VANESSA PEREIRA DE ABREU

SYSTEMATIC OF FOLIICOLOUS AND PHYTOPATHOGENIC FUNGI ASSOCIATED WITH NATIVE PLANTS OF THE BRAZILIAN CERRADO *STRICTO SENSU*

Tese apresentada à Universidade Federal de Viçosa, como parte das exigências do Programa de Pós-Graduação em Microbiologia Agrícola, para obtenção do título de *Doctor Scientiae*.

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BIOGRAFIA

VANESSA PEREIRA DE ABREU, filha de Damião Barbosa de Abreu e Tânia Maria Pereira Abreu, nasceu em Viçosa, Minas Gerais, no dia 02 de agosto de 1990.

Em 2009 ingressou no curso de graduação em Agroecologia no Instituto Federal de Educação, Ciência e Tecnologia do Sudeste de Minas Gerais – Campus Rio Pomba, graduando-se em janeiro de 2013.

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Em março de 2015, iniciou o curso de Doutorado em Microbiologia Agrícola na Universidade Federal de Viçosa, continuando seus estudos nas áreas de etiologia de doenças fúngicas de plantas e micologia (taxonomia e filogenia molecular de fungos folícolas e fitopatogênicos).

SUMÁRIO

RESUMO

ABREU, Vanessa Pereira de, D.Sc., Universidade Federal de Viçosa, fevereiro de 2019. **Sistemática de fungos folícolas e fitopatogênicos associados a plantas nativas do Cerrado Brasileiro *stricto sensu***. Orientador: Olinto Liparini Pereira. Coorientadora: Meiriele da Silva.

O Cerrado abriga uma enorme diversidade de espécies endêmicas de plantas e animais, sendo assim, considerado um *hotspot* mundial de biodiversidade. Porém, ele é o bioma brasileiro que mais perdeu cobertura vegetal nativa nos últimos anos. Estudos recentes ressaltam que o Cerrado poderá sofrer o maior processo de extinção de espécies de plantas e consequentemente, os fungos sofrem os mesmos efeitos por estarem associados a vegetação e ao solo. Os mesmos podem também estar ameaçados e poucos estudos foram realizados para descobrir a diversidade fúngica associada a espécies de plantas do Cerrado. O conhecimento da micodiversidade do Cerrado começou com as atividades de coletores europeus no final do século XIX e as descrições de novas espécies e gêneros foram baseadas apenas na morfologia dos fungos, mesmo as descrições mais recentes foram baseadas apenas em dados morfológicos, sem informação molecular, a qual permitiria a comparação e análises filogenéticas com outras espécies no mundo. Diante disso, o objetivo deste trabalho foi determinar e descrever a micobiota folícola e fitopatogênica associada a plantas nativas do Cerrado, com base em análises morfológicas e moleculares, além de estabelecer o posicionamento filogenético das espécies encontradas e iniciar uma coleção de culturas fúngicas desse bioma. Um total de 82 materiais vegetais foram coletados e 92 fungos pertencentes a vários gêneros foram isolados, quando possível, armazenados e desses, 6 gêneros foram selecionados para os estudos de taxonomia e filogenia molecular. Este estudo relata 3 possíveis gêneros novos (*Paraopeba*, *Dictyosporina* e *Trochilispora*); 5 possíveis espécies novas (*Mastigosporella pigmentata*, *Pseudocercospora styracina*, *Trochilispora schefflerae*, *Dictyosporina ferruginea* e *Paraopeba schefflerae*) e uma possível epitificação (*Uleomyces sanguineus*) será proposta. Estes resultados corroboram com a grande diversidade de espécies fúngicas encontradas por outros pesquisadores no bioma Cerrado e representa uma contribuição para o conhecimento da diversidade de fungos folícolas e fitopatogênicos associados a diferentes plantas nativas da Floresta Nacional de Paraopeba (FLONA - Paraopeba).

ABSTRACT

ABREU, Vanessa Pereira de, D.Sc., Universidade Federal de Viçosa, February, 2019. **Systematic of foliicolous and phytopathogenic fungi associated with native plants of the Brazilian Cerrado *stricto sensu*** Adviser: Olinto Liparini Pereira. Co-adviser: Meiriele da Silva.

Cerrado is a home of huge diversity of endemic species of plants and animals. Therefore, it is considered a global biodiversity hotspot, however it is the Brazilian biome that has lost most native vegetation cover in recent years. Recent studies emphasize that the Cerrado may suffer the greatest extinction of plant species and consequently, the fungi suffer the same effects, because they are associated with vegetation and soil. They may also be threatened, and few studies have been carried out to discover the fungal diversity associated with Cerrado plant species. Knowledge of Cerrado micodiversity began with the activities of European collectors in the late 19th century and descriptions of new species and genera were based only on fungi morphology. Even the most recent descriptions were based only on morphological data without molecular information, which would allow the comparison and phylogenetic analyzes with other species in the world. The objective of this work was to determine and describe the foliicolous and phytopathogenic mycobiota associated with Cerrado native plants, based on morphological and molecular analyzes, as well as to establish the phylogenetic positioning of the species found and to initiate a fungal culture collection of this biome. A total of 82 plant materials were collected and 92 fungi belonging to several genera were isolated, when possible, and of these, six genera were selected for the taxonomy and molecular phylogeny studies. This study reports 3 possible new genera (*Paraopeba*, *Dictyosporina* and *Trochilispora*); 5 possible new species (*Mastigosporella pigmentata*, *Pseudocercospora styracina*, *Trochilispora schefflerae*, *Dictyosporina ferruginea* and *Paraopeba schefflerae*) and a possible epitypification (*Uleomyces sanguineus*) will be proposed. These results corroborate the great diversity of fungal species found by other researchers in the Cerrado biome and represent a contribution to the knowledge of the diversity of follicolous and phytopathogenic fungi associated with different native plants of the Floresta Nacional de Paraopeba (FLONA - Paraopeba).

INTRODUÇÃO GERAL

O Cerrado originou-se há pelo menos 40 milhões de anos, sendo considerado o mais antigo dos biomas atuais do planeta (Barbosa 2017). Entretanto, o Cerrado que nós conhecemos atualmente configurou-se como tal há cerca de 4 milhões de anos e certamente mudou muito ao longo desse período. A presença de seres humanos no Cerrado também pode ser considerada antiga, visto que, registros fósseis encontrados nesse bioma datam de 13 mil anos (Fernandes 2016).

O termo Cerrado é comumente utilizado para designar um conjunto de ecossistemas que ocorrem no Brasil Central (Eiten 1977; Ribeiro et al. 1981). Depois da Amazônia, o Cerrado é considerado o segundo maior bioma brasileiro em extensão, e segundo a classificação de Ribeiro e Walter (1998), compreende formações vegetais campestres (campo sujo, campo rupestre e campo limpo), savânicas (cerrado sentido restrito, parque de cerrado, palmeiral e vereda) e florestais (mata ciliar, mata de galeria, mata seca e cerradão).

O relevo do domínio do Cerrado é, em geral, plano ou suavemente ondulado, estendendo-se por imensos planaltos ou chapadões. Os solos são profundos e bem drenados, porém são pobres em nutrientes, frequentemente ácidos e com alto teor de alumínio. A radiação solar geralmente é intensa com temperatura média anual de 24 °C, mas durante a primavera e o verão, pode alcançar os 40 °C. A precipitação anual varia entre 1.250 mm a 2.000 mm (Coutinho 2002).

O Cerrado abriga uma enorme diversidade de espécies endêmicas, sendo assim, considerado um *hotspot* mundial de biodiversidade, ou seja, ele é uma área prioritária para conservação. No Brasil existem apenas dois *hotspots*: a Mata Atlântica e o Cerrado (Mittermeier et al. 2005).

Atualmente, aproximadamente 12 mil espécies de plantas no Cerrado são conhecidas, número que o torna um dos biomas mais diversos do mundo. Dessas espécies, apenas cerca de 200 podem ser produzidas em viveiros, pois, ainda não se consegue reproduzir em laboratório as complexas interações entre os elementos do bioma, moldadas desde a era Cenozoica. Muitas plantas do Cerrado têm sementes que são ativadas apenas em situações bem específicas. Algumas dessas plantas só têm a dormência quebrada quando ingeridas por certos mamíferos e expostas a substâncias presentes em seus intestinos e ainda a dormência da semente é quebrada pelo fogo ou por microrganismos (Barbosa 2017).

O Cerrado já atingiu seu clímax evolutivo e precisa, para o seu desenvolvimento, de uma série de fatores que já não existem mais, por exemplo, existem plantas no Cerrado que só são polinizadas por um ou outro tipo de abelhas ou vespas nativas, várias das quais foram extintas pelo uso de agrotóxicos nas lavouras. Essas plantas poderão sobreviver, mas não serão capazes de se reproduzir. Outras plantas do Cerrado levam séculos para se desenvolver e desempenhar plenamente suas funções ecológicas (Barbosa 2017).

Em termos gerais, o Cerrado, é o bioma brasileiro que mais perdeu cobertura vegetal nativa sendo que, nos últimos 50 anos, perdeu aproximadamente 46% de sua vegetação original e isso é devido à destruição provocada pelo desmatamento, pelas extensas monoculturas, pela ocupação antrópica, pela introdução de espécies exóticas que se tornam invasoras, pela exploração de minérios e pelo desrespeito às normas ambientais (Fernandes 2016; Strassburg et al. 2017).

Há relatos de que o bioma Cerrado poderá sofrer o maior processo de extinção de espécies de plantas já registrado na história, com três vezes mais perdas de flora do que houve desde 1500 (Strassburg et al. 2017). Juntamente com a vegetação, os fungos sofrem os mesmos efeitos, por estarem associados a ela e ao solo (Rocha et al. 2010; de Castro 2015; Silva et al. 2016; de Araujo et al. 2018).

Os fungos são organismos importantes e que influenciam cotidianamente a vida dos seres vivos, seja diretamente como alimento ou gerando produtos para a indústria farmacêutica, alimentícia e de fermentação. São potencialmente importantes no controle biológico de insetos e nematoides, em associações micorrízicas e simbioses com insetos. Entretanto, podem ser extremamente prejudiciais para a agricultura, causando mais de 70% das doenças de plantas cultivadas, além de produzirem micotoxinas em grãos armazenados, nocivas ao homem e aos animais. Do ponto de vista ecológico, são responsáveis pela ciclagem e mineralização da matéria orgânica (Alexopoulos et al. 1996).

Reunir evidências que justifiquem o reconhecimento de espécies fúngicas como ameaçadas são em parte responsáveis pela virtual ausência de fungos nas listas de espécies ameaçadas e nas medidas de conservação. A maior e mais importante rede de conservação no mundo (Red List) lista apenas 43 espécies fúngicas, e dessas, 12 estão ameaçadas de extinção (IUCN 2018). Esses números evidenciam uma elevada negligência com relação aos microrganismos, visto que os mesmos podem também estar ameaçados de extinção, especialmente os fungos que estão associados a plantas ameaçadas de extinção.

Neste contexto, Minter (2010) referiu-se aos fungos, como "os órfãos do Rio", por terem sido negligenciados na "Conferência das Nações Unidas sobre Ambiente e Desenvolvimento Sustentável", também conhecida como ECO 92 ou Rio 92. Um grupo de fungos para os quais seria, possível reunir evidências científicas sobre a condição de ameaça iminente de extinção é o dos fungos fitopatogênicos/folícolas altamente específicos em suas relações com espécies de plantas hospedeiras ameaçadas de extinção (Rocha et al. 2010; de Castro 2015; Silva et al. 2016).

O conhecimento da micodiversidade do Cerrado começou com as atividades de coletores europeus no final do século XIX. Os trabalhos pioneiros do alemão Paul Hennings, foram importantes. Ele estudou os materiais obtidos pelo coletor botânico Ernst Ule, um alemão naturalizado brasileiro vinculado ao Museu Nacional do Rio de Janeiro. Os micologistas de instituições brasileiras A. C. Batista e A. P. Viégas contribuíram muito para o conhecimento dos fungos do Cerrado, ambos alimentados por importantes coletas realizadas pelo botânico Ezechias Paulo Heringer, ex-professor da Universidade de Brasília e principal consultor ambiental do Distrito Federal na época da implantação de Brasília (Viégas 1944; Viégas 1945; Viégas 1961; Silva e Minter 1995; Dianese et al. 1997; Dianese 2000).

Desde 1993, a pesquisa micológica da Universidade de Brasília (UnB) tem focado suas pesquisas em fungos associados com a vegetação do Cerrado brasileiro. Na década de 90, o micologista que retomou os estudos sobre a micodiversidade do Cerrado foi o professor Dianese. Entretanto, apesar da enorme importância dos seus trabalhos, não foram feitos isolamentos dos fungos, então não se tem um banco de germoplasma disponível para acessar esse material genético. Descrições de novas espécies e gêneros eram baseadas apenas na morfologia dos fungos, mesmo as descrições mais recentes foram baseadas apenas em características morfológicas, sem informação molecular, a qual permitiria a comparação e análises filogenéticas com outras espécies no mundo

(Dianese et al. 1993; Dianese e Santos 1995; Rezende e Dianese 2003; Dornelo-Silva e Dianese 2003; Souza et al. 2008; Inácio et al. 2012; Hernández-Gutiérrez e Dianese 2014; Hernández-Gutiérrez et al. 2015).

Oito gêneros novos de hifomicetos em tricomas de plantas nativas que crescem no Cerrado brasileiro foram descritos (Pereira-Carvalho et al. 2009). Essas descobertas sugerem que os tricomas de plantas são uma fonte inexplorada de diversidade de fungos, e merecem mais atenção nas pesquisas (inventários) de biodiversidade. Após a publicação desse trabalho, o professor Dianese e outros micologistas que trabalham com micodiversidade, publicaram uma revisão intitulada: "Unusual fungal niches" (Cantrell et al. 2011), onde os autores descreveram cinco habitats fúngicos incomuns, incluindo os tricomas de plantas do Cerrado. Muitos desses nichos incomuns são considerados ambientes extremos e têm sido extensivamente estudados para as bactérias e arqueas. No entanto descobertas recentes revelaram também a presença de fungos e outras espécies eucarióticas (Cantrell et al. 2011). Recentemente o grupo liderado pelo professor Dianese iniciou trabalhos envolvendo isolamento, análises filogenéticas e disponibilização de sequências de fungos do Cerrado em bancos de dados públicos (Santos et al. 2016; Guterres et al. 2018).

Um estudo com fungos associados a plantas do Cerrado mostrou a descoberta de gêneros e espécies novas para a ciência e que alguns deles são supostamente específicos de uma planta ameaçada de extinção (*Dimorphandra wilsonii*) e, por consequência, são espécies também ameaçadas e deveriam passar a ser consideradas em programas de proteção, por exemplo, de uma determinada área ou de uma determinada planta (Silva et al. 2016).

Alveariospora é um exemplo de um gênero novo e raro de um hifomiceto encontrado no Cerrado, mas que não tem nenhuma informação molecular a seu respeito (Silva et al. 2012). Como a maioria dos trabalhos, não foram realizados isolamentos em cultura, dessa forma, não foi possível realizar nenhuma inferência filogenética para resolver os grupos, nem o armazenamento dos fungos para futuros estudos de aplicação biotecnológica para a agricultura, indústria e meio ambiente.

Visto que, o Cerrado é um bioma ameaçado e de elevada diversidade e que já foram encontrados muitos gêneros e espécies novas, inclusive alguns fungos hifomicetos muito raros associados a plantas endêmicas faz-se necessário a realização de um inventário e a construção de um banco de culturas pioneiro desses fungos no Brasil. Por isso, estudos visando a ampliação do conhecimento sobre as espécies fúngicas associadas a plantas nativas do Cerrado, é de suma importância.

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Systematic of foliicolous and phytopathogenic fungi associated with native plants of the Brazilian Cerrado *stricto sensu*

Abstract

Cerrado is a home of huge diversity of endemic species of plants and animals. Therefore, it is considered a global biodiversity hotspot, however it is the Brazilian biome that has lost most native vegetation cover in recent years. Knowledge of Cerrado micodiversity began with the activities of European collectors in the late 19th century and descriptions of new species and genera were based only on fungi morphology. Even the most recent descriptions were based only on morphological data without molecular information, which would allow the comparison and phylogenetic analyzes with other species in the world. The objective of this work was to determine and describe the foliicolous and phytopathogenic mycobiota associated with Cerrado native plants, based on morphological and molecular analyzes, as well as to establish the phylogenetic positioning of the species found and to initiate a fungal culture collection of this biome.
The objective of this work was to determine and describe the foliicolous and phytopathogenic mycobiota associated with Cerrado native plants, based on morphological and molecular analyzes, as well as to establish the phylogenetic positioning of the species found and to initiate a fungal culture collection of this biome.
A total of 82 plant materials were collected and 92 fungi belonging to several genera were isolated, when possible, and of these, six genera were selected for the taxonomy and molecular phylogeny studies. This study reports 3 possible new genera (*Paraopeba*, *Dictyosporina* and *Trochilispora*); 5 possible new species (*Mastigosporella pigmentata*, *Pseudocercospora styracina*, *Trochilispora schefflerae*, *Dictyosporina ferruginea* and *Paraopeba schefflerae*) and a possible epitypification (*Uleomyces sanguineus*) will be proposed. These results corroborate the great diversity of fungal species found by other researchers in the Cerrado biome and represent a contribution to the knowledge of the diversity of follicolous and phytopathogenic fungi associated with different native plants of the Floresta Nacional de Paraopeba (FLONA - Paraopeba).

