

**SÃO PAULO STATE UNIVERSITY** INSTITUTE OF BIOSCIENCES AT RIO CLARO



# **GRADUATE PROGRAM IN BIOLOGICAL SCIENCES (APPLIED MICROBIOLOGY)**

# **SYSTEMATICS AND EVOLUTION OF** *ESCOVOPSIS* **AND HYPOCREALEAN RELATIVES ASSOCIATED WITH ATTINE ANT COLONIES**

# **QUIMI VIDAURRE MONTOYA**

**Rio Claro, SP December – 2020**

### **SYSTEMATICS AND EVOLUTION OF** *ESCOVOPSIS* **AND HYPOCREALEAN RELATIVES ASSOCIATED WITH ATTINE ANT COLONIES**

# **QUIMI VIDAURRE MONTOYA**

A thesis submitted to the Institute of Biosciences at Rio Claro, from the São Paulo State University (UNESP), in fulfilment of the requirements for the degree of Doctor in Biological Sciences (Applied Microbiology).

Advisor: Dr. Andre Rodrigues

Co-advisor: Dr. Maurício Bacci Jr.

**Rio Claro, SP December – 2020**

M798s Montoya, Quimi Vidaurre Systematics and evolution of Escovopsis and hypocrealean relatives associated with attine ant colonies / Quimi Vidaurre Montoya. -- Rio Claro, 2020 205 p. : il., tabs., fotos Tese (doutorado) - Universidade Estadual Paulista (Unesp), Instituto de Biociências, Rio Claro Orientador: Andre Rodrigues Coorientador: Maurício Bacci Jr. 1. Hypocreales. 2. Taxonomy. 3. Phylogeny. 4. Symbiosis. 5. Evolution. I. Título.

Sistema de geração automática de fichas catalográficas da Unesp. Biblioteca do Instituto de Biociências, Rio Claro. Dados fornecidos pelo autor(a).

Essa ficha não pode ser modificada.





**Câmpus de Rio Claro** 



# **CERTIFICADO DE APROVAÇÃO**

# TÍTULO DA TESE: SYSTEMATICS AND EVOLUTION OF ESCOVOPSIS AND HYPOCREALEAN RELATIVES ASSOCIATED WITH ATTINE ANT COLONIES

# **AUTOR: QUIMI VIDAURRE MONTOYA ORIENTADOR: ANDRÉ RODRIGUES**

Aprovado como parte das exigências para obtenção do Título de Doutor em CIÊNCIAS BIOLÓGICAS (MICROBIOLOGIA APLICADA), área: Microbiologia Aplicada pela Comissão Examinadora:

Prof. Dr. ANDRÉ RODRIGUES (Participação Virtual) Departamento de Biologia Geral e Aplicada / IB Rio Claro relis

Profa. Dra. DERLENE ATTILI DE ANGELIS (Participação Virtual) Centro Pluridisciplinar de Pesquisas Químicas, Biológicas e Agrícolas / Universidade Estadual de Campinas

Jadion D.P.Begovie Departamento de Biociências e Tecnologia / Universidade Federal de Goiás

Profa. Dra. ESTER GAYA BELLES (Participação Virtual) Comparative Plant and Fungal Biology / Royal Botanic Gardens Kew

Prof. Dr. HUZEFA A RAJA (Participaçao Virtual) Department of Chemistry and Biochemistry / University of North Carolina

Rio Claro, 18 de dezembro de 2020

 **To my mother…**

### **ACKNOWLEDGMENTS**

First of all, I am very grateful to Brazil for giving me the opportunity to develop myself and improve my skills as a professional and as a person. These four years were simply incredible. Much to learn and little time to achieve it. Many achievements and many frustrations. Exciting field trips, and much more beautiful days marvelling myself with the beauty of *Escovopsis*. Many successful experiments, many broken plates, and many but many failed PCRs. However, I can say that in sum it was gratifying. For all of that, I would like to thank all people that collaborated with me and helped me to grow.

I would like to thank Dr. Andre Rodrigues for the opportunity to work in his laboratory, for his trust, his constant support during the development of my study, and for all the knowledge he shared with me. Likewise, I would like to thank the Laboratory of Ecology and Fungi Systematics (LESF) team, for all their support and friendship.

I would like to thank the São Paulo Research Foundation (FAPESP), for the graduate (# 2016/04955-3) and visiting (BEPE - # 2018/07931-3) scholarships granted and for the financial assistance granted to the thematic project (grant # 2012/25299-6), to which the present study is part of. In the same way, I am grateful to the Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq for all the financial assistance to our laboratory and for the development of my study. "This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001".

I would like to thank the Graduate Program in Biological Sciences (Applied Microbiology), and to all their professors and professionals who are part of the program for the good and kind scientific environment, they provided to me, and to the Department of General and Applied Biology, especially the Laboratory of Industrial and Environmental Microbiology (LAMAI), and the Laboratory of Dr. Maurício Bacci Junior for all their support.

Evidently, none of this would have been possible without the constant support of my mother Rosa E. Montoya Castro, my fiancé Maria Jesus Sutta Martiarena, my mother-in-law Josefina Sutta Martiarena, and my friends Lia Costa Pinto, Juliana Aparecida Dos Santos, Marcela Cristina Silva Caixeta, and Lucas Andrade Meirelles. So, I would like to thank all of them for being the people who showed me the way when I was wrong.

*Science is born from ideas, crawls and pronounces its first words on the arms of hypothesis, feeds and nourishes itself on discussion, and makes its way guided by the light of the evidence.*

### **ABSTRACT**

*Escovopsis* is a group of fungi that inhabit the colonies of fungus-growing ants. The study of this fungal genus has been based on several assumptions that became dogmas. For instance, i) many fungi associated with attines were treated as *Escovopsis*, without taxonomic support, ii) the genus was considered a specialized mycoparasite of the attines' mutualistic fungi, and iii) it was thought that the genus coevolved with attines based on the assumption of its parasitic lifestyle. However, for many years the *Escovopsis* taxonomy, its relationship with the ants and its phylogeographic distribution were almost an empty space for the scientific community. In addition, the origin of the genus was never addressed. Therefore, the main objective of this study was to build the systematics of the *Escovopsis* and shed light on its origin, evolution, diversification, and phylogeographic distribution. Three manuscripts are the result of this study and are presented here as chapters. The first manuscript presents the description of two new *Escovopsis* species (published in MycoKeys). The second manuscript brings the reassessment of the *Escovopsis* taxonomy, provides a suitable taxonomic and phylogenetic framework for the systematics of the genus, and describes two new Hypocreaceae genera (submitted to IMA Fungus). The third manuscript shows the origin, evolution, phylogeographic distribution and the trait adaptations experienced by *Escovopsis* since its entry in fungus-growing ant colonies. This study fills an important gap in the taxonomy, systematics, and evolution of *Escovopsis* and related genera which certainly will help researchers to better understand the evolution of the attines' system.

**Key-words:** Hypocreales, Taxonomy, Phylogeny, Symbiosis, Evolution

#### **RESUMO**

*Escovopsis* é um interessante grupo de fungos que habita as colônias das formigas atíneas. O estudo desse fungo se baseou em diversos pressupostos que, por muito tempo, se tornaram dogmas. Por exemplo, i) vários fungos associados à essas formigas foram tratados como *Escovopsis*, porém sem nenhum suporte taxonômico, ii) o gênero foi considerado um micoparasita especializado da associação formiga - fungo cultivado, e iii) acreditou-se que o gênero co-evoluiu com as atíneas, pois parasita o parceiro fúngico dessas formigas desde a origem da associação. No entanto, a taxonomia de *Escovopsis*, bem como sua relação com as formigas e sua distribuição filogeográfica foram quase um espaço vazio para a comunidade científica. Além disso, a origem do gênero nunca foi abordada. Nesse contexto, o objetivo deste estudo foi construir a sistemática do gênero *Escovopsis* e angariar evidências sobre sua origem, evolução, diversificação e distribuição filogeográfica. Três manuscritos são o resultado deste estudo e são apresentados como capítulos. O primeiro manuscrito traz a descrição de duas novas espécies de *Escovopsis* (publicado na MycoKeys). O segundo manuscrito apresenta a reavaliação da taxonomia de *Escovopsis*, fornece um marco taxonômico e filogenético robusto para a sistemática do gênero e descreve dois novos gêneros dentro da família Hypocreaceae (submetido na IMA Fungus). O terceiro manuscrito mostra a origem, evolução, distribuição filogeográfica e as adaptações experimentadas pelo gênero desde seu ingresso nas colônias das atíneas. Este estudo preenche uma lacuna importante na taxonomia, sistemática e evolução de *Escovopsis* e gêneros próximos e, certamente, ajudará os pesquisadores a compreender melhor a evolução do sistema das formigas atíneas.

**Palavras-chave**: Hipocreales, Taxonomia, Filogenia, Simbiose, Evolução

# **SUMMARY**







### <span id="page-12-0"></span>**Introduction**

Sixty-five million years ago, after the massive extinction of the dinosaurs, fungusgrowing ants (subfamily Myrmicinae, Attini tribe, Attina subtribe, "the attines") started producing their own food. Finding food is a constant and demanding struggle to organisms, and sometimes it leads them to certain death. Thus, the emergence of fungus-growing behaviour was not only a safer way to deal with lack of food, but directly influenced the evolutionary success of the attines and established the beginning of one of the most interesting and complex insect-fungus associations we know on earth.

Fungiculture performed by attine ants can be divided into five types: i) the fungiculture practiced by the genera in the basal attines, *Cyphomyrmex*, *Mycetophylax*, *Mycocepurus*, *Apterostigma auriculatum* group that grow fungi from the tribe Leucocoprinae (Agaricaceae); ii) the fungiculture practiced by species of the *Apterostigma pilosum* group that cultivate fungi of the Pterulaceae family, named coral fungi; iii) the fungiculture practiced by ant species of the *Cyphomyrmex rimosus* group, which cultivate yeasts (in Leucocoprinae); iv) the fungiculture practiced by the genera *Trachymyrmex* and *Sericomyrmex* that cultivate other fungi in Leucocoprinae, and v) the fungiculture of leafcutting ants, which cultivate *Leucoagaricus gongylophorus*.

Attine ants are restricted to the American continent and comprise 17 genera with more than 250 species phylogenetically divided into Neoattini and Paleoattini. The genera *Atta* and *Acromyrmex*, in the Neoattini group (more derived clades) are known as leaf-cutting ants, and they are important crop pests, because the large amounts of fresh plant material they collect to feed their fungal partner. In return, the fungal cultivar *L. gongylophorus* produces vesicles called gongylidia which are used by the ants as food source. On the other hand, the less derived attini genera, known as non-leaf-cutting ants (comprising ant genera in both Neoattini and Paleoattini) use other substrates like seeds, insect carcasses, and dry plant material to nourish their fungal partners. In addition, for millions of years attines have been introducing into their colonies a great diversity of microorganisms along with the substrates they collect and also microorganisms attached to their bodies. Consequently, complex symbiotic networks made their way slowly in attine colonies.

Though several symbiotic relationships have been described between the microorganisms living in the attine ant fungus garden, the mutualism between attines and the fungi they cultivate is the backbone of this ecosystem. With the constant entrance of microorganisms into the colonies, attine's environment is prone to parasites that are able to take advantage of the system. Indeed, ecological factors suggest that several parasites could have arrived at the fungus-farming ant colonies. However, the genus *Escovopsis*  (Ascomycota: Hypocreales, Hypocreaceae) was proposed as the only and specialized parasite in this system.

Due to the ecological importance that a parasite represents within the attine system, many studies turned their efforts to the study of the *Escovopsis*-mutualistic fungus interaction. However, the study of this diverse and interesting group of fungi has been based on several assumptions that became dogmas, since its discovery. For instance, it was proposed that: i) all fungi producing brown conidia found in attine colonies belong to *Escovopsis*. However, the *Escovopsis* taxonomy was almost an empty space for the scientific community and most that we know about its taxonomy was raised by non-taxonomic studies; ii) the genus is a specific and specialized mycoparasite. Nonetheless, our knowledge on the parasitic mechanisms used by *Escovopsis* to overcome the fungal cultivar defences and the ant colonies barriers is still limited. The conclusion that *Escovopsis* is a parasite was based on the evaluation of few strains from one of the 26 clades of the genus; and iii) *Escovopsis* had coevolved with the attines and their mutualistic fungi. However, the origin of *Escovopsis* is a complete mystery, as it is its phylogenetic relationship with the attine and the fungal cultivars.

Under this scenario, this study aimed to build the systematics of the *Escovopsis* showing its origin, diversification, and phylogeographic distribution. To reach this goal we used the following approach: i) increase the number of *Escovopsis* strains in our collection, ii) standardize the taxonomy of the genus to access its morphological features, iii) create a phylogenetic framework to perform the *Escovopsis* tree of life, iv) combine the taxonomic and phylogenetic analysis to build the *Escovopsis* systematics, v) estimate the origin of the genus, vi) evaluate its relationship with the ants, and vii) unravel its phylogeographic distribution.

The first two years, we gathered a collection of 365 strains [153 strains already deposited in the Laboratory of Fungal Ecology and Systematics (LESF - UNESP, Rio Claro, SP) and 212 obtained in this study]. In addition, we carried out an in-depth study of the taxonomy of this genus to know more about its taxonomic and to plan a strategy to standardize it. The main issues of the *Escovopsis* taxonomy were presented in the paper "**More pieces to a huge puzzle: Two new** *Escovopsis* **species from fungus gardens of attine ants**" which is the first chapter of this thesis. This study introduced *Escovopsis clavata* and *E. multiformis* within a well detailed taxonomic and phylogenetic framework, and emphasized the non-standardized taxonomy and the phylogenetic incongruities of the genus.

Some suggestions to reach a better view of the *Escovopsis* systematics were proposed in this paper.

Moving on to which was suggested in that study, we sequenced five molecular markers (ITS, LSU, *tef1*, *rpb*1, and *rpb*2) to start building the phylogenetic tree of life of *Escovopsis*. Our results suggested that the *Escovopsis* clade is composed by more than one genus. Based on these results we raised the hypothesis that: If more than one genus is living in attines fungus garden, then it would suppose the possibility that more than one fungus would have co-evolved with the attines colonies in a multiparasitism relationship. To answer these questions, we aimed to build the most comprehensive phylogenetic tree of *Escovopsis*  and infer the divergence time of the genus to access its evolutionary history and to shed light on our hypothesis. This part of the study was developed at Emory University, Department of Biology, O. Wayne Rollins Research Center, Atlanta, USA.

We assembled samples from LESF and from Dr. Nicole M. Gerardo' Laboratory (Emory University, Atlanta, USA) and carried out the broadest phylogenetic analysis of the genus *Escovopsis*. This analysis comprehended a total of 584 strains from different regions across America (Argentina, Brazil, Ecuador, Panama, and Costa Rica) spanning several biomes. The results supported our previous hypothesis that *Escovopsis* comprehends more than one genus. Then, we reassessed the taxonomy of *Escovopsis* by using standardized parameters including a select and informative set of morphological characters and a comprehensive multilocus phylogeny which is explained in the manuscript **"Fungi of the strong conidial form" in attine ant colonies: taxonomic and phylogenetic reassessment of the genus** *Escovopsis*". This manuscript was submitted to IMA Fungus and is presented here as the second chapter.

The reassessment of *Escovopsis* and the comprehensive phylogeny of the genus provided the ground to estimate the origin of the genus as well as its phylogenetic relationship with the attines and its phylogeographic distribution. Our findings support that the origin of *Escovopsis* and the beginning of the attine fungus domestication correspond in time. However, *Escovopsis* appears to have reached the ant colonies of just few attine genera during the last 38 million of years, along with the plant material collected to nourish the fungus gardens. These results are presented in the manuscript "**Digging into the past of a fungus-growing ant guest: origin and evolution of** *Escovopsis*", which is presented here as the third chapter. Interesting fungal trait adaptations and hypothesis about the origin and the evolutionary history of the genus are discussed in this manuscript.

### <span id="page-16-0"></span>**Objectives**

### <span id="page-16-1"></span>**General**

To build the systematics of the genus *Escovopsis* showing its origin, diversification, and phylogeographic distribution

### <span id="page-16-2"></span>**Specific**

- ❖ To standardize the conditions to assess the taxonomy of *Escovopsis*
- ❖ To infer the phylogenetic tree of life of *Escovopsis* and associated fungal genera
- ❖ To infer the *Escovopsis-*attine ant co-cladogenesis
- ❖ To infer the evolutionary history of *Escovopsis* within the attine ant-fungus system

# **Chapter I**

**Manuscript published in Mycokeys**

<span id="page-17-0"></span>**DOI: https://doi.org/10.3897/mycokeys.46.30951**

# **More pieces to a huge puzzle: Two new** *Escovopsis* **species from fungus gardens of attine ants**

Quimi Vidaurre Montoya<sup>1</sup>, Maria Jesus Sutta Martiarena<sup>1</sup>, Danilo Augusto Polezel<sup>1</sup>, Sérgio Kakazu<sup>2</sup>, Andre Rodrigues<sup>1,2\*</sup>

<sup>1</sup> Department of Biochemistry and Microbiology, UNESP – São Paulo State University, Rio Claro, SP, Brazil.

<sup>2</sup> Center for the Studies of Social Insects, UNESP – São Paulo State University, Rio Claro,

SP, Brazil.

Manuscript published in Mycokeys

DOI: https://doi.org/10.3897/mycokeys.46.30951

\* Corresponding author:

Andre Rodrigues [\(andrer@rc.unesp.br\)](mailto:andrer@rc.unesp.br)

Universidade Estadual Paulista – UNESP, Departamento de Bioquímica e Microbiologia

Avenida 24-A, n. 1515, Bela Vista, Rio Claro, SP, Brazil, Zip code: 13.506-900

Phone #: +55 19 3526-4364

### <span id="page-19-0"></span>**Abstract**

*Escovopsis* (Ascomycota: Hypocreales, Hypocreaceae) is the only known parasite of the mutualistic fungi cultivated by fungus-growing ants (Formicidae: Myrmicinae: Attini: Attina, the "attines"). Despite its ecological role, the taxonomy and systematics of *Escovopsis* have been poorly addressed. Here, based on morphological and phylogenetic analyses with three molecular markers (internal transcribed spacer, large subunit ribosomal RNA and the translation elongation factor 1-alpha), we describe *Escovopsis clavatus* and *E. multiformis* as new species isolated from fungus gardens of *Apterostigma* ant species. Our analysis shows that *E. clavatus* and *E. multiformis* belong to the most derived *Escovopsis* clade, whose main character is the presence of conidiophores with vesicles. Nevertheless, the most outstanding feature of both new species is the presence of a swollen region in the central hypha of the conidiophore named swollen cell, which is absent in all previously described *Escovopsis* species. The less derived *Escovopsis* clades lack vesicles and their phylogenetic position in the Hypocreaceae still remains unclear. Considering the high genetic diversity in *Escovopsis*, the description of these new species adds barely two new pieces to a huge taxonomic puzzle; however, this discovery is an important piece to the building of the systematics of this group of fungi.

**Key-words:** Hypocreales, Taxonomy, Phylogeny, Parasitic fungi, Symbiosis.

### <span id="page-20-0"></span>**Introduction**

Microorganisms play important roles in the stability of social insect colonies (Hughes et al. 2008, Joop and Vilcinskas 2016, Vanderpool et al. 2018). The environment of these insects has a high potential to harbour unique fungal species (Attili-Angelis et al. 2014, Harrington et al. 2014, Menezes et al. 2015, Montoya et al. 2016). The evolutionary success of the fungus garden of the fungus-farming ants (Formicidae: Myrmicinae: Attini: Attina, the "attines") depends on complex symbiotic interactions amongst bacteria, fungi and the ants (Currie et al. 2003, Gerardo et al. 2006a, Kost et al. 2007). The association between attine ants and their mutualistic fungi (Basidiomycota: Agaricales) is the core of the attine colonies; however, *Escovopsis* (Ascomycota: Hypocreales: Hypocreaceae) can exploit this association. Although no specialised parasitic structures were found, studies showed that this parasite is able to kill its native host as well as the ants and its mutualistic bacteria by chemical compounds (Currie 2001, Varanda-Haifig et al. 2017, Custodio and Rodrigues 2018, Dhodary et al. 2018, Heine et al. 2018). Despite the ecological relevance of *Escovopsis* as parasites of attine ant colonies, the taxonomy of this genus has been neglected.

Attine ants are classified in two sister clades: the Palaeoattina and Neoattina (Branstetter et al. 2017). Leafcutter ants (*Atta* and *Acromyrmex*) are considered the most derived attines within the Neoattina. Their behaviour is characterised by collecting fresh leaves and flowers to feed several cultivars from two clades of fungi in the Agaricaceae (Mueller et al. 2017, 2018). On the other hand, non-leafcutter ants also occur in both the Neoattina and Palaeoattina clades. Distinct from *Atta* and *Acromyrmex*, non-leafcutter ants forage on seeds, insect frass and dry leaves to nourish a wide range of fungal cultivars in the Agaricaceae and Pterulaceae (Villesen et al. 2004, Schultz and Brady 2008).

The attine ant-fungus cultivar-*Escovopsis* symbiosis has been widely studied in leafcutter ants (Mueller and Gerardo 2002, Currie et al. 2003, Gerardo et al. 2004, 2006a,b). In addition to their contributions on the biology of *Escovopsis*, these studies also revealed considerable diversity of the parasite. Considering the variety of mutualistic fungi that nonleafcutter ants may cultivate, as well as the different substrates used for that purpose, a high diversity of *Escovopsis* species is unsurprising. This is especially true for *Apterostigma*  (Gerardo et al. 2006b), a genus of non-leafcutter attine with species that cultivate different cultivars including *Leucoagaricus gongylophorus*, the domesticated fungus cultivated by many higher attine ant species, mostly leafcutter ants (Sosa-Calvo and Schultz 2010, Schultz et al. 2015, Ješovnik et al. 2016, Sosa-Calvo et al. 2017, Mueller et al. 2017, 2018).

While *Escovopsis* species exploiting gardens of *Atta*, *Acromyrmex*, *Trachymyrmex* and *Mycetophylax* were formally described, the morphological characters of the species associated with *Apterostigma* are unknown. A previous study associated clades of the parasite with the colour pattern of *Escovopsis* colonies (brown, yellow, white and pink; Gerardo et al. 2006b). However, no taxonomic studies were undertaken to formally describe these clades. Here, we describe *Escovopsis clavatus* and *E. multiformis* as new species isolated from the fungus garden of *Apterostigma*. The distinctive feature of these lineages is the presence of swollen cells at the base of the conidiophore branches. This phenotype differentiates these two new species from previously described *Escovopsis*. Considering that previous studies showed a high genetic diversity within *Escovopsis*, the description of these species adds two pieces to the enormous taxonomic puzzle which is *Escovopsis*.

### <span id="page-21-0"></span>**Material and Methods**

### <span id="page-22-0"></span>**Sampling sites and** *Escovopsis* **isolation**

Five *Escovopsis* isolates were obtained from fungus gardens of five different colonies of *Apterostigma* spp. (Table S1). The isolates LESF 847, LESF 853, LESF 854 and LESF 855 were obtained from colonies found in the Atlantic Rain Forest in Florianópolis, State of Santa Catarina, Brazil (October 2015). The isolate LESF 1136 was obtained from a single colony found in the Amazon Forest in Cotriguaçu, State of Mato Grosso, Brazil (October 2017). The nests were found inside or under rotten logs. Fungus gardens, along with tending workers and brood, were collected in UV-sterilised plastic containers using sterilised spoon and forceps. Samples were taken to the Laboratory of Fungal Ecology and Systematics (LESF) at the UNESP – São Paulo State University, Rio Claro, Brazil.

For fungal isolation, seven garden fragments  $(0.5-1 \text{ mm}^3)$  were inoculated on plates (three plates per colony) containing potato dextrose agar (PDA, Neogen Culture Media, Neogen<sup>®</sup>) supplemented with the antibacterial antibiotic chloramphenicol [150  $\mu$ g ml<sup>-1</sup>, Sigma] and incubated at 25°C in darkness. Plates were monitored daily for fungal growth and, when *Escovopsis* mycelia sprouted from garden fragments, they were transferred to new PDA plates. All isolates were prepared as axenic (monosporic) cultures and stored under sterile distilled water kept at 8°C (Castellani 1963) and at −80°C (as conidia suspensions in 10% glycerol).

### <span id="page-22-1"></span>**Morphological analysis**

The morphological characters of the five isolates (LESF 847, LESF 853, LESF 854, LESF 855 and LESF 1136) were examined. Due to the lack of standardisation of culture conditions for *Escovopsis*, the macroscopic characters of the colonies, i.e. radial growth,

mycelium colour, morphology and presence of soluble pigments, were evaluated on eight different media: PDA, malt agar 2% [MA2%: 2% of malt extract (Neogen Culture Media) and 1.5% of agar (Neogen Culture Media)], cornmeal agar (CMD, Neogen Culture Media), synthetic nutrient agar [SNA: 1 g of  $KH_2PO_4$  (Labsynth®), 1 g of KNO<sub>3</sub> (Labsynth®), 0.5 g of MgSO<sub>4</sub>(7H<sub>2</sub>O) (Labsynth®), 0.5 g of KCl (Labsynth®), 0.2 g of Glucose (Labsynth®), 0.2 g of Sucrose (Labsynth®) and 15 g of Agar (Neogen Culture Media)], oatmeal agar (OA), potato carrot agar (PCA, HiMedia®), malt extract agar 2% [MEA: 30 g  $1^{-1}$  of malt extract (Neogen Culture Media), 5 g  $1^{-1}$  of bacteriological peptone (Neogen Culture Media), 20 g  $1^{-1}$ of glucose (Labsynth<sup>®</sup>) and 15 g  $l^{-1}$  of Agar (Neogen Culture Media)] and Czapek yeast extract agar [CYA; 30 g of Sucrose (Labsynth®), 5 g of Yeast extract (Neogen Culture Media), 1 g of  $KH_2PO_4$  (Labsynth®), 0.3 g of NaNO<sub>3</sub> (Synth), 0.05 g of KCl (Labsynth®), 0.05 g of MgSO<sub>4</sub>(7H<sub>2</sub>O) (Labsynth<sup>®</sup>), 0.001 g of FeSO<sub>4</sub> (Labsynth<sup>®</sup>), 0.001 g of ZnSO<sub>4</sub> (Labsynth<sup>®</sup>), 0.0005 g of CuSO<sub>4</sub> (Labsynth<sup>®</sup>), 15 g of Agar (Neogen Culture Media)] at five temperatures (10°C, 20°C, 25°C, 30°C and 35°C). These temperatures correspond to the conditions used in previous studies that described *Escovopsis* species (Seifert et al. 1995, Augustin et al. 2013, Masiulionis et al. 2015, Meirelles et al. 2015a). For this purpose, 200 μl of conidia were spread on plates with water-agar (WA) and incubated for seven days at 25°C in darkness. Then, mycelium fragments of 0.5 cm diameter were cut from the WA plates and inoculated in the centre of the plates (90 x 15 mm) containing the eight culture media. All the strains examined showed better development in the dark and with unsealed Petri dishes to allow air passage; therefore, incubation was carried out in the darkness and without sealing the plates, for 14 days. Three replicate plates were inoculated for each media and for each incubation temperature.

To examine the microscopic characters, i.e. the morphology, size, branching patterns, vesicles and swollen cells of the conidiophores, as well as phialides and conidia, slide cultures on PDA and MEA were performed. Briefly, we placed a  $5 \text{ mm}^2$  fragment of culture medium on a microscopic slide and then we inoculated the fungus at the centre of the fragment. Then, the inoculated medium was covered with a coverslip and incubated at 25°C for 4-7 days in the dark. After that, the coverslips, where the fungus grew, were removed and placed in new slides with a drop of lactophenol. Finally, the slides were examined under a light microscope (DM750, Leica, Germany). Fungal microscopic structures were photographed and measured (with 30 measurements per structure) in LAS EZ v.4.0 (Leica Application Suite).

Microscopic structures were also examined under scanning electron microscopy (SEM). Fungal samples (five days old cultures on PDA) were fixed in osmium tetroxide vapour for 72 h. Then, samples were dehydrated using a series of acetone concentrations (50, 75, 90, 95 and 100%) and dried to critical point using liquid CO<sup>2</sup> (Balzers CPD030). The dried material was sputtered with gold (Balzers SCD050) and examined under the scanning electron microscope (TM3000, Hitachi).

### <span id="page-24-0"></span>**DNA extraction, PCR and sequencing**

DNA extraction of the five strains was performed, following the steps published in Meirelles et al. (2015a). Three molecular markers were amplified: the internal transcribed spacer (ITS) region (White et al. 1990, Schoch et al. 2012); translation elongation factor 1 alpha (*tef*1) (Taerum et al. 2007); and the large subunit ribosomal RNA (LSU) (White et al. 1990, Haugland and Heckman 1998, Currie et al. 2003) (Table S2).

PCR and sequence reaction conditions followed the steps published in Meirelles et al. (2015b) for the ITS region, Meirelles et al. (2015a) for *tef*1 and Augustin et al. (2013) for LSU. The final amplicons were cleaned up with Wizard SV Gel and PCR Clean-up System kit (Promega), following the manufacturer's protocol. Sequences (forward and reverse) were generated in ABI3500 (Life Technologies). The LSU of 29 strains previously used in Meirelles et al. (2015b) also was amplified and sequenced for this study (Table S1). The sequences were assembled in contigs in BioEdit v. 7.1.3 (Hall 1999) and deposited in GenBank (Table S1 for accession numbers).

### <span id="page-25-0"></span>**Phylogenetic analyses**

To infer the phylogenetic position of the new species in the *Escovopsis* clade, sequences from previous studies were retrieved from the GenBank and aligned with our new sequences in a dataset for each marker (Chaverri et al. 2003, Spatafora et al. 2007, Jaklitsch and Samuels 2011, Põldmaa 2011, Meirelles et al. 2015b). This data included sequences from the seven *Escovopsis* ex-type strains, from *Escovopsioides nivea* and some species from *Hypomyces* and *Trichoderma*, as the phylogenetic closest relatives of *Escovopsis*. First, the three datasets [46 sequences of ITS (621 bp), LSU (531 bp) and *tef*1 (758 bp)] were aligned separately in MAFFT v.7 (Katoh and Standley 2013). The end parts of each alignment were removed manually by considering a point where the sequences presented greater homogeneity (all alignments are deposited in Treebase: **<http://purl.org/phylo/treebase/phylows/study/TB2:S23689>**). Then, a phylogenetic tree was inferred using each dataset separately (Fig. 6). The nucleotide substitution model was selected by independent runs in jModelTest 2 (Darriba et al. 2012) using the Akaike Information Criterion (AIC) with a 95% confidence interval. Second, the three datasets were concatenated using Winclada v.1.00.08 (Nixon 2002). The final file comprised 40 sequences totalling 1911 bp. All phylogenetic trees were reconstructed using maximum likelihood (ML) in RAxML v.8 (Stamatakis 2014 with 1000 independent trees and 1000 bootstrap replicates; MLB) and Bayesian Inference (BI) in MrBayes v.3.2.2. (Ronquist et al. 2012). The ML phylogenetic trees were reconstructed using the GTR+ G substitution model and the BI phylogenetic trees were performed with the GTR  $+ I + G$  substitution model. In the case of BI, two separate runs were carried out, each consisting of three hot chains and one cold chain and a Markov Chain Monte Carlo (MCMC) sampling for two million generations to obtain Bayesian posterior probability (PP) values for the clades. Convergence occurred when the standard deviation (SD) of split frequencies fell below 0.01 and the first 25% of the generations of MCMC sampling were discarded as burn-in. The final phylogenetic trees were edited in FigTree v.1.4 and in Adobe Illustrator CC v.17.1. *Lecanicillium antillanum* CBS 350.85 was used as the outgroup in all trees, because it belongs to a family phylogenetically close to Hypocreaceae (Spatafora et al. 2007).

### <span id="page-26-0"></span>**Results**

### <span id="page-26-1"></span>**Taxonomy**

<span id="page-26-2"></span>*Escovopsis clavatus* Q.V. Montoya, M.J.S. Martiarena, D.A. Polezel, S. Kakazu & A. Rodrigues sp. nov. Figs. 1-3 MycoBank: MB828328

*Etymology*: "*clavatus*" in reference to the predominantly clavate shape of vesicles.

*Typification*: BRAZIL. Santa Catarina, Florianópolis, (27°44'39.6''S, 48°31'10.14''W), elev. 46 m, Fungus garden, 08, 2015. *A. Rodrigues*. Holotype: CBS H-23845 (dried culture on PDA). Ex-type strain LESF 853 (= CBS 145326).

*Sequences*: ITS (MH715096), *tef*1 (MH724270) and LSU (MH715110).

*Colonies* grow only at 20 and 25°C (Fig. 1). At both temperatures, growth starts on the third day on CMD, CYA, MA 2%, MEA, OA, PCA, PDA; and on the sixth day on SNA. Colonies have floccose aerial mycelia with a pale-brown colour after seven days. Faster growth was observed on MA2% and heavy sporulation was identified on MA2%, PDA and OA. At  $20^{\circ}$ C, colonies reached  $0.5 - 0.7$  cm,  $1.5 - 2.5$  cm and  $0.5 - 1$  cm on CMD, CYA and SNA, respectively. At this temperature, colonies reached the edge of the plate after 10 days on MA 2% and PCA; after 12 days on OA and MEA; and after 14 days on PDA and CYA. At 25°C, colonies reach 2 cm, 3 – 3.2 cm and 2 cm on CMD, CYA and SNA, respectively, after 14 days. At this temperature, colonies reached the plate edge after seven days on OA and PCA; and after 10 days on MA2%, MEA and PDA. Concentric rings were observed only on PCA at 20°C (Fig. 1). No pustule-like structures were observed.

*Conidiophores* arising from aerial hypha alternated or opposite (Fig. 3A), with the main axis of  $50 - 780$  μm in length, some without branching and often with  $1 - 2$  levels of branching (Figs. 2A and E, 3A and E). Branches arise from the main axis of the conidiophore in an alternated or opposite pattern, with a septum near to the central axis and before the vesicle, usually with 1-2 branches at each branching point  $(16 - 138 \,\mu m \log)$  or 2-4 branches arising from swollen cells  $(28 - 35 \mu m \log)$ , mostly forming angles less than 90<sup>°</sup> and less frequently right angles, usually straight and sometimes slightly curved up or down. Each branch terminates in a vesicle, with 1-8 fertile heads per conidiophore. Swollen cells are present in the 15% of the total of conidiophores examined (Figs. 2C-D and 3E) and can measure 10 – 18 μm long x 7 – 9 μm wide. *Vesicles* with only a septum at the base, in various shapes: globose (8%), subglobose (24%), broadly ellipsoidal (33%), ellipsoidal (27%), cylindrical (8%) (Figs. 2E-G and 3F-G); and reaching  $9 - 27 \mu m$  long x  $7 - 20 \mu m$  wide. *Phialides* lageniform formed on vesicles (Fig. 3H), with  $5 - 8 \mu m$  in total length, elongated base  $(0.5 - 1.5 \mu m \times 0.5 - 1 \mu m)$ , followed by a swollen section  $(1.5 - 2.5 \mu m \times 1 - 3 \mu m)$ and a thin neck  $(1.5 - 4 \mu m \times 0.5 \mu m)$ . *Conidia* with 1.5  $\mu m - 2.5 \mu m$  long x 0.5  $\mu m - 1.5$ μm wide, in various shapes: broadly ellipsoidal (5%), ellipsoidal (43.3%), cylindrical (51.7%); brown, with smooth and slightly thickened walls and in chains (Figs. 2H and 3I). *Habitat*: Isolated from fungus gardens of *Apterostigma* sp.

*Additional specimens examined*: BRAZIL. Santa Catarina, Florianópolis, (27°44'38.94''S, 48°31'9.3''W), elev. 32 m, fungus garden, 08, 2015. *A. Rodrigues*. LESF 854 (ITS - MH715097, *tef*1 - MH724271 and LSU - MH715111). Santa Catarina, Florianópolis, (27°44'39.49''S; 48°31'9.72''W), elev. 38 m, fungus garden, 08, 2015. *A. Rodrigues*. LESF 855 (ITS - MH71509), *tef*1 - MH724272 and LSU - MH715112).

*Notes*: *Escovopsis clavatus* is phylogenetically closely related to *E. multiformis* and its most distinctive characters are its growth temperatures, the conidiophore branching and the swollen cells. It grows at 20 and 25°C; nevertheless, *E. multiformis* grows at 10, 20, 25 and 30°C. The conidiophore of *E. clavatus* is larger and more branched than the conidiophore of *E. multiformis*. In addition, the swollen cells of *E. clavatus* are less frequent and shorter than in *E. multiformis*. The character distinguishing *E. clavatus* from other species of *Escovopsis*  is the swollen cell on the conidiophores.

<span id="page-28-0"></span>*Escovopsis multiformis* Q.V. Montoya, M.J.S. Martiarena, D.A. Polezel, S. Kakazu & A. Rodrigues sp. nov. Figs. 1, 4 and 5

#### Mycobank: MB828329

*Etymology*: "*multiformis*" in relation to the different vesicle shapes found in the same isolate. *Typification*: BRAZIL. Santa Catarina, Florianópolis, (27°28'11.28''S, 48°22'39.48''W), elev. 119 m, Fungus garden, 08, 2015. *A. Rodrigues*. Holotype: CBS H-23846 (dried culture on PDA). Ex-type strain LESF 847 (= CBS 145327).

*Sequences*: ITS (MH715091), *tef*1 (MH724265) and LSU (MH715105).

*Colonies* grow at 10, 20, 25 and 30°C (Fig. 1). The best growth temperature was 30°C. At this temperature, colonies reached  $1.2 - 1.4$  cm,  $2.7 - 3$  cm,  $2.6 - 3$  cm,  $3.3 - 3.5$  cm,  $2.5$  $-2.8$  cm,  $2.7 - 2.9$  cm and  $1.9 - 2.5$  cm in radius on CMD, CYA, MA2%, MEA, OA, PCA and PDA, after 14 days, respectively. Colonies exhibit light-brown floccose mycelia (colony edge usually lighter or white). The colour shades and the character of the aerial mycelium vary on each culture medium (Fig. 1). Colonies present concentric rings with a hardened ring similar to a crust in the centre of the colony on CYA (Fig. 1) and the sporulation is more abundant on PCA and PDA. At 20°C, on CMD, CYA, MA2%, MEA, OA, PCA, PDA and SNA, colonies attain 0.5 - 0.8 cm, 1.1 - 2.2 cm, 2 - 2.5 cm, 2.1 - 2.3 cm, 2 - 2.5 cm, 2.8 cm, 1.9 - 2.4 cm and 0 - 0.1 cm in radius, respectively. At 25°C, colonies reach 1 cm, 2.1 - 2.3 cm, 2 - 2.4 cm, 2.5 - 2.6 cm, 2.2 - 2.7 cm, 2.8 - 3 cm, 1.8 - 2 cm and 0.1 - 0.2 cm in radius on CMD, CYA, MA2%, MEA, OA, PCA, PDA and SNA, respectively. Pustule-like structures are observed on OA and CMD at 20, 25 and 30 $^{\circ}$ C. At 10 $^{\circ}$ C, the colony growth was inconspicuous, reaching  $0.2 - 0.3$  cm,  $0.2 - 0.4$  cm,  $0.3$  cm,  $0.6 - 0.8$  cm,  $0.8$  cm and  $0.3 -$ 0.5 cm in radius on CYA, MA2%, MEA, OA, PCA and PDA, respectively, after 14 days. At this temperature, growth started in these culture media after seven days and sporulation occurred only after the  $12<sup>th</sup>$  day. No growth was observed at  $35<sup>o</sup>C$ .

*Conidiophores* arising from aerial hypha alternated or opposite (Fig. 3A), with the main axis of  $41 - 293$  µm in length, some without branching and most of them with one level of branching. Rarely, branches form two levels branching (Figs. 4A-C and 5A-B). Branches arise from the main axis of the conidiophore alternated, with a septum near the central axis and before the vesicle, usually with one branch at each branching point  $(32 – 84 \mu m \log)$  or 2-4 branches arising from swollen cells  $(17 - 86 \mu m \text{ long})$ , mostly forming right angles, usually slightly curved up. Each branch terminates in a vesicle, with 1-4 fertile heads per conidiophore. Swollen cells are present in 27% of the total of conidiophores examined (Figs.  $4D-G$  and  $5C-F$ ) and can measure  $16-34 \mu m \log x$  9 – 20  $\mu m$  wide. Sometimes, one swollen cells' branch gives rise to another swollen cell with more branches (Figs. 2F and 3C). *Vesicles* with only a septum at the base, in various shapes: globose (22%), subglobose (37%), broadly ellipsoidal (26%), ellipsoidal (10%), cylindrical (5%) (Figs. 4H-I and 5G-H); and reaching 12 – 27 μm x 9 – 17 μm wide. *Phialides* lageniform formed on vesicles (Fig. 5I), with 6 – 10 μm in total length, elongated base  $(1 – 2.5 \mu m \times 0.5 – 1 \mu m)$ , followed by a swollen section  $(2.5 - 4.5 \mu m \times 2 - 3.5 \mu m)$  and a thin neck  $(1 - 4.5 \mu m \times 0.5 - 1 \mu m)$ . *Conidia* are  $2.5 - 3.5$ μm long x 1.5 – 2.5 μm wide, in various shapes: globose (2%), subglobose (3%), broadly ellipsoidal (33%), ellipsoidal (47%), cylindrical (15%); brown, with smooth and slightly thickened walls and in chains (Figs. 4 and 5J).

*Habitat*: Isolated from fungus garden of *Apterostigma* sp.

*Additional specimens examined*: BRAZIL. Mato Grosso, Cotriguaçu, (09°49'22.74''S, 58°15'32.04''W), elev. 252 m, Fungus garden, 10, 2017. *Q. V. Montoya*. LESF 1136 (ITS - MH715092, *tef*1 - MH724266 and LSU - MH715106).

*Notes*: *Escovopsis multiformis* is closely related to *E*. *clavatus*. Different from *E*. *clavatus*  that grow at 20 and 25°C, *E*. *multiformis* grow at 10, 20, 25 and 30°C. The optimum growth temperature of *E. multiformis* is 30°C and that of *E*. *clavatus* is 25°C. The conidiophores of *E. multiformis* are smaller and less branched than *E*. *clavatus* and the swollen cells are more frequent and larger than those found in *E*. *clavatus*. *E. multiformis* differs from other described species by the presence of conidiophores with a swollen cell, the presence of different vesicles shapes and because it is phylogenetically placed in a distinct clade.

### <span id="page-31-0"></span>**Morphological analyses**

The isolates LESF 853 (*Escovopsis clavatus*, Figs. 1-3) and LESF 847 (*Escovopsis multiformis*, Figs. 1, 4 and 5) differed from the seven previously described *Escovopsis* species, mainly in micro-morphological structures. All isolates had white colonies with a floccose appearance on all culture media, but *E. clavatus* had the most floccose colonies. After 5-7 days incubation, the centre of the colonies turned pale brown and, after 7 days, the entire colony gradually turned from white to light brown (not always from the middle to the edge in *E. multiformis*).

*Escovopsis multiformis* showed growth at wide ranges of temperature (from 10- 30°C); nonetheless, *E. clavatus* showed growth only at 20 and 25°C (Fig. 1). None of the isolates grew at 35°C. On all culture media, the best growth was obtained at 25°C for *E. clavatus* and at 30°C for *E. multiformis*. In all cases where growth was observed, it started between 24 to 36 hours and sporulation started on the third day.

All strains of both species have a unique type of conidiophore with a swollen cell, from which branches emerge (Figs. 2C-D, 3E, 4D-F and 5C-F). These conidiophores were more frequent in *E. multiformis* than *E. clavatus* (27% and 15%, respectively). Mono or polycephalous conidiophores, without the swollen cells, that were described in the other *Escovopsis* species, were also present but with some differences in the size and branching pattern (Figs. 2A-B, 3A-D, 4A-C and 5A-B). Conidiophores with cruciform or opposed branches were rarely observed. On the other hand, the two new species had basipetal and smooth-walled conidia with slightly thickened walls, formed from phialides. No chlamydospores were observed in the aerial or submersed mycelia of the three strains.

### <span id="page-32-0"></span>**Phylogenetic analyses**

Separate phylogenetic analyses with the three molecular markers showed topological differences because of the incongruity placement of the formal described *Escovopsis* species and some strains that form new phylogenetic clades within the genus (Fig. 6). The phylogenetic placement of *E. multiformis* and *E. clavatus* also presented conflicts amongst the three molecular markers; however, the position of each strain that made up both new species was concordant through the three genealogies ( $PP= 1$ ; MBL= 100%, Fig. 6).

The combined analysis also confirmed *E*. *multiformis* and *E*. *clavatus* as two new phylogenetic species in *Escovopsis* (PP= 1; MLB= 100%, Fig. 7) and showed the strain LESF018 (a vesiculated *Escovopsis* species) as the closest relative of both. Nevertheless, the concatenated BI and ML trees also presented few differences between them with respect to the position of the *E. aspergilloides* and *E. lentecrescens*. The BI analysis placed *E. aspergilloides* and *E. lentecrescens* separate from *E*. *multiformis* and *E*. *clavatus* (Fig. 7); however, the ML analysis showed the former species as sister clades of *E*. *multiformis* and *E*. *clavatus*.

It is important to highlight that the concatenated analysis, as well as the trees inferred with ITS and LSU, showed the vesiculated *Escovopsis* (*E. aspergilloides, E. clavatus, E. lentecrescens, E. microspora, E. moelleri, E. multiformis, E. weberi*) as the most derived group, separated from the non-vesiculated *Escovopsis* (*E. kreiselii* and *E. trichodermoides*).

In addition, both the combined and the analysis performed with ITS and *tef*1 showed some *Escovopsis* species (*E. aspergilloides, E. kreiselii, E. lentecrescens* and *E. trichodermoides*) often clustering with other Hypocreaceae genera or falling outside the *Escovopsis* clade, which reveals that *Escovopsis* is apparently paraphyletic (Figs. 6 and 7).

### <span id="page-33-0"></span>**Discussion**

The attine ants have persisted for millions of years because of the biological relationships that these insects maintain with the beneficial microorganisms that inhabit their colonies. Several studies tried to understand how these biological relationships sculptured the evolutionary history of the attine ants (Mueller et al. 1998, Currie et al. 2003, Gerardo et al. 2006ab, Nygaard et al. 2016, Mueller et al. 2018). Nevertheless, the taxonomy of *Escovopsis*, the only known parasite in the attine's environment, has been poorly addressed. Considering that *Escovopsis* co-evolved with the attine ants' cultivar, improved knowledge about the taxonomy and systematics of this genus could shed light on the evolutionary success of these insects. Therefore, the discovery and description of new *Escovopsis* species is an important advance in understanding this system.

Subsequent to the formal description of *Escovopsis* (Muchovej and Della Lucia 1990), several studies showed a high genetic diversity of this genus in the colonies of both leafcutter and non-leafcutter attine ants (Gerardo et al. 2006a, Meirelles et al. 2015b). Only seven species of the parasite have been described so far (Seifert et al. 1995, Augustin et al. 2013, Masiulionis et al. 2015, Meirelles et al. 2015a) and the morphological diversity and physiology of the parasite remain unknown. In addition, a lack of standardised conditions for describing the morphology of *Escovopsis* hinders researchers from identifying morphological characters that might help to distinguish *Escovopsis* species from one another and from the other related genera from the Hypocreaceae. Unfortunately, this fact made it difficult to describe new species of the parasite. Studies showed that the expressed phenotypic characters (phenotypic plasticity) of fungi are directly influenced by growth conditions (Slepecky and Starmer 2009, Sharma and Pandey 2010, Wrzosek et al. 2017, Kim et al. 2017). As the morphological plasticity of *Escovopsis* species is still poorly understood, the standardisation of cultivation conditions is imperative. The strains described as new species here were evaluated on eight different culture media (those used in the description of the seven previous species) and at five temperatures (to establish cardinal growth temperatures). Due to the lack of standard culture conditions, the comparison with each species previously described was only partial. Nonetheless, we are providing characters of these two new species in all the conditions previously used, to help future researchers to standardise the taxonomy of the genus.

Recent attempts to expand the morphological concept of *Escovopsis* generated inconsistencies in the taxonomy and systematics of this genus (Masiulionis et al. 2015, Meirelles et al. 2015a). The morphologic characters that initially gave rise to the concept of *Escovopsis* (presence of terminal vesicles and phialidic conidiogenesis, see Muchovej and Della Lucia 1990) are distinctive to delineate *Escovopsis*, because no other genus in the Hypocreaceae family has such combined characters. However, some *Escovopsis* species described recently, namely *E. trichodermoides* and *E. kreiselii*, lack vesicles and each has a different kind of conidiogenesis (synchronous and sympodial, respectively). Besides, the results of the phylogenetic analysis performed in previous studies (Meirelles et al. 2015b, Masiulionis et al. 2015, Augustin et al. 2013), as well as the results from our analysis, reveals that *Escovopsis* is paraphyletic (Figs. 6 and 7). Therefore, future studies will have to reconsider if both species indeed belong to *Escovopsis*. For this purpose, the taxonomic conditions need to be delimited and additional molecular markers will have to be included to help us resolve those phylogenetic incongruities. Then the generic concept of *Escovopsis*  species should be revisited.

Our study shows that the ex-type strains LESF 853 (*E. clavatus*) and LESF 847 (*E. multiformis*) form a monophyletic clade within most derived *Escovopsis* (vesiculated *Escovopsis*) (PP = 1, BML = 100%). Most interesting, unlike the other *Escovopsis* species, the two new species present a unique type of conidiophore with a swollen cell, from which one to four branches arise. The newly described species also possess smooth conidia with slightly thickened walls. A recent study suggests the possibility that conidia ornamentation could be associated with the mechanism for horizontal transmission of *Escovopsis* between ant colonies and with the latency of the parasite conidia. This hypothesis was based on observations of some conidia adhering to the ant legs and in spore dormancy in vitro bioassays (Augustin et al. 2017). The same authors also argued that such character could be used as morphological markers for the taxonomy of the genus. However, because of scarce knowledge of the morphological features of the *Escovopsis* species, it is difficult to decipher which phenotypic character could be considered diagnostic for this genus. Therefore, future researchers need to carefully evaluate the phenotypic characters of each *Escovopsis* clade to determine which of characters are homologous versus those that are homoplasious to build taxonomic keys.

Considering the high genetic diversity of *Escovopsis* and the poor knowledge of its taxonomic diversity, the description of these new species are merely two small pieces of a complex puzzle. Nonetheless, our work should help future researchers to build the framework for the systematics of this parasitic fungus. In addition, our study also suggests that the
fungus gardens of attine ants could host a high diversity of *Escovopsis* that has yet to be discovered.

#### **Acknowledgements**

We are grateful to ''Fundação de Amparo à Pesquisa do Estado de São Paulo'' (FAPESP) for financial support (Grants # 2014/24298-1 and #2017/12689-4) conceded to AR and for the scholarship (# 2016/04955-3) to QVM. We also would like to thank Antônio Teruyoshi Yabuki (UNESP, Rio Claro) for SEM assistance, Lia Costa Pinto Wentzel, Rodolfo Bizarria Jr and Caitlin Conn for valuable comments on this manuscript. In addition, we are grateful to Dr. Huzefa Raja (reviewer #1), Keith Seifert (reviewer #2) and the editor Thorsten Lumbsch for providing constructive comments on this study.

#### **References**

Attili-Angelis D, Duarte APM, Pagnocca FC, Nagamoto NS, de Vries M, Stielow JB, de Hoog GS (2014) Novel *Phialophora* species from leaf-cutting ants (tribe Attini). Fungal Divers 65 (1): 65–75. https://doi.org/10.1007/s13225-013-0275-0

Augustin JO, Groenewald JZ, Nascimento RJ, Mizubuti ESG, Barreto RW, Elliot SL, Evans HC (2013) Yet more "weeds" in the garden: Fungal novelties from nests of leafcutting ants. PLoS One 8 (12): e82265. https://doi.org/10.1371/journal.pone.0082265

Augustin JO, Simões TG, Dijksterhuis J, Elliot SL, Evans HC (2017) Putting the waste out: a proposed mechanism for transmission of the mycoparasite *Escovopsis* between leafcutter ant colonies. R Soc Open Sci 4(5): 161013. https://doi.org/10.1098/rsos.161013

Branstetter MG, Ješovnik A, Sosa-Calvo J, Lloyd MW, Faircloth BC, Brady SG, Schultz TR (2017) Dry habitats were crucibles of domestication in the evolution of agriculture in ants. Proc R Soc B Biol Sci 284(1852): 20170095. https://doi.org/10.1098/rspb.2017.0095 Castellani AMD (1963) Further researches on the long viability and growth of many pathogenic fungi and some bacteria in sterile distilled water. Mycopathol. Mycol. Appl. 20: 1-6. https://doi.org/10.1007/BF02054872

Chaverri P, Castlebury LA, Samuels GJ, Geiser DM (2003) Multilocus phylogenetic structure within the *Trichoderma harzianum*/*Hypocrea lixii* complex. Mol Phylogenet Evol 27(2):302-313. https://doi.org/10.1016/S1055-7903(02)00400-1

Currie CR, Wong B, Stuart AE, Schultz TR, Rehner SA, Mueller UG, Sung GH, Spatafora JW, Straus NA (2003) Ancient tripartite coevolution in the attine ant-microbe symbiosis. Science 299 (5605): 386-388. https://doi.org/10.1126/science.1078155

Currie CR (2001) Prevalence and impact of a virulent parasite on a tripartite mutualism. Oecologia 128(1): 99-106. https://doi.org/10.1007/s004420100630

Custodio BC, Rodrigues A (2018) Escovopsis kreiselii specialization to its native hosts in the fungiculture of the lower attine ant Mycetophylax morschi. Antonie Van Leeuwenhoek https://doi.org/10.1007/s10482-018-1158-x.

Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: more models, new heuristics and parallel computing. Nat Methods 9: 772. https://doi: 10.1038/nmeth.2109

Dhodary B, Schilg M, Wirth R, Spiteller D (2018) Secondary metabolites from *Escovopsis weberi* and their role in attacking the garden fungus of leaf-cutting ants. Chem - A Eur J 24(17): 4445–4452. https://doi.org/10.1002/chem.201706071

Gerardo NM, Jacobs SR, Currie CR, Mueller UG (2006a) Ancient host-pathogen associations maintained by specificity of chemotaxis and antibiosis. PLoS Biol 4(8): e235. https://doi.org/10.1371/journal.pbio.0040235

Gerardo NM, Mueller UG, Currie CR (2006b) Complex host-pathogen coevolution in the *Apterostigma* fungus-growing ant-microbe symbiosis. BMC Evol Biol 6:88. https://doi.org/10.1186/1471-2148-6-88

Gerardo NM, Mueller UG, Price SL, Currie CR (2004) Exploiting a mutualism: parasite specialization on cultivars within the fungus-growing ant symbiosis. Proc R Soc B Biol Sci 271(1550): 1791-1798. https://doi.org/10.1098/rspb.2004.2792

Harrington TC, McNew D, Mayers C, et al (2014) *Ambrosiella roeperi* sp. nov. is the mycangial symbiont of the granulate ambrosia beetle, *Xylosandrus crassiusculus*. Mycologia 106(4): 835-845. https://doi.org/10.3852/13-354

Haugland RL, Heckman JL (1998) Identification of putative sequence specific PCR primers for detection of the toxigenic fungal species *Stachybotrys chartarum*. Molecular and Cellular Probes 12(6): 387-396. https://doi.org/10.1006/mcpr.1998.0197

Heine D, Holmes NA, Worsley SF, Santos ACA, Innocent TM, Scherlach K, Patrick EH, Yu DW, Murrell JC, Vieria PC, Boomsma JJ, Hertweck C, Hutchings M, Wilkinson B (2018) Chemical warfare between leafcutter ant symbionts and a co-evolved pathogen. Nat Commun 9(1): 2208. https://doi.org/10.1038/s41467-018-04520-1

Hughes DP, Pierce NE, Boomsma JJ (2008) Social insect symbionts: evolution in homeostatic fortresses. Trends Ecol Evol 23(12): 672-677. https://doi.org/10.1016/j.tree.2008.07.011

Jaklitsch WM, Põldmaa K, Samuels GJ (2011) Reconsideration of *Protocrea* (Hypocreales , Hypocreaceae). Mycologia 100(6): 962-984.

Ješovnik A, González VL, Schultz TR (2016) Phylogenomics and divergence dating of fungus-farming ants (Hymenoptera: Formicidae) of the genera *Sericomyrmex* and *Apterostigma*. PLoS One 11(7): e0151059. https://doi.org/10.1371/journal.pone.0151059 Joop G, Vilcinskas A (2016) Coevolution of parasitic fungi and insect hosts. Zoology 119(4): 350-358. https://doi.org/10.1016/j.zool.2016.06.005

Katoh K, Standley DM (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Mol Biol Evol 30(4): 772-780. https://doi.org/10.1093/molbev/mst010

Kim YK, Xiao CL, Rogers JD (2005) Influence of culture media and environmental factors on mycelial growth and pycnidial production of *Sphaeropsis pyriputrescens*. Mycologia 97(1): 25-32. https://dori.org[/10.1080/15572536.2006.11832835](https://doi.org/10.1080/15572536.2006.11832835)

Kost C, Lakatos T, Böttcher I, Arendholz WR, Redenbach M, Wirth R (2007) Non-specific association between filamentous bacteria and fungus-growing ants. Naturwissenschaften 94(10): 821-828. https://doi.org/10.1007/s00114-007-0262-y

Kwong WK, Medina LA, Koch H, Sing KW, Soh EJY, Ascher JS, Jaffé R, Moran NA (2017) Dynamic microbiome evolution in social bees. Sci Adv 3(3):e1600513. https://doi.org/10.1126/sciadv.1600513

Masiulionis VE, Cabello MN, Seifert KA, Rodrigues A, Pagnocca FC (2015) *Escovopsis trichodermoides* sp. nov., isolated from a nest of the lower attine ant *Mycocepurus goeldii*. Antonie van Leeuwenhoek 107(3): 731-40. https://doi.org/ 10.1007/s10482-014-0367-1

Meirelles LA, Montoya QV, Solomon SE, Rodrigues A (2015a) New light on the systematics of fungi associated with attine ant gardens and the description of *Escovopsis kreiselii* sp. nov. PLoS One 10(1): e0112067. https://doi: 10.1371/journal.pone.0112067

Meirelles LA, Solomon SE, Bacci M, Wright AM, Mueller UG, Rodrigues A (2015b) Shared *Escovopsis* parasites between leaf-cutting and non-leaf-cutting ants in the higher attine fungus-growing ant symbiosis. R Soc Open Sci 2(9):150257. https://doi.org/

Menezes C, Vollet-Neto A, Marsaioli AJ, Zampieri D, Fontoura IC, Luchessi AD, Imperatriz-Fonseca VL (2015) A Brazilian social bee must cultivate fungus to survive. Curr Biol 25(21): 2851-2855. https://doi.org/10.1016/j.cub.2015.09.028

Montoya QV, Meirelles LA, Chaverri P, Rodrigues A (2016) Unraveling *Trichoderma* species in the attine ant environment: description of three new taxa. Antonie van Leeuwenhoek 109(5): 633-651. https://doi.org/10.1007/s10482-016-0666-9

Moriya S, Inoue T, Ohkuma M, Yaovapa T, Johjima T, Suwanarit P, Sangwanit U, Vongkaluang C, Noparatnaraporn N, Kudo T (2005) Fungal community analysis of fungus gardens in termite nests. Microbes Environ 20 (4): 243-252. https://doi.org/10.1264/jsme2.20.243

Muchovej, J.J.; Della Lucia TC (1990) *Escovopsis*, a new genus from leaf-cutting ant nests to replace *Phialocladus* nomen invalidum. Mycotaxon 37, 191–195.

Mueller UG, Rehner SA, Schultz TR (1998) The evolution of agriculture in ants. Science 281(5385): 2034-2038.

Mueller UG, Gerardo N (2002) Fungus-farming insects: multiple origins and diverse evolutionary histories. Proc Natl Acad Sci USA 99(24): 15247-15249. https://doi.org/10.1073/pnas.242594799

Mueller UG, Ishak HD, Bruschi SM, Smith CC, Herman JJ, Solomon SE, Mikheyev AS, Rabeling C, Scott JJ, Cooper M, Rodrigues A, Ortiz A, Brandão CRF, Lattke JE, Pagnocca FC, Rehner SA, Schultz TR, Vasconcelos HL, Adams RMM, Bollazzi M, Clark RM, Himler AG, LaPolla JS, Leal IR, Johnson RA, Roces F, Sosa-Calvo J, Wirth R, Bacci M Jr. (2017) Biogeography of mutualistic fungi cultivated by leafcutter ants. Mol Ecol 26(24): 6921-6937. https://doi.org/10.1111/mec.14431

Mueller UG, Kardish MR, Ishak HD, Wright AM, Solomon SE, Bruschi SM, Carlson AL, Bacci M Jr (2018) Phylogenetic patterns of ant-fungus associations indicate that farming strategies, not only a superior fungal cultivar, explain the ecological success of leafcutter ants. Mol Ecol 27(10): 2414-2434. https://doi.org/10.1111/mec.14588

Nixon KC (2002) WinClada ver. 1.0000. Ithaca, NY: Published by the author.

Nygaard S, Hu H, Li C, Schiøtt M, Chen Z, Yang Z, Xie Q, Ma C, Deng Y, Dikow RB, Rabeling C, Nash DR, Wcislo WT, Brady SG, Schultz TR, Zhang G, Boomsma JJ (2016) Reciprocal genomic evolution in the ant–fungus agricultural symbiosis. Nat Commun 7: 12233. https://doi.org/10.1038/ncomms12233

Põldmaa K (2011) Tropical species of *Cladobotryum* and *Hypomyces* producing red pigments. Stud Mycol 68: 1-34. https://doi.org/10.3114/sim.2011.68.01

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. Syst Biol 61(3): 539-542. https://doi.org/10.1093/sysbio/sys029

Sharma G, Pandey RR (2010) Influence of culture media on growth, colony character and sporulation of fungi isolated from decaying vegetable wastes. J Yeast Fungal Res 1(8): 157 - 164.

Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Fungal Barcoding Consortium (2012) Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proc Natl Acad Sci USA 109(16): 6241–6246. https://doi.org./10.1073/pnas.1117018109

Schultz TR, Brady SG (2008) Major evolutionary transitions in ant agriculture. Proc Natl

Acad Sci USA 105(14):5435-5440. https://doi.org/10.1073/pnas.0711024105

Schultz TR, Sosa-Calvo J, Brady SG, Lopes CT, Mueller UG, Bacci M Jr, Vasconcelos HL (2015) The Most Relictual Fungus-Farming Ant Species Cultivates the Most Recently Evolved and Highly Domesticated Fungal Symbiont Species. Am Nat 185(5):693-703. https://doi.org/10.1086/680501

Seifert KA, Samson RA, Chapela IH (1995) *Escovopsis aspergilloides*, a rediscovered hyphomycete from leaf-cutting ant nests. Mycologia 87(3): 407-413. https://doi.org/10.2307/3760838

Slepecky RA, Starmer WT (2009) Phenotypic plasticity in fungi: a review with observations on *Aureobasidium pullulans*. Mycologia 101(6):823-832. https://doi.org/10.3852/08-197

Sosa-Calvo J, Ješovnik A, Lopes CT, Rodrigues A, Rabeling C, BacciJr M, Vasconcelos HL, Schultz T (2017) Biology of the relict fungus-farming ant *Apterostigma megacephala* Lattke, including descriptions of the male, gyne, and larva. Insect Soc 64 (3): 329-346. https://doi.org/10.1007/s00040-017-0550-2

Sosa-Calvo J, Schultz TR (2010) Three remarkable new fungus-growing ant species of the genus *Myrmicocrypta* (Hymenoptera: Formicidae), with a reassessment of the characters that define the genus and its position within the attini. Ann Entomol Soc 103(2): 181-195. https://doi.org/10.1603/AN09108

Spatafora JW, Sung GH, Sung JM, Hywel-Jones NL, White JF Jr (2007) Phylogenetic evidence for an animal pathogen origin of ergot and the grass endophytes. Mol Ecol 16(8):1701-11. https://doi.org/10.1111/j.1365-294X.2007.03225.x

Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30:1312–1313.

https://doi.org/10.1093/bioinformatics/btu033

Taerum SJ, Cafaro MJ, Little AE, Schultz TR, Currie CR (2007) Low host-pathogen specificity in the leaf-cutting ant-microbe symbiosis. Proc R Soc B Biol Sci 274(1621):1971-1978. https://doi.org/10.1098/rspb.2007.0431

Thomas A. Hall (1999) Bioedit a user-friendly biological sequence alignment editor an analysis program for windows 95/98/NT. Nucleic Acids Symp 41: 95-98

Vanderpool D, Bracewell RR, McCutcheon JP (2018) Know your farmer: ancient origins and multiple independent domestications of ambrosia beetle fungal cultivars. Mol Ecol 27(8): 2077-2094. https://doi.org/10.1111/mec.14394

Varanda-Haifig SS, Albarici TR, Nunes PH, Haifig I, Vieira PC, Rodrigues A (2017) Nature of the interactions between hypocrealean fungi and the mutualistic fungus of leafcutter ants. Antonie Van Leeuwenhoek 110(4): 593-605. https://doi.org/10.1007/s10482- 016-0826-y

Villesen P, Mueller UG, Schultz TR, Adams RMM, Bouck AC (2004) Evolution of antcultivar specialization and cultivar switching in *Apterostigma* fungus-growing ants. Evolution 58(10): 2252-2265.

White TJ, Bruns T, Lee SH, Taylor JW (1990) PCR protocols: a guide to methods and application. Academic Press 315−322. http://dx.doi.org/10.1016/b978-0-12-372180- 8.50042-1

Wrzosek M, Ruszkiewicz-Michalska M, Sikora K, Damszel M, Sierota Z (2017) The plasticity of fungal interactions. Mycol Prog 16(2): 101-108. https://doi.org/10.1007/s11557-016-1257-x

**Figure legends**

Fig 1. Colony macroscopic characters of *Escovopsis clavatus* and *Escovopsis multiformis* on CMD, CYA, MA2%, MEA, OA, PCA, PDA and SNA media after 14 days at 10, 20, 25 and 30°C.



Fig 2. *Escovopsis clavatus*. A-B: Conidiophores without "swollen cells". C-D: Conidiophores with "swollen cells" (red arrow). E-G: Vesicles in various shapes with phialides pattern. G: Conidia.



Fig 3. *Escovopsis clavatus*. SEM images A-D: Conidiophores without "swollen cells". E: Conidiophore with "swollen cells" (red arrow). F-G: Vesicles. H: Phialides. G: Conidia.



Fig 4. *Escovopsis multiformis*. A-C: Conidiophores mono- and polycephalous without "swollen cells". D-G: Conidiophores mono and polycephalous with "swollen cells" (red arrow). H-I: Vesicles in various shapes. J: Conidia.





Fig 6. Phylogenetic position of *Escovopsis clavatus* and *Escovopsis multiformis* considering each molecular marker separately (ITS, LSU and *tef1*). The trees were reconstructed under Bayesian and Maximum Likelihood inferences. The numbers on branches indicate the posterior probabilities and the bootstrap support values, respectively. The seven *Escovopsis* ex-type strains are denoted in bold and the new species are highlighted in green (*E. clavatus*) and light brown (*E. multiformis*). The trees include a total of 40 *Escovopsis* sequences of each marker (ITS - 621 bp, LSU - 531 bp and *tef*1 - 758 bp) and *Escovopsioides*, *Hypomyces*, *Sphaerostilbella*, *Trichoderma* and *Protocrea* were included as the closest phylogenetic relatives of *Escovopsis*. *Lecanicillium antillanum* CBS 350.85 was used as the outgroup. ET: ex-type.



Fig 7. Phylogenetic position of *Escovopsis clavatus* and *Escovopsis multiformis*. The phylogenetic analysis is based on the concatenated sequences of ITS, LSU and *tef1*; and the tree was reconstructed using Bayesian and Maximum Likelihood inferences. Numbers on branches indicate the posterior probabilities and the bootstrap support values, respectively. All *Escovopsis* species previously described are denoted in bold and the new species are highlighted in green for *E. clavatus* and light brown for *E. multiformis*. The tree includes a total of 40 *Escovopsis* sequences with 1911 bp (ITS - 621 bp, LSU - 531 bp and *tef*1 - 758 bp). The data also included sequences from *Escovopsioides*, *Hypomyces*, *Sphaerostilbella*, *Trichoderma* and *Protocrea* as the closest phylogenetic relatives of the parasite. *Lecanicillium antillanum* CBS 350.85 was used as the outgroup. ET: ex-type strains. Bar: 0.04 substitutions per nucleotide position.



# **Supporting information**



Table S1. *Escovopsis* strains used in the phylogenetic analyses and their associated metadata.





<sup>ET</sup> Ex-type; <sup>&</sup> tef1 sequences obtained by Meirelles et al. (2015a); \* tef1 sequences obtained by Currie et al. (2003); <sup>\$</sup> LSU sequences obtained by Osti and Rodrigues (2018); \* LSU sequences obtained in this study.

Table S2. Molecular markers, primers and PCR conditions used in this study.



# **References**

Augustin JO, Groenewald JZ, Nascimento RJ, Mizubuti ESG, Barreto RW, Elliot SL, Evans HC (2013) Yet more "weeds" in the garden: Fungal novelties from nests of leaf-cutting ants. PLoS One 8 (12): e82265. https://doi.org/10.1371/journal.pone.0082265

Chaverri P, Castlebury LA, Samuels GJ, Geiser DM (2003) Multilocus phylogenetic structure within the *Trichoderma harzianum* / *Hypocrea lixii* complex. Mol Phylogenet Evol 27(2): 302-313. https://doi.org/10.1016/S1055-7903(02)00400-1

Currie CR, Wong B, Stuart AE, Schultz TR, Rehner SA, Mueller UG, Sung GH, Spatafora JW, Straus NA (2003) Ancient tripartite coevolution in the attine ant-microbe symbiosis. Science 299 (5605): 386-388. https://doi.org/10.1126/science.1078155

Haugland RL, Heckman JL (1998) Identification of putative sequence specific PCR primers for detection of the toxigenic fungal species *Stachybotrys chartarum*. Molecular and Cellular Probes 12(6): 387-396. https://doi.org/10.1006/mcpr.1998.0197

Jaklitsch WM, Põldmaa K, Samuels GJ (2011) Reconsideration of *Protocrea* ( Hypocreales , Hypocreaceae ). Mycologia 100(6): 962- 984.

Masiulionis VE, Cabello MN, Seifert KA, Rodrigues A, Pagnocca FC (2015) *Escovopsis trichodermoides* sp. nov., isolated from a nest of the lower attine ant *Mycocepurus goeldii*. Antonie van Leeuwenhoek 107(3): 731-40. https://doi: 10.1007/s10482-014-0367-1

Meirelles LA, Montoya QV, Solomon SE, Rodrigues A (2015a) New light on the systematics of fungi associated with attine ant gardens and the description of *Escovopsis kreiselii* sp. nov. PLoS One 10(1): e0112067. https://doi: 10.1371/journal.pone.0112067

Meirelles LA, Solomon SE, Bacci M, Wright AM, Mueller UG, Rodrigues A (2015b) Shared *Escovopsis* parasites between leafcutting and non-leaf-cutting ants in the higher attine fungus-growing ant symbiosis. R Soc Open Sci 2(9):150257. https://doi: 10.1098/rsos.150257

Osti JF, Rodrigues A (2018) *Escovopsioides* as a fungal antagonist of the fungus cultivated by leafcutter ants. BMC Microbiol 18(1):130. https://doi.org/doi./10.1186/s12866-018-1265-x.

Põldmaa K (2011) Tropical species of *Cladobotryum* and *Hypomyces* producing red pigments. Stud Mycol 68: 1-34. https://doi: 10.3114/sim.2011.68.01

Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Fungal Barcoding Consortium (2012) Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proc Natl Acad Sci USA 109(16): 6241–6246. https://doi.org./10.1073/pnas.1117018109

Spatafora JW, Sung GH, Sung JM, Hywel-Jones NL, White JF Jr (2007) Phylogenetic evidence for an animal pathogen origin of ergot and the grass endophytes. Mol Ecol 16(8):1701-1711. https://doi: 10.1111/j.1365-294X.2007.03225.x

Taerum SJ, Cafaro MJ, Little AE, Schultz TR, Currie CR (2007) Low host-pathogen specificity in the leaf-cutting ant-microbe symbiosis. Proc R Soc B Biol Sci 274(1621):1971-1978. https://doi.org/10.1098/rspb.2007.0431

White TJ, Bruns T, Lee SH, Taylor JW (1990) PCR protocols: a guide to methods and application. Academic Press 315−322. http://dx.doi.org/10.1016/b978-0-12-372180-8.50042-1

# **Chapter II**

**Manuscript submitted to IMA Fungus**

**"Fungi of the strong conidial form" in attine ant colonies: taxonomic and phylogenetic reassessment of the genus** *Escovopsis*

Quimi Vidaurre Montoya<sup>1,2\*</sup>, Maria Jesus Sutta Martiarena<sup>1,2</sup>, Rodolfo Bizarria Júnior<sup>1,2</sup>, Nicole Marie Gerardo<sup>3</sup>, Andre Rodrigues<sup>1,2\*</sup>

<sup>1</sup> Department of General and Applied Biology, São Paulo State University (UNESP), Rio Claro, SP, Brazil.

<sup>2</sup> Center for the Studies of Social Insects, São Paulo State University (UNESP), Rio Claro, SP, Brazil.

<sup>3</sup> Emory University, Department of Biology, O. Wayne Rollins Research Center, Atlanta, USA

Submitted to IMA Fungus

\* Corresponding author:

Andre Rodrigues [\(andrer@rc.unesp.br\)](mailto:andrer@rc.unesp.br), Quimi Vidaurre Montoya [\(quimivimo@gmail.com\)](mailto:quimivimo@gmail.com) Universidade Estadual Paulista (UNESP), Centro de Estudos de Insetos Sociais Avenida 24-A, n. 1515, Bela Vista, Rio Claro, SP, Zip code: 13.506-900

Phone #: 55 19 3526-4364

# **Abstract**

*Escovopsis* (Ascomycota: Hypocreales, Hypocreaceae) is a fascinating group of fungi, members of which are considered specialized parasites of the fungal cultivars of fungus-growing ants (Formicidae: Myrmicinae: Attini: Attina, the "attines"). The lack of a suitable taxonomic framework and phylogenetic inconsistencies have long hampered *Escovopsis*research. The aim of this study was to create a standardized taxonomic framework and provide a comprehensive multilocus phylogenetic analysis, in order to set the basis of the *Escovopsis* systematics, and the stage for future *Escovopsis* research. Morphological and phylogenetic analyses support the separation of *Escovopsis* into three distinct genera. In light of this, we redefine *Escovopsis* and place *E. kreiselii* and *E. trichodermoides* into two new genera (*Sympodiorosea* and *Luteomyces*, respectively). Furthermore, we propose *Escovopsis microspora* as a synonym of *E. weberi*, and we recombined *E. kreiselii* and *E. trichodermoides* as *Sympodiorosea kreiselii* and *Luteomyces trichodermoides*, respectively. This study significantly expands our understanding of the systematics of *Escovopsis* and related genera, thereby facilitating future research on the evolutionary history, taxonomic diversity, and ecological roles of *Escovopsis*, *Sympodiorosea*, and *Luteomyces*.

**Keywords:** *Hypocreaceae*, Phylogenetics, Attines, Symbiosis, Evolution, fungus-growing ants

# **Introduction**

Fungi can exhibit bewildering morphological and genetic diversity (Mueller and Schmit 2007; Hawksworth and Lücking 2017). Through systematic approaches, taxonomists have developed mechanisms to categorize organisms based on their phenotypic and genetic characters (Komarek and Beutel 2006; Pavlinov 2018). Classification of organism demands that a selected set of morphological characters be evaluated under standardized parameters (Komarek and Beutel 2006). The lack of standardization precludes detailed study of many fungal groups, as is the case for the genus *Escovopsis*. *Escovopsis* is a diverse group of Hypocrealean fungi (Ascomycota: Hypocreales, Hypocreaceae), members of which are presumed to have evolved parasitizing the mutualistic fungus of fungus-growing ants (Formicidae: Myrmicinae: Attini: Attina, the "attines") (Yek et al. 2012). Besides, *Escovopsis* has only been found associated with fungus-growing ant colonies, suggesting that the genus has evolved in relation to these ants' system, potentially for millions of years. Despite their fascinating biology in relation to a canonical system for the study of coevolution and symbiosis, the paucity of taxonomic studies and unresolved phylogenetic inconsistencies have prevented the development of a comprehensive understanding of the systematics, ecology, and evolution of these fungi.

More than a century has passed since Möller (1893) observed a group of "fungi of the strong conidial form" in attine gardens, which 80 years later would be named *Phialocladus* (Kreisel 1972). Almost two decades later, *Phialocladus* was considered an invalid name because of the lack of the type specimen of the genus, and consequently, it was renamed as *Escovopsis* (*Escova*- Portuguese for brush, -*opsis* Greek for like), with *Escovopsis weberi* designated as the type species of the genus (Muchovej and Della Lucia 1990). Although the macroscopic characters of *E. weberi* were not fully described by the authors, the description of this species established the foundation for *Escovopsis* taxonomy. In 1995, Seifert et al. (1995) described *Escovopsis aspergilloides* in a detailed taxonomic study, providing a suitable framework to standardize the conditions for assessment of the the morphological features of *Escovopsis*. However, after this study, the taxonomy of *Escovopsis* was set aside for eighteen years.

Unlike taxonomic studies, the relationship between *Escovopsis* and the attine ants' mutualistic fungi has been the topic of numerous studies (Currie et al. 2003; Gerardo et al. 2006a,b; Taerum et al. 2007; Folgarait et al. 2011; Elizondo Wallace et al. 2014; Marfetán et al. 2015; Birnbaum and Gerardo 2016; de Man et al. 2016; Heine et al. 2018). Through these studies, a great diversity of *Escovopsis* was revealed and the first ideas about the phylogenetic position of this fungal group were gradually emerging (Gerardo et al. 2006b; Augustin et al. 2013; Masiulionis et al. 2015; Meirelles et al. 2015a,b). Initially, some authors suggested that *Escovopsis* belonged to Hypocreales, although, at the time no phylogenetic evidence was provided to support that hypothesis (Currie et al. 1999a,b). The first phylogenetic analysis of *Escovopsis* confirmed the genus to be within Hypocreales and place it as a sister clade of the Hypocreaceae (Currie et al. 2003). However, a more extensive phylogenetic analysis of *Escovopsis* strains associated with fungus gardens of *Apterostigma* ants indicated that the genus belonged to the Hypocreaceae (Gerardo et al. 2006b).

Augustin et al. (2013) were the first authors to combine morphological and phylogenetic approaches to study *Escovopsis*. Based on internal transcribed spacer (ITS) and large subunit ribosomal RNA (LSU) sequences, the authors described *Escovopsis lentecrescens*, *E. microspora*, and *E. moelleri*, which formed a monophyletic clade with *E*. *weberi* and *E*. *aspergilloides*. The most remarkable character of these newly named species was the presence of conidiophores with vesicles, as previously described by Muchovej and Della Lucia (1990) and Seifert et al. (1995). Nonetheless, for the description of the new species, Augustin et al. (2013) used different culture media from those used by Seifert et al. (1995), hindering a clear comparison of interspecific morphological differences. Furthermore, while phylogenetic analyses of Augustin et al. (2013) based ITS and LSU sequences suggested that *Escovopsis* formed a monophyletic clade, the analysis based on translation elongation factor 1-alpha (*tef*1) (where the new species were not included) suggested that *Escovopsis* may not be monophyletic. Furthermore, the authors also introduced the genus *Escovopsioides* (Ascomycota: Hypocreales, Hypocreaceae) which formed a polytomic clade with all Hypocreaceae.

For almost thirty years, the genus *Escovopsis* was morphologically defined by the presence of conidiophores with vesicles that support the phialides (i.e., determinate growth conidiogenous cells), from which conidia are produced (phialidic conidiogenesis). This changed with the introduction of *Escovopsis trichodermoides* (Masiulionis et al. 2015) and *Escovopsis kreiselii* (Meirelles et al. 2015a). These species have conidiophores without vesicles and with synchronous (*E. trichodermoides*) and sympodial (*E. kreiselii*) conidiogenous cells instead of phialides. Therefore, Meirelles et al. (2015a) amended the morphological description of *Escovopsis* to insert the morphological features of *E. kreiselii*. However, because Masiulionis et al. (2015) and Meirelles et al. (2015a) were published at nearly the same time, the new definition did not include *E. trichodermoides.* Furthermore, as with Augustin et al. (2013), the parameters used to describe *E. kreiselii* and *E.* 

*trichodermoides* were different from those used in previous studies, making comparisons with other *Escovopsis* species difficult.

The insertion of *E. trichodermoides* and *E. kreiselii* within *Escovopsis* not only meant changes to the morphological description of the genus but also intensified the phylogenetic uncertainties. In the phylogenies produced by Masiulionis et al. (2015) and Meirelles et al. (2015a,b), it was clear that vesiculate *Escovopsis* were closely related to *Escovopsioides* (Augustin et al. 2013) than to *E. trichodermoides* and *E. kreiselii*. Nonetheless, both Masiulionis et al. (2015) and Meirelles et al. (2015a,b) preferred to maintain *E. trichodermoides*, *E. kreiselii* and the vesiculate *Escovopsis* as being in the same genus.

Recently, Montoya et al. (2019) used the ITS, LSU, and *tef*1 markers in a multilocus phylogenetic approach to describe *Escovopsis clavata* and *E. multiformis*. The authors noticed that disagreements in *Escovopsis* taxonomy occurred between vesiculate *Escovopsis*, *E. trichodermoides* and *E. kreiselii*. Therefore, they highlighted the need to establish a standardized taxonomic framework and to utilize new molecular markers to resolve the phylogeny of the genus. Nevertheless, subsequent description of five new *Escovopsis* species (Marfetán et al. 2019) further complicated *Escovopsis* taxonomy because the phenotypic characters of these species were assessed under different conditions than those used in previous studies. Moreover, interpretation of the phylogenetic analyses carried out by Marfetán et al. (2019) had several limitations: i) it was based on the LSU and *tef*1 genes separately; ii) the *tef*1 sequences obtained in the study do not align with the *tef*1 sequences in previously published studies; and, iii) some of the new species (*Escovopsis atlas*, *E. catenulata*, *E*. *longivesica* and *E. pseudoweberi*) fall in the same clade yet strains of *E. atlas*  fall in different, non-monophyletic clades.

Given this complicated and piecemeal research history, the aim of this study is to reassess the taxonomy of *Escovopsis* by using standardized taxonomic parameters, a select and informative set of morphological characters, and a comprehensive multilocus phylogeny. Our results fill an important gap in mycology and will help future researchers to access the diversity and the evolutionary history of *Escovopsis* and related genera that inhabit the colonies of fungus-growing ants.

# **Methods**

#### **Phylogenetic placement of all strains previously named as** *Escovopsis*

The target of this first analysis was to show the phylogenetic placement of the strains currently treated as *Escovpsis*. It is difficult to performe a multilocus analysis because there are few strains on the literature that were sequenced for more than one molecular marker. Nonetheless, the *tef* gene was the one used in most of the studies already published (Currie et al. 2003; Gerardo et al. 2006; Taerum et al. 2007, 2010; Augustin et al. 2013; Meirelles et al. 2015a, b; Masiulionis et al. 2015; Montoya et al. 2019). Accordingly, we gather all *tef* sequences from the literature and combined it with our *tef* data set to reconstruct a phylogenetic tree. The final data set contained a total of 415 *tef* sequences (754 bp), that included vesiculate-*Escovopsis* (n= 281), non-vesiculate *Escovopsis* (n= 70), 63 strains from five *Hypocreaceae* genera (*Escovopsioides*, *Hypomyces*, *Protocrea, Sphaerostilbella,* and *Trichoderma*); and *Lecanicillium antillanum* CBS 35085 as the outgroup (Table S1). The *tef*1 sequences of species described in Marfetán et al. (2019) were not included in our analysis because they do not align with the *Escovopsis* sequences from the previous studies.

The data set was first aligned in MAFFT v.7 (Katoh and Standley 2013), and phylogenetic trees were reconstructed using maximum likelihood (ML) and Bayesian inferences (BI) in RAxML (Stamatakis 2014) and MrBayes v.3.2.2 (Ronquist et al. 2012), respectively. The nucleotide substitution model was GTR for ML and K80 + G for BI and was calculated in jModelTest 2 (Darriba et al. 2012), using the Akaike Information Criterion (AIC) with 95% confidence intervals. For ML analysis, 1000 independent trees and 1000 bootstrap replicates were performed, while for BI two separate runs (each consisting of three hot chains and one cold chain) were carried out. In last case, five million generations of the Markov Chain Monte Carlo (MCMC) were enough to reach convergence (standard deviation (SD) of split frequencies fell below 0.01). To generate final BI tree, the first 25% of trees were discarded as burn-in. The final tree was edited in FigTree v.1.4 [\(http://tree.bio.ed.ac.uk/software/figtree/\)](http://tree.bio.ed.ac.uk/software/figtree/) and Adobe Illustrator CC v.17.1.

#### **Phylogenetic and taxonomic framework for** *Escovopsis***' systematics**

## **Isolates**

A total of 103 strains (vesiculate  $[n=65]$ , and non-vesiculate  $[n=38]$ ) were included in this study (Table S2). Of these, 31 strains were obtained from previous studies (Augustin et al. 2013, Masiulionis et al. 2015, Meirelles et al. 2015b, Montoya et al. 2019), and the remaining (n= 72) were isolated from three regions in Brazil (Anavilhanas, state of Amazonas; Camp 41, state of Amazonas; and Botucatu, state of São Paulo - Table S2). The process of isolation, purification, and preservation of the strains followed methods outlined in Montoya et al. (2019). Briefly, from each attine colony, 21 garden fragments  $(0.5-1 \text{ mm}^3)$ were inoculated on potato dextrose agar (PDA, Neogen Culture Media, Neogen®) plates

supplemented with chloramphenicol [150 µg mL-1, Sigma] (seven garden fragments per plate). The plates were incubated at 25 °C in darkness. Plates were monitored daily for seven days, and, when *Escovopsis* mycelia sprouted out, it was transferred to new PDA plates without chloramphenicol. Axenic cultures were prepared (monosporic cultures) and stored in sterile distilled water kept at  $8 - 10$  °C (Castellani 1963), and in 10% glycerol at -80 °C.

#### **DNA extraction, PCR and sequencing**

The genomic DNA of the strains was extracted using a modified CTAB method (Möller et al. 1992). Briefly, fungal aerial mycelia, grown for seven days at 25 ° C on PDA, was crushed with the aid of glass microspheres (Sigma) in lysis solution and incubated at 65 ° C for 30 minutes. The organic phase was separated using a solution of chloroform-isoamyl alcohol (24: 1). Then, the material was centrifuged (10,000 g for 10 minutes), and the supernatant with the genomic DNA was collected. This extract was precipitated with 3M sodium acetate and isopropanol and purified with two successive washes of 70% ethanol. The DNA was suspended in 30  $\mu$ L of Tris-EDTA solution and stored at -20 °C.

Five molecular markers were amplified for all newly isolated *Escovopsis* strains: the internal transcribed spacer (ITS), the large subunit ribosomal RNA (LSU), the translation elongation factor 1-alpha (*tef*1), and the RNA polymerase II protein-coding genes (*rpb*1 and *rpb*2, Table S3). For strains from previous publications, we utilized previously published ITS, LSU and *tef*1 sequences, when available, and generated missing sequences for other molecular markers (Table S2). Sequences of *rpb*1 and *rpb*2 for 23 strains in the genus *Escovopsioides* were also generated in this study to complete our dataset (Table S2).

PCR reactions were carried out following Meirelles et al. (2015b) for ITS, Meirelles et al. (2015a) for *tef*1 and Augustin et al. (2013) for LSU (Table S3). PCRs for the *rpb*1 and *rpb*2 genes (Table S3) were performed in a final volume of 25 µL (4 µL of dNTPs [1.25 mM each]; 5  $\mu$ L of 5X buffer; 1  $\mu$ L of BSA [1 mg mL<sup>-1</sup>]; 2  $\mu$ L of MgCl<sub>2</sub> [25 mM]; 1  $\mu$ L of each primer [10  $\mu$ M]; 0.5  $\mu$ l of Taq polymerase [5 U  $\mu$ L<sup>-1</sup>], 2  $\mu$ L of diluted genomic DNA [1:100] and 8.5  $\mu$ L of sterile ultrapure water). When amplification was difficult, we added 1.5  $\mu$ L of dimethyl sulfoxide (DMSO), decreasing the volume of sterile ultrapure water to 7.0 µL, or we used the PuReTaq™ Ready-to-Go™ PCR kit (illustra™) following the manufacturer's protocol. Touchdown PCR conditions were used for *rpb*1 and *rpb2*: 1) 96 °C for 5 min; 2) 15 cycles of 94 °C for 30s, 65 °C for 1.5 min for *rpb*1 and for 1 min for *rpb*2 (the annealing temperature gradually decreased 1 °C per cycle) and 72 °C for 1.5 min for *rpb*1 and for 1 min for *rpb*2; and then 3) 35 cycles of 94 $\degree$ C for 30s, 50  $\degree$ C for 1min and 72  $\degree$ C for 1 min (Table S3).

Final amplicons were purified with the Wizard SV Gel and PCR Clean-up System (Promega) following the manufacturer's protocol. Sequences (forward and reverse) were generated on an ABI3500 (Life Technologies), and the consensus sequences were assembled in BioEdit v. 7.1.3 (Hall 1999) and Geneious (Kearse et al. 2012). All sequences are deposited in GenBank (Table S2 for accession numbers).

#### **Phylogenetic analyses**

Phylogenetic analyses were performed at family, genus and species levels. The objective of the analyses at the family level was to investigate whether all clades formally described as *Escovopsis* belong to *Hypocreaceae*. The objective of the analyses at the genus level was to investigate whether vesiculate *Escovopsis* forms a monophyletic clade, separating them from the non-vesiculate *Escovopsis,* as previously observed by Montoya et al. (2019). Besides, we wanted to know if the monophyly of all those clades remains constant considering the analysis using the five molecular markers separately as well as combined. The analyses at the species level aimed to clarify whether *E*. *weberi* and *E*. *microspora* are two different species based on the phylogenetic species concept.

Species described in Marfetán et al. (2019) were not included in our analyses because of the inavailability of ITS, *rpb*1, and *rpb*2 sequences, and because the *tef*1 sequences provided by the authors do not align with the *Escovopsis* sequences from other studies (Augustin et al. 2013; Masiulionis et al. 2015; Meirelles et al. 2015a, b; Montoya et al. 2019). Nonetheless, the LSU sequences generated by Marfetán et al. (2019) were combined with our LSU data to show phylogenetic placement of these strains (Fig. S1).

For the 'family-level', we used a concatenated data set that included 145 sequences for LSU (625 bp), 143 for *rpb*1 (851 bp), 144 for *rpb*2 (980 bp), and 145 for *tef*1 (849 bp) from six families of the Hypocreales order. For this analysis, we generated the *rpb*1 and *rpb*2 sequences for *Escovopsis* (including the nine ex-type strains) and *Escovopsioides* (including the ex-type strain). All other sequences were obtained from the NCBI GenBank database (Currie et al. 2003; Sung et al. 2008; Augustin et al. 2013; Masiulionis et al. 2015; Meirelles et al. 2015a, b; Montoya et al. 2019, Table S4). The *Stachybotrys* clade was used to root the tree (Sung et al. 2008).

Multiple loci were used to address the 'genus-level' questions, and all possible combinations of ITS, LSU, *tef*1, and *rpb*2 (25 combinations) were analyzed. Data sets included 134 sequences of ITS (661 bp), LSU (593 bp), *tef*1 (758 bp), and *rpb*2 (1023 bp); and 132 sequences of *rpb*1 (766 bp). The sequences represented 103 strains from the *Escovopsis* clade (vesiculate ( $n = 65$ ) and non-vesiculate ( $n = 38$ ), including the nine ex-type strains), 31 strains from five *Hypocreaceae* genera (*Escovopsioides*, *Hypomyces*, *Protocrea, Sphaerostilbella,* and *Trichoderma*); and *Lecanicillium antillanum* CBS 35085 as the outgroup (Table S2).

For the 'species-level', we used a concatenated data set that consisted of only sequences from vesiculate *Escovopsis* (65 sequences of ITS [661 bp], LSU [593 bp], *tef*1 [758 bp], *rpb*1 [766 bp], and *rpb*2 [1023 bp]). *E. kreiselii* (CBS 139320) was used to root the tree (Table S2).

For all analyses, data sets were first aligned separately for each gene in MAFFT v.7 (Katoh and Standley 2013). The nucleotide substitution model for each alignment was calculated in jModelTest 2 (Darriba et al. 2012), using the Akaike Information Criterion (AIC) with 95% confidence intervals. Then, the data sets were concatenated in Winclada v.1.00.08 (Nixon 2002). All phylogenetic trees were constructed using Maximum Likelihood (ML) in RAxML v.8 (Stamatakis 2014) and Bayesian Inference (BI) in MrBayes v.3.2.2 (Ronquist et al. 2012). For ML, we estimated 1000 independent trees and performed 1000 bootstrap replicates using the GTR model for each partition independently. For BI analyses, we carried out two separate runs (each consisting of three hot chains and one cold chain) using the GTR+I+G model for each partition independently; for all analyses, two million generations of the Markov Chain Monte Carlo (MCMC) were enough to reach convergence

(standard deviation (SD) of split frequencies fell below 0.01). To generate BI trees, the first 25% of trees were discarded as burn-in. Trees were edited in FigTree v.1.4 [\(http://tree.bio.ed.ac.uk/software/figtree/\)](http://tree.bio.ed.ac.uk/software/figtree/) and Adobe Illustrator CC v.17.1.

## **Morphology and Growth**

Here, we used nine *Escovopsis* ex-type species (*E. aspergilloides*, *E. clavata*, *E. kreiselii*, *E. lentecrescens*, *E. microspora*, *E. moelleri*, *E. multiformis*, *E. trichodermoides*, and *E. weberi*), representing the known diversity of the genus, to i) develop standardized conditions for evaluating the macroscopic and microscopic features of *Escovopsis*; ii) determine if morphological features support the results observed in phylogenetic analyses; and iii) create a taxonomic key for the genus, including illustrations of key microscopic structures.

Macroscopic characters (i.e. radial growth, mycelium colour, morphology and presence of soluble pigments) of the nine *Escovopsis* species were evaluated on eight different media (Table S5) at five temperatures (10 °C, 20 °C, 25 °C, 30 °C and 35 °C). These media and temperatures correspond with those previously used for the description of the known *Escovopsis* species (Seifert et al. 1995; Augustin et al. 2013; Masiulionis et al. 2015; Meirelles et al. 2015a, b; Montoya et al. 2019). After evaluation under these conditions, a set of media was selected based on the i) ability to evaluate growth rate; ii) expression of unique phenotypic characters of each species, iii) feasibility of comparison of morphological features of *Escovopsis* with other *Hypocreaceae*, and iv) ease of access to media in most laboratories. To obtain the inoculum, 200  $\mu$ L of 10<sup>6</sup> conidia per 1 uL sterile water from

colonies with seventh days of growth were homogeneously spread on Petri dishes (90 x 15 mm) with water-agar (WA) and incubated for seven days at 25 °C in darkness. Then, for all assays, 0.5 cm diameter fragments of WA with mycelia were inoculated in the center of Petri dishes (90 x 15 mm) containing each culture media. Dishes were not sealed and were incubated in the darkness following Montoya et al. (2019), which documented better development of *Escovopsis* under these conditions. We performed three replicates on each media and temperature, and we examined the morphological characters of all species every 24 hours for 14 days. After this evaluation, the optimal time for measuring growth and evaluating macroscopic characters was determined. Both parameters were standardized based on the point at which we were able to observe the most significant differences in growth and morphological characters between species.

Microscopic structures (i.e., conidiophores, conidiophores' branches, conidiophores' swollen cells, vesicles, conidiogenous cells, chlamydospores, and conidia) and their features (i.e., shape, size, colour, and pattern) were evaluated on PDA because *Escovopsis* species form such structures in greater numbers and much faster than in other media. To assess the microscopic structures, we carried out slide culture preparations. To do so, we placed three fragments of 0.5 mm<sup>3</sup> PDA on a microscopic slide, and we then inoculated each fragment with conidia of the fungus. Each inoculated fragment was covered with a coverslip and incubated at 25°C for 4-7 days in the dark. After that, the fragments of PDA were removed and the coverslips with fungal mycelia were placed on slides with a drop of lactophenol. The slides were examined under a light microscope (DM750, Leica, Germany), and the microscopic fungal structures were photographed and measured (30 measurements per structure) using LAS EZ v.4.0 (Leica Application Suite).
### **Taxonomic Key to Escovopsis species, Luteomyces, and Sympodiorosea**

Thirty-six morphological features (Table S6) from *E. aspergilloides*, *E. clavata*, *E. lentecrescens*, *E. microspora*, *E. moelleri*, *E. multiformis*, *E. weberi*, *E. kreiselii* and *E. trichodermoide*s were analyzed using the "rpart" library (Therneau and Atkinson 2019) in R 3.6.3 . Seven out of the 36 characters were selected using a recursive partitioning algorithm (with the information gain as a measure for deciding between alternative splits) as the most informative features to build the dichotomous key (Williams 2011). Finally, a dichotomous key (in cladogram format) was constructed using a decision tree that started with a single node root that split into multiple branches to end in the leaves corresponding to each species. The final cladogram was manually edited using Adobe Illustrator CC v.17.1, and the information on branches were used to perform the Taxonomic Key.

# **Results**

# **Phylogenetic placement of all strains previously named as** *Escovopsis*

The *tef* phylogenetic tree showed *Escovopsis* as a paraphyletic clade (Fig. 1, S2). While vesiculate *Escovopsis* and *E*. *trichodermoides* are sister clades, they are away from *E*. *kreiselii*. *E*. *kreiselii* formes a monophyletic clade close to *Hypomyces* (Fig. 1, and S2). It is important to note that the strains from the brown clade of the phylogeny performed by Gerardo et al. (2006b) are placed withing the vesiculate *Escovopsis* clade (mostly close to *E. clavata* and *E. multiformis*). On the other hand, the pink and yellow clades formed well supported monophyletic clades separated from vesiculate *Escovopsis*, *E*. *trichodermoides*  and *E*. *kreiselii* (Fig. 1, and S2).

# **Phylogenetic and taxonomic framework for** *Escovopsis***' systematics**

### **Phylogenetic analyses**

Phylogenetic analyses (BI and ML) at the family level placed both the vesiculate and non-vesiculate *Escovopsis* within the *Hypocreaceae* (Fig. 2). Vesiculate *Escovopsis* (*E. aspergilloides*, *E. clavata*, *E. lentecrescens*, *E. microspora*, *E. molleri*, *E. multiformis* and *E. weberi*) formed a monophyletic clade in both the BI and ML analysis (BI Posterior Probability (PP) = 1; ML bootstrap value (MLB) = 100) (Fig. 2). Furthermore, non-vesiculate *Escovopsis* (*E. kreiselii* and *E. trichodermoides*) formed well-supported, monophyletic clades (PP = 1, MLB = 100, each one) outside of the vesiculate *Escovopsis* and separate from all other *Hypocreaceae* genera (Fig. 2).

Analyses at the genus level revealed that *Hypomyces*, *Escovopsioides*, *E. kreiselii*, *E. trichodermoides*, and vesiculate-*Escovopsis* each form separate, monophyletic clades (Fig. 3). The phylogenetic placement of the five clades varies depending on the molecular marker used for analysis. The analyses made separately with ITS, LSU, and *rpb*1 (Fig. 3A, B, D), as well as the concatenated analysis based on the five markers (Fig. 3F) indicate vesiculate-*Escovopsis*, and *E. kreiselii* as sister clades. The analyses made separately with *tef*1 and *rpb*2 (Fig. 3C, E), and the concatenated analysis based on four markers (LSU, *tef*1, *rpb*1, and *rpb*2 - Fig. 3G) indicate vesiculate-*Escovopsis* and *E. trichodermoides* as forming sister clades. In addition, the analyses performed with ITS and the five concatenated-markers showed *Escovopsioides* and *E. trichodermoides* forming a monophyletic clade (PP = 1, MLB = 100 - Fig. 3A). The analysis based on *rpb*1, however, indicated *Escovopsioides* forming a monophyletic clade with *Hypomyces*, while analysis based on *tef*1 placed *Hypomyces* between *Escovopsioides* and *E. kreiselii* (Fig. 3C). Finally, the analyses carried out with LSU, *tef*1, and *rpb*2 separately (Fig. 3B, C, E), and the concatenated analysis (LSU, *tef*1, *rpb1* and *rpb*2 - Fig. 3G, 3A) placed *Hypomyces*, *Escovopsioides*, *E. kreiselii*, *E. trichodermoides*, and vesiculate-*Escovopsis* in well-supported, monophyletic clades (clearly separated from each other).

At the species level, *E. moelleri*, *E. aspergilloides*, *E. lentecrescens*, *E. clavata*, and *E. multiformis* formed well-supported clades that were clearly separated from each other. However, the ex-type strains of *E. weberi* and *E. microspora* grouped together with 45 other isolates in the same well-supported clade (Fig. 4A, B). This result was also observed at both the family and genus level trees.

Regarding the five species described by Marfetán et al. (2019), our analysis of the available LSU data indicates that they form two different clades closely related to *E. aspergilloides* and *E. lentecrescens* (Fig. S1). Specifically, the four strains of *E. primorosea* formed a well-supported monophyletic clade (Fig. S1), however *E. atlas*, *E. catenulata*, *E. longivesica*, *E. pseudoweberi*, and five strains named by the authors as *E. weberi* formed a single well-supported monophyletic clade (Fig. S1). Future research will need to reassess the morphology of these strains under standardized conditions and construct phylogenies based on additional markers.

### **Macroscopic features and conditions**

Vesiculate *Escovopsis* spp. were able to grow between 10 °C and 30 °C. In isolates that grew at 10 °C (*E. clavata*, *E. microspora*, *E. moelleri*, and *E. weberi*), growth was limited and inconspicuous, so at this temperature, growth was only reported as, present or absent. Strains grew better at 20, 25, and 30 °C. No strains grew at 35 °C. Between 20 to 30 °C, colonies started growing between the first (*E. lentecrescens*, *E. microspora*, *E. moelleri*, and *E. weberi*) and fourth day (*E. aspergilloides*, *E. clavata*, *E. multiformis*). Some fast-growing species (*E. weberi*, *E. microspora*, and *E. moelleri*) covered the entirety of the Petri dishes by the third day. Based on these results, we selected the fourth day as the best time to record the presence or absence of growth at 10  $^{\circ}$ C and to measure the radius of growth at 20, 25, and  $30^{\circ}$ C.

Evaluation on the eight media types (Fig. 5) demonstrated that the media influence growth rate and growth form. Growth on CYA, PCA, and PDA resulted in similar morphology for both *E. weberi* and *E. microspora*. Likewise, MA resulted in similar growth patterns as CYA, MEA, OA, and PDA for *E. moelleri*, CYA for *E. aspergilloides*, and PCA and PDA for *E. lentecrescens*, *E. clavata*, *E. multiformis*, *E. kreiselii* and *E. trichodermoides*. In contrast, none of the isolates grew well on SNA (all strains exhibited inconspicuous aerial mycelia, and the morphological patterns were difficult to observe until 14 days post inoculation). OA was also not ideal because the growth of strains was difficult to measure as a result of the medium's opacity. Except to *E. aspergilloides*, all strains exhibited vigorous growth and good expression of colour on MEA. Importantly, differences in growth rate were most apparent on CMD, and, on this medium, some species (e.g., *E. weberi* and *E. microspora*) produced hyphal agglomerations (pustule-like) on which conidiophores were often produced (similar to the pustules produced by *Trichoderma*). Based on these results, we selected CMD, MEA, and PDA as the most suitable media to evaluate macroscopic features of *Escovopsis* species. It is important to highlight that these media are also used for the morphological assessment of other genera in the *Hypocreaceae.*

On CMD, MEA, and PDA, most of the *Escovopsis* strains grew best at 25 °C (Fig. 5). At this temperature, the differences in macroscopic characters, especially colony colour, were most apparent on day seven. For instance, white to light and dark-brown (*E. clavata*, *E. lentecrescens*, *E. microspora*, *E. moelleri*, *E. multiformis*, and *E. weberi*), and light-yellow to light-brown colony colours (*E. aspergilloides*) were clearly distinguishable. Although less clear, other colours (greenish-brown, pink, pinkish-brown, and reddish-brown) were observed on colonies of *E. weberi* and *E. microspora* on PDA and MEA. Between the seventh and tenth day, most of species became dark-brown on the three media, and the distintion between them became less clear (except for *E. lentecrescens*). After the tenth day, the aerial mycelia of all species started to deteriorate. Therefore, seven days of growth at 25 °C appears to be the most suitable condition to evaluate the macroscopic characters of these species.

*E*. *kreiselii* and *E*. *trichodermoides* (non-vesiculate *Escovopsis*) exhibited slower growth than vesiculate *Escovopsis*. These species start growing between the second and fourth day, reaching the edge of Petri dishes after ten (*E*. *kreiselii*) and seven days (*E*. *trichodermoides*), respectively, with variation depending on the media and temperature. Furthermore, *E*. *kreiselii* and *E*. *trichodermoides* exhibit the clearest distinguishable growth forms and colony colour (light brown, pink, pinkish-brown, dark-brown, for *E*. *kreiselii*; and beige, pale-yellow, yellow, yellowish-brown, for *E*. *trichodermoides*) after 14 days (Fig. 5). Before this time, colonies are usually white to pale-pink (*E. kreiselii*) or white to pale-yellow

(*E*. *trichodermoides*). Therefore, for both *E*. *kreiselii* and *E*. *trichodermoides*, we suggest day seven as the best time to evaluate the colonies' growth radius and day 14 for colony morphology assessment.

### **Microscopic features and conditions**

Two well separated groups were observed based on microscopic characters: i) the vesiculate group, composed of *E. weberi*, *E. microspora*, *E. moelleri*, *E. aspergilloides*, *E. lentecrescens*, *E. clavata*, and *E. multiformis*; and ii) the non-vesiculate group, composed of *E. kreiselii*, and *E. trichodermoides*.

Vesiculate *Escovopsis* spp. present conidiophores with one vesicle (mono-vesiculate) or 2 - 53 vesicles (poly-vesiculate) (Fig. 6). Mono-vesiculate conidiophores (Fig. 6A-B) emerge from aerial mycelia in an alternating and opposite pattern in all species of this group. Poly-vesiculate conidiophores (Fig. 6C-H) also emerge from the aerial mycelia and can present short branches composed of one or two cells (most frequent for *E. moelleri*, *E. aspergilloides*, and *E. lentecrescens*) or long branches with multiple cells (most frequent for *E. clavata*, *E. microspora*, *E. multiformis,* and *E. weberi*). *E. weberi* and *E. microspora* have the largest and most branched conidiophores of the genus (Fig. 6G). In these clades, it is fairly common to find up to three levels of conidiophore branching. Some poly-vesiculate conidiophores have a swollen cell from were branches emerge (*E. clavata*, and *E. multiformis* – Fig. 6F). Vesicles, mostly composed of a single cell (non-septate vesicles - Fig. 6I-S), and rarely of two cells (septate vesicles - Fig. 6U-V), can emerge from the conidiophore's apex, the apex of the conidiophore's branches (usually only one vesicle in the short branches and two or more in long branches), as well as directly from the main axis of both the conidiophores and conidiophore's branches. Vesicles emerge directly separated by a septum (most common for *E. weberi* and *E. microspora*) or form a peduncle made up of one or two cells (most common for *E. moelleri*, *E. aspergilloides*, *E. lentecrescens*, *E. clavate* and *E. multiformis*). Vesicles can exhibit different shapes (globose, sub-globose, capitate, obovoid, prolate, spatulate, clavate, cymbiform, oblanceolate, subulate, cylindric, filiform, clavateseptate, cylindric-septate) (Fig. 6I-V) and sizes, depending of the species. Phialides (conidiogenous cells in the vesiculate *Escovopsis* – Fig. 6W-Z) emerge mainly from the vesicles and less frequently from the aerial mycelia (only observed in *E. weberi* and *E. microspora*). These structures give rise to the conidia and present a lageniform and ampulliform shape. The main differences between the phialides of the different species are mostly related to the sizes of the base, the widened part and the neck (Fig. 6V-Z). Conidia are single cells produced in chains in the phialides (enteroblastic conidiogenesis) and can vary in shape (globose, sub-globose, ellipsoidal, oblong, and oblong-ornamented) (Fig. 6ae). Most of the species have smooth conidia, but *E. moelleri* have conidia with ornamentations on cell walls (Fig. 6e). Of the vesiculate *Escovopsis* spp., only *E. weberi* and *E. microspora* have chlamydospores, but these are rarely observed.

The non-vesiculate groups form conidiophores remarkably different from those of the vesiculate group. Conidiophores of *E. kreiselii* lack vesicles and are formed on the aerial mycelium in an alternated or opposite pattern, and are more branched (with irregular branching conformation) than those of vesiculate *Escovopsis* (Fig. 23A, B). Conidiogenous cells of *E. kreiselii* are holoblastic sympodial (i.e., have indeterminate growth; Fig. 23C-H), and they are formed at the apex and at both the main and branch axis of the conidiophore (Fig. 23B). Conidia of *E. kreiselii* are solitary, globose to sub-globose, smooth but with thickwalled, light brown to dark brown, and sometimes with a denticle (Fig. 23I) or with a lesion (when the denticle remains in the conidiogenous cell – Fig. 23J). In contrast to *E*. *kreiselii*, the conidiophores of *E. trichodermoides* are pyramidal (*Trichoderma*-like), with one to six short levels of branches arising at more or less right angles from the conidiophore axis. They also lack vesicles (Fig. 25 A, B). This species has synchronous conidiogenous cells (Fig. 25B-F) with ampulliform shapes producing either solitary (Fig. 25C) or up to three conidia (Fig. 25D-F). The conidia are sub-globose to ovate, yellow-brown and ornamented (verrucose – Fig. 25G). Unlike the vesiculate *Escovopsis* spp., *E*. *kreiselii* and *E*. *trichodermoides* regularly form chlamydospores on all culture media and at all temperature at which they grow (Fig. 23K and 14I).

# **Taxonomy**

Phylogenetic analyses in this study unambiguously demonstrate that species previously treated as *Escovopsis* form three distinct clades. These groups also differ significantly from each other both in colony morphology and in microscopic characters. The first clade includes the ex-type strains of *E. aspergilloides*, *E. clavata*, *E. lentecrescens*, *E. microspora*, *E. moelleri*, *E. multiformis*, and *E. weberi*, which are all vesiculate species. Based on the similarity of their sequences, and their morphological characters, we synonymise *E. microspora* with *E. weberi*. The five other species in this group can regularly be distinguished from *E. weberi* and each other (Fig. S3). We treat these five species, together with *E. weberi*, as *Escovopsis*. Therefore, we restrict, and redefine *Escovopsis* to include only vesiculate species.

The two remaining clades (*E. kreiselii* and *E. trichodermoides*) included only nonvesiculate *Escovopsis* species. Below, we reassign these two clades into two, new genera, *Sympodiorosea* and *Luteomyces*. The descriptions of all the species are emended and aligned with each other based on the criteria established in this study. A taxonomic key is provided to facilitate the recognition of these genera and species.

# *Escovopsis* **J. J. Muchovej & Della Lucia, Mycotaxon 37: 192 (1990) Fig. 6** MycoBank: MB11249

*Etymology*: *Escova*- Portuguese for brush, -*opsis* Greek for like (brush like due to the bottlebrush appearance of the sporophore)

*Previous genus description*: vesiculate; vesicles cylindrical to globose, evanescent; phialides hyaline, swollen at base, extending to a narrow neck; conidia in short basipetal chains, aseptate, hyaline at first becoming pigmented with an ornamented or mucilaginous brown outer coat or sheath, phoretic. Non-vesiculate conidiophores are present in less derived strains, with non-phialidic conidigenous cells producing solitary conidia.

*Genus redescription*: Monophyletic Hypocreaceae genus that presents mono- and polyvesiculate conidiophores formed on hyaline aerial mycelia (Fig. 6A-H). Vesicles are terminal, mostly non-septate (Fig. 6I-S) and rarely with one septum (Fig. 6T-U), and of different shapes (globose, sub-globose, capitate, obovoid, prolate, spatulate, clavate, cymbiform, oblanceolate, subulate, cylindric, filiform, clavate-septate, cylindric-septate – Fig. 6I-U). Phialides hyaline, with a thin base, a swollen section and a thin neck (Fig. 6V-Z), are formed on vesicles. Conidia in chains, smooth or ornamented, aseptate, hyaline to brown, and in different shapes (globose, sub-globose, ellipsoidal, cylindric), are produced in phialides (Fig. 6a-e).

Notes: *Escovopsis* is phylogenetically placed within Hypocreaceae as a sister clade of *Luteomyces*. *Escovopsis* exhibits faster growth and different colony colour (brown) than *Luteomyces* (yellow). Unlike *Luteomyces*, which presents synchronous conidiogenous cells, *Escovopsis* forms phialides. The main feature of this genus is the presence of conidiophores with terminal vesicles that differentiate it from its sister clade and from all other known Hypocreaceae.

*Escovopsis weberi* J.J. Muchovej and Della Lucia, Mycotaxon 37: 192 (1990). Fig. *7*

MycoBank: MB127786

= *Escovopsis microspora* H.C. Evans and J.O. Augustin, PLoS One 8 (12): e82265, 5 (2013) MycoBank: MB800442

*Etymology*: "*weberi*" in honour of Neal A. Weber, American entomologist who found the fungus in the 1960's.

*Typification*: BRAZIL. Minas Gerais: Viçosa, T. M. Dela Lucia, isolated from ant colony (ex-type culture, ATCC 64542).

*Sequences*: ITS (KF293285), *tef*1 (AY172623), LSU (KF293281), *rpb*1 (MT305412), and *rpb*2 (MT305537).

*Colonies* growing at 10, 20, 25, and 30 °C on CMD, PDA, and MEA. After four days at 10 °C, inconspicuous growth only on inoculum, on the three media. At 20, 25, and 30 °C, growth starts on the first day on all media. After four days at 20 °C, radial growth of colonies reaches  $2 - 2.4$  cm,  $3 - 4$  cm, and 4 cm, on CMD, MEA, and PDA, respectively. At 25 °C, colonies reach plate edge on third day on PDA, and after four days radial growth of colonies reaches  $1.7 - 3.6$  cm, and  $2.4 - 4$  cm, on CMD and MEA, respectively. After four days at 30  $^{\circ}$ C, radial growth of colonies reaches 3.7 – 4 cm, 1.2 – 1.5 cm, and 3.7 – 4 cm on CMD, MEA and PDA, respectively. After seven days at 25 °C on CMD, colonies exhibit diffuse aerial mycelia spread by stolon and forming short pustules-like structures with white to brown conidia (Fig. 7C). On MEA, colonies form abundant aerial mycelia and different conidia colours (usually light-brown to brown in centre, followed by pinkish to light-brown and beige to greenish-brown regions, and white to pale - yellow on edge - Fig. 7B). On MEA, colonies can also display other colours, like yellow and reddish-brown, and eventually submerged mycelium forming dense circular zones and white to brown pustules-like. On PDA, colonies form abundant aerial mycelia spread by stolons, and white to brown conidia (Fig. 7A), and can also display other colours, like yellow to greenish-brown and pinkish to reddish-brown, and eventually pustule-like formations. Soluble pigments are not observed.

*Conidiophores* mono and poly-vesiculate (2 – 20 vesicles), hyaline, usually pyramidal, less frequent with irregular shape, smooth-walled, and arising alternated or opposite (less frequent) from aerial mycelia (Fig. 7D-E). Mono-vesiculate conidiophores reach  $20 - 60$  μm, and poly-vesiculate ones  $30 - 577$  μm, in length. Conidiophore stipes 45 – 90 μm long x 5 – 7 μm wide, separated by septum  $2 - 5$  μm from food cell (basal cell). Conidiophore branches, 34 – 127 μm long, mostly alternated and less opposite, at more or less right angles and slightly curved up and in one to two levels. Stipes on branches 10 – 36 μm long, separated by septum 1.5 – 3 μm from conidiophore axis. *Vesicles* in various shapes (cylindrical [predominant], clavate, and filiform – Fig. 9F-H),  $21 - 63 \mu m$  long x  $6 - 12 \mu m$ wide, predominantly non-septate and less frequent septate (Fig. 7F), separated from conidiophore axis or branch axis by stipe 1 – 12 μm long with one to two septa. *Phialides* formed on vesicles (Fig. 7F-I), total length  $7 - 9 \mu m$ , lageniform with wide base  $(0.5 - 1 \mu m)$ long x  $1 - 1.5$  μm wide), followed by swollen section  $(2.5 - 3 \mu m \times 2.5 - 3 \mu m)$  and long thin neck (3 – 4 μm x 0.5 – 0.8 μm). *Conidia* formed in chains on phialides, ellipsoidal to oblong  $(2.5 \text{ µm} - 3 \text{ µm} \text{ long x } 1.5 \text{ µm} - 2.5 \text{ µm} \text{ wide})$ , brown, with smooth and thickened walls (Fig. 7J).

Notes: *E. weberi* is the most derived clade of the genus and is phylogenetically close to *E. moelleri*. *E. weberi* grows faster than *E. moelleri* and other known *Escovopsis* species and exhibits the most variable colony colours in the genus. Unlike the strains of its sister clade, *E. weberi* forms smooth conidia in long chains, without ornamentations, and presents cylindric, filiform, and septated vesicles.

*Escovopsis aspergilloides* Seifert, Samson and Chapela, Mycologia 87: 408 (1995). Fig. 8

### MycoBank: MB413060

*Etymology*: *Aspergillus*-like. The etymology of this species was not clearly specified by Seifert et al. (1995). However, the authors implied that the name of the species was chosen because of its similarity with the vesicles of *Aspergillus*, previously observed by Möller 1893.

*Typification*: Trinidad, near ASA Wright Nature Center, in wet, dense, secondary tropical rainforest, in a nest of *Trachymyrmex ruthae*, from a nest chamber 15-20 cm below the soil surface, T. R. Schultz, 9 Nov. 1992. Isolated in June 1993 from mycelium in the living nest in Ithaca, New York by I. H. Chapela, no. 92110905C (holotype, DAOM 216382; ex-type culture, CBS 423.93 and DAOM 216382).

*Sequences*: ITS (NR\_137160), *tef*1 (AY172632), LSU (KF293283), *rpb*1 (MT305421), and *rpb*2 (MT305546).

*Colonies* growing at 20 and 25 °C on CMD, PDA, and MEA. At 20 °C, growth starts on second day on PDA, on third day on MEA, and on fourth day on CMD. After four days at 20 °C, radial growth of colonies reaches  $0 - 0.1$  cm,  $0.2 - 0.5$  cm, and  $0.5 - 0.8$  cm, on CMD, MEA, and PDA, respectively. At 25 °C, growth starts on second day on MEA and PDA, and on third day on CMD. After four days at 25 °C, radial growth of colonies reaches  $0.1 - 0.3$  cm,  $0.5 - 0.7$  cm, and  $0.5 - 1$  cm on CMD, MEA, and PDA, respectively. Colonies do not grow at 10 and 30 °C. After seven days at 25 °C, colonies exhibit diffuse aerial mycelia spread by stolons, and pale-yellow to brown conidia on CMD (Fig. 8C). On MEA, submerged mycelia form a dense circular zone, and diffuse aerial mycelia in circular-sector shapes form white to yellow and yellowish-brown conidia (white on edge and yellow-brown in centre - Fig. 8B). On PDA, abundant aerial mycelia, spread by stolons, form pale-yellow to lightbrown conidia (Fig. 8A). Pustule-like formations and soluble pigments are not observed.

*Conidiophores* mono and poly-vesiculate (1-15 vesicles), hyaline, with irregular shape, smooth-walled and arising alternated or opposite from aerial mycelia (Fig. 8D-F). Mono-vesiculate conidiophores reach  $40 - 72 \mu m$ , and poly-vesiculate ones  $80 - 300 \mu m$ , in length. Conidiophore stipes  $24 - 101 \mu m \log x 5 - 6 \mu m$  wide, separated by septum  $4 - 6 \mu m$ μm from food cell (basal cell). Conidiophore branches, 32 – 161 μm long, alternated, at more or less right angles, and from one to three levels. Second branching level usually longer than other branching levels. Stipes on branches  $10 - 49$  μm long, separated by septum  $2 - 4$  μm from conidiophore axis. *Vesicles* in various shapes (globose [predominant], sub-globose, capitate, ovoboid, prolate and spatulate - Fig. 8D-G),  $14 - 22 \mu m \log x 10 - 22 \mu m$  wide, usually separated from conidiophore axis or branch axis by stipe  $10 - 40$  µm long with one to two septa. *Phialides* formed on vesicles (Fig. 8G-H), total length 6 – 10 μm, ampulliform, with truncated pyramid shape base  $(1-2 \mu m \log x 0.5 - 1.5 \mu m \text{ wide})$  followed by swollen section  $(3.5 - 4 \mu m \log x 2 - 3 \mu m \text{ wide})$  and long thin neck  $(4 \mu m \log x 2 \mu m \text{ wide})$ . *Conidia* formed in chains on phialides, globose to oblong  $(2.5 - 3 \mu m)$  long x  $2 - 2.5 \mu m$ wide), brown, with smooth and slightly thickened walls (Fig. 8H-I). *Chlamydospores* intercalar, hyaline,  $11 - 22 \mu m \log x 8 - 14 \mu m$  wide (Fig. 8J).

Notes: *E. aspergilloides* is phylogenetically close to *E*. *lentecrescens*. *E. aspergilloides* grows faster than *E*. *lentecrescens*. However, the most remarkable feature of *E. aspergilloides* is its pale-yellow to yellowish-brown colonies, which differentiate it from the brown colonies of *E*. *lentecrescens*.

*Escovopsis clavata* Q.V. Montoya, M.J.S. Martiarena, D.A. Polezel, S. Kakazu and A. Rodrigues, Mycokeys 46: 102 (2019). Fig. 9

MycoBank: MB828328

*Etymology*: "*clavata*" in reference to the predominantly clavate shape of vesicles.

*Typification*: BRAZIL. Santa Catarina, Florianópolis, GPS: 27°44'39.6''S; 48°31'10.14''W, elev. 46 m, fungus garden of *Apterostigma* sp, 08, 2015. *A. Rodrigues*. Holotype: CBS H-23845 (dried culture on PDA). Ex-type strain LESF 853 (= CBS 145326).

*Sequences*: ITS (MH715096), *tef*1 (MH724270) and LSU (MH715110), *rpb*1 (MT305419), and *rpb*2 (MT305544).

*Colonies* growing at 20 and 25 °C on CMD, PDA, and MEA. At both temperatures, growth starts on third day on all media. After four days at 20 °C, radial growth of colonies reaches  $0 - 0.3$  cm,  $0.1 - 0.4$  cm, and  $0.3 - 0.5$  cm on CMD, MEA, and PDA, respectively. After four days at 25 °C, radial growth of colonies reaches  $0.2 - 0.8$  cm,  $0.4 - 0.6$  cm, and  $0.6 - 1.1$  cm on CMD, MEA, and PDA, respectively. No growth is observed at 10 and 30 °C. After seven days at 25 °C, colonies exhibit diffuse aerial mycelia and form beige to palebrown conidia on CMD (Fig. 9C). On MEA (Fig. 9B) and PDA (Fig. 9A), colonies grow in circular shape with dense, floccose aerial mycelia, with beige conidia near the edge and beige to pale brown conidia in the center. Stolons are rare. Pustule-like formations and soluble pigments are not observed.

*Conidiophores* mono and poly-vesiculate (2 – 8 vesicles), hyaline, with irregular shape, smooth-walled, and arising alternated or opposite from aerial mycelia (Fig. 9D-G). Mono-vesiculate conidiophores reach  $10 - 50 \mu m$ , and poly-vesiculate ones up to 780  $\mu$ m, in length. Conidiophore stipes  $10 - 40$  μm long x  $5 - 8$  μm wide, separated by septum  $2 - 9$  μm from food cell (basal cell). Conidiophore axis usually ends in terminal vesicle (Fig. 9D-E), sometimes in elongated, infertile hypha (Fig. 9F) and less frequently in terminal swollen cell

 $10 - 18$  μm long x  $7 - 9$  μm wide (Fig. 9G). Conidiophore branches, usually short and sometimes as long as conidiophore axis,  $16 - 138 \mu m$  long, alternated or opposite, usually at right angles and sometimes slightly curved up or down, and with one to two branching levels. Conidiophores with swollen cells from two to four branches only on swollen cell,  $28 - 35$ μm long, mostly curved up and less frequently at right angles (Fig. 9G). Stipes on branches 9 – 38 μm long, separated by septum 2 – 6 μm from conidiophore axis. *Vesicles* in various shapes (globose, sub-globose, capitate, obovoid, prolate, spatulate, clavate [predominant-Fig. 9H], cymbiform, and cylindric),  $9 - 27 \mu m$  long x  $7 - 20 \mu m$  wide, separated from conidiophore axis or branch axis by stipe 10 – 30 μm long with two to six septa. *Phialides* formed on vesicles (Fig. 9H-I), total length  $5 - 8 \mu m$ , lageniform with elongated base (0.5 – 1.5 μm long x  $0.5 - 1$  μm wide) followed by swollen section  $(1.5 - 2.5 \mu m \log x 1 - 3 \mu m$ wide) and thin neck (1.5 – 4 μm long x 0.5 μm wide). *Conidia* formed in chains on phialides, ellipsoidal to oblong  $(1.5 \mu m - 2.5 \mu m)$  long x 0.5  $\mu m - 1.5 \mu m$  wide), brown, with smooth and slightly thickened walls (Fig. 9J).

Notes: *E. clavata* is phylogenetically close to *E. multiformis*. Unlike strains of *E. multiformis*, which grows at 10, 20, 25 and 30 °C, *E. clavata* grows only at 20 and 25 °C. Conidiophores of *E. clavata* are usually larger and more branched than those of *E. multiformis*. *E. clavata* and *E. multiformis* are the only species in the genus that form conidiophores with swollen cells, though these structures are less frequent and shorter in *E. clavata* than in *E. multiformis*.

*Escovopsis lentecrescens* H.C. Evans and J.O. Augustin, PloS ONE 8 (12): e82265, 5 (2013). *Fig. 10*

### MycoBank: MB800441

*Etymology*: Based on the markedly slow growth rate *in vitro* compared to all other described species.

*Typification*: BRAZIL. Minas Gerais: Viçosa, Mata do Paraíso, 700 m, Apr 2010, J.O. Augustin & H.C. Evans, isolated from fungal garden of *Acromyrmex subterraneus subterraneus* (holotype IMI 501179; isotype DOA628-VIC 31755, CBS 135750).

*Sequences*: ITS (JQ815079), *tef*1 (JQ855714), LSU (JQ855717), *rpb*1 (MT305415), and *rpb*2 (MT305540).

*Colonies* growing at 20, and 25 °C on CMD, PDA, and MEA. At 20 °C, growth starts on third day on all media. After four days at 20  $^{\circ}$ C, radial growth of colonies reaches  $0 - 0.2$ cm on CMD, and  $0 - 0.1$  cm on both MEA and PDA. At 25 °C, growth starts on the second day on all three media. After four days at 25 °C, radial growth of colonies reaches  $0.2 - 0.3$ cm,  $0.2 - 0.5$  cm, and  $0.2 - 0.3$  cm on CMD, MEA and PDA, respectively. No growth is observed at 10 and 30 °C. After seven days at 25 °C on CMD, colonies with diffuse aerial mycelia spread by stolons, and pinkish to pale-brown conidia (Fig. 10C). On MEA, colonies form circular shape, with dense cottony aerial mycelia, and white to beige conidia (Fig. 20B). On PDA, colonies form circular shape, with dense cottony aerial mycelia, and white to darkbrown conidia (white on edge and pale to dark-brown in center - Fig. 10A). Conidia are more abundant on PDA than on CMD and MEA. Stolons are rare. Pustule-like formations and soluble pigments are not observed.

*Conidiophores* mono and poly-vesiculate (1-10 vesicles), hyaline, with irregular shape, smooth-walled and arising alternated or opposite from aerial mycelia (Fig. 10D-E). Mono-vesiculate conidiophores reach  $36 - 150$  um, and poly-vesiculate ones  $57 - 200$  µm, in length. Conidiophore stipes  $28 - 49$  μm long x  $5 - 7$  μm wide, separated by septum  $2 - 6$ μm from food cell (basal cell). Conidiophore branches, 20 – 80 μm long, alternated at more or less right angles, and from one to three levels. The second branching level is usually much longer than other branching levels. Stipes on branches  $7 - 31$  µm long, separated by septum up to 9 μm from conidiophore axis. *Vesicles* in various shapes (globose [predominant], subglobose, spathulate, oblanceolate and cylindric - Fig. 10D-H),  $14 - 27 \mu m$  long x  $13 - 27 \mu m$ wide, usually separated from the conidiophore axis or branch axis by stipe  $10 - 94 \mu m$  long with one to six septa. *Phialides* formed on vesicles (Fig. 10F-I), total length  $6 - 8.5 \mu m$ , ampulliform, with truncated pyramid shape base  $(0.5-1 \mu m \log x 1 - 1.5 \mu m \text{ wide})$  followed by swollen section  $(4 - 5 \mu m \log x 2.5 - 3 \mu m \text{ wide})$  and long thin neck  $(2 - 3 \mu m \log x$ 0.5 – 0.6 μm wide). *Conidia* formed in chains on phialides, globose to oblong (2 – 3.5 μm long  $x \approx 1.5 - 2 \mu m$  wide), brown, with smooth and slightly thickened walls (Fig. 10J). *Chlamydospores* intercalary, hyaline, 9.5 – 23 μm long x 8.5 – 16 μm wide (Fig. 10K).

Notes: *E*. *lentecrescens* is phylogenetically close to *E. aspergilloides*. *E*. *lentecrescens*  grows slower than *E. aspergilloides* and the other known species in the genus. The feature that differenciates *E*. *lentecrescens* from *E. aspergilloides* is the brown colour of its colonies in comparison to the pale-yellow to yellowish-brown colonies of *E. aspergilloides*. *Escovopsis moelleri* H.C. Evans and J.O. Augustin, PloS ONE 8 (12): e82265, 5 (2013). Fig. 11.

### MycoBank: MB800440

*Etymology*: Named in honour of A.F.W. Möller, who pioneered work on fungal gardens of ants and provided the first illustrations of *Escovopsis*.

*Typification*: BRAZIL. Minas Gerais: Viçosa, Mata do Paraíso, 700 m, Apr 2010, J.O. Augustin & H.C. Evans, isolated from fungal garden of *Acromyrmex subterraneus molestans* Forel (holotype IMI 501176; isotype DOA626-VIC 31753, CBS 135748).

Sequences: ITS (JQ815077), tef1 (JQ855712), LSU (JQ855715), *rpb*1 (MT305413), and *rpb*2 (MT305538).

*Colonies* growing at 10, 20, and 25 °C on CMD, PDA and MEA. After fourth days at 10 °C on all three media, growth inconspicuous and only on inoculum. At 20 °C, growth starts between first and second day on all three media. After four days at 20 °C, radial growth of colonies reaches  $2.3 - 3.8$  cm,  $3.5 - 4$  cm and  $3.1 - 4$  cm on CMD, MEA and PDA, respectively. At 25 °C, growth starts on the first day, and reaches the plate edge between the third and fourth day on all three media. No growth is observed at 30 °C. After seven days at 25 °C on CMD, colonies form thin aerial mycelia spread by stolon and submerged mycelia, and beige to pale-brown conidia (Fig. 11C). On MEA, colonies form short aerial mycelia, mostly spread by submerged mycelia, and white to beige conidia (Fig. 21B). On PDA, form cottony aerial mycelia, spread predominantly by submerged mycelia and less by stolons, and form beige to brown conidia (brown conidia on plate edge - Fig. 11A). Pustule-like formations and soluble pigments are not observed.

*Conidiophores* mono and poly-vesiculate (2 – 9 vesicles), hyaline, usually pyramidal and less frequent with irregular shape, smooth-walled, and arising mostly alternated and less frequent opposite from aerial mycelium (Fig. 11D-E). Mono-vesiculate conidiophores are rare and reach  $34 - 54$  µm, and poly-vesiculate ones reach  $70 - 236$  µm, in length. Monovesiculate conidiophores stipes with only one septum  $(2 – 23 \mu m \log x 6 – 10 \mu m \text{ wide})$  or up to five septa (up to 144  $\mu$ m long), separated by septum  $2 - 7 \mu$ m from food cell (basal cell). Poly-vesiculate conidiophores stipes  $8 - 52 \mu m$  long x  $6 - 10 \mu m$  wide, separated by septum  $2 - 5$  μm from the basal cell. Conidiophore branches  $30 - 89$  μm long, mostly alternated and less opposite, at more or less right angles and slightly curved up, and from one to two levels. Stipes on branches  $2 - 20 \mu m$  long, separated by septum  $2 - 8.5 \mu m$  from conidiophore axis. *Vesicles* in various shapes (Subulate, oblanceolate, and clavate - Fig. 11F-H),  $22 - 60$  μm long x  $5 - 10$  μm wide, mostly non-septate and rarely with one septum (clavate-septate), separated from conidiophore axis or branch axis by stipe  $1.5 - 17 \mu m$  long with one to three septa. *Phialides* formed on vesicles (Fig. 11I), total length  $5 - 7 \mu m$ , ampulliform, with short and wide base  $(1.7 – 3 \mu m \log x 0.5 – 1 \mu m \text{ wide})$ , followed by swollen section  $(4.4 - 5.6 \,\mu m \log x \, 3.6 - 4.8 \,\mu m \,\text{wide})$  and short thin neck  $(1 - 1.7 \,\mu m \log x \, 3.6 - 4.8 \,\mu m \,\text{wide})$  $x \lt 1 - 2 \mu m$  wide). *Conidia* formed on phialides, mostly solitary and less in short chains, oblong-ornamented  $(6 - 7 \mu m \log x 3.0 - 3.8 \mu m \text{ wide})$ , brown, with ornamentation and thickened walls (Fig. 11J).

Notes: *E. moelleri* is phylogenetically close to *E. weberi*. *E. moelleri* grows slower than *E. weberi*. Unlike strains of its sister clade, *E. moelleri* forms mainly clavate vesicles. However, the most remarkable feature that differentiates *E. moelleri* from all known *Escovopsis* species is the ornamented conidia formed in short chains.

*Escovopsis multiformis* Q.V. Montoya, M.J.S. Martiarena, D.A. Polezel, S. Kakazu and A. Rodrigues, Mycokeys 46: 106 (2019). Fig. 12.

Mycobank: MB828329

*Etymology*: "*multiformis*" in relation to the different vesicle shapes found in the same isolate.

*Typification*: BRAZIL. Santa Catarina, Florianópolis, GPS: 27°28'11.28''S; 48°22'39.48''W, elev. 119 m, Fungus garden of *Apterostigma* sp, 08, 2015. *A. Rodrigues*. Holotype: CBS H-23846 (dried culture on PDA). Ex-type strain LESF 847 (= CBS 145327).

*Sequences*: ITS (MH715091), *tef*1 (MH724265) and LSU (MH715105), *rpb*1 (MT305420), and *rpb*2 (MT305545).

*Colonies* growing at 10 °C on PDA and MEA, and at 20, 25 and 30 °C on CMD, PDA and MEA. After four days at 10 °C, inconspicuous growth only on inoculum, on both PDA and MEA. At 20 °C, growth starts on second day on CMD and on third day on MEA and PDA. After four days at 20 °C, radial growth of colonies reaches  $0.4 - 1$  cm,  $0.3 - 0.6$  cm, and  $0.2 - 0.5$  cm on CMD, MEA and PDA, respectively. At 25  $^{\circ}$ C, growth starts on second day on all media. After four days at 25 °C, radial growth of colonies reaches  $0.6 - 1$  cm on CMD, and  $0.4 - 0.7$  cm on MEA and PDA. At 30 °C, growth starts on second day on CMD and on third day on MEA and PDA. After four days, at 30 °C, radial growth of colonies reaches  $0.4 - 0.7$  cm,  $0 - 0.3$  cm and  $0 - 0.2$  cm on CMD, MEA and PDA, respectively. After seven days at 25 °C on CMD, colonies exhibit submerged mycelia forming a dense circular

zone, diffuse aerial mycelia spread by stolons, and beige to pale-brown conidia (Fig. 12C). On MEA, mycelia form dense, cottony colonies with beige exudates and white to beige conidia (Fig. 12B). On PDA, colonies exhibit cottony raised growth, with white to brown conidia (white on edge and brown in center - Fig. 12A). Stolons are rare on MEA and PDA. Pustule-like formations on CMD at 20, 25, and 30 °C. Soluble pigments are not observed.

*Conidiophores* mono and poly-vesiculate (2 – 9 vesicles), hyaline, usually with irregular shape, smooth-walled, and arising alternated or opposite from aerial mycelia (Fig. 12D-G). Mono-vesiculate conidiophores reach  $66 - 136$  µm, and poly-vesiculate ones  $82 -$ 293 μm, in length. Conidiophore stipes  $16 - 56$  μm long x  $7 - 9$  μm wide, with one to three septa, separated by septum  $1 - 2$  μm from food cell (basal cell). Conidiophore axis usually ends in terminal vesicle, and sometimes in terminal swollen cell  $16 - 34 \mu m \log x$  9 – 20 μm wide (Fig. 12G). Conidiophore branches, usually short and sometimes as long as conidiophore axis,  $32 - 84$  µm long, alternated, usually at right angles and sometimes slightly curved up, and from one to three branching levels. Conidiophores with swollen cells from two to six branches only on swollen cell,  $28 - 35$  µm long, mostly curved up and less frequently at right angles (Fig. 12G). Each swollen cell branch usually ends in one vesicle, but sometimes it forms another swollen cell with two to four new branches. Stipes on branches 22 – 70 μm long, separated by septum 1 – 2 μm from conidiophore axis. *Vesicles* in various shapes (globose, sub-globose [predominant], capitate, obovoid, prolate, spatulate, cymbiform, and cylindric),  $12 - 27 \mu m \log x$  9 – 17  $\mu m$  wide, separated from conidiophore axis or branch axis by stipe 22 – 70 μm long with one to four septa. *Phialides* formed on vesicles (Fig. 12H-I), total length  $6 - 10 \mu m$ , lageniform with elongated base  $(1 - 2.5 \mu m x)$  $0.5 - 1 \,\mu\text{m}$ ), followed by swollen section  $(2.5 - 4.5 \,\mu\text{m} \times 2 - 3.5 \,\mu\text{m})$  and thin neck  $(1 - 4.5 \,\mu\text{m} \times 2)$ 

μm x  $0.5 - 1$  μm). *Conidia* formed in chains on phialides, globose to oblong  $(2.5 - 3.5 \mu m)$ long  $x \times 1.5 - 2.5 \mu m$  wide), brown, with smooth and slightly thickened walls (Fig. 12J).

Notes: *E. multiformis* is phylogenetically close to *E. clavata*. Unlike strains of *E. clavata,* which grows only at 20 and 25 °C, *E. multiformis* can grow at 10, 20, 25, and 30 °C. Conidiophores of *E. multiformis* are usually shorter and less branched than those of *E. clavata*. *E. multiformis* and *E. clavata* are the only species in the genus that form conidiophores with swollen cells, though these structures are more frequent and larger in *E. multiformis* than in *E. clavata*.

*Sympodiorosea* Q.V. Montoya and A. Rodrigues, gen. *nov*. MycoBank: MB 835147. Fig. 13

*Etymology*: "*Sympodio*" refers to the sympodial conidiogenous cells, and "*rosea*" to the colony colour.

*Colonies* form inconspicuous mycelia at 10 and 30 °C, and floccose, white, palebeige, pink, and brown aerial mycelia at 20 and 25 °C. *Conidiophores* formed on aerial mycelia, alternated or opposite, usually at right angles, and with irregular branching conformation. Sympodial conidiogenous cells solitary, in pairs or in verticils at conidiophore and branch apices, and solitary, alternated and opposite, at both conidiophore and branch axes. *Conidia* solitary, globose to sub-globose, smooth or rough (thick-walled), light-brown to dark-brown and with denticles or lesions (like holes). Chlamydospores are common.

*Habitat:* isolated from fungus gardens of *Mycetophylax morchi* (Hymenoptera: Formicidae: tribe Attini).

Notes: *Sympodiorosea* is phylogenetically placed within Hypocreaceae near *Luteomyces* and *Escovopsis*. *Sympodiorosea* presents slower growth and different colony colour (pink) than *Luteomyces* (yellow) and *Escovopsis* (brown). The main feature of this genus is the presence of conidiophores with sympodial conidiogenous cells that differentiate it from all known Hypocreaceae.

*Sympodiorosea kreiselii* (Meirelles, Montoya, Solomon and Rodrigues) Montoya et al. Journal. XX: XX. 2020, comb. nov. Fig. 14.

MycoBank: MB 835148.

*Etymology*: "*kreiselii*" in honour of Hanns Kreisel, who first described the *Phialocladus* currently known as *Escovopsis* (Meirelles et al. 2015a).

*Typification*: BRAZIL. Santa Catarina, Florianópolis, Praia da Joaquina, GPS: 27°37' 50.01'' S; 48° 27' 3.64'' W, elev. 1 m, Fungus garden of *Mycetophylax morchi*, 03, 2009. A. Rodrigues. Ex-type strain LESF53 (= CBS 139320, = CBMAI 1691). Holotype: CBS H-22062 (dried culture on PDA).

*Basionym*: *Escovopsis kreiselii* L.A. Meirelles, Q.V. Montoya, S.E. Solomon and A. Rodrigues, PLoS One. 10: 1–14, 2015.

*Sequences*: ITS (KJ808767), *tef*1 (KJ 808766), LSU (HJ808765), *rpb*1 (MT305418), and *rpb*2 (MT305543).

*Colonies* growing at 10, 20, 25 and 30 °C on CMD, PDA and MEA. After seven days at 10  $\degree$ C, inconspicuous growth, and sometimes no growth is observed. At 20  $\degree$ C, growth starts on fourth day on all media. After seven days at 20 °C, radial growth of colonies reaches  $0.7 - 1.5$  cm,  $0.4 - 0.8$  cm, and  $1 - 1.5$  cm on CMD, MEA and PDA, respectively. At 25 °C, growth starts on second day on all media. After seven days at 25 °C, radial growth of colonies reaches  $1 - 1.5$  cm,  $0.9 - 1.5$  cm, and  $1.2 - 1.6$  cm on CMD, MEA and PDA, respectively. At 30 ºC, growth only on CMD, starting on second day. After seven days at 30 °C, radial growth of colonies reaches 0.8 cm. After 14 days at 25 °C, colonies floccose, and pale-beige to -pink, on CMD (Fig. 14C); cottony, beige to pinkish-brown in centre and white to light yellow on edge, and eventually forming concentric rings on MEA (Fig. 14B); and floccose, light-pink to pinkish-brown in center and white to light-pink on edge, usually forming concentric rings on PDA (Fig. 14A). Pustule-like, stolons, and soluble pigments are not observed.

*Conidiophores* 29 – 229 μm long, hyaline, with irregular shape, smooth-walled, alternated or opposite, at more or less right angles (Fig. 24D-F). Conidiophore stipes  $6 - 40$ μm long x  $3.5 - 5.5$  μm wide, separated by septum  $0.5 - 2$  μm from the food cell (basal cell). Conidiophore branches  $14 - 40$  µm long, solitary, opposite (two branches) or in verticils (three to four branches), at more or less right angles, and from one to three levels. Stipes on branches  $6 - 14$  µm long, separated by septum  $1.5 - 2.5$  µm from conidiophore axis. Second level branches always formed by stipe (similar to the supporting cells in *Trichoderma*) and conidiogenous cells on apex (Fig. 14D). *Sympodial* conidiogenous cells 5.3–13.4 μm long x 2.5–3.5 μm wide, formed at conidiophore apex or at axis and apex from branches (Fig. 14F), hyaline, ampulliform to lageniform, solitary or in verticils (up to 6 cells), and with numerous

denticles (Fig. 14G). *Conidia* globose to sub-globose  $(2.4 - 3.2 \mu m \log x 2 - 2.7 \mu m \text{ wide})$ , solitary (Fig. 14G), light-brown to dark-brown, smooth or rough surface, thick-walled, and with one denticle (coming from conidiogenous cell) or one hole (when denticle remains on conidiogenous cell) (Fig. 14I). *Chlamydospores* globose to sub-globose  $(3 - 3.5 \mu m)$  long x  $2.5 - 3$  µm wide), hyaline, and with smooth walls (Fig. 14H).

*Luteomyces* Q.V. Montoya and A. Rodrigues, gen. nov. MycoBank: MB 835150. Fig. 15 *Etymology:* "*Luteomyces*" in relation to the colour exhibited by the colonies of the strains that make up the genus.

*Colonies* form surface mycelia at 10 and 30 °C; and floccose, white, beige and yellow aerial mycelia at 20 and 25 ºC. Stolons, and beige to yellow soluble pigments are exhibit at all temperatures. *Conidiophores* formed on aerial mycelia, alternated, usually arising at right angles, smooth-walled, and pyramidal shape. *Synchronous* conidiogenous cells on apex and axis from conidiophore and branches, solitary, ampulliform to lageniform. *Conidia* solitary, dry, ornamented, and yellow to light-brown. *Chlamydospores* abundant, hyaline, and smooth.

*Habitat:* Isolated from fungus gardens of *Mycocepurus goeldii* (Hymenoptera: Formicidae: tribe Attini).

Notes: *Luteomyces* is phylogenetically placed within Hypocreaceae as a sister clade of *Escovopsis* (Fig. 2, 2G). *Luteomyces* grows more slowly and has different colony colour (mainly yellow) than *Escovopsis* (mainly brown). The main feature of this genus is the presence of conidiophores with synchronous conidiogenous cells that differentiate it from its sister clade and all other known Hypocreaceae.

*Luteomyces trichodermoides* (Cabello, Masiulionis, Seifert, Rodrigues and Pagnocca) Montoya et al. Journal. XX: XX. 2020, comb. nov. Fig. 16.

MycoBank: MB 835152.

*Etymology*: "*trichodermoides*" referring to the branching pattern, which resembles that of *Trichoderma* spp.

*Typification*: Brazil. Rio Claro, Sao Paulo, isolated from the upper part of a fungus garden of *M. goeldii* (Hymenoptera: Formicidae: tribe Attini). Isolation number VEM001, ex-type CBS 137343 and CBMAI 1620 and LPSC 1176.

*Basionym*: *Escovopsis trichodermoides* Cabello, Masiulionis, Seifert, Rodrigues and Pagnocca, Antonie van Leeuwenhoek, Int J Gen Mol Microbiol. 107: 731–740, 2015.

*Sequences*: ITS (KJ485699), *tef*1 (KF033128), LSU (MF116052), *rpb*1 (MT305417), and *rpb*2 (MT305542).

*Colonies* can grow at 10, 20, 25 and 30 °C on CMD, PDA and MEA. After seven days at 10 °C, inconspicuous growth, only on inoculum. At 20 ºC, growth starts on third day on all media. After seven days at 20 °C, radial growth of colonies reaches  $0.3 - 1.1$  cm,  $0.3$  $-0.5$  cm, and  $0.5 - 1.1$  cm on CMD, MEA and PDA, respectively. At 25 °C, growth starts on second day on all media. After seven days at 25 °C, radial growth of colonies reaches 2.1  $-4$  cm, 2.9 – 4 cm, and 2.7 – 4 cm on CMD, MEA and PDA, respectively. At 30 °C, growth starts on second day on all media and reaches the plate edge between the fifth and sixth day on PDA and MEA. After seven days at 30  $^{\circ}$ C, radial growth of colonies reaches 1.3 – 3.3 cm on CMD. After fourteen days at 25 °C, colonies floccose, and white to beige, on CMD (Fig.

16C); dense cottony, white to pale-yellow in center and yellow on the edge, and forming concentric rings and diffuse yellow pigment on MEA (Fig. 16B); and floccose, yellow, with stolons and diffuse yellow pigment on PDA.

*Conidiophores* 16 – 300 μm long, hyaline, with pyramidal or irregular shape, smoothwalled, alternated or opposite and at right angles (Fig. 16D-E). Conidiophore stipes measuring  $5 - 10$  μm long x  $2 - 3$  μm wide, separated by septum  $2 - 3$  μm from the food cell (basal cell). Conidiophore branches, 7 – 56 μm long, alternated, at right angles**,** longer at the base and shorter towards the apex, and from one to four levels. Stipes on branches  $2 - 7 \mu m$ long x  $1.5 - 2$  μm wide, separated by septum  $1.5 - 2$  μm from conidiophore axis. *Synchronous* conidiogenous cells  $10 - 20 \mu m$  long x  $7 - 8.5 \mu m$  wide, formed at apex and axis from conidiophore and branches (Fig. 16F), hyaline, ampulliform to lageniform. *Conidia* globose to sub-globose  $(2.5 - 3.5 \mu m \log x 2 - 3 \mu m \text{ wide})$ , formed on conidiogenous cells and directly from conidiophore and branch axes (Fig. 16E-F), solitary, yellow to yellowishbrown, and with verrucose cell wall (Fig. 16H). *Chlamydospores* globose to sub-globose  $(11.5 - 18 \,\mu m)$  long and  $10 - 18 \,\mu m$  wide), hyaline, and with smooth walls (Fig. 16G).

### **Taxonomic key to species of** *Escovopsis***,** *Luteomyces***, and** *Sympodiorosea*

Morphological characters described at each node of the dichotomous cladogram clearly distinguish the six *Escovopsis* species in just seven steps (Fig. S3). Interestingly, topologies of the phylogenetic tree of the genus based on DNA sequence markers (Fig. 4A, B) and the cladogram performed based on morphological features (Fig. S3) are congruent.





# **Discussion**

Here, we provide a starting point for the systematics of *Escovopsis* and related genera using a standardized taxonomic framework, a set of morphological characters, and comprehensive multilocus phylogenetic analyses. Our results supported the separation of species previously treated as *Escovopsis* into three distinct genera. Accordingly, we redefine and restrict *Escovopsis* to vesiculate species, and we describe *Sympodiorosea* to accommodate *E. kreiselii* and *Luteomyces* to accomodate *E. trichodermoides*. This study provides a long-awaited revision of *Escovopsis* systematics and related genera, thus helping future researchers to assess the diversity and evolutionary history of these fungus-growing ant associates.

Genera of Hypocreaceae have morphological features that differentiate them from each other (Jaklitsch and Samuels 2011; Põldmaa 2011). Due to the morphological plasticity of fungi (Slepecky and Starmer 2009; Wrzosek et al. 2017), variations in the shades of colours expressed by these organisms are highly expected. Nonetheless, the prevalent brown colour of *Escovopsis* colonies is a unique feature of this genus within the family. Curiously, other genera in the same family also exhibit unique colours, as is the case for the genus *Trichoderma,* which is characterized by its mostly green colonies (Jaklitsch 2009), and *Escovopsioides,* which is characterized by its white colour (Augusting et al. 2013). Colours exhibited by *Sympodiorosea* (pink) and *Luteomyces* (yellow) are also unique within Hypocreaceae. Interestingly, the separation of these clades by the colour patterns was previously observed by other authors (Gerardo et al. 2006b; Meirelles et al. 2015b), but the lack of a deep morphological analysis prevented reaching the conclusion that they were different genera.

Microscopic features also differentiate *Escovopsis* from other genera in the Hypocreaceae. Conidiophores with terminal-vesicles producing phialides, present in *Escovopsis*, are a unique feature for this family. *Escovopsioides* also presents vesicles, however they are formed intercalated on aerial mycelia and solitary on the apex of the conidiophores. Furthermore, the vesicles of this genus are smaller and have fewer phialides than those of *Escovopsis* (Augustin et al. 2013). On the other hand, *Sympodiorosea* and *Luteomyces* are the only groups within Hypocreaceae that present sympodial and synchronous conidiogenous cells, respectively. Interestingly, only a distant group of entomopathogenic fungi, as is the case of *Beauveria* (Hypocreales, Cordicipetaceae), has sympodial conidiogenesis (Rehner et al. 2011), and there are no other groups of fungi within the Hypocreales that form synchronous conidiogenous cells. Future studies will hopefully shed light on the evolutionary pressures that led *Escovopsis*, *Sympodiorosea*, and *Luteomyces* to form these unique microscopic characters.

The consideration of all fungi producing brown conidia in the attine ant's colonies as *Escovopsis* (without taxonomic and phylogenetic analyses) made of *Escovopsis* a paraphyletic clade (Fig. 1, S2). Lack of a comprehensive phylogenetic analysis has precluded resolving the phylogenetic uncertainties of *Escovopsis* (Montoya et al. 2019). In light of our results, we considered two hypotheses to disentangle the phylogenetic disagreements of this group of fungi: First, *Escovopsis*, *Luteomyces*, and *Sympodiorosea* belong to the same genus. In this case, *Escovopsioides* (sister clade of *Luteomyces*, Fig. 3A, F) and *Hypomyces* (sister clade of *Sympodiorosea*, Fig. 3 C, D) would have to belong to the same genus to enforce monophyly (Baun and Smith, 2013). Nonetheless, both *Escovopsioides* and *Hypomyces* are well supported, separate monophyletic clades (Fig. 2,2) and present unique morphological characters that differentiate them from other Hypocreaceae. *Escovopsioides*, for instance, is the only Hypocreaceae that forms one type of conidia on phialides and another direct from aerial mycelia (without conidiogenous cells). In contrast, *Hypomyces* forms septate conidia and sexual structures, which is not observed in *Escovopsis*, *Luteomyces*, *Sympodiorosea* or *Escovopsioides*. Second, *Escovopsis*, *Luteomyces*, and *Sympodiorosea* represent taxa within different genera. In this case, considering that the same genes, in different genera, follow different evolutionary paths (Gompel and Prud'homme 2009), the variation of the phylogenetic position of the three clades (Fig. 3) could be better explained if they were diffent genera. Most important, regardless of the molecular markers used in this study, each clade preserves its monophyly within Hypocreaceae. In light of this evidence, and the unique derived morphological characters expressed by *Escovopsis*, *Luteomyces*, and *Sympodiorosea* (Fig. 4-7), we propose the second hypothesis as the most parsimonious. Future research, using genome-based phylogenetic methods, may resolve the relationship of these genera to each other.

The circumscription of *Escovopsis* raises important questions for the genus. How diverse is *Escovopsis*? What is its host range? How is the genus phylogeographically distributed? And, what is its role in attine gardens? For many years, *Escovopsis* was considered a diverse group of fungi (Gerardo et al. 2006a,b; Rodrigues et al. 2008, 2011; Caldera et al. 2009; Pagnocca et al. 2012; Yek et al. 2012; Meirelles et al. 2015a,b). However, that assumption was based on considering *Sympodiorosea*, *Luteomyces* and other clades (Fig. 1, and S2) within *Escovopsis*. Currently, *E. weberi*, *E. aspergilloides*, *E. clavata*, *E. lentecrescens*, *E. microspora* (synonym of *E. weberi*), *E. moelleri*, and *E. multiformis* are the only species described under standardized taxonomical conditions. The species introduced by Marfetán et al. (2019) also belong to *Escovopsis* (Fig. S1), nonetheless, the taxonomy and phylogeny of these species are still unclear. Therefore, future studies should consider that both the genetic diversity and the number of known species of the genus were overestimated. Likewise, future studies will unveil the geographical distribution of *Escovopsis* and its phylogenetic correspondence with the ants, and the mutualistic fungi. Finally, several studies suggested that *Escovopsis* is a mycoparasite (Currie et al. 1999a, 2003; Currie 2001; Gerardo et al. 2004; Little and Currie 2007; de Man et al. 2016). However, the parasitic mechanisms of *Escovopsis* species are poorly understood, and this hypothesis was also raised considering *Sympodiorosea* and *Luteomyces* within the same genus. Therefore, the mechanisms of the parasitism of *Escovopsis* should be carefully addressed.

Similar questions as those raised for *Escovopsis* must be addressed in future studies for *Sympodiorosea*, *Luteomyces* and the other clades (Fig.1, and S2). The genetic and morphological diversity, as well as the geographical distribution of both genera, are still a mystery. Some authors suggested that *Sympodiorosea* and *Luteomyces* are more likely to be associated with the colonies of lower attine ants than higher attine (e.g., leaf-cutting) ants (Gerardo et al. 2006b), but more evidence is necessary to confirm this hypothesis. Recent studies have shown that some strains of *Sympodiorosea* behave as antagonists of the mutualistic fungus of *Mycetophylax morschi* being able to kill it under laboratory conditions (Custodio and Rodrigues 2019). However, the mechanisms by which it manages to kill the cultivars are completely unknown. On the other hand, Bizarria et al. (2020) demonstrated that *Luteomyces* had little negative impact on the mutualistic fungus of *Mycocepurus goeldii*, being just able to inhibit the fungus cultivars *in-vitro* and unable to overcome defenses of the ant colonies. The ecology and lifestyle of the other clades previously treated as *Escovopsis* (Fig. 1, and S2) is a completely mistery. Therefore, the assumption of a parasitic lifestyle for these groups of fungi should be reconsidered and examined carefully.

Since Alfred Möller (1893) observed the "fungi of the strong conidial form" within the fungus gardens of fungus-growing ants, several groups of fungi that share the same niche were classified as *Escovopsis*. Many taxonomic and phylogenetic incongruities have been reported in the last two decades, and the lack of taxonomic studies for this genus have hampered scientists to recognize the root of the problem. After a detailed systematic study, we conclude that taxonomic disagreements in the *Escovopsis* genus were caused due to the inclusion of two groups of fungi that belong to different genera (*Luteomyces* and *Sympodiorosea*) within the same genus. This discovery not only solves the taxonomic and phylogenetic disagreements of the genus but significantly expands our understanding of the systematics of *Escovopsis*, and related genera, and provides a stable foundation from which to build future research on the evolutionary history, taxonomic diversity, and ecological roles of these unique fungi.

# **Declarations**

## **Ethics approval and consent to participate**

Not applicable

# **Adherence to national and international regulations**

Not applicable

## **Consent for publication**

### Not applicable

### **Availability of data and material**

The data set used in this study will available in the NCBI-GenBank (Table S1, S2, and S3). The alignments used to perform the phylogenetic trees will be deposited in Treebase as soon as the reviewers' comments were addressed and the final trees were generated.

### **Competing interests**

The authors declare that they have no competing interests.

# **Authors' contributions**

QVM and AR designed the study. QVM carried out the morphological and phylogenetic analyses. QVM, MJSM, RBJ carried out *in vitro* growth experiments. QVM, AR, MSJM and NMG wrote the manuscript. All authors read and approved the final manuscript.

# **Acknowledgments**

We are grateful to Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) for financial support (grants # 2014/24298-1, # 2017/12689-4 and #2019/03746-0) of AR and for scholarships (# 2016/04955-3 and # 2018/07931-3) to QVM. We are also grateful to the National Science Foundation for financial support of NMG (NSF DEB-1754595 and DEB-1927161). AR also thanks Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq for a fellowship (grant # 305269/2018-6). Likewise, we would like to thank the Laboratory of Fungal Ecology and Systematics (LESF - São Paulo State University, Rio Claro, SP, Brazil) and Gerardo Laboratory (Emory University, Atlanta, USA) research teams, especially Dr. Aileen Berasategui Lopez, Dr. Caitlin Conn, Dr. Pepijn Kooij and MSc. Mariana Barcoto, for valuable comments on this manuscript. In addition, we are grateful to the anonymous reviewers and the editor, Marco Bonete, for providing constructive comments on this study.

# **References**

- Augustin JO, Groenewald JZ, Nascimento RJ, et al (2013) Yet more "weeds" in the garden: Fungal novelties from nests of leaf-cutting ants. PLoS One 8:. doi: 10.1371/journal.pone.0082265
- Birnbaum SSL, Gerardo NM (2016) Patterns of Specificity of the Pathogen *Escovopsis* across the Fungus-Growing Ant Symbiosis. Am Nat 188:52–65. doi: 10.1086/686911
- Bizarria R, Nagamoto NS, Rodrigues A (2020) Lack of fungal cultivar fidelity and low virulence of *Escovopsis trichodermoides*. Fungal Ecol 45:100944. doi: 10.1016/j.funeco.2020.100944
- Caldera EJ, Poulsen M, Suen G, Currie CR (2009) Insect Symbioses: A Case Study of Past, Present, and Future Fungus-growing Ant Research\*. Environ Entomol 38:78–92. doi: http://dx.doi.org/10.1603/022.038.0110
- Currie CR (2003) Ancient Tripartite Coevolution in the Attine Ant-Microbe Symbiosis. Science (80- ) 299:386–388. doi: 10.1126/science.1078155
- Currie CR (2001) Prevalence and impact of a virulent parasite on a tripartite mutualism. Oecologia 128:99–106. doi: 10.1007/s004420100630
- Currie CR, Mueller UG, Malloch D (1999a) The agricultural pathology of ant fungus gardens. Proc Natl Acad Sci U S A 96:7998–8002. doi: 10.1073/pnas.96.14.7998
- Currie CR, Scott J a., Summerbell RC, Malloch D (1999b) Fungus-growing ants use antibioticproducing bacteria to control garden parasites. Nature 398:701–704. doi: 10.1038/nature01563
- Currie CR, Wong B, Stuart AE, et al (2003) Ancient Tripartite Coevolution in the Attine Ant-Microbe Symbiosis. Science (80- ) 299:386–388. doi: 10.1126/science.1078155
- Custodio BC, Rodrigues A (2019) *Escovopsis kreiselii* specialization to its native hosts in the fungiculture of the lower attine ant *Mycetophylax morschi*. Antonie van Leeuwenhoek, Int J Gen Mol Microbiol 112:305–317. doi: 10.1007/s10482-018-1158-x
- Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: more models, new heuristics and parallel computing. Nat Methods 9:772–772. doi: 10.1038/nmeth.2109
- de Man TJB, Stajich JE, Kubicek CP, et al (2016) Small genome of the fungus *Escovopsis weberi* , a specialized disease agent of ant agriculture. Proc Natl Acad Sci 113:3567–3572. doi:
10.1073/pnas.1518501113

- Elizondo Wallace DE, Vargas Asensio JG, Pinto Tomás AA (2014) Correlation between virulence and genetic structure of *Escovopsis* strains from leaf-cutting ant colonies in Costa Rica. Microbiol (United Kingdom) 160:1727–1736. doi: 10.1099/mic.0.073593-0
- Folgarait P, Gorosito N, Poulsen M, Currie CR (2011) Preliminary in vitro insights into the use of natural fungal pathogens of leaf-cutting ants as biocontrol agents. Curr Microbiol 63:250–258. doi: 10.1007/s00284-011-9944-y
- Gerardo NM, Jacobs SR, Currie CR, Mueller UG (2006a) Ancient host-pathogen associations maintained by specificity of chemotaxis and antibiosis. PLoS Biol 4:1358–1363. doi: 10.1371/journal.pbio.0040235
- Gerardo NM, Mueller UG, Currie CR (2006b) Complex host-pathogen coevolution in the Apterostigma fungus-growing ant-microbe symbiosis. BMC Evol Biol 6:88. doi: 10.1186/1471-2148-6-88
- Gerardo NM, Mueller UG, Price SL, Currie CR (2004) Exploiting a mutualism: parasite specialization on cultivars within the fungus-growing ant symbiosis. Proc R Soc B Biol Sci 271:1791–1798. doi: 10.1098/rspb.2004.2792
- Gompel N, Prud'homme B (2009) The causes of repeated genetic evolution. Dev Biol 332:36–47. doi: 10.1016/j.ydbio.2009.04.040
- Hall (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser 41:
- Hawksworth DL, Lücking R (2017) Fungal Diversity Revisited : 2 . 2 to 3 . 8 Million Species. Microbiol Spectr 1:1–17. doi: 10.1128/microbiolspec.FUNK-0052-2016.Correspondence
- Heine D, Holmes NA, Worsley SF, et al (2018) Chemical warfare between leafcutter ant symbionts and a co-evolved pathogen. Nat Commun 9:2208:1–11. doi: 10.1038/s41467-018-04520-1
- Jaklitsch WM (2009) European species of Hypocrea Part I. The green-spored species. Stud Mycol 63:1–91. doi: 10.3114/sim.2009.63.01
- Jaklitsch WM, Samuels GJ (2011) Europe PMC Funders Group Reconsideration of *Protocrea* ( Hypocreales , Hypocreaceae ). 100:962–984
- Katoh K, Standley DM (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Mol Biol Evol 30:772–780. doi: 10.1093/molbev/mst010
- Kearse M, Moir R, Wilson A, et al (2012) Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647– 1649. doi: 10.1093/bioinformatics/bts199
- Komarek A, Beutel R (2006) Problems in taxonomy and suggestions for a standardized description of new insect taxa. Entomol Probl 36:55
- Kreisel H (1972) Pilze aus Pilzgärten von Atta insularis in Kuba. Z Allg Mikrobiol 12:643–654. doi: 10.1002/jobm.19720120805
- Little AEF, Currie CR (2007) Symbiotic complexity: discovery of a fifth symbiont in the attine ant– microbe symbiosis. Biol Lett 3:501–504. doi: 10.1098/rsbl.2007.0253
- Marfetán JA, Romero AI, Cafaro MJ, Folgarait PJ (2018) Five new *Escovopsis* species from Argentina. Mycotaxon 133:569–589. doi: 10.5248/133.569
- Marfetán JA, Romero AI, Folgarait PJ (2015) Pathogenic interaction between *Escovopsis weberi* and *Leucoagaricus* sp.: Mechanisms involved and virulence levels. Fungal Ecol 17:52–61. doi: 10.1016/j.funeco.2015.04.002
- Masiulionis VE, Cabello MN, Seifert KA, et al (2015) *Escovopsis trichodermoides* sp. nov., isolated from a nest of the lower attine ant *Mycocepurus goeldii*. Antonie van Leeuwenhoek, Int J Gen Mol Microbiol 107:731–740. doi: 10.1007/s10482-014-0367-1
- Meirelles LA, Montoya QV, Solomon SE, Rodrigues A (2015a) New light on the systematics of fungi associated with attine ant gardens and the description of *Escovopsis kreiselii* sp. nov. PLoS One 10:. doi: 10.1371/journal.pone.0112067
- Meirelles LA, Solomon SE, Bacci M, et al (2015b) Shared *Escovopsis* parasites between leafcutting and non-leaf-cutting ants in the higher attine fungus-growing ant symbiosis. R Soc Open Sci 2:. doi: 10.1098/rsos.150257
- Moller A As hortas de fungos de algumas formigas sul-Americanas, 1st edn. Rio de Janeiro, Brasil
- Möller EM, Bahnweg G, Sandermann H, Geiger HH (1992) A simple and efficient protocol for isolation of high molecular weight DNA from filamentous fungi, fruit bodies, and infected plant tissues. Nucleic Acids Res 20:6115–6
- Montoya QV, Martiarena MJS, Polezel DA, et al (2019) More pieces to a huge puzzle: Two new *Escovopsis* species from fungus gardens of attine ants. MycoKeys 46:97–118. doi: 10.3897/mycokeys.46.30951
- Muchovej, J.J.; Della Lucia TC (1990) *Escovopsis*. A new genus from leaf-cutting ants nests to replace Phailocladus nomem invalidum
- Mueller GM, Paul ÆJ (2007) Fungal biodiversity : what do we know ? What can we predict ? Biodivers Conserv 16:1–5. doi: 10.1007/s10531-006-9117-7

Nixon KC (2002) WinClada ver. 1.0000. Publ by author, Ithaca, New York, USA

Pagnocca FC, Masiulionis VE, Rodrigues A (2012) Specialized fungal parasites and opportunistic

fungi in gardens of attine ants. Psyche (Stuttg) 2012:. doi: 10.1155/2012/905109

Pavlinov IY (2018) Foundations of Biological Systematics : History and Theory

- Põldmaa K (2011) Tropical species of *Cladobotryum* and *Hypomyces* producing red pigments. Stud Mycol 68:1–34. doi: 10.3114/sim.2011.68.01
- Rehner SA, Minnis AM, Sung GH, et al (2011) Phylogeny and systematics of the anamorphic, entomopathogenic genus *Beauveria*. Mycologia 103:1055–1073. doi: 10.3852/10-302
- Rodrigues A, Bacci M, Mueller UG, et al (2008) Microfungal "weeds" in the leafcutter ant symbiosis. Microb Ecol 56:604–614. doi: 10.1007/s00248-008-9380-0
- Rodrigues A, Mueller UