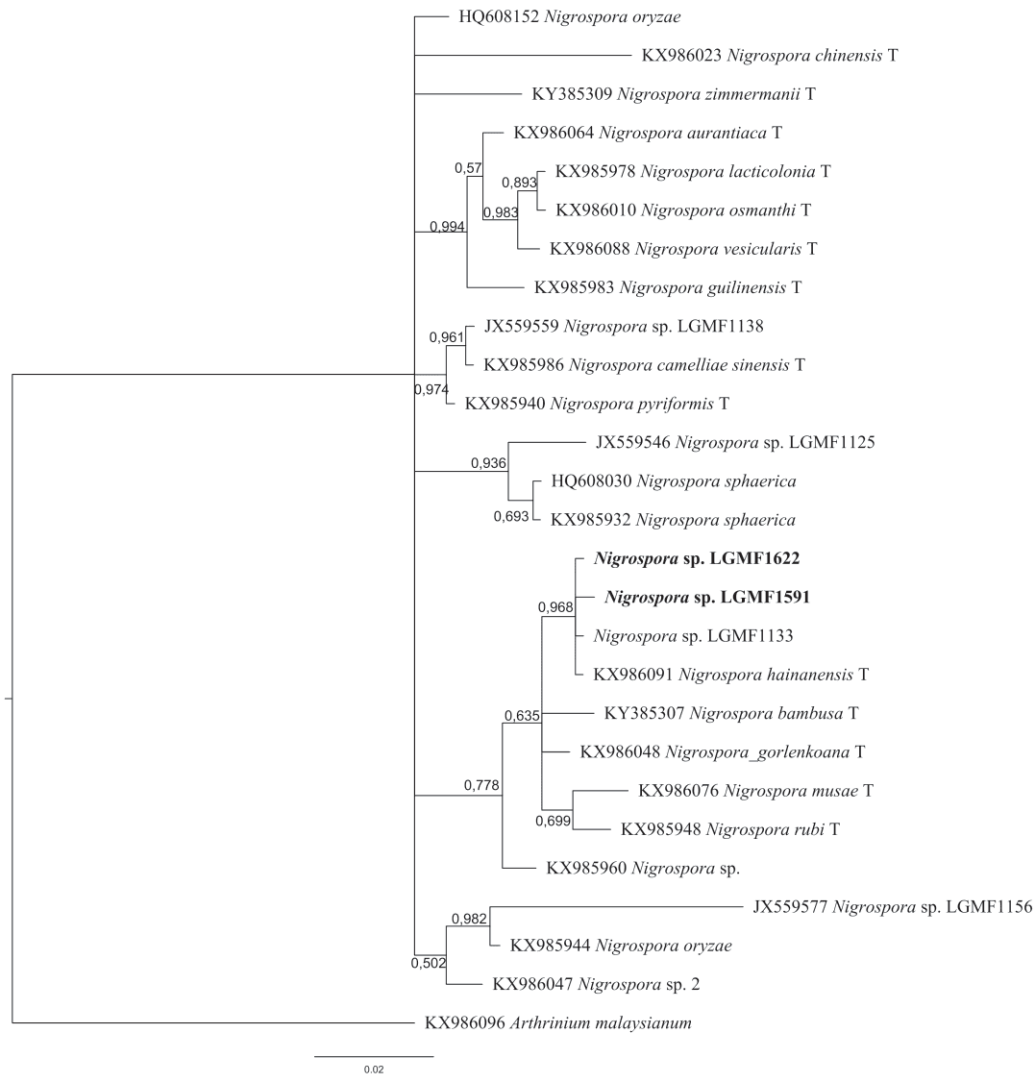


Figure S21-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1622 and LGMF1591 (bold) identified as *Nigrospora hainanensis* and sequences of all accepted species from *Nigrospora* genus. The data matrix had 27 taxa and 500 characters. The tree was rooted to *Arthrinium malaysianum* (KX986096). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

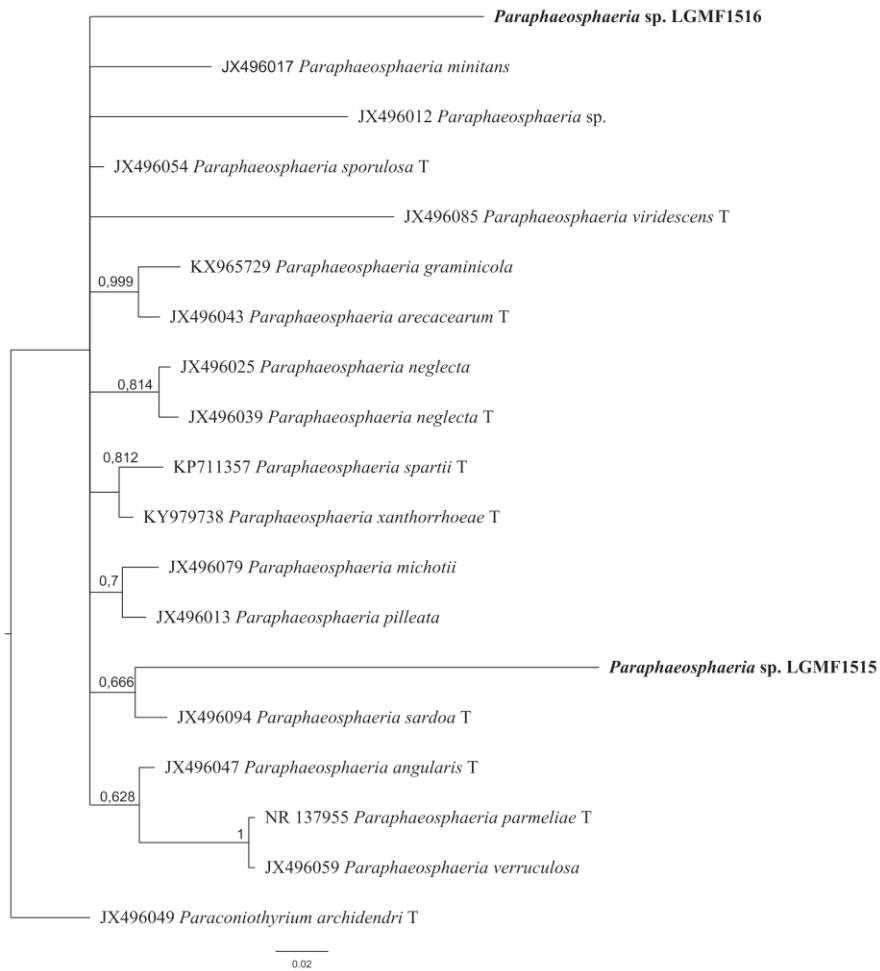


Figure S22-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1515 and LGMF1516 (bold) identified as *Paraphaeosphaeria* sp. and sequences of all accepted species from *Paraphaeosphaeria* genus. The data matrix had 19 taxa and 488 characters. The tree was rooted to *Paraconiothyrium archidendri* (JX496049). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

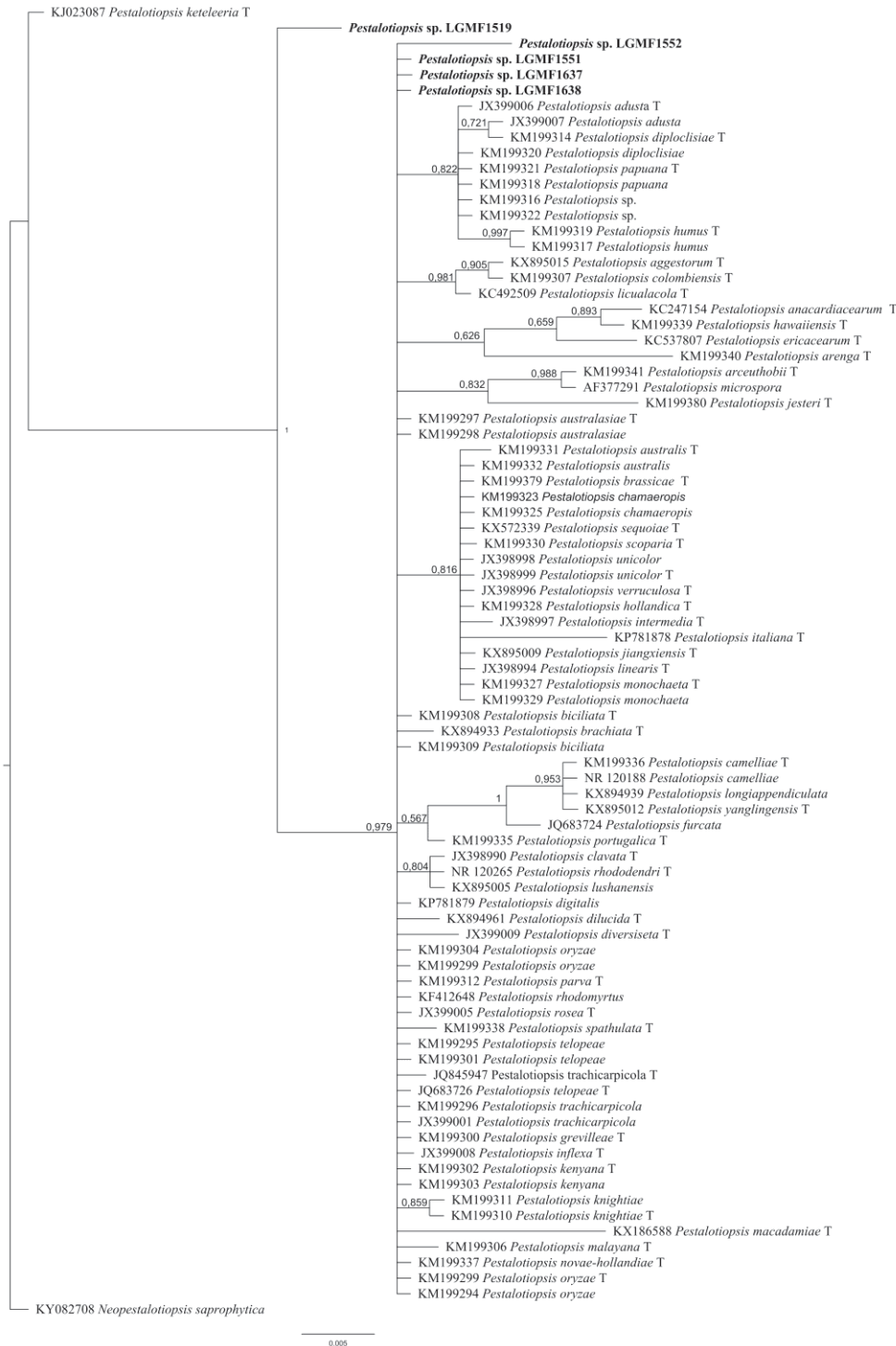


Figure S23-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1519, LGMF1552, LGMF1551, LGMF1637 and LGMF1638 (bold) identified as *Pestalotiopsis* sp. and sequences of all accepted species from *Pestalotiopsis* genus. The data matrix had 84 taxa and 376 characters. The tree was rooted to *Neopestalotiopsis saprophytica* (KY082708). Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

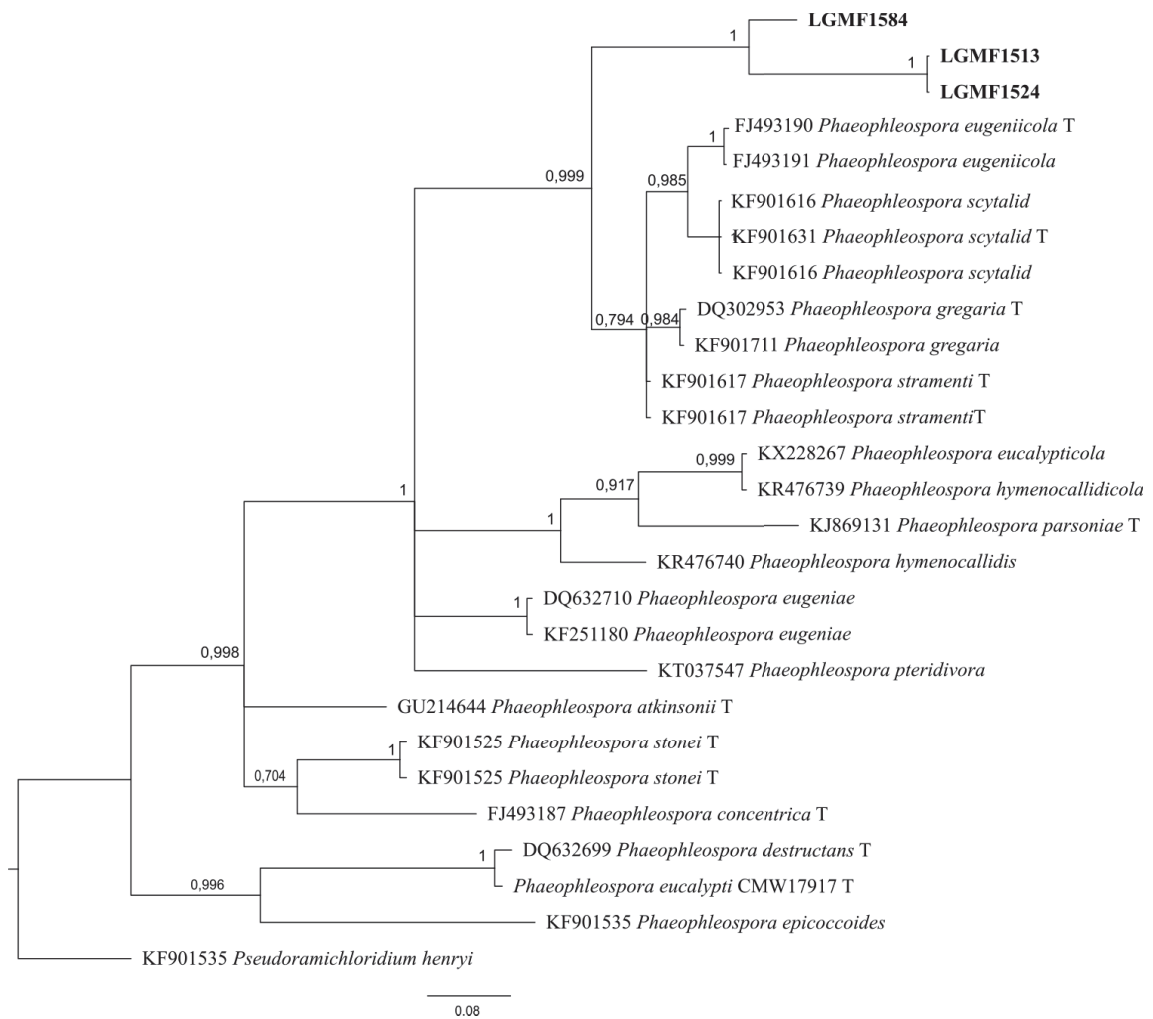


Figure S24-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1584, LGMF1513 and LGMF1524 (bold) identified as *Phaeophleospora* sp. and sequences of all accepted species from *Phaeophleospora* genus. The data matrix had 27 taxa and 496 characters. The tree was rooted to *Pseudoramichloridium henryi* (KF901535). Scale bar shows 0.08 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain

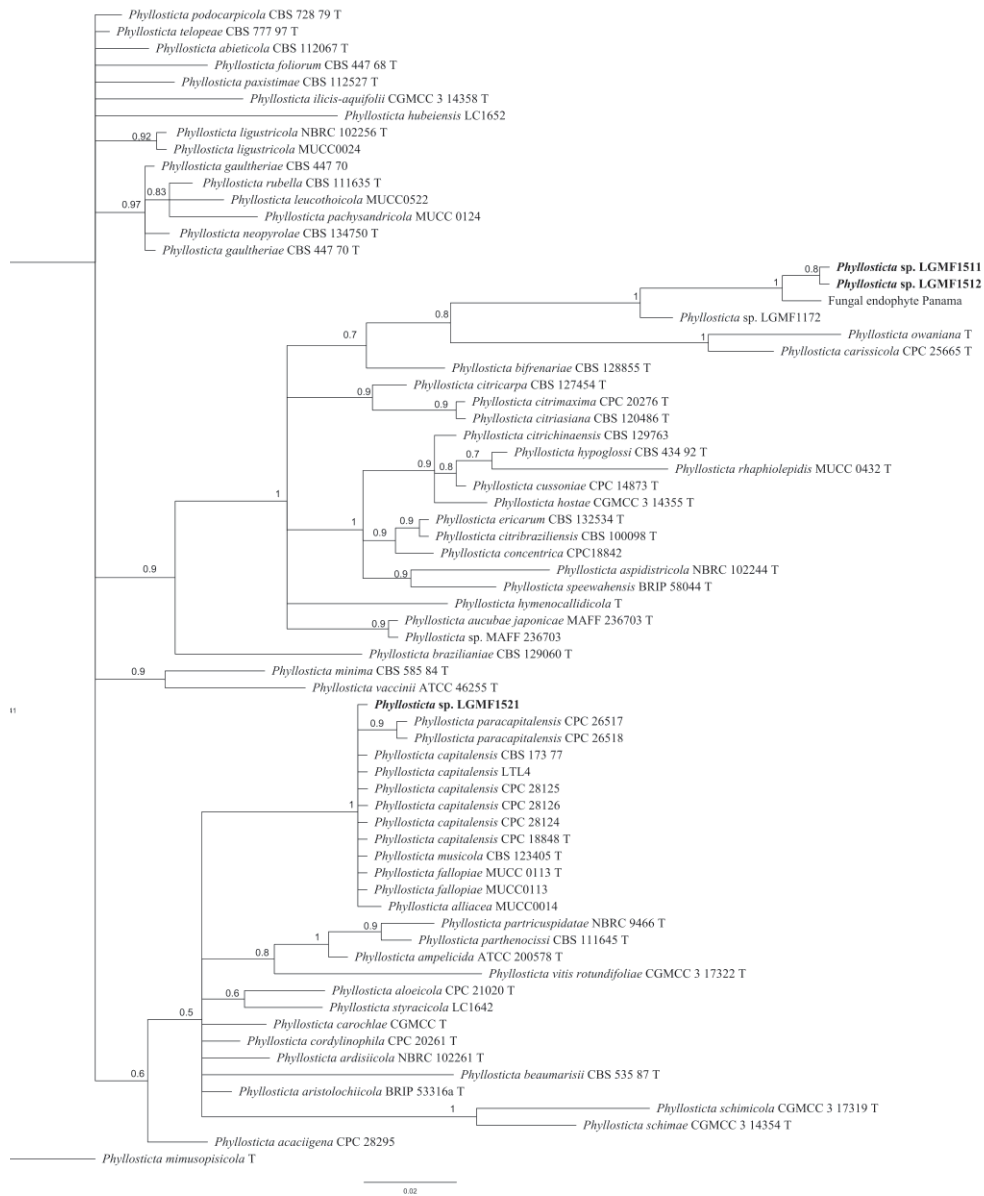


Figure S25-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1584, LGMF1513 and LGMF1524 (bold) identified as *Phyllosticta* sp. and sequences of all accepted species from *Phyllosticta* genus. The data matrix had 69 taxa and 358 characters. The tree was rooted to *Phyllosticta mimosopiscicola*. Scale bar shows 0.02 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

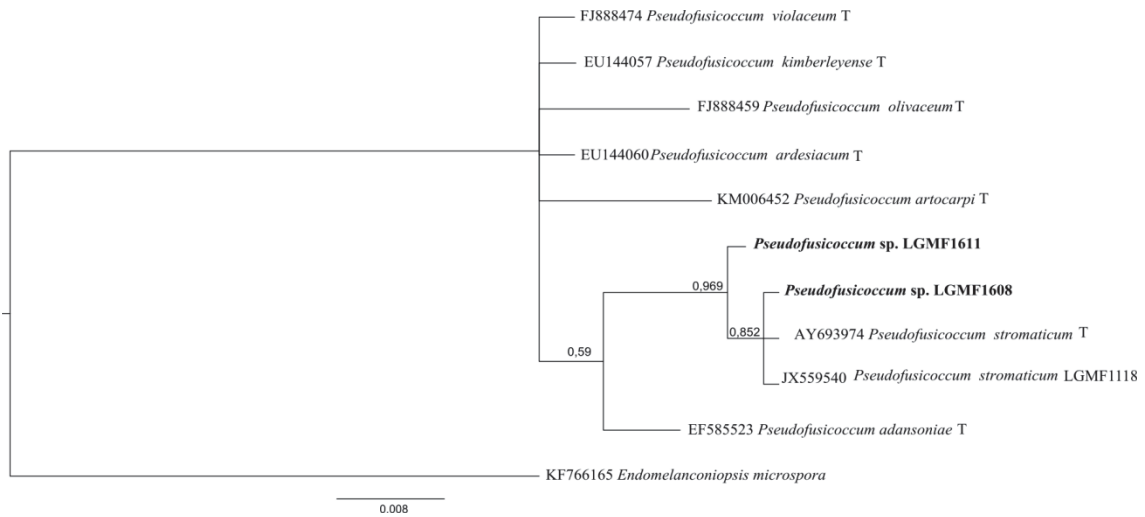


Figure S26-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1611 and LGMF1608 (bold) identified as *Pseudofusicoccum stromaticum* and *Pseudofusicoccum* sp. and sequences of all accepted species from *Pseudofusicoccum* genus. The data matrix had 11 taxa and 519 characters. The tree was rooted to *Endomelanconiopsis microspora* (KF766165). Scale bar shows 0.008 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

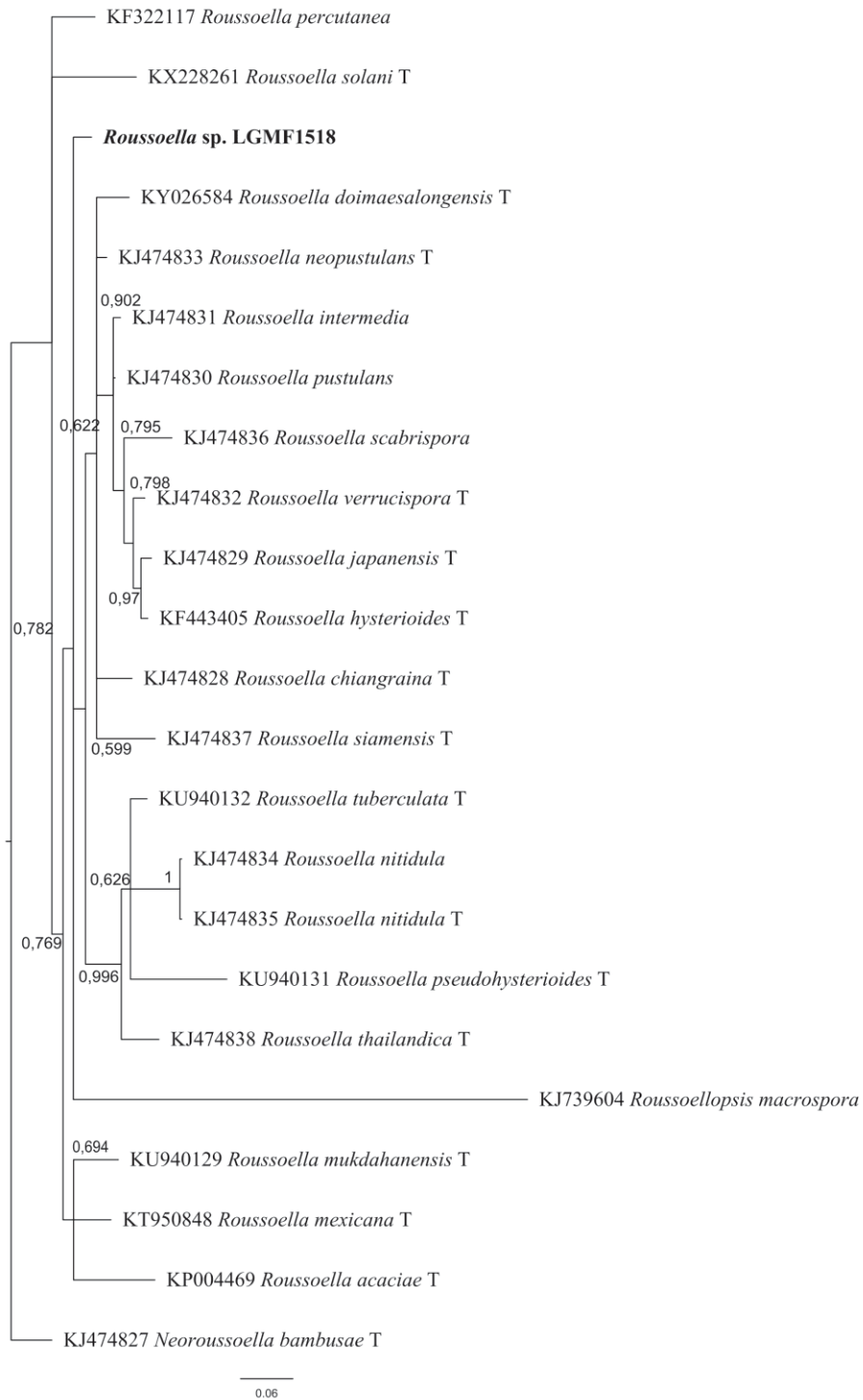


Figure S27-Bayesian phylogenetic tree based on ITS partial sequence of LGMF1518 (bold) identified as *Roussoella* sp. and sequences of all accepted species from *Roussoella* genus. The data matrix had 23 taxa and 388 characters. The tree was rooted to *Neorousoella bambusae* (KJ474827). Scale bar shows 0.06 changes and Bayesian posterior probability values are indicated at the nodes. T: type strain.

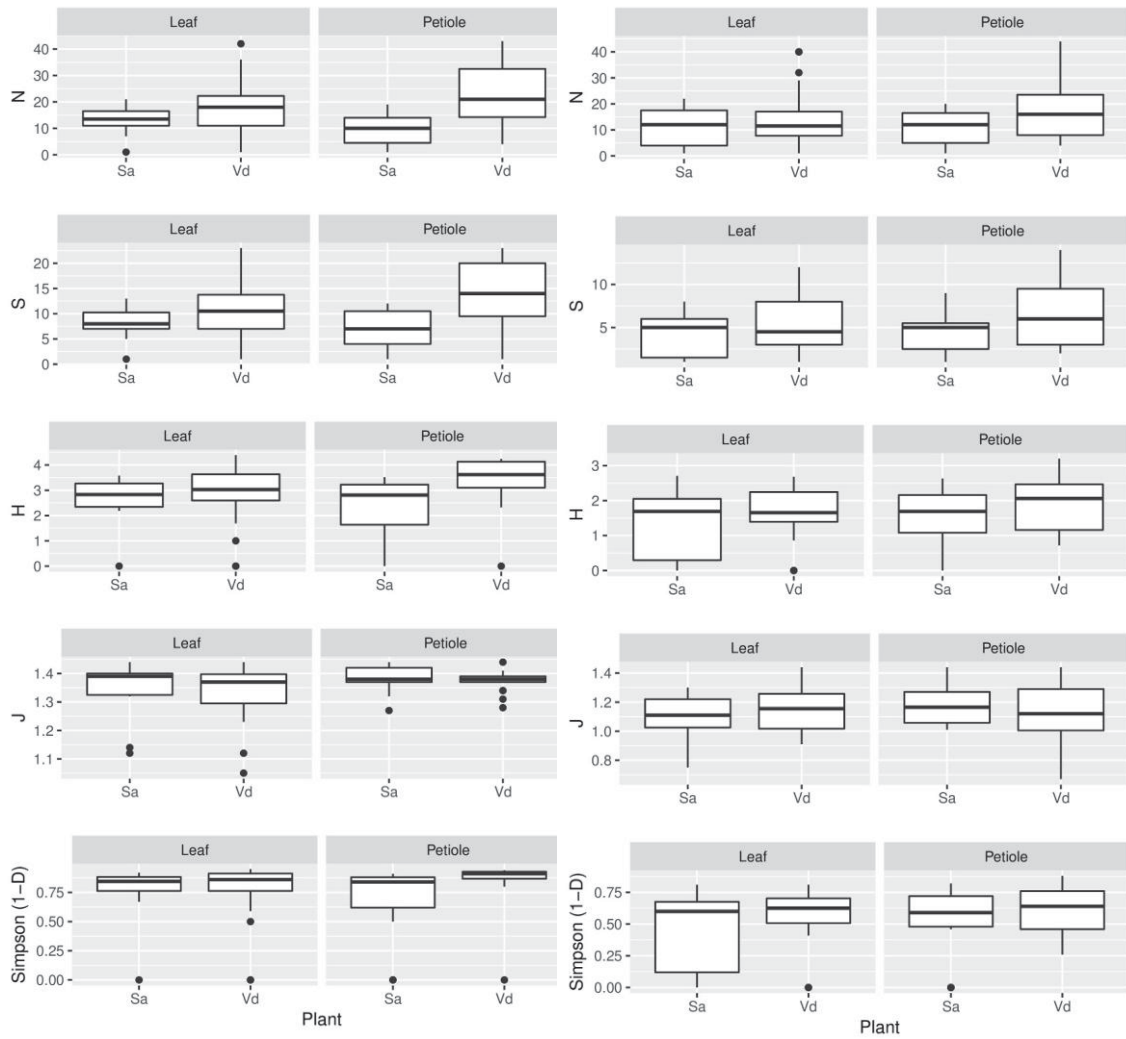


Figure S28-Boxplot graphic showing median, quartiles and outliers for diversity indexes, abundance and richness A) in Morphotype and B) in Genera. Note: Vd for *Vochysia divergens* and Sa for *Stryphnodendron adstringens*.

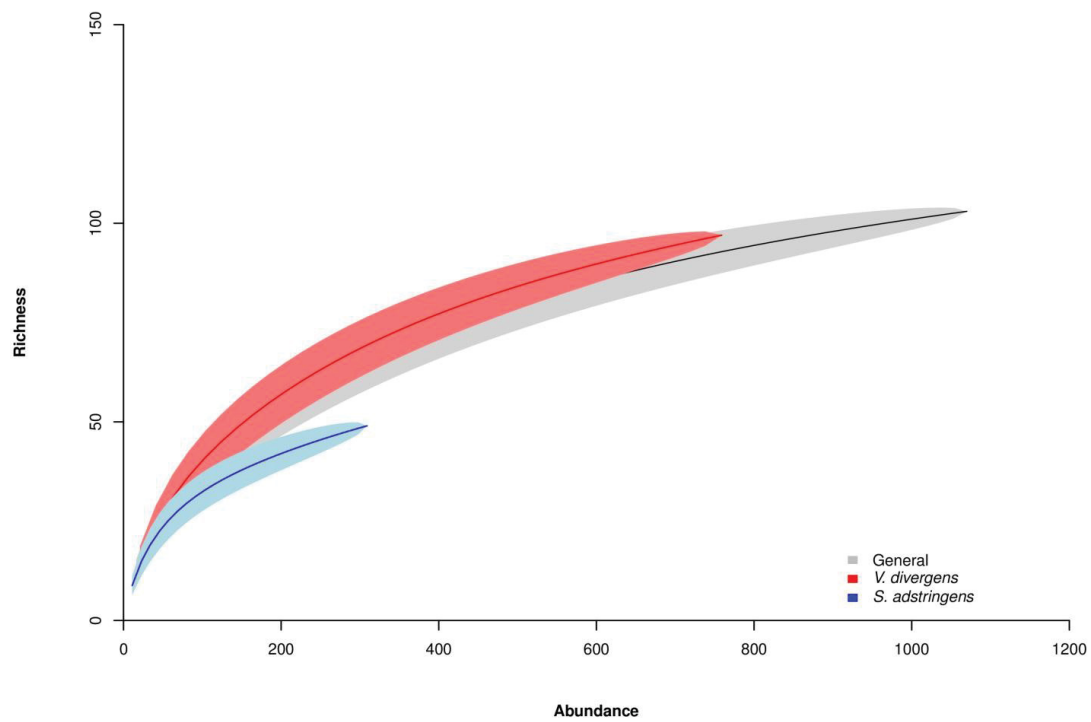


Figure S29-Rarefaction curve of richness and abundance per morphotype of endophytic fungi associated with *Vochysia divergens* (blue), *Stryphnodendron adstringens* (green) and both (grey).

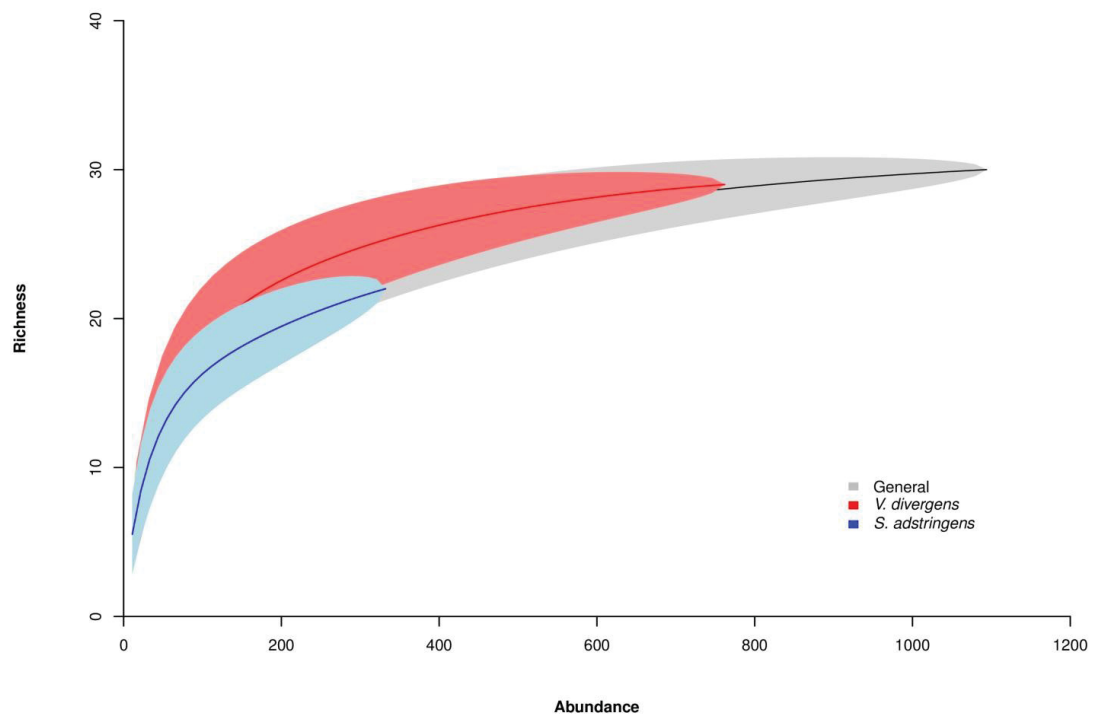


Figure S30-Rarefaction curve of richness and abundance per genus of endophytic fungi associated with *Vochysia divergens* (blue), *Stryphnodendron adstringens* (green) and both (grey).

4. CONSIDERAÇÕES FINAIS

No presente estudo foi realizado um levantamento da diversidade de fungos endofíticos presentes nas plantas medicinais *V. divergens* e *S. adstringens*. As análises filogenéticas evidenciam a presença de novas espécies e possíveis gêneros ainda desconhecidos, agregando valor à riqueza de endófitos nessas plantas.

Foi também caracterizada a comunidade de fungos endofíticos de *V. divergens* e *S. adstringens*, demonstrando que a presença dos grupos dominantes não é hospedeiro-dependente, e conseqüentemente, não é bioma-dependente.

Além disso, os isolados obtidos demonstraram potencial biotecnológico nas análises de bioprospecção, com destaque para o gênero *Diaporthe*. A linhagem *Diaporthe* sp. LGMF1631 apresentou elevada atividade frente aos fitopatógenos avaliados, principalmente contra *P. citricarpa* com inibição de 90% do crescimento. Contra os patógenos clínicos, os isolados *Diaporthe* sp. LGMF1548 e LGMF1583 apresentaram uma atividade de amplo espectro frente a diferentes linhagens, como *S. maltophilia*, KPC, *E. cloacae* MRSA e *C. albicans*. Futuros estudos são necessários para aplicação dos metabólitos produzidos por esses endófitos, como a caracterização química e análise de citotoxicidade dos compostos ativos presente nos extratos.

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