Keywords: Biome, Epitypification, Phylogeny, Taxonomy

Introduction

Cerrado is the second largest biome in Brazil, with approximately 2 million km^2 and occupies about 24% of the national territory (Klink and Machado 2005; Sawyer et al. 2017). The climate of this biome is seasonal and characterized by the presence of two well-defined seasons: dry winters (from April to September) and rainy summers (from October to March) (Bayma et al. 2003; da Silva et al. 2008).

This biome is considered a global biodiversity hotspot, with 1,500 animal species and more than 12,000 plant species, of which 4,800 species of plants and vertebrates are endemic. In addition, it has the richest flora among the savannas of the world, with a high rate of endemism (Myers et al. 2000; Mendonça et al. 2008; Queiroz 2009; Strassburg et al. 2017; Bolson 2018). However, the natural vegetation of Cerrado has been replaced by the expansion of agribusiness, low legal protection, incentives limited to conservation and anthropic occupation (Ribeiro and Walter 1998; Sano et al. 2010; Lenza et al. 2011; Strassburg et al. 2017) being considered currently one of the most threatened biomes of the country (Strassburg et al. 2017; MMA 2018; de Araujo et al. 2018).

Cerrado lost about 46% of its native vegetation cover and only 19.8% remain unchanged (Strassburg et al. 2017). If the exploitation of these native areas continues at a strong expansion rate, the vegetation of the Cerrado will be restricted to the areas of Conservation Units, indigenous lands and areas unfit for agriculture, causing many species of plants as well as animals to be extinguished (Queiroz 2009).

The transformations that they see occurring in the landscapes of the Cerrado and the threat of extinction of many of their plant and animal species is alarming (Strassburg et al. 2017). When discussing the preservation of endangered species in Brazil or abroad, the focus is always given to elements of fauna and flora. However, little known and highly diversified and specialized organisms such as fungi are no less vulnerable to extinction. For this reason, some studies have been discussing the importance of preserving mycobiota (Thor 1998; Moore et al. 2001; Berlund and Jonsson 2005; Rocha et al. 2010; Griffith 2012; de Castro 2015; Silva et al. 2016).

The neglect of microorganisms is mainly due to the fact that they are not seen with the naked eye and by the false idea that microorganisms, in general, have facilitated dispersion and consequently wide geographical distribution (Griffith 2012). However, especially after the use of molecular tools in the study of microbial ecology, it is known that microbial populations may have defined and endemic population structure (Rodriguez et al. 2004).

A study published in the journal Nature shows that increasing knowledge about soil biodiversity is obtained in regions dominated by agriculture, especially in Europe and North America, while the soil biodiversity of the southern hemisphere, such as in the tropical Cerrado, is very little studied (de Araujo et al. 2018). Recently, microbial groups present in the soil, including bacteria (Araujo et al. 2012; de Castro et al. 2016; de Araujo et al. 2017), archaea (de Araujo et al. 2018) and fungi (de Castro et al. 2016; de Araujo et al. 2017), are being investigated in the Cerrado biome. These studies revealed differences in the composition of the community of microbial groups depending on the type of predominant vegetation, with a higher number of microorganisms in climactic regions of the tree vegetation. However, the systematics of foliicolous and phytopathogenic fungi associated with native plants in the Brazilian Cerrado remains poorly studied.

Dianese et al. (1997) reported that the Brazilian Cerrado fungi have been shown to be very specific to host plants, varying approximately from 1 to 6 fungi per plant species. Due to this, the loss by the extinction of a plant species can lead to a coextinction event, that is, to the extinction of specialized organisms that depend on this plant. Therefore, studies aiming to broaden the knowledge about the fungal species associated to native plants of the Cerrado is of sum importance.

Hence, the objectives of this study were: I) to initiate a taxonomic survey and reassessment of fungi of the Cerrado biome based on a combination of morphological and molecular analyses; II) to identify and describe the foliicolous and phytopathogenic mycobiota associated with native plants of the Cerrado biome; III) to establish the phylogenetic positioning of the species found; IV) to start a collection of fungal cultures of the Cerrado biome.

Material and Methods

The work was carried out in the Laboratório de Micologia e Etiologia de Doenças Fúngicas de Plantas, belonging to the Departamento de Fitopatologia, Universidade Federal de Viçosa (UFV), Viçosa, Minas Gerais, Brazil.

Collection area

Sampling were carried out in the Floresta Nacional de Paraopeba (FLONA - Paraopeba), located in the municipality of Paraopeba, in the state of Minas Gerais. They were carried out at different times and areas of FLONA - Paraopeba in order to favor the greater quantity and diversity of fungal species.

Sample collection and isolation

Plants were sampled both with disease symptoms (phytopathogenic fungi) and by the presence of colonies on the leaf surface (foliicolous fungi). The collections were carried out in the morning, due to the high temperature in the Cerrado *senso stricto* in the afternoon. There were four collections in this area (two in January and two in September 2016), for these collections were acquired the necessary licenses and the permission of the ICMBio to carry them out.

Leaves were observed with the aid of a pocket magnifier, cut with pruning shears or manually and placed in plastic bags. The botanical identifications of the materials were carried out by means of specialized literature and the aid of botanicals. The plants were herborized in botanical press for the deposit in the VIC Herbarium, at the Universidade Federal de Viçosa (UFV).

Two methodologies were applied for the isolation of fungi, direct isolation (Alfenas and Mafia 2016) for five genera (*Mastigosporella*, *Pseudocercospora*, *Trochilispora*, *Dictyosporina*, and *Paraopeba*) and ejection of ascospores (Alfenas and Mafia 2016) for the genus *Uleomyces*.

The direct isolation consisted of the transfer, with the aid of a stylet, of fungal structures directly from the leaves to Petri dishes containing Malt Extract Agar (MEA) (20 g of malt extract, 20 g of agar and 1000 mL of distilled water) with antibiotic, chloramphenicol (Sigma - Aldrich). Each framework was placed at four points approximately equidistant in Petri dishes containing MEA.

For ascospore ejection, pieces of leaves with fungal structures were cut and placed in an inverted Petri dish lid containing Water Agar (WA) (20 g of agar and 1000 mL of distilled water). After ascospores were ejected into the surface of the WA, the pieces of leaves were removed and the plates were incubated at 25 ºC for about 12 hours until ascospores germinated. A single ascospore germinated was transferred to Petri dishes containing MEA under a stereomicroscope [Motic® SMZ-168 (20X)]. The plates were incubated at 25 ºC until the colonies appeared.

Those cultures were purified by the single-ascospore or single hyphal-tip method prepared on 2% WA (Dhingra and Sinclair 1995) and maintained on PDA (39 g of potato dextrose agar, and 1000 mL of distilled water). All isolates were stored in anhydrous silica gel at 4 ºC (Mota et al. 2003) and in sterile distilled water, as described by Castellani (1939).

DNA extraction, sequencing, and phylogenetic analyses

For cultivable fungi (*Mastigosporella*, *Pseudocercospora*, *Trochilispora*, *Dictyosporina*, and *Paraopeba*), single-spore or single hyphal-tip isolates were grown on Potato Dextrose Agar (PDA) at 25 °C under a 12-h photoperiod for 7 days. The surfaces of cultures were scraped off using a sterile toothpick, and approximately 40 mg of mycelium were transferred to a sterile 1.5 mL microcentrifuge tube. For non-cultivable fungi (*Uleomyces*), direct method for extraction of fungal genomic DNA was used (Pinho et al. 2013). Ascomata present in the each collected leaf were cut out and placed into a microcentrifuge tube for DNA extraction. Ascomata were ground in liquid nitrogen to a fine powder using a microcentrifuge tube pestle. The crushing continued after adding 100 µl of Nuclei Lysis Solution of the Wizard Genomic DNA Purification Kit (Promega Corporation, WI). After the first grinding, more 500 µl of the above-mentioned solution was added. The extraction was continued as described by Pinho et al. (2013). The samples were deposited in the "Collection of DNA" (CDA), housed at Laboratório de Micologia e Etiologia de Doenças Fúngicas de Plantas.

The primers used in the amplification are listed in Table 1.

Table 1. Primers used to amplify the internal transcribed spacer regions 1 and 2 (including the 5.8S rRNA gene) (ITS), part of the gene nuclear large subunit ribosomal

DNA (LSU), translation elongation factor 1-α (TEF-1α), β-tubulin (βt), and actin (ACT) of the fungal genera studied.

Locus	Primers	Reference	Genera
ITS	ITS1 and ITS4	White et al. 1990	*Mastigosporella*, *Pseudocercospora*, *Trochilispora*, *Dictyosporina*, and *Paraopeba*
ITS	ITS5 and ITS4	White et al. 1990	*Uleomyces*
LSU	LR0R and LR5	Vilgalys and Hester 1990	*Mastigosporella*, *Pseudocercospora*, *Trochilispora*, *Dictyosporina*, *Paraopeba*, and *Uleomyces*
TEF1-α	983F and 2218R	Rehner 2001	*Mastigosporella*, *Pseudocercospora*, and *Trochilispora*
ACT	ACT-512F and ACT-783R	Carbone and Kohn 1999	*Pseudocercospora*
βt	Bt2a and Bt2b	Glass and Donaldson 1995	*Trochilispora*

Polymerase chain reactions (PCR) included the following ingredients for each 25 µL reaction: 12.5 µl of Dream Taq TM PCR Master Mix 2× (MBI Fermentas, Vilnius, Lithuania); 1 µl of 10 pmol/µl of each forward and reverse primer synthesized by Invitrogen (Carlsbad, CA); 1 µl of dimethyl sulfoxide (DMSO, Sigma–Aldrich, St. Louis, MO); 5 µl of 100× (10 mg/mL) Bovine Serum Albumin (BSA, Sigma–Aldrich, St. Louis, MO); 2.5 µl of nuclease-free water and 2 µl of genomic DNA (25 ng/µl). Negative controls with sterile water instead of DNA were performed at each PCR.

The amplifications were performed in the thermal cycler C1000™ Thermal Cycler (BIO-RAD). The thermal cycling programs were an initial denaturation at 95 ºC for 60s. Followed by 30 cycles of denaturation at 95 ºC for 30 s, primer annealing at 55 ºC, 60 ºC, 55 ºC, 56 ºC, 54 ºC, 55 ºC for 30 s, primer extension at 72 ºC for 60 s, 30 s or 45 s and a final extension at 72 ºC for 5 min for ITS1/ITS4, ITS5/ITS4, LSU, TEF1-α, ACT, and βt, respectively.

The PCR products were analyzed by electrophoresis on 2% agarose gels stained with GelRed™ (Biotium Inc., Hayward, CA, U.S.A.) in a 1× Tris-acetate-EDTA buffer and visualized under UV light on a transilluminator (L-Pix Touch, Loccus

Biotechnology) to check for the amplification size and purity. PCR products were purified and sequenced by Macrogen Inc., Korea (http://www.macrogen.com).

The nucleotide sequences were read with FinchTV v.1.4.0 (Geospiza Inc.). All the sequences were checked manually, and new sequences were deposited in GenBank (http://www.ncbi.nlm.nih.gov). The sequences were compared against the GenBank database using their Mega BLAST program for preliminary identification of the isolates. Sequence data of ex-type or ex-epitype cultures obtained from reference articles and the closest hits of GenBank database were included in this study.

The sequences of the isolates from this study were aligned with the additional sequences using MEGA v. 6 software (Tamura et al. 2013) employing the MUSCLE® algorithm (Edgar 2004). The alignments were checked, and manual adjustments were made, when necessary. The resulting alignment will be deposited into TreeBASE (http://www.treebase.org).

The best nucleotide substitution model for each gene/region was determined using the Akaike Information Criterion (AIC) implemented in MrMODELTEST 2.3 (Posada and Buckley 2004) (Table 2).

Table 2. Genera and models of evolution selected for ITS, LSU, TEF1-α, and ACT.

Gêneros	**Modelos**			
	ITS	**LSU**	**TEF1-α**	**ACT**
Dictyosporina	GTR+G	GTR+I+G	-	-
Mastigosporella	SYM+I+G	GTR+I	-	-
Paraopeba	-	GTR+I+G	-	-
Pseudocercospora	SYM+G	-	GTR+I+G	SYM+I+G
Trochilispora	HKY+G	GTR+I+G	-	-

- These genes/region were not used in phylogenetic analyses.

Bayesian inference (BI) analyses employing Markov Chain Monte Carlo method were performed with the selected sequences, first with each region separately, then with the combined dataset, when possible.

The phylogenetic analysis of each region and of the concatenated dataset were conducted in MrBayes on XSEDE v.3.2.6 (Heulsenbeck et al. 2015) at the CIPRES Science Gateway (Miller et al. 2010). In MrBayes, the data were partitioned by gene, and the parameters of the nucleotide substitution models for each partition were set as described in the table above (Table 2). Four MCMC chains were run simultaneously, starting from random trees for 10,000,000 generations. Trees were sampled every 1,000 generation, resulting in 10,001 trees. The first 2,500 trees were discarded as the burn-in phase of each analysis. The posterior probabilities (Rannala and Yang 1996) were determined from a majority-rule consensus tree that was generated from the remaining trees. The trees were visualized in FigTree v. 1.3.1 (Rambaut 2009), exported and edited using the graphics programs. The phylogenetic tree of *Paraopeba* was rooted with *Venturia inaequalis* CBS 176.42. The phylogenetic tree of *Dictyosporina* was rooted with *Xenostigmina zilleri* CBS 115686 and *Xenostigmina zilleri* CBS 124108. The phylogenetic tree of *Trochilispora* was rooted with *Immersidiscosia eucalypti* MAFF 242781. The phylogenetic tree of *Mastigosporella* was rooted with *Immersiporthe knoxdaviesiana* NR 120111 (ITS) and *Aurifilum marmelostoma* HQ 730873 (LSU). The phylogenetic tree of *Pseudocercospora* was rooted with *Passalora eucalypti* CBS 111318.

Morphological studies

Representative isolates identified in the phylogenetic analyses were used for morphological characterization. Slides were mounted in lactoglycerol with the fungal structures present in leaves. Images were obtained with an Olympus BX53 light microscope equipped with a digital camera, (Olympus Q-Color5™) and edited using the graphics programs. Thirty measurements of relevant morphological characteristics were made using Olympus cellSens software.

Representative isolates of each taxon were deposited in the culture collection of fungi "Coleção Octávio Almeida Drummond" (COAD) and deposited at VIC Herbarium, both located at the Universidade Federal de Viçosa (Minas Gerais, Brazil).

Results and Discussion

A total of 82 plant materials were collected and 92 isolates/samples belonging to several genera/species were obtained, when possible, and stored (Table 3).

Table 3. Host, family, Brazilian name plant and fungal genera or species found in an area of Cerrado *stricto sensu* of the Floresta Nacional de Paraopeba (FLONA - Paraopeba), Minas Gerais, Brazil.

Host	**Family**	**Brazilian name**	**Fungal genera or species**
Anacardium humile	Anacardiaceae	Cajuzinho-anão	*Cercospora* sp.
Baccharis dracunculifolia	Asteraceae	Alecrim-do-campo	Not identified/Not isolated
Banisteriopsis gardneriana	Malpighiaceae	_	*Puccinia banisteriae*
Brosimum gaudichaudii	Moraceae	Mama-cadela	*Passalora* sp.
Brosimum gaudichaudii	Moraceae	Mama-cadela	*Alternaria* sp.
Brosimum gaudichaudii	Moraceae	Mama-cadela	*Cladosporium* sp.
Byrsonima sp.	Malpighiaceae	Murici	*Passalora* sp.
Byrsonima sp.	Malpighiaceae	Murici	*Pestalotiopsis* sp.
Byrsonima sp.	Malpighiaceae	Murici	*Phyllosticta* sp.
Byrsonima sp.	Malpighiaceae	Murici	*Pseudocercosporella* sp.
Byrsonima sp.	Malpighiaceae	Murici	Not identified/Not isolated
Byrsonima sp.	Malpighiaceae	Murici	Not identified/Not isolated
Caryocar brasiliense	Caryocaraceae	Pequi	Not identified/Not isolated
Caryocar brasiliense	Caryocaraceae	Pequi	Not identified/Not isolated
Caryocar brasiliense	Caryocaraceae	Pequi	*Glomerella* sp.
Caryocar brasiliense	Caryocaraceae	Pequi	Not identified/Not isolated
Curatella americana	Dilleniaceae	Lixeira	*Cercospora* sp.
Davilla rugosa	Dilleniaceae	Cipó caboclo	*Passalora* sp.
Davilla rugosa	Dilleniaceae	Cipó caboclo	*Asterina* sp.
Davilla rugosa	Dilleniaceae	Cipó caboclo	Not identified/Not isolated
Dimorphandra mollis	Fabaceae	Faveira-do-campo	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Erythroxylum sp.	Erythroxylaceae	_	Not identified/Not isolated
Eugenia dysenterica	Myrtaceae	Cagaita	*Cladosporium* sp.
Guapira noxia	Nyctaginaceae	Maria-mole	Not identified/Not isolated
Unidentified host	Unidentified family	_	*Phoma* sp.
Unidentified host	Aristoloquiaceae	_	Not identified/Not isolated
Unidentified host	Leguminosae	_	Not identified/Not isolated
Unidentified host	Leguminosae	_	Not identified/Not isolated
Unidentified host	Rubiaceae	_	Not identified/Not isolated
Unidentified host	Rubiaceae	_	Not identified/Not isolated
Unidentified host	Verbenaceae	_	*Pseudocercosporella* sp.
Unidentified host	Vochysiaceae	_	Not identified/Not isolated
Unidentified host	Malphighiaceae	_	Not identified/Not isolated
Unidentified host	Bignoneaceae	_	Not identified/Not isolated

Unidentified host	Leguminosae	_	Not identified/Not isolated
Unidentified host	Rubiaceae	_	Not identified/Not isolated
Unidentified host	Myrtaceae	_	Not identified/Not isolated
Unidentified host	Vochysiaceae	_	Not identified/Not isolated
Hymenaea stigonocarpa	Fabaceae	Jatobá-do-cerrado	*Phomopsis* sp.
Hymenaea stigonocarpa	Fabaceae	Jatobá-do-cerrado	Not identified/Not isolated
Inga sp.	Fabaceae	Ingá	Not identified/Not isolated
Kielmeyera coriacea	Calophyllaceae	Pau-santo	*Dictyosporina ferruginea*
Kielmeyera coriacea	Calophyllaceae	Pau-santo	*Mycosphaerella* sp.
Kielmeyera coriacea	Calophyllaceae	Pau-santo	*Asterina* sp.
Kielmeyera coriacea	Calophyllaceae	Pau-santo	Not identified/Not isolated
Manihot tripartita	Euphorbiaceae	Mandioca-de-veado	Not identified/Not isolated
Miconia albicans	Melastomataceae	Canela-de-velha	*Cladosporium* sp.
Miconia albicans	Melastomataceae	Canela-de-velha	Not identified/Not isolated
Miconia albicans	Melastomataceae	Canela-de-velha	Not identified/Not isolated
Miconia albicans	Melastomataceae	Canela-de-velha	Not identified/Not isolated
Miconia albicans	Melastomataceae	Canela-de-velha	Not identified/Not isolated
Miconia albicans	Melastomataceae	Canela-de-velha	Not identified/Not isolated
Miconia albicans	Melastomataceae	Canela-de-velha	*Cladosporium* sp.
Miconia albicans	Melastomataceae	Canela-de-velha	Not identified/Not isolated
Phoradendron sp.	Loranthaceae	_	*Pseudocercospora* sp.
Qualea parviflora	Vochysiaceae	Pau-terra-roxo	*Mastigosporella pigmentata*
Roupala montana	Proteaceae	Carne-de-vaca	*Mycosphaerella* sp.
Roupala montana	Proteaceae	Carne-de-vaca	*Stenella* sp.
Roupala montana	Proteaceae	Carne-de-vaca	Not identified/Not isolated
Roupala montana	Proteaceae	Carne-de-vaca	*Phyllachora* sp.
Schefflera morototoni	Araliaceae	Morototó	*Cladosporium* sp.
Schefflera morototoni	Araliaceae	Morototó	*Paraopeba schefflerae*
Schefflera morototoni	Araliaceae	Morototó	*Fusarium* sp.
Schefflera morototoni	Araliaceae	Morototó	*Trochilispora schefflerae*
Schefflera morototoni	Araliaceae	Morototó	Not identified/Not isolated
Schefflera morototoni	Araliaceae	Morototó	Not identified/Not isolated
Schinus terebinthifolius	Anacardiaceae	Aroeira-vermelha	*Alternaria* sp.
Serjania sp.	Sapindaceae	_	*Pseudocercospora* sp.
Siparuna guianensis	Monimiaceae	Maria fedentina	Not identified/Not isolated
Siparuna guianensis	Monimiaceae	Maria fedentina	*Septoria* sp.
Siparuna guianensis	Monimiaceae	Maria fedentina	*Pseudocercospora* sp.
Styrax ferrugineus	Styracaceae	Laranjinha-do-cerrado	*Pseudocercospora styracina*
Styrax ferrugineus	Styracaceae	Laranjinha-do-cerrado	*Uleomyces sanguineus*
Styrax ferrugineus	Styracaceae	Laranjinha-do-cerrado	Not identified/Not isolated

Styrax ferrugineus	Styracaceae	Laranjinha-do-cerrado	*Parmularia* sp.
Styrax ferrugineus	Styracaceae	Laranjinha-do-cerrado	Not identified/Not isolated
Styrax ferrugineus	Styracaceae	Laranjinha-do-cerrado	Not identified/Not isolated
Styrax ferrugineus	Styracaceae	Laranjinha-do-cerrado	Not identified/Not isolated
Syagrus flexuosa	Arecaceae	Coqueiro-do-campo	*Passalora* sp.
Vernonia sp.	Asteraceae	_	Not identified/Not isolated
Xylopia aromatica	Annonaceae	Pimenta-de-macaco	Not identified/Not isolated
Xylopia aromatica	Annonaceae	Pimenta-de-macaco	*Elsinoe* sp.
Xylopia aromatica	Annonaceae	Pimenta-de-macaco	Not identified/Not isolated
Xylopia aromatica	Annonaceae	Pimenta-de-macaco	*Phyllosticta* sp.
Xylopia aromatica	Annonaceae	Pimenta-de-macaco	*Aecidium* sp.

Twenty-seven plant families were identified and only one family was not identified, twenty-eight host plant genera/species were identified and fourteen were not identified, twenty-five fungal genera/species were identified and fifty were not identified/analyzed.

Six genera/species were selected for the studies of taxonomy and phylogenetic analyses.

Systematic

Paraopeba *V.P. Abreu, A.A.M. Gomes, A.L. Firmino & O.L. Pereira*

(Published in Persoonia v.39, p.348-349, 2017).

Etymology. Name refers to the city of Paraopeba, state of Minas Gerais, Brazil, where the fungus was first found.

Classification — Asterinaceae, Asterinales, Dothideomycetes.

Leaf spots epiphyllous, circular to irregular, single to confluent, brown. *Hyphae* straight to slightly flexuous, brown, septate, smooth. *Appressoria* numerous, entire, globose to cylindrical, alternate to unilateral, unicellular, brown, penetration peg central on the appressorial cell. *Conidiogenous cells* schizolytic, cylindrical to elliptical, light brown to brown, smooth. *Conidia* cylindrical, multicellular, brown, smooth, rounded ends, septate. *Sexual morph* unknown.

Type species. *Paraopeba schefflerae* V.P. Abreu, A.A.M. Gomes, A.L. Firmino & O.L. Pereira. MycoBank MB821209.

Paraopeba schefflerae *V.P. Abreu, A.A.M. Gomes, A.L. Firmino & O.L. Pereira*

Etymology. Named after its host genus, *Schefflera*.

Leaf spots epiphyllous, circular to irregular, single to confluent, brown, 2–8 mm diam. *Hyphae* straight to slightly flexuous, brown, septate, 1.5–3.5 µm diam, smooth. *Appressoria* numerous, entire, globose to cylindrical, alternate to unilateral, unicellular, 3–6 × 4.5–6.5 µm, brown, penetration peg central on the appressorial cell. *Conidiogenous cells* schizolytic, cylindrical to elliptical, 4.5–10 × 3.5–6.5 µm, pale brown to brown, smooth. *Conidia* cylindrical, multicellular (3–14-cells), brown, smooth, rounded ends, 18–85 × 4.5–7 µm, 2–13-septate. *Sexual morph* unknown.

Culture characteristics — The colony grows slowly on malt extract agar, reaching 7 mm diam after 40 d at 25 ºC with a photoperiod of 12 h; margins irregular, with aerial mycelium sparse, black, colonies fertile.

Typus. BRAZIL, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA - Paraopeba), on leaves of *Schefflera morototoni* (Araliaceae), 30 Jan. 2016, V.P. Abreu & O.L. Pereira (VIC 44232, COAD 2249; ITS sequence GenBank KY952164, LSU sequence GenBank KY952165, MycoBank MB821409).

Notes — The order Asterinales is characterized by epiphytic fungi, biotrophic parasites, with superficial non-ostiolate ascomata, opening irregularly at maturity; surface mycelium and haustoria are present in several genera (Bezerra 2004). Asterinales is composed by two families, Asterinaceae and Parmulariaceae (Guatimosim et al. 2015; Giraldo et al. 2017). Members of Asterinaceae are characterized by producing black colonies consisting of a brown mycelium on the leaf surface (Guatimosim et al. 2015). Asexual morphs (hyphomycetous and coelomycetous) have been observed in some Asterinaceae (Summerell et al. 2006; Hongsanan et al. 2016). The conidia of *Paraopeba schefflerae* are formed in schizolytic conidiogenous cells while conidia of *Alysidiella*, *Blastacervulus* and *Asterostomula* are formed in sporodochial, acervular and pycnothyrial conidiomata, respectively (Summerell et al. 2006; Giraldo et al. 2017). Additionally, the appressorial cells are present in *Paraopeba* but have not been observed in *Alysidiella*, *Blastacervulus*, and *Asterostomula*

(Summerell et al. 2006; Giraldo et al. 2017). Bayesian inference analysis (alignment and tree were deposited into TreeBASE under accession number S21280) suggests that *Paraopeba schefflerae* is related to members of Asterinaceae and represents a different genus in this family. *Paraopeba schefflerae* is phylogenetically close but clearly distinct from *Prillieuxina baccharidincola*. Phylogenetic analysis and morphological comparisons support the introduction of *Paraopeba* as a new genus of Asterinaceae, and *Paraopeba schefflerae* as the type species of this genus. To our knowledge, this is the first Asterinaceae member described colonizing *Schefflera morototoni* leaves. In addition, *Paraopeba schefflerae* is a rare case of Asterinaceae known from culture (ex-type COAD 2249).

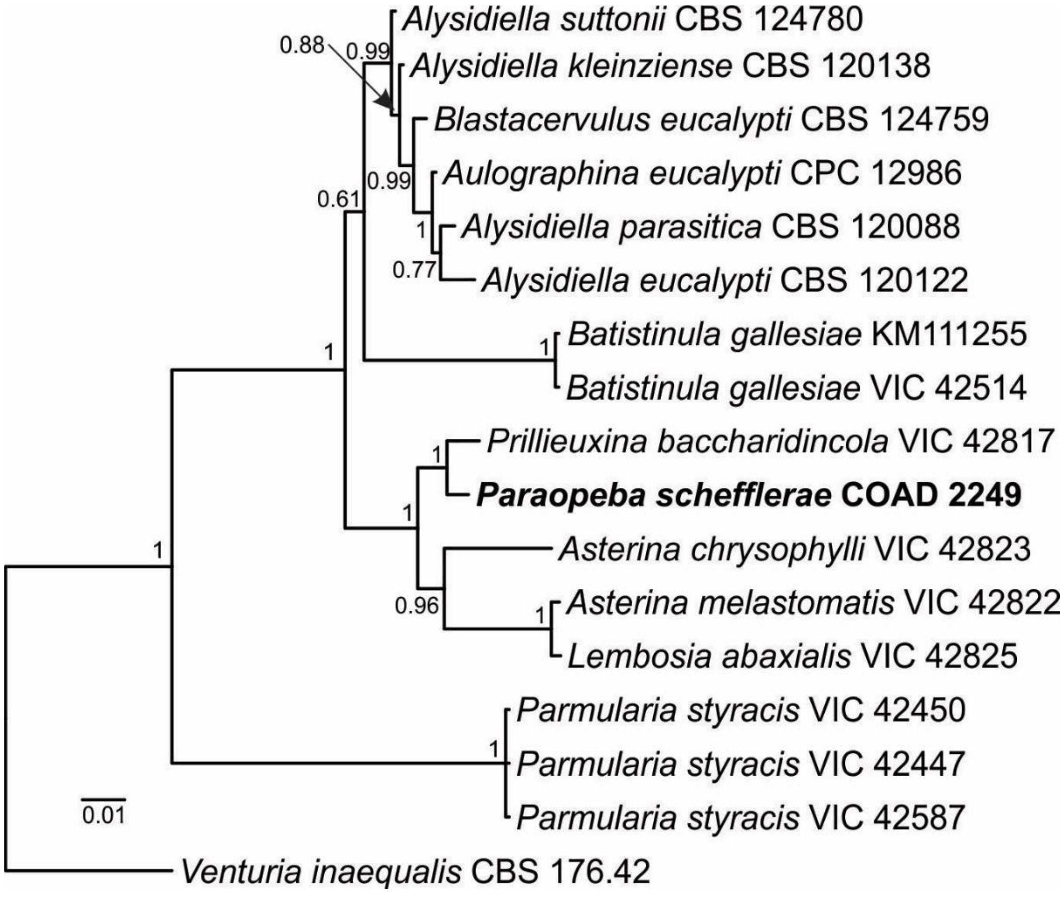


Fig. 1. Phylogenetic tree inferred from Bayesian analysis based on LSU sequences. The analysis was performed with 10 M generations in MrBayes v. 3.2.6. The Bayesian posterior probability values are indicated at the nodes. The tree was rooted to *Venturia inaequalis* CBS 176.42. The new species is highlighted in bold face.

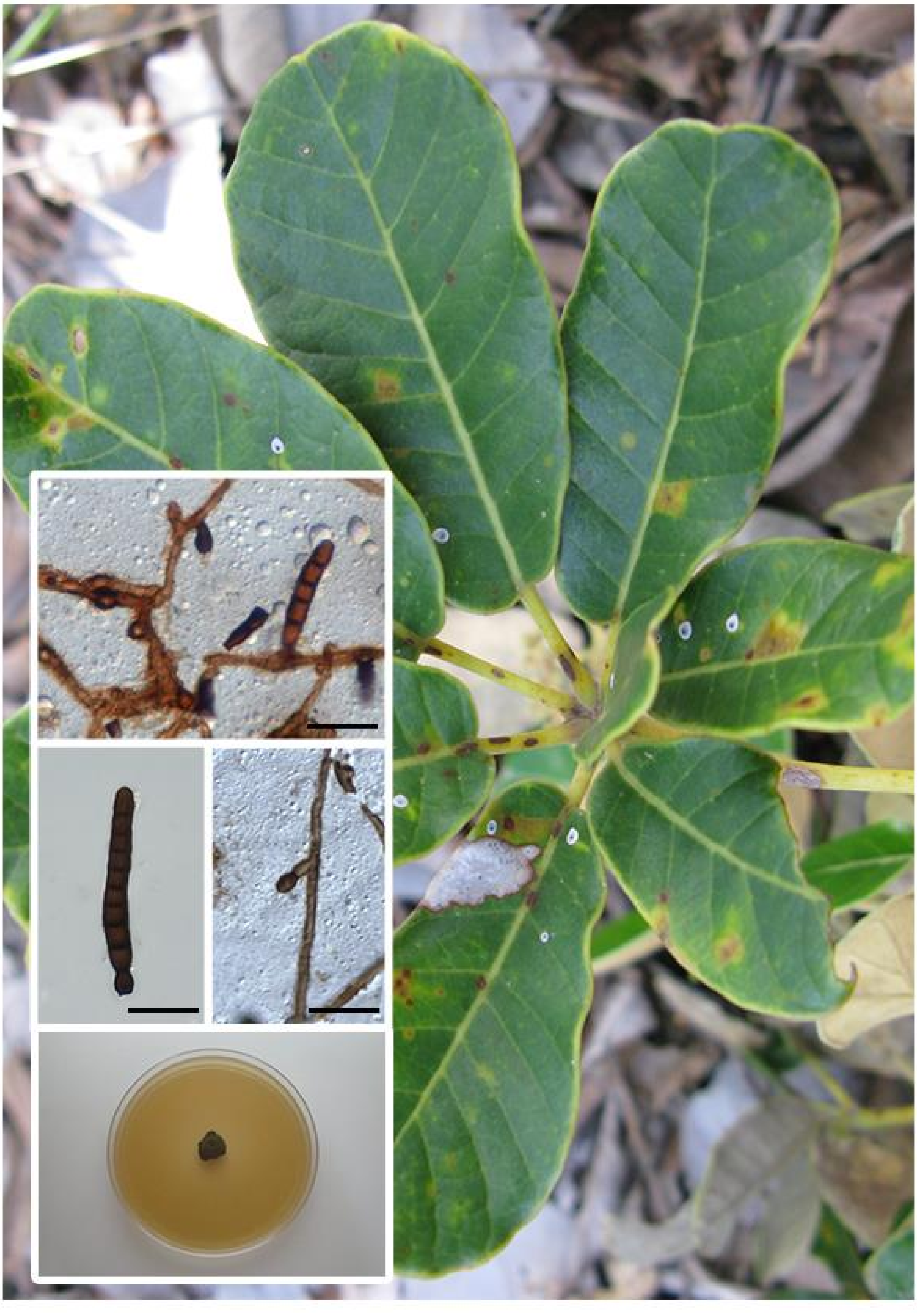


Fig. 2. Leaves of *Schefflera morototoni* in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil; conidia formed on superficial mycelium; thick-walled pigmented conidium; conidium being formed in the conidiogenous cell; colony on MEA after 40 d at 25 ºC. Scale bars = 20 µm.

Dictyosporina *V.P. Abreu, R.F. Castañeda-Ruiz & O.L. Pereira*

(Published in Fungal Diversity v.87, p.63-65, 2017).

Etymology. Refers to the dictyosporous conidia.

Classification — Mycosphaerellaceae, Capnodiales, Dothideomycetes.

Leaf spots epiphyllous, circular to irregular, single, black. *Sporodochia* reddish-brown. *Conidiophores* reduced to conidiogenous cells (Castañeda-Ruiz et al. 2012; Sutton and Pascoe 1989). *Sexual morph* unknown.

Type species. *Dictyosporina ferruginea* V.P. Abreu, R.F. Castañeda-Ruiz & O.L. Pereira. MycoBank MB 821781. Facesoffungi number FoF 03438.

Dictyosporina ferruginea *V.P. Abreu, R.F. Castañeda-Ruiz & O.L. Pereira*

Etymology. Refers to its reddish-brown sporodochia.

Leaf spots epiphyllous, circular to irregular, single, black, with the presence of sporodochia. *Internal mycelium* indistinct. *External mycelium* absent. *Sporodochia* 14−35 × 25−55 µm, reddish-brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8−20 × 4−8 µm, monoblastic, terminal integrated, determinate, reddish-brown. Almost the outer wall layer(s) breaks first, and several conidia are observed attached only by the inner wall layer(s) and miniscule portion of the outer wall layer(s), as can be confirmed by the pale or colorless pigmentation of the conidiogenous cells apex just below each attached conidium and a ridge or frill of outer wall material some distance from the truncate base of the conidium observed at the conidiogenous loci. *Conidia* 20−34 × 14−23 µm, solitary, muriform, cylindrical rounded at the ends, reddish-brown and the secession of each conidium is schizolytic, but the outer and inner wall layers do not separate simultaneously as in most related conidial fungi. *Sexual morph* unknown.

Culture characteristics — The colony grows slowly on malt extract agar 6 mm diam after 40 days at 25 ºC, margins irregular, with dark-brown colonies (Fig 4e).

Typus. BRAZIL, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA - Paraopeba), on leaves of *Kielmeyera coriacea* (Calophyllaceae), 31 Jan. 2016, V.P. Abreu & O.L. Pereira (VIC 44241, COAD 2272; ITS and LSU sequences

GenBank MF344901 and MF344902, MycoBank MB 821782; Facesoffungi number FoF 03439).

Notes — *Dictyosporina* is introduced as a new genus based on morphology and phylogenetic support (LSU and ITS sequence data). Seifert et al. (2011) described five foliicolous, dictyosporous genera with sporodochial conidiomata: *Dictyorostrella*, *Stigmina*, *Thyrostroma*, *Thyrostromella* and *Xenostigmina*, these genera share morphologically comparable sporodochia and conidia with *Dictyosporina*. However, *Dictyorostrella*, typified by *D. caricicola* (U. Braun & Melnik) U. Braun, has a conspicuous, immersed, or erumpent, dark brown stromata and monoblastic, indeterminate, annellidic conidiogenous cells after several enteroblastic percurrent elongations, the conidia are euseptate, obclavate, abruptly rostrate, obconical truncate at the base (Braun 1999). The genus *Stigmina*, typified by *S. platani* (Fuckel) Sacc., is distinguished by a well-developed, immersed or superficial, *textura angularis*, brown stromata and conidiogenous cells monoblastic, indeterminate, annellidic, with several enteroblastic percurrent elongations; the conidia distoseptate and euseptate, clavate, cylindrical, obclavate or oblong (Ellis 1971; Sutton and Pascoe 1989). The genus *Stigmina* is considered interpreted, with a broad generic concept that needs to be re-evaluated (Sutton and Pascoe 1989) and still near 100 recorded names are registered under the same genus (Index Fungorum 2017). *Thyrostroma* typified by *T. compactum* (Sacc.) Höhn. has superficial and immersed, pale brown stromata, conidiogenous cells monoblastic, indeterminate, annellidic, with 1–3 enteroblastic percurrent elongations, also sympodial extensions of the conidiogenous cells have been described. The conidia are ellipsoidal, cylindrical or clavate, euseptate, phragmo- or dictyoseptate pale to mid brown (Ellis 1971; Sutton and Pascoe 1989; Seifert et al. 2011). The genus *Thyrostromella*, typified by *T. myriana* (Desm.) Höhn., is characterized by erumpent stromata, and polyblastic, indeterminate, with few sympodial elongations and cicatrized conidiogenous cells. The conidia are euseptate, dictyoseptate, brown to olivaceous brown (Ellis 1971; Seifert et al. 2011). *Xenostigmina* typified by *X. zilleri* (A. Funk) Crous is distinguished by terminal and intercalary, tapering to flat tipped loci, with sympodial and enteroblastic percurrent elongations conidiogenous cells. The conidia are ellipsoidal to navicular, frequently with an apical beak to obtuse at the apex, and subobtuse basal appendage and basal marginal frill, dictyoseptate, pale to mid brown (Crous et al. 2009; Seifert et al. 2011). Our phylogenetic trees built by using LSU and

ITS corroborated that our fungus represents a new genus and a new species belonging to Mycosphaerellaceae (Fig. 3).

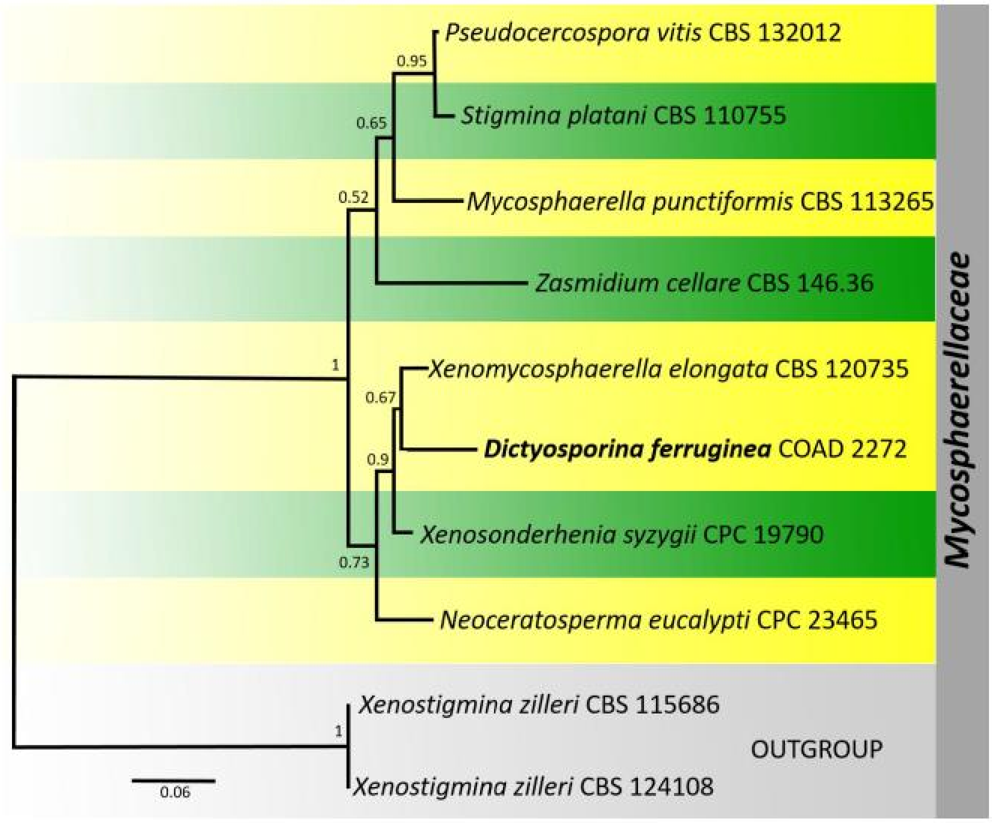


Fig. 3. Phylogenetic tree obtained from Bayesian Inference analysis based on a combined dataset of ITS and LSU sequences. Bayesian posterior probabilities are shown above the nodes. The tree is rooted to *Xenostigmina zilleri* CBS115686 and *Xenostigmina zilleri* CBS124108. Bold indicates ex-type strain COAD 2272.

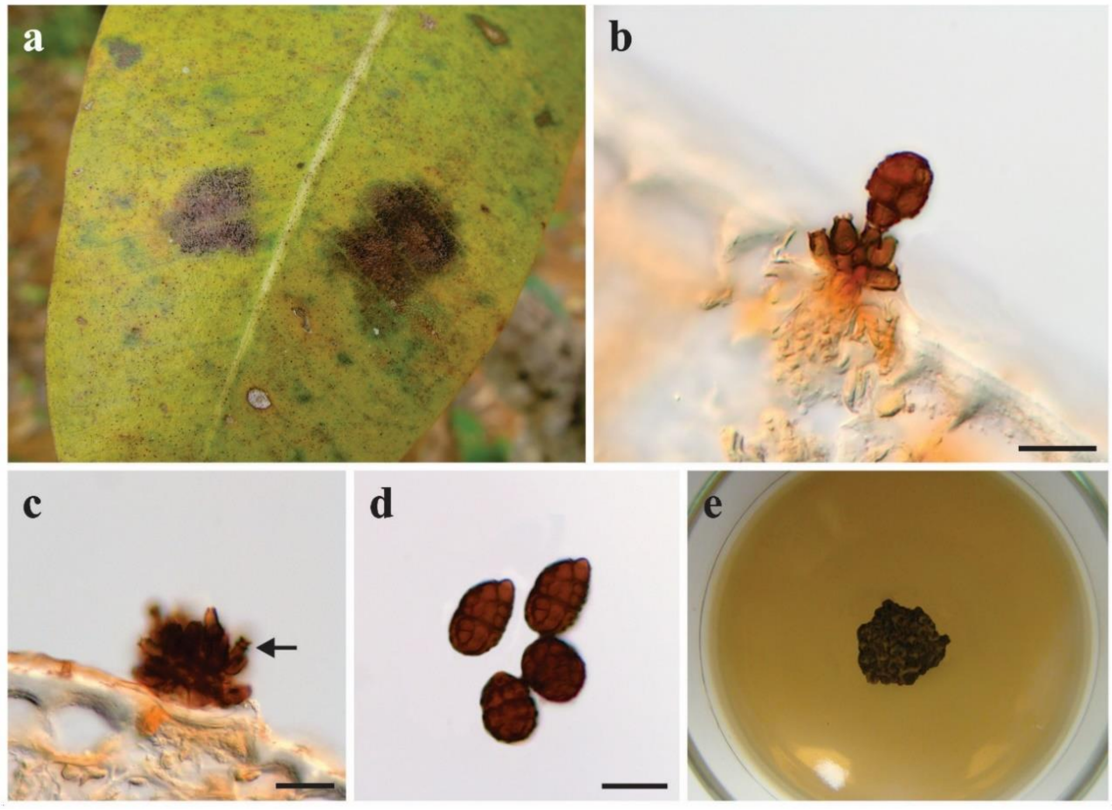


Fig. 4. *Dictyosporina ferruginea* (VIC 44241, holotype). a Leaf spot symptoms on *Kielmeyera coriacea*. b Sporodochial conidiomata with dictyosporous conidia attached. c Detail of frill of outer wall material observed at the conidiogenous loci (arrow). d Dictyosporous conidia. e Colony grows slowly on malt extract agar 6 mm diam after 40 days at 25 ºC (COAD 2272). Scale bars b–d = 20 µm.

Trochilispora *V.P. Abreu, A.W.C. Rosado & O.L. Pereira* (to be proposed as a new genus)

Etymology. From the family Trochilidae (hummingbirds) and –spora.

Classification — Amphisphaeriaceae, Xylariales, Sordariomycetes.

Asexual morph associated with leaf spot disease on *Schefflera morototoni* (Fig. 6a). *Conidioma* acervular (Fig. 6c), epiphyllous, scattered and occasionally confluent, subepidermal in origin, erumpent, rounded to oval in outline, unilocular, brown or black, basal stroma thick, of *textura angularis*, cells thick-walled and almost colourless; lateral walls thick, cells thick-walled, pale brown to brown. *Conidiophores* cylindrical to subcylindrical, formed in the concavity of the conidioma, unbranched, hyaline, smooth-walled. *Conidiogenous cells* discrete, annellidic with 2 annellations, hyaline, thin- and smooth-walled. *Conidia* fusiform, straight or slightly curved, 3–4-septate, concolourous, smooth, bearing apical appendage tubular, filiform, single, not centric, unbranched and basal appendage absent; basal cell hyaline to subhyaline, obconic to conic, smooth and thin-walled; 2–3 median cells doliiform, smooth, concolourous, brown, septa darker than the rest of the cell; apical cell hyaline to subhyaline, subconical to hemisphaerical, thin- and smooth-walled (Fig. 6d–g). *Sexual morph* unknown.

Type species. *Trochilispora schefflerae* V.P. Abreu, A.W.C. Rosado & O.L. Pereira. MycoBank MB 824655. Facesoffungi number FoF 04859

Trochilispora schefflerae *V.P. Abreu, A.W.C. Rosado & O.L. Pereira* (to be proposed as a new species)

Etymology. Name derived from its host genus, *Schefflera*.

Asexual morph conidiomata acervular, epiphyllous, scattered and occasionally confluent, subepidermal in origin, erumpent, rounded to oval in outline, 49–88 × 79–235 µm diam., unilocular, brown or black, basal stroma thick, of *textura angularis*, cells thick-walled and almost colourless; lateral walls 3–5 cells thick, cells thick-walled, pale brown to brown. *Conidiophores* cylindrical to subcylindrical, (8.5–15.5 × 1.5–2 µm), formed in the concavity of the conidioma, unbranched, hyaline, smooth-walled. *Conidiogenous cells* discrete, annellidic with 2 annellations, (3.5–11.5 × 1.5–3 µm), hyaline, thin- and smooth-walled. *Conidia* fusiform, straight or slightly curved, concolourous, smooth, bearing apical appendage, and basal appendage absent; 3-septate (13–19 × 3.5–5), bearing: [basal cell obconic to conic, hyaline to subhyaline, smooth and thin-walled, 2–4 µm long; two median cells doliiform, 8.5–12.5 µm long, smooth, concolourous, brown, septa darker than the rest of the cell (second cell from base brown, 3.5–5.5 µm long; third cell brown, 4.5–7 µm long); apical cell 2–3.5 µm long, hyaline to subhyaline, subconical to hemispherical, thin- and smooth-walled; with 1 tubular apical appendage, arising from the apical crest, not centric, unbranched, filiform, 2–6.5 µm long; basal appendage absent], or 4-septate (15.5–21 × 4–5), bearing: [basal cell obconic to conic, hyaline to subhyaline, smooth and thin-walled, 2–5 µm long; three median cells doliiform, 10–13 µm long, smooth, concolourous, brown, septa darker than the rest of the cell (second cell from base brown, 4–6 µm long; third cell brown, 2.5–4 µm long; fourth cell brown, 2.5–4.5 µm long); apical cell 2.5–3.5 µm long, hyaline to subhyaline, subconical to hemisphaerical, thin- and smooth-walled; with 1 tubular apical appendage, arising from the apical crest, not centric, unbranched, filiform, 2.5–7.5 µm long; basal appendage absent]. *Sexual morph* unknown.

Culture characteristics — Colonies cultured on PDA reaching 38 mm diam after 1 wk at 25 °C with a photoperiod of 12 hours, regularly margins, with dense aerial mycelium, white, colonies fertile (Fig. 6b). Colonies cultured on MEA reaching 40 mm diam after 1 wk at 25 °C with a photoperiod of 12 hours, regularly and submerged margins, with scarce and sebaceous aerial mycelium, pale yellowish, colonies fertile.

Typus. BRAZIL, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA - Paraopeba), on leaves of *Schefflera morototoni* (Araliaceae), 30 Jan. 2016, V.P. Abreu & O.L. Pereira (VIC 44384, COAD 2371; ITS, LSU, *tef1* and *tub2* sequences GenBank MH128360, MH084761, MH231216 and MH231215, MycoBank MB824656, Facesoffungi number FoF 04860).

Notes — *Trochilispora* is introduced as a new genus based on morphology and phylogenetic support (LSU and ITS DNA sequence data). Based on phylogenetic analyses, *Trochilispora schefflerae* COAD 2371 grouped in a well-supported clade including *Hymenopleella hippophaeicola* CBS 140410 (Fig. 5), but different genera can be grouped in the same clade, as for example: *Morinia* and *Zetiasplozna*, *Truncatella* and *Broomella*, among others. Unfortunately, Jaklitsch et al. (2016) did not observed the asexual morph of *Hymenopleella hippophaeicola*, but the authors cite the *Hymenopleella sollmannii* species reported by Shoemaker and Müller (1965). The phylogenetic position of the *Trochilispora* family is still unclear. Morphologically, *Trochilispora schefflerae* COAD 2371 differs from *Hymenopleella sollmannii* by having conidia formed in conidiomata acervular with lateral walls 3–5 cells thick of brown hyphae, conidiophores smaller, conidiogenous cells discrete, annellidic with 2 annellations; conidia fusiform, straight or slightly curved, 3–4-septate, with medium brown central cells and hyaline to subhyline end cells, apical cell with an appendage tubular, filiform, single, not centric, unbranched, not septum and basal cell without appendage basal. Our phylogenetic tree built using LSU and ITS data, and morphological features corroborated that our isolate represents a new genus and a new species belonging to Amphisphaeriaceae (Fig. 5).

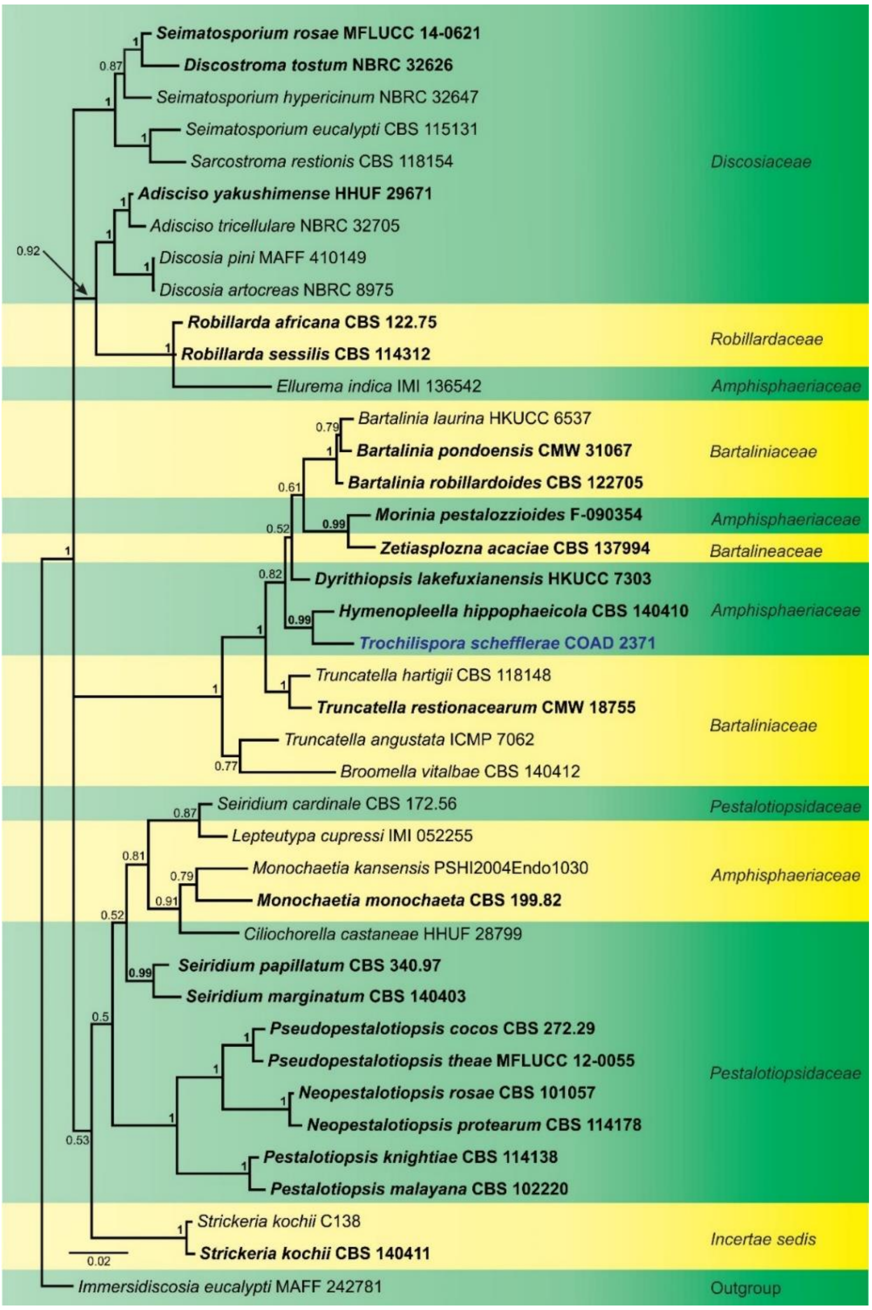


Fig. 5. Phylogram generated from Bayesian Inference analysis based on combined ITS and LSU sequence data for several closely related genera in Amphisphaeriales. Sequence data of ex-type or ex-epitype cultures obtained from Senanayake et al. (2015) and the closest hits of GenBank database were included in this study. The combined genes sequence analysis included 40 taxa, which comprise a total 1405 characters (591 characters for ITS, 814 characters for LSU), and outgroup taxon *Immersidiscosia eucalypti* MAFF 242781. Bayesian posterior probabilities are indicated at the nodes and values equal or greater than 0.95 are in bold. Isolate numbers are indicated after species names. Ex-type or ex-epitype strains are in bold. New sequence data is in bold and blue.

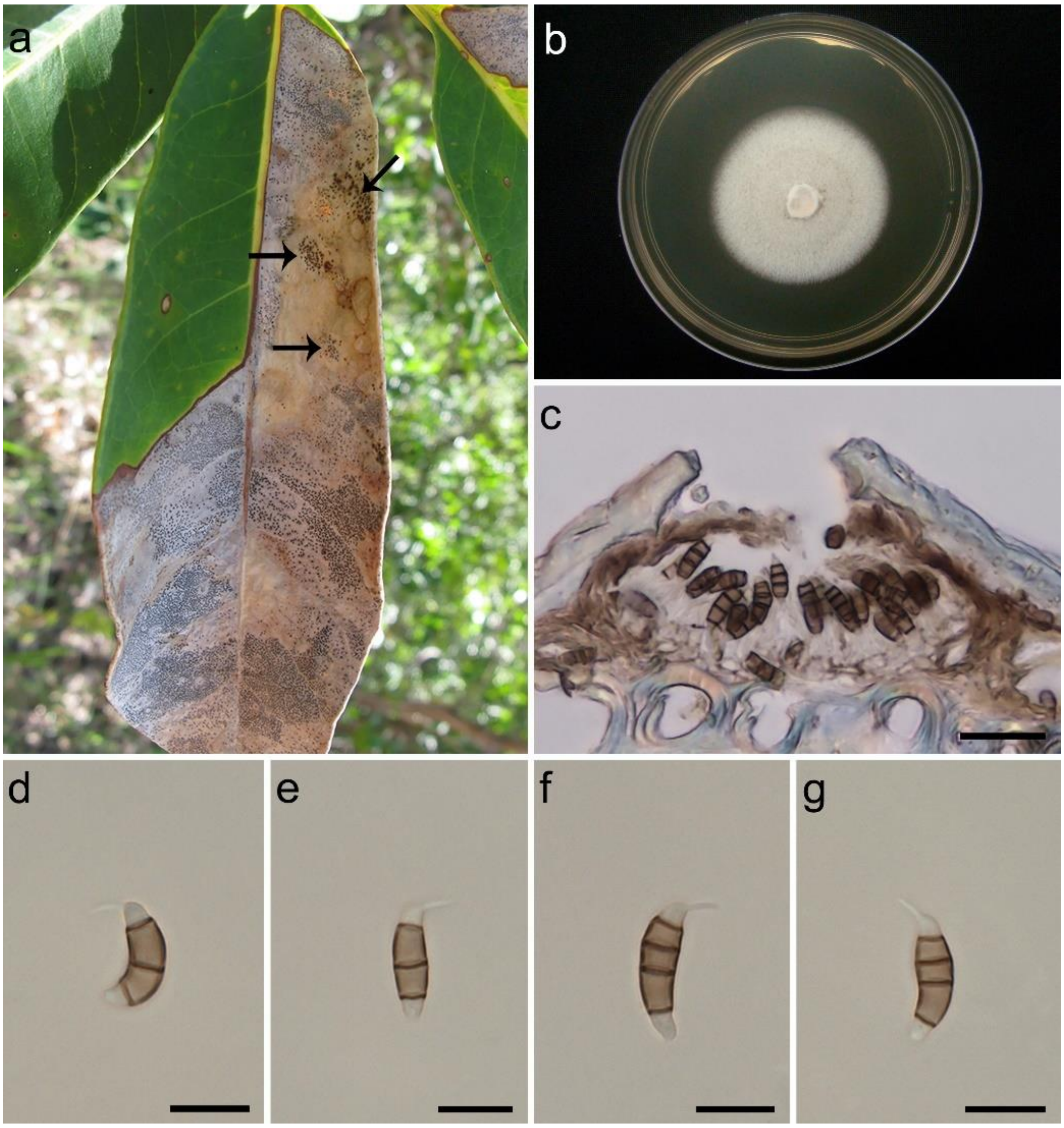


Fig. 6. *Trochilispora schefflerae* (VIC 44384, holotype) a Leaves of *Schefflera morototoni* in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil. The arrows indicate the reproductive structures of the fungus. b Colony on PDA (Potato dextrose agar) after 1 wk at 25 °C with a photoperiod of 12 hours in the dark in Petri dishes (90 x 15 mm) (COAD 2371). c Cross section of the conidioma. d-g Conidia. Scale bars: c = 50 µm, d-g = 10 µm.

Mastigosporella pigmentata *V.P. Abreu & O.L. Pereira*

(Published in Persoonia v.39, p.348-349, 2017).

Etymology. Refers to the pigmented conidia of the species.

Classification — Harknessiaceae, Diaporthales, Sordariomycetes.

Conidiomata immersed, pycnidial, up to 160 µm diam, pale brown on host tissue; wall of 4–6 layers of pale brown to brown *textura globulosa*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* pale brown, smooth, ampulliform or doliiform, 4.5–9 × 4–7 µm. *Conidia* solitary, aseptate, ellipsoid to fusiform, unicellular, pale brown, sometimes slightly darker at the ends, smooth, thick-walled, developing a solitary apical appendage (cellular, type A1 *sensu* Nag Raj 1993), which is part of the conidial body, developing while still attached to the conidiogenous cell, attenuating into an acutely rounded tip; conidium body 21–33 × 6.5–9.5 µm (excluding appendage); basal hilum truncate, 1.5–2 µm diam, apical appendage developing as continuation of conidium body, containing cytoplasm, 11–28 µm.

Culture characteristics — Colonies on malt extract agar 63 mm diam after 5 d at 25 ºC with a photoperiod of 12 h, margins irregular, white aerial mycelium, colonies fertile.

Typus. BRAZIL, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA - Paraopeba), on leaves of *Qualea parviflora* (Vochysiaceae), 31 Jan. 2016, V.P. Abreu & O.L. Pereira (VIC 44383, COAD 2370; ITS, LSU and *tef1* sequences GenBank MG587929, MG587928 and MH020056, MycoBank MB823670).

Notes — Species of the coelomycete genus *Mastigosporella* are characterised by yellowish brown to dark brown pycnidial conidiomata and hyaline conidiogenous cells with enteroblastic-percurrent proliferation to produce additional narrowly ellipsoid to fusiform conidia bearing an appendage of type A1 (appendage initially arising as a tubular extension of the conidium body) (Nag Raj 1993). Currently, the genus *Mastigosporella* is known from three species, *M. hyalina*, *M. anisophylleae* and *M. georgiana* (Nag Raj 1993; Crous et al. 2013a; Rossman et al. 2015; Senanayake et al. 2017). Only one species of *Mastigosporella* (*M. anisophylleae*) is known from culture and DNA sequence data (Crous et al. 2013a; Senanayake et al. 2017). *Mastigosporella pigmentata* clearly differs from *M. hyalina*, *M. anisophylleae*, and *M. georgiana* by having pale brown conidia and conidiogenous cells. *Mastigosporella pigmentata* presents larger and wider conidia than *M. hyalina* and *M. georgiana*. *Mastigosporella pigmentata* has conidia similar in length to *M. anisophylleae*, but distinguishable from it by being wider. In addition, the conidia of *Mastigosporella pigmentata* presents apical appendages longer than *M. anisophylleae* and *M. hyalina*. Members of this genus were reported from the USA and Zambia on leaves of *Quercus coccinea*; on leaves and petioles of *Nyssa biflora*, *Nyssa sylvatica* and on *Anisophyllea* sp. (Nag Raj 1993; Crous et al. 2013a; Senanayake et al. 2017). To our knowledge, this is the first report of the occurrence of the genus *Mastigosporella* in Brazil. Phylogenetic analysis and morphological comparisons support the introduction of *Mastigosporella pigmentata* as a new species within this genus.

Table 4. Morphological characteristics (sizes in µm) of *Mastigosporella* spp.

Species	**Conidia**	**Conidiogenous cells**	**Apical appendage**	**References**
Mastigosporella anisophylleae	(21–)27–30(–32) × (4.5–)5–5.5(–6)	5–12 × 3–5	(5–)6–7(–8)	Crous et al. (2013a)
Mastigosporella georgiana	16–25 × 5–7	5–10 × 2.5–6	12–26 × 1	Nag Raj (1993); Rossman et al. (2015)
Mastigosporella hyalina	18–28 × 3.5–5	7–11 × 3–4(–5)	5–10(–12)	Nag Raj (1993)
Mastigosporella pigmentata	**21–33 × 6.5–9.5**	**4.5–9 × 4–7**	**11–28**	**This study**

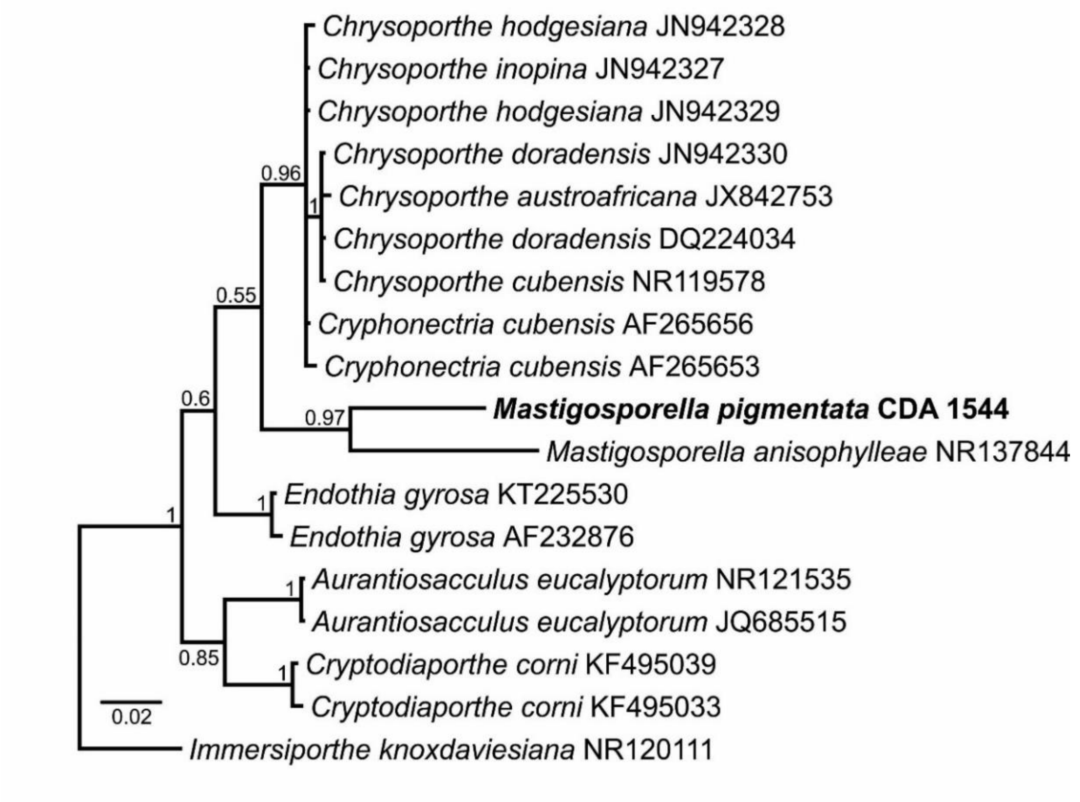


Fig. 7. Phylogenetic tree obtained from Bayesian Inference analysis based on the ITS sequences. The Bayesian posterior probabilities are indicated next to the nodes. The tree was rooted with *Immersiporthe knoxdaviesiana* NR120111. The species in this study is highlighted in bold.

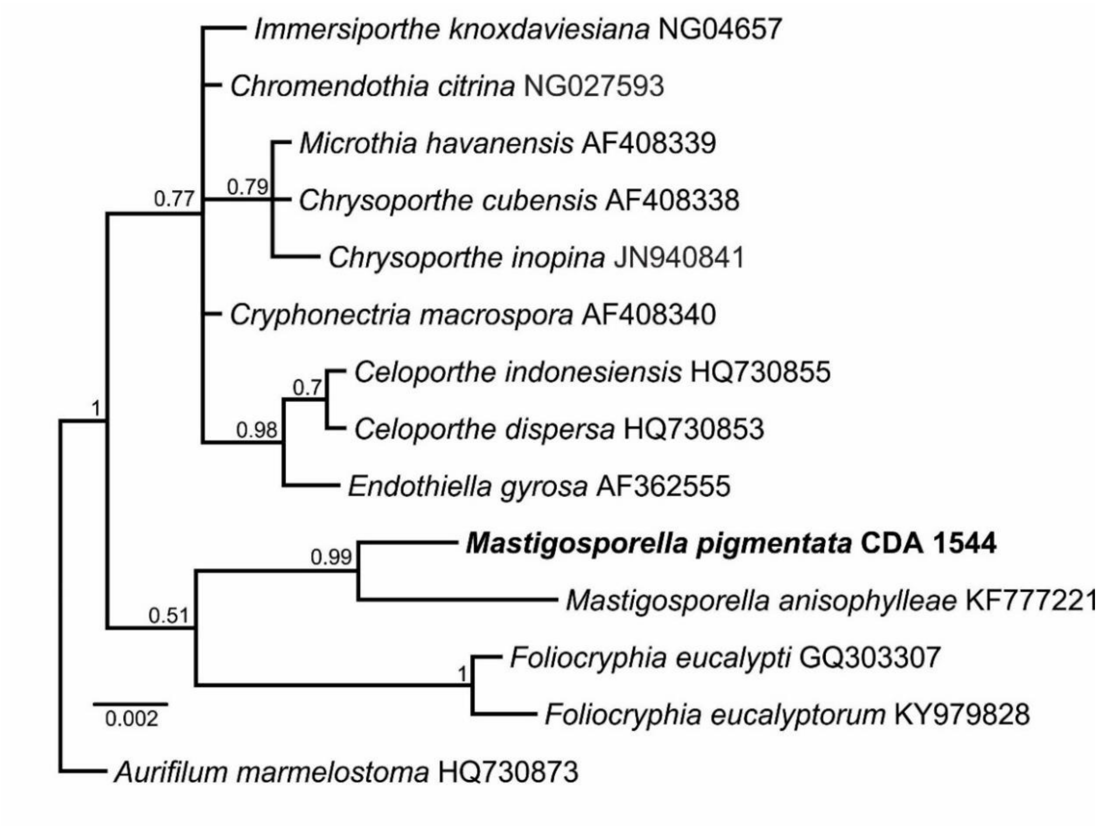


Fig. 8. Phylogenetic tree obtained from Bayesian Inference analysis based on the LSU sequences. The Bayesian posterior probabilities are indicated next to the nodes. The tree was rooted with *Aurifilum marmelostoma* HQ730873. The species in this study is highlighted in bold.

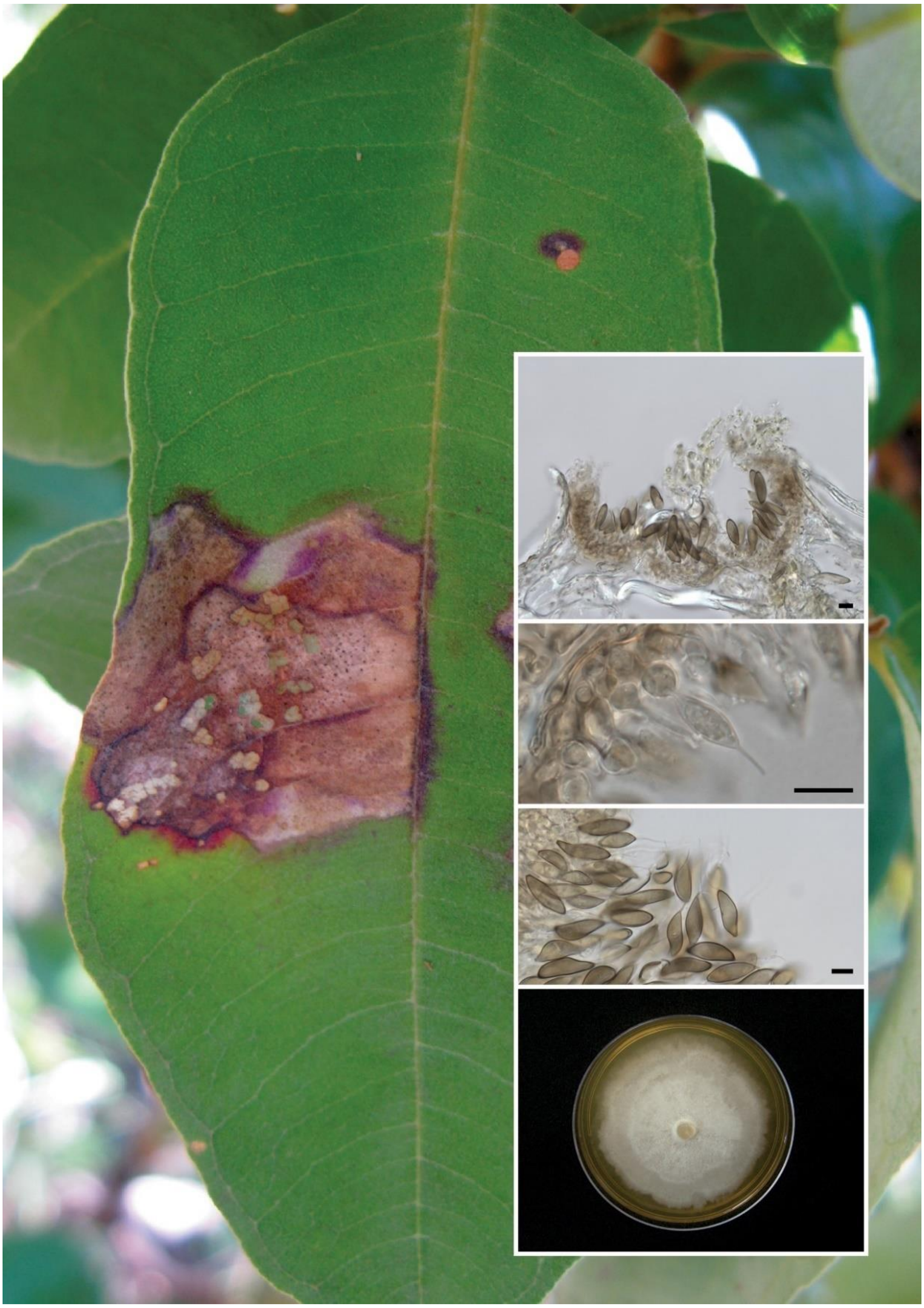


Fig. 9. Leaf spot symptoms on *Qualea parviflora* (Vochysiaceae) in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil; vertical section of conidioma; conidiogenous cell with developing pigmented conidia; mature pale brown conidia with apical appendages; colony on MEA after 5 d at 25 ºC. Scale bars = 10 µm.

Pseudocercospora styracina *V.P. Abreu & O.L. Pereira*

(Published in Persoonia v.41, p.238-417, 2018).

Etymology. Name derived from its host genus, *Styrax*.

Classification — Mycosphaerellaceae, Capnodiales, Dothideomycetes.

Leaf spots amphigenous, circular to irregular, initially chlorotic, becoming brown with age, 4–10 mm diam. *Internal mycelium* indistinct. *External mycelium* brown, septate, branched, smooth, 1.5–2.5 µm diam, colonising the trichomes. *Stromata* absent. *Conidiophores* hypophyllous, cylindrical, branched, solitary, 19–57 × 2–4.5 µm, 1−7-septate, straight or geniculate, brown, smooth, sometimes restricted to conidiogenous cells. *Conidiogenous cells* terminal, 7–13.5 × 2.5–4.5 µm, or conidiophores reduced to conidiogenous cells, 3.5–12.5 × 2–4 µm, subcylindrical, brown, smooth, proliferating sympodially. *Conidiogenous loci* inconspicuous, unthickened, not darkened. *Conidia* solitary, guttulate, pale brown to brown, smooth, subcylindrical, straight to slightly curved, 22.5–47.5 × 2–3 µm, base truncate, 1–3-septate, hila neither unthickened nor darkened, 1–1.5 µm diam.

Culture characteristics — Colonies on PDA 34 mm diam after 20 d at 25 ºC with a photoperiod of 12 h; with aerial mycelium sparse, grey, reverse iron-grey, sterile.

Typus. BRAZIL, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA - Paraopeba), on leaves of *Styrax* sp. (Styracaceae), 31 Jan. 2016, V.P. Abreu & O.L. Pereira (VIC 44382, COAD 2369; ITS, LSU, *tef1* and *actA* sequences GenBank MH397664, MH480643, MH480642 and MH480641, MycoBank MB824660).

Notes — Cercosporoid fungi include several genera of microfungi with cosmopolitan distribution and are highly diverse, especially in tropical and subtropical countries (Crous et al. 2013b; Bakhshi et al. 2014; Silva et al. 2016). *Pseudocercospora* species can be found as saprobes, endophytes, hyperparasites, being very common as plant pathogens - causing mainly leaf spots (Crous et al. 2013b; Braun et al. 2016; Guatimosim et al. 2016). Cercosporoid fungi have been reported as host-specific (Guatimosim et al. 2016; Silva et al. 2016). Four cercosporoid fungi have been described from *Styrax* spp.: *Passalora styracis*, *Cercospora apii* s. lat. (= *Cercospora styracicola*), *Pseudocercospora fukuokaensis* and *Cercoramularia koreana* (Crous and Braun 2003; Videira et al. 2017). Morphologically, *P. styracina* clearly differs from *P. fukuokaensis* and *P. brackenicola* by having external mycelium colonising the trichomes and stromata absent. Additionally, the conidia length of *P. styracina* (22.5–47.5 µm) are shorter than *P. fukuokaensis* (30–70 µm) and *P. brackenicola* (20–77 µm) (Chupp 1954; Guatimosim et al. 2016). *Pseudocercospora styracina* does not correspond to any sequences available in GenBank at present. Hence, it is described here as a new species.

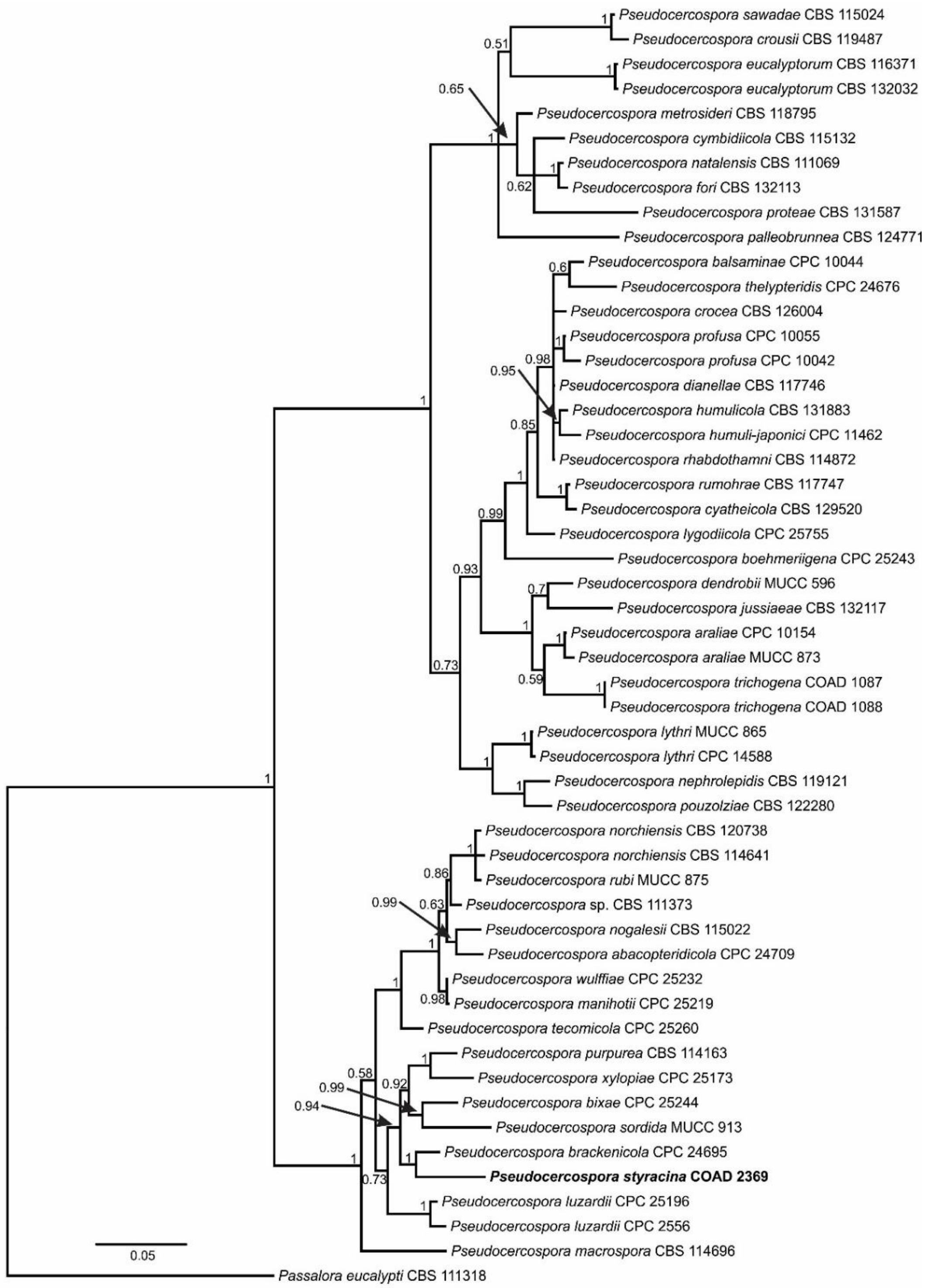


Fig. 10. Bayesian inference tree obtained by phylogenetic analyses of the combined ITS, *actA* and *tef1* sequences conducted in MrBayes on XSEDE at the CIPRES Science Gateway (Miller et al. 2010). Bayesian posterior probability values are indicated at the nodes. The new species is indicated in bold face. *Passalora eucalypti* (CBS 111318) was used as an outgroup.

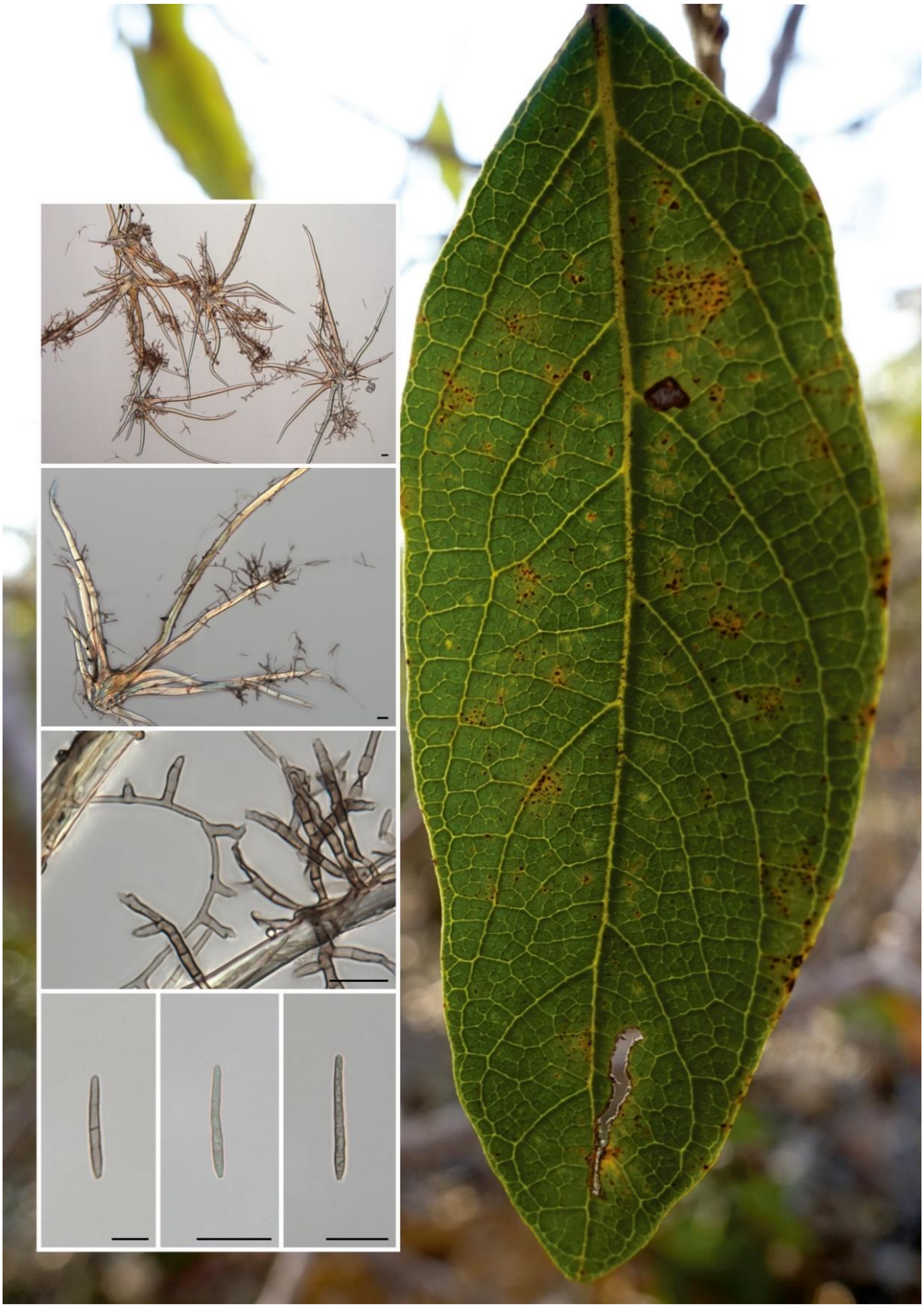


Fig. 11. Chlorotic leaf spots symptoms on *Styrax* sp. (Styracaceae) in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil; external mycelium with conidiophores and conidiogenous cells colonising the trichomes and pigmented conidia with inconspicuous, unthickened, not darkened conidiogenous loci. Scale bars = 20 µm.

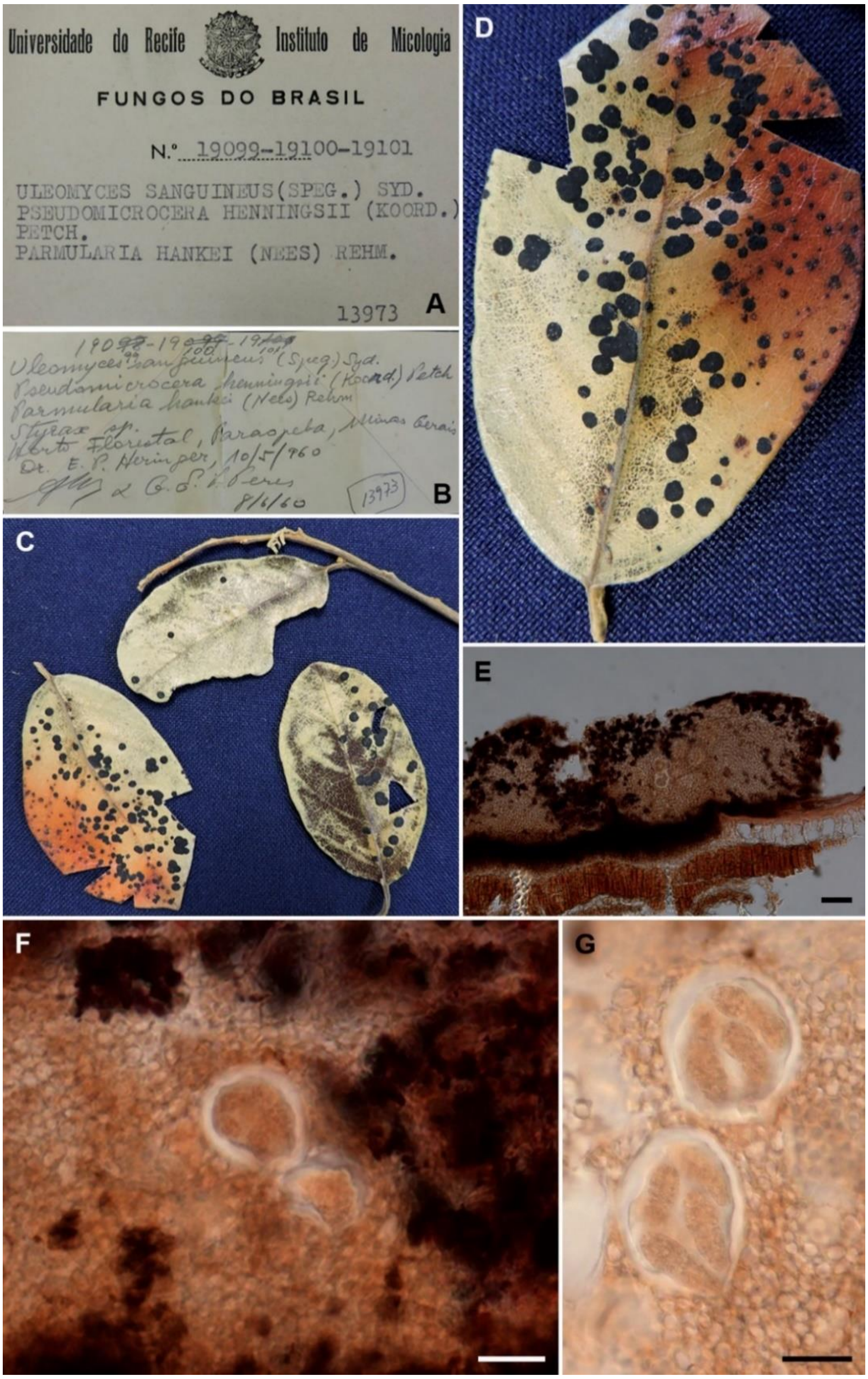
Uleomyces sanguineus (to be proposed as an epitype)

Classification — Cookellaceae, *incertae sedis*, Dothideomycetes.

Colonies epiphyllous 1–2 mm, located along the midrid and secondary veins, solitary, forming a dark scab on the adaxial face of leaves. *Ascomata* 435.5–1310.5 × 175–207.5 µm, crustose, superficial or erumpent, pulvinate, circular to irregular, solitary, dark red to brown, multilocular, forming two layers of monoascal locules. *Hypostroma* foot-like, short, epidermal and immersed, connected to the host. *Asci* globose-saccate, sessile, eight-spored, persistent, bitunicate, ectotunica 41.5–57 × 26–43 µm, endotunica 24–49 × 26–43 µm, embedded singly and irregularly in the fertile pseudoparenchyma; dehiscence indistinct. Interthercial filaments absent. *Ascospores* 23.5–34 × 8.5–13.5 µm, dictyoseptate, constricted at the septa, mainly at median septa, with 5–7 transversal septa and 1 longitudinal septum, yellowish. *Asexual morph* not seen.

Epitype: BRAZIL. Minas Gerais: Paraopeba, Floresta Nacional de Paraopeba, on leaves of *Styrax* sp. (Styracaceae), 31 Jan. 2016, V.P. Abreu & O.L. Pereira (VIC44416).

Notes — *Uleomyces parasiticus* was first described in 1895 by P. Henn. However, *Phymatosphaeria sanguinea* had already been described in 1883 by Speg. As *P. sanguinea* is older than *U. parasiticus*, *P. sanguinea* becomes synonymous (species was used to describe *U. sanguineus*) and *U. sanguineus* becomes the type of genus. *Uleomyces* is within the Cookellaceae (von Arx and Müller 1975), but according to Hyde et al. (2013), there are only two accepted families within Myriangiales (Myriangiaceae and Elsinoaceae) and Cookellaceae is misplaced in Dothideomycetes, and it should be treated as *incertae sedis*. There are no molecular data available for Cookellaceae (Hyde et al. 2013; Fan et al. 2017), and we were not able to get the cultures and DNA sequences of our isolate. Furthermore, we tried the direct extraction, however, without sucess. Then, we agree to keep the Cookellaceae as *incertae sedis* and perform a new collection and extraction of DNA in future studies. *Uleomyces sanguineus* was found on leaves of *Styrax* sp. (Styracaceae), associated with *Parmularia hankei*, in the Floresta Nacional de Paraopeba, Minas Gerais, however, the taxonomy of *Uleomyces sanguineus* has been uncertain due to deterioration of the sexual structures over the time of the type species. Based on the comparison morphological made between our isolate and the type species currently deposited in the herbarium Pe. Camille Torrend (URM) of the Universidade Federal de Pernambuco, in Recife, Pernambuco, Brazil (In the past, Universidade do Recife – Instituto de Micologia – IMUR), we propose here that our isolate become the type species of the genus *Uleomyces*.



Universidade do Recife Instituto de Micologia

FUNGOS DO BRASIL

N.º 19099-19100-19101

ULEOMYCES SANGUINEUS(SPEG.) SYD.
PSEUDOMICROCERA HENNINGSII (KOORD.)
PETCH.
PARMULARIA HANKEI (NEES) REHM.

13973

190~~98~~ 99-19~~099~~ 100-19~~100~~ 101
Uleomyces sanguineus (Speg.) Syd.
Pseudomicrocera henningsii (Koord.) Petch
Parmularia hankei (Nees) Rehm
Styrax sp.
Horto Florestal, Paraopeba, Minas Gerais
Dr. E. P. Heringer, 10/5/960
& G. S. L. Peres
8/6/60
13973

Fig. 12. *Uleomyces sanguineus* (type). A. Stored type at Universidade Federal de Pernambuco – Instituto de Micologia (IMUR). B. Collector notes. C. All the leaves of *Styrax* sp. deposited. D. Only one of the leaves has structures of *Uleomyces sanguineus.* E. A cross section of the ascomata. F. Detail of the asci inside the ascomata tissue. G. Details of the degraded ascospores. Scale bars: E = 50 µm, F-G = 20 µm.

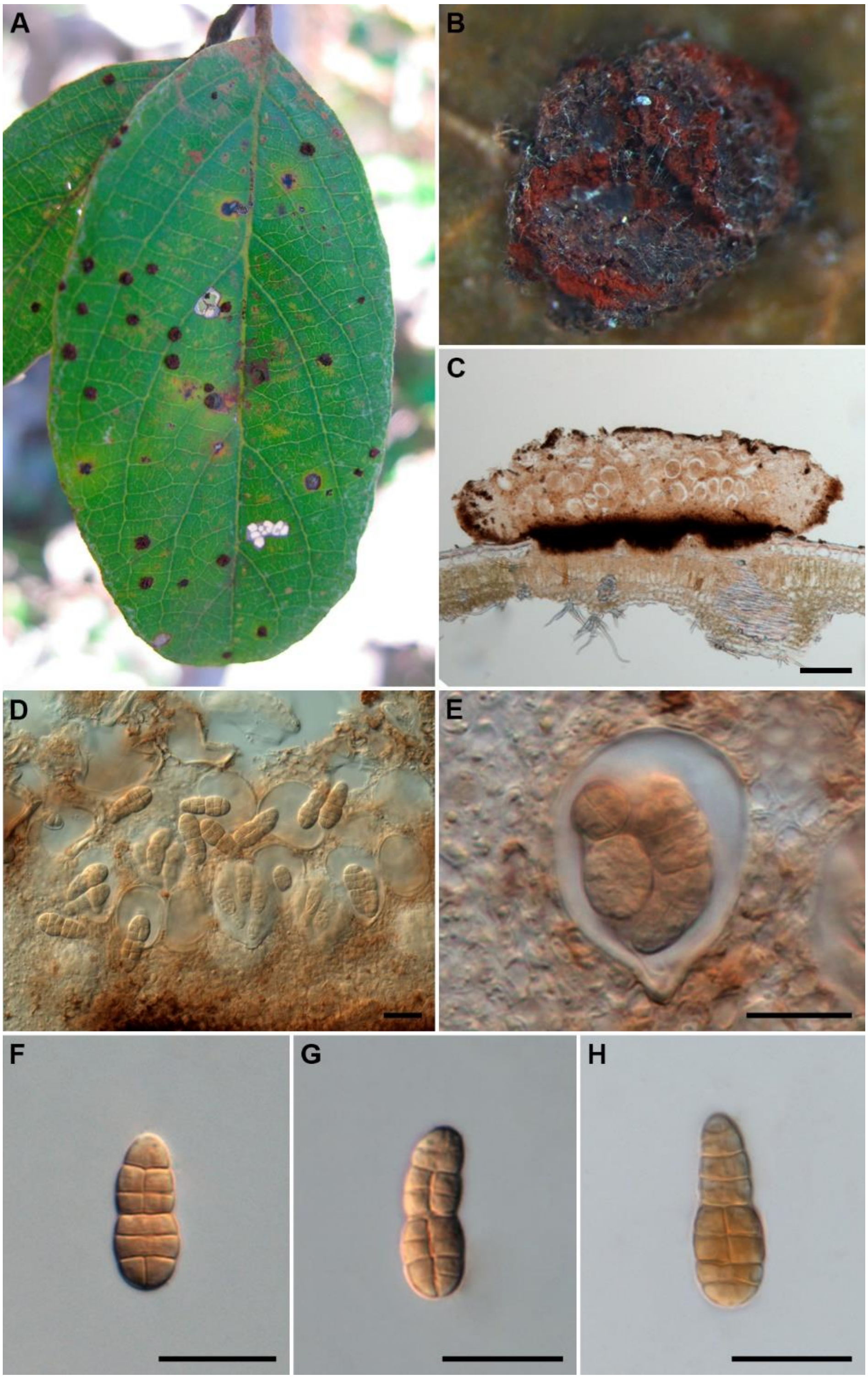


Fig. 13. *Uleomyces sanguineus* VIC44416 (to be proposed as epitype). A. Leaf of *Styrax* sp. showing the structures of *Uleomyces sanguineus*. B. Detail of ascomata. C. A cross section of the ascomata. D. Asci and ascospores spread by the ascomata tissue. E. Detail of an ascus with ascospores. F-H. Muriform ascospores. Scale bars: C = 50 µm, D-H = 20 µm.

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CONCLUSÕES GERAIS

Este estudo representa uma contribuição para o conhecimento da diversidade de fungos folícolas e fitopatogênicos associados a diferentes plantas nativas da Floresta Nacional de Paraopeba (FLONA - Paraopeba).

Três possíveis gêneros novos (*Paraopeba*, *Dictyosporina* e *Trochilispora*); cinco possíveis espécies novas (*Mastigosporella pigmentata*, *Pseudocercospora styracina*, *Trochilispora schefflerae*, *Dictyosporina ferruginea* e *Paraopeba schefflerae*) e uma possível epitificação (*Uleomyces sanguineus*) foram/serão propostos.

Uma coleção de culturas de fungos do Cerrado foi iniciada e futuros estudos de aplicação biotecnológica para a agricultura, indústria e meio ambiente poderão ser iniciados.

O presente trabalho corrobora com a grande diversidade de espécies fúngicas encontradas por outros pesquisadores nas regiões de Cerrado e dessa forma outros estudos são necessários para aumentar o conhecimento sobre esses importantes fungos folícolas e fitopatogênicos e responder a questões sobre valor taxonômico de caracteres morfológicos em ordens/famílias/gêneros de fungos tropicais pouco pesquisados.

ANEXOS

Fungal Diversity (2017) 87:1–235
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Fungal diversity notes 603–708: taxonomic and phylogenetic notes on genera and species

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Abstract

This is the sixth in a series of papers where we bring collaborating mycologists together to produce a set of notes of several taxa of fungi. In this study we introduce a new family *Fuscostagonosporaceae* in Dothideomycetes. We also introduce the new ascomycete genera *Acericola*, *Castellaniomyces*, *Dictyosporina* and *Longitudinalis* and new species *Acericola italica*, *Alternariaster trigonosporus*, *Amarenomyces dactylidis*, *Angustimassarina coryli*, *Astrocystis bambusicola*, *Castellaniomyces rosae*, *Chaetothyrina artocarpi*, *Chlamydotubeufia krabiensis*, *Colletotrichum lauri*, *Collodiscula chiangraiensis*, *Curvularia palmicola*, *Cytospora mali-sylvestris*, *Dictyocheirospora cheirospora*, *Dictyosporina ferruginea*, *Dothiora coronillae*, *Dothiora spartii*, *Dyfrolomyces phetchaburiensis*, *Epicoccum cedri*, *Epicoccum pruni*, *Fasciatispora calami*, *Fuscostagonospora cytisi*, *Grandibotrys hyalinus*, *Hermatomyces nabanheensis*, *Hongkongmyces thailandica*, *Hysterium rhizophorae*, *Jahnula guttulaspora*, *Kirschsteiniothelia rostrata*, *Koorchalomella salmonispora*, *Longitudinalis nabanheensis*, *Lophium zalerioides*, *Magnibotryascoma mali*, *Meliola clerodendri-infortunati*, *Microthyrium chinense*, *Neodidymelliopsis moricola*, *Neophaeocryptopus spartii*, *Nigrograna thymi*, *Ophiocordyceps cossidarum*, *Ophiocordyceps issidarum*, *Ophiosimulans plantaginis*, *Otidea pruinosa*, *Otidea stipitata*, *Paucispora kunmingense*, *Phaeoisaria microspora*, *Pleurothecium floriforme*, *Poaceascoma halophila*, *Periconia aquatica*, *Periconia submersa*, *Phaeosphaeria acaciae*, *Phaeopoacea muriformis*, *Pseudopithomyces kunmingnensis*, *Ramgea ozimecii*, *Sardiniella celtidis*, *Seimatosporium italicum*, *Setoseptoria scirpi*, *Torula gaodangensis* and *Vamsapriya breviconidiophora*. We also provide an amended account of *Rhytidhysteron* to include apothecial ascomata and a J+ hymenium. The type species of *Ascotrichella*

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Key words

ITS nrDNA barcodes
LSU
novel fungal species
systematics

Abstract Novel species of fungi described in this study include those from various countries as follows: **Antarctica**: *Cadophora antarctica* from soil. **Australia**: *Alfaria dandenongensis* on *Cyperaceae*, *Amphosoma persooniae* on *Persoonia* sp., *Anungitea nullicana* on *Eucalyptus* sp., *Bagadiella eucalypti* on *Eucalyptus globulus*, *Castanediella eucalyptigena* on *Eucalyptus* sp., *Cercospora dianellicola* on *Dianella* sp., *Cladoriella kinglakensis* on *Eucalyptus regnans*, *Cladoriella xanthorrhoeae* (incl. *Cladoriellaceae* fam. nov. and *Cladoriellales* ord. nov.) on *Xanthorrhoea* sp., *Cochlearomyces eucalypti* (incl. *Cochlearomyces* gen. nov. and *Cochlearomycetaceae* fam. nov.) on *Eucalyptus obliqua*, *Codinaea lambertiae* on *Lambertia formosa*, *Diaporthe obtusifoliae* on *Acacia obtusifolia*, *Didymella acaciae* on *Acacia melanoxylon*, *Dothidea eucalypti* on *Eucalyptus dalrympleana*, *Fitzroyomyces cyperi* (incl. *Fitzroyomyces* gen. nov.) on *Cyperaceae*, *Murramarangomyces corymbiae* (incl. *Murramarangomyces* gen. nov., *Murramarangomycetaceae* fam. nov. and *Murramarangomycetales* ord. nov.) on *Corymbia maculata*, *Neoanungitea eucalypti* (incl. *Neoanungitea* gen. nov.) on *Eucalyptus obliqua*, *Neoconiothyrium persooniae* (incl. *Neoconiothyrium* gen. nov.) on *Persoonia laurina* subsp. *laurina*, *Neocrinula lambertiae* (incl. *Neocrinulaceae* fam. nov.) on *Lambertia* sp., *Ochroconis podocarpi* on *Podocarpus grayae*, *Paraphysalospora eucalypti* (incl. *Paraphysalospora* gen. nov.) on *Eucalyptus sieberi*, *Pararamichloridium livistonae* (incl. *Pararamichloridium* gen. nov., *Pararamichloridiaceae* fam. nov. and *Pararamichloridiales* ord. nov.) on *Livistona* sp., *Pestalotiopsis dianellae* on *Dianella* sp., *Phaeosphaeria gahniae* on *Gahnia aspera*, *Phlogicylindrium tereticornis* on *Eucalyptus tereticornis*, *Pleopassalora acaciae* on *Acacia obliquinervia*, *Pseudodactylaria xanthorrhoeae* (incl. *Pseudodactylaria* gen. nov., *Pseudodactylariaceae* fam. nov. and *Pseudodactylariales* ord. nov.) on *Xanthorrhoea* sp., *Pseudosporidesmium lambertiae* (incl. *Pseudosporidesmiaceae* fam. nov.) on *Lambertia formosa*, *Saccharata acaciae* on *Acacia* sp., *Saccharata epacridis* on *Epacris* sp., *Saccharata hakeigena* on *Hakea sericea*, *Seiridium persooniae* on *Persoonia* sp., *Semifissispora tooloomensis* on *Eucalyptus dunnii*, *Stagonospora lomandrae* on *Lomandra longifolia*, *Stagonospora victoriana* on *Poaceae*, *Subramaniomyces podocarpi* on *Podocarpus elatus*, *Sympoventuria melaleucae* on *Melaleuca* sp., *Sympoventuria regnans* on *Eucalyptus regnans*, *Trichomerium eucalypti* on *Eucalyptus tereticornis*, *Vermiculariopsiella eucalypticola* on *Eucalyptus dalrympleana*, *Verrucoconiothyrium acaciae* on *Acacia falciformis*, *Xenopassalora petrophiles* (incl. *Xenopassalora* gen. nov.) on *Petrophile* sp., *Zasmidium dasypogonis* on *Dasypogon* sp., *Zasmidium gahniicola* on *Gahnia sieberiana*. **Brazil**: *Achaetomium lippiae* on *Lippia gracilis*, *Cyathus isometricus* on decaying wood, *Geastrum caririense* on soil, *Lycoperdon demoulinii* (incl. *Lycoperdon* subg. *Arenicola*) on soil, *Megatomentella cristata* (incl. *Megatomentella* gen. nov.) on unidentified plant, *Mutinus verrucosus* on soil, *Paraopeba schefflerae* (incl. *Paraopeba* gen. nov.) on *Schefflera morototoni*, *Phyllosticta catimbauensis* on *Mandevilla catimbauensis*, *Pseudocercospora angularis* on *Prunus persica*, *Pseudophialophora sorghi* on *Sorghum bicolor*, *Spumula piptadeniae* on *Piptadenia paniculata*. **Bulgaria**: *Yarrowia parophonii* from gut of *Parophonus hirsutulus*. **Croatia**: *Pyrenopeziza velebitica* on *Lonicera borbasiana*. **Cyprus**: *Peziza halophila* on coastal dunes.

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P.W. Crous[1,2], M.J. Wingfield[3], T.I. Burgess[4], G.E.St.J. Hardy[4], J. Gené[5], J. Guarro[5], I.G. Baseia[6], D. García[5], L.F.P. Gusmão[7], C.M. Souza-Motta[8,13], R. Thangavel[9], S. Adamčík[10], A. Barili[11], C.W. Barnes[12], J.D.P. Bezerra[13], J.J. Bordallo[14], J.F. Cano-Lira[5], R.J.V. de Oliveira[13], E. Ercole[15], V. Hubka[16,17], I. Iturrieta-González[5], A. Kubátová[16], M.P. Martín[18], P.-A. Moreau[19], A. Morte[14], M.E. Ordoñez[11], A. Rodríguez[14], A.M. Stchigel[5], A. Vizzini[15], J. Abdollahzadeh[20], V.P. Abreu[21], K. Adamčíková[22], G.M.R. Albuquerque[8], A.V. Alexandrova[23,24], E. Álvarez Duarte[37], C. Armstrong-Cho[25], S. Banniza[25], R.N. Barbosa[8], J.-M. Bellanger[26], J.L. Bezerra[13], T.S. Cabral[27], M. Caboň[10], E. Caicedo[11], T. Cantillo[7], A.J. Carnegie[28], L.T. Carmo[7], R.F. Castañeda-Ruiz[29], C.R. Clement[30], A. Čmoková[17], L.B. Conceição[7], R.H.S.F. Cruz[6], U. Damm[31], B.D.B. da Silva[32], G.A. da Silva[13], R.M.F. da Silva[13], A.L.C.M. de A. Santiago[13], L.F. de Oliveira[34], C.A.F. de Souza[13], F. Déniel[33], B. Dima[35], G. Dong[36], J. Edwards[38], C.R. Félix[39], J. Fournier[40], T.B. Gibertoni[13], K. Hosaka[42], T. Iturriaga[43], M. Jadan[44], J.-L. Jany[33], Ž. Jurjević[45], M. Kolařík[16,17], I. Kušan[44], M.F. Landell[39], T.R. Leite Cordeiro[13], D.X. Lima[13], M. Loizides[46], S. Luo[36], A.R. Machado[13], H. Madrid[47], O.M.C. Magalhães[13], P. Marinho[48], N. Matočec[44], A. Mešić[44], A.N. Miller[43], O.V. Morozova[49], R.P. Neves[13], K. Nonaka[50], A. Nováková[17], N.H. Oberlies[51], J.R.C. Oliveira-Filho[13], T.G.L. Oliveira[13], V. Papp[52], O.L. Pereira[53], G. Perrone[54], S.W. Peterson[55], T.H.G. Pham[24,41], H.A. Raja[51], D.B. Raudabaugh[43], J. Řehulka[56], E. Rodríguez-Andrade[5], M. Saba[57], A. Schauflerová[58], R.G. Shivas[59], G. Simonini[60], J.P.Z. Siqueira[5], J.O. Sousa[61], V. Stajsic[62], T. Svetasheva[49,63], Y.P. Tan[64], Z. Tkalčec[44], S. Ullah[65], P. Valente[66], N. Valenzuela-Lopez[5,67], M. Abrinbana[68], D.A. Viana Marques[34], P.T.W. Wong[36], V. Xavier de Lima[13], J.Z. Groenewald[1]

Key words

ITS nrDNA barcodes
LSU
new taxa
systematics

Abstract Novel species of fungi described in this study include those from various countries as follows: **Australia**, *Chaetopsina eucalypti* on *Eucalyptus* leaf litter, *Colletotrichum cobbittiense* from *Cordyline stricta* × *C. australis* hybrid, *Cyanodermella banksiae* on *Banksia ericifolia* subsp. *macrantha, Discosia macrozamiae* on *Macrozamia miquelii, Elsinoë banksiigena* on *Banksia marginata, Elsinoë elaeocarpi* on *Elaeocarpus* sp., *Elsinoë leucopogonis* on *Leucopogon* sp., *Helminthosporium livistonae* on *Livistona australis*, *Idriellomyces eucalypti* (incl. *Idriellomyces* gen. nov.) on *Eucalyptus obliqua*, *Lareunionomyces eucalypti* on *Eucalyptus* sp., *Myrotheciomyces corymbiae* (incl. *Myrotheciomyces* gen. nov., *Myrotheciomycetaceae* fam. nov.), *Neolauriomyces eucalypti* (incl. *Neolauriomyces* gen. nov., *Neolauriomycetaceae* fam. nov.) on *Eucalyptus* sp., *Nullicamyces eucalypti* (incl. *Nullicamyces* gen. nov.) on *Eucalyptus* leaf litter, *Oidiodendron eucalypti* on *Eucalyptus maidenii*, *Paracladophialophora cyperacearum* (incl. *Paracladophialophoraceae* fam. nov.) and *Periconia cyperacearum* on leaves of *Cyperaceae*, *Porodiplodia livistonae* (incl. *Porodiplodia* gen. nov., *Porodiplodiaceae* fam. nov.) on *Livistona australis*, *Sporidesmium melaleucae* (incl. *Sporidesmiales* ord. nov.) on *Melaleuca* sp., *Teratosphaeria sieberi* on *Eucalyptus sieberi*, *Thecaphora australiensis* in capsules of a variant of *Oxalis exilis.* **Brazil**, *Aspergillus serratalhadensis* from soil, *Diaporthe pseudoinconspicua* from *Poincianella pyramidalis*, *Fomitiporella pertenuis* on dead wood, *Geastrum magnosporum* on soil, *Marquesius aquaticus* (incl. *Marquesius* gen. nov.) from submerged decaying twig and leaves of unidentified plant, *Mastigosporella pigmentata* from leaves of *Qualea parviflorae*, *Mucor souzae* from soil, *Mycocalia aquaphila* on decaying wood from tidal detritus, *Preussia citrullina* as endophyte from leaves of *Citrullus lanatus*, *Queiroziella brasiliensis* (incl. *Queiroziella* gen. nov.) as epiphytic yeast on leaves of *Portea leptantha*, *Quixadomyces cearensis* (incl. *Quixadomyces* gen. nov.) on decaying bark, *Xylophallus clavatus* on rotten wood. **Canada**, *Didymella cari* on *Carum carvi* and *Coriandrum sativum.* **Chile**, *Araucasphaeria foliorum* (incl. *Araucasphaeria* gen. nov.) on *Araucaria araucana*, *Aspergillus tumidus* from soil, *Lomentospora valparaisensis* from soil. **Colombia**, *Corynespora pseudocassiicola* on *Byrsonima* sp., *Eucalyptostroma eucalyptorum* on *Eucalyptus pellita*, *Neometulocladosporiella eucalypti* (incl. *Neometulocladosporiella* gen. nov.) on *Eucalyptus grandis* × *urophylla*, *Tracylla eucalypti* (incl. *Tracyllaceae* fam. nov., *Tracyllalales* ord. nov.) on *Eucalyptus urophylla.* **Cyprus**, *Gyromitra anthracobia* (incl. *Gyromitra* subg. *Pseudoverpa*) on burned soil. **Czech Republic**, *Lecanicillium restrictum* from the surface of the wooden barrel, *Lecanicillium testudineum* from scales of *Trachemys scripta elegans*. **Ecuador**, *Entoloma yanacolor* and *Saproamanita quitensis* on soil. **France**, *Lentithecium carbonneanum* from submerged decorticated *Populus* branch. **Hungary**, *Pleuromyces hungaricus* (incl. *Pleuromyces* gen. nov.) from a large *Fagus sylvatica* log. **Iran**, *Zymoseptoria crescenta* on *Aegilops triuncialis.* **Malaysia**, *Ochroconis musicola* on *Musa* sp. **Mexico**, *Cladosporium michoacanense* from soil. **New Zealand**, *Acrodontium metrosideri* on *Metrosideros excelsa, Polynema podocarpi* on *Podocarpus totara, Pseudoarthrographis phlogis* (incl. *Pseudoarthrographis* gen. nov.) on *Phlox subulata.* **Nigeria**, *Coprinopsis afrocinerea* on soil. **Pakistan**, *Russula mansehraensis* on soil under *Pinus roxburghii*. **Russia**, *Baoran-*

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Key words

ITS nrDNA barcodes
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Abstract Novel species of fungi described in this study include those from various countries as follows: **Angola**, *Gnomoniopsis angolensis* and *Pseudopithomyces angolensis* on unknown host plants. **Australia**, *Dothiora corymbiae* on *Corymbia citriodora, Neoeucasphaeria eucalypti* (incl. *Neoeucasphaeria* gen. nov.) on *Eucalyptus* sp., *Fumagopsis stellae* on *Eucalyptus* sp., *Fusculina eucalyptorum* (incl. *Fusculinaceae* fam. nov.) on *Eucalyptus socialis, Harknessia corymbiicola* on *Corymbia maculata, Neocelosporium eucalypti* (incl. *Neocelosporium* gen. nov., *Neocelosporiaceae* fam. nov. and *Neocelosporiales* ord. nov.) on *Eucalyptus cyanophylla, Neophaeomoniella corymbiae* on *Corymbia citriodora*, *Neophaeomoniella eucalyptigena* on *Eucalyptus pilularis, Pseudoplagiostoma corymbiicola* on *Corymbia citriodora, Teratosphaeria gracilis* on *Eucalyptus gracilis, Zasmidium corymbiae* on *Corymbia citriodora.* **Brazil**, *Calonectria hemileiae* on pustules of *Hemileia vastatrix* formed on leaves of *Coffea arabica*, *Calvatia caatinguensis* on soil, *Cercospora solani-betacei* on *Solanum betaceum*, *Clathrus natalensis* on soil, *Diaporthe poincianellae* on *Poincianella pyramidalis*, *Geastrum piquiriunense* on soil, *Geosmithia carolliae* on wing of *Carollia perspicillata*, *Henningsia resupinata* on wood, *Penicillium guaibinense* from soil, *Periconia caespitosa* from leaf litter, *Pseudocercospora styracina* on *Styrax* sp., *Simplicillium filiforme* as endophyte from *Citrullus lanatus*, *Thozetella pindobacuensis* on leaf litter, *Xenosonderhenia coussapoae* on *Coussapoa floccosa.* **Canary Islands (Spain)**, *Orbilia amarilla* on *Euphorbia canariensis.* **Cape Verde Islands**, *Xylodon jacobaeus* on *Eucalyptus camaldulensis.* **Chile**, *Colletotrichum arboricola* on *Fuchsia magellanica.* **Costa Rica**, *Lasiosphaeria miniovina* on tree branch. **Ecuador**, *Ganoderma chocoense* on tree trunk. **France**, *Neofitzroyomyces nerii* (incl. *Neofitzroyomyces* gen. nov.) on *Nerium oleander.* **Ghana**, *Castanediella tereticornis* on *Eucalyptus tereticornis*, *Falcocladium africanum* on *Eucalyptus brassiana*, *Rachicladosporium corymbiae* on *Corymbia citriodora.* **Hungary**, *Entoloma silvae-frondosae* in *Carpinus betulus-Pinus sylvestris* mixed forest. **Iran**, *Pseudopyricularia persiana* on *Cyperus* sp. **Italy**, *Inocybe roseascens* on soil in mixed forest. **Laos**, *Ophiocordyceps houaynhangensis* on *Coleoptera* larva. **Malaysia**, *Monilochaetes melastomae* on *Melastoma* sp. **Mexico**, *Absidia terrestris* from soil. **Netherlands**, *Acaulium pannemaniae*, *Conioscypha boutwelliae*, *Fusicolla septimanifiniscientiae*, *Gibellulopsis simonii*, *Lasionectria hilhorstii*, *Lectera nordwiniana, Leptodiscella rintelii, Parasarocladium debruynii* and *Sarocladium dejongiae* (incl. *Sarocladiaceae* fam. nov.) from soil. **New Zealand**, *Gnomoniopsis rosae* on *Rosa* sp. and *Neodevriesia metrosideri* on *Metrosideros* sp. **Puerto Rico**, *Neodevriesia coccolobae* on *Coccoloba uvifera*, *Neodevriesia tabebuiae* and *Alfaria tabebuiae* on *Tabebuia chrysantha.* **Russia**, *Amanita paludosa* on bogged soil in mixed deciduous forest, *Entoloma tiliae* in forest of *Tilia* × *europaea*, *Kwoniella endophytica* on *Pyrus communis.* **South Africa**, *Coniella diospyri* on *Diospyros mespiliformis, Neomelanconiella combreti* (incl. *Neomelanconiellaceae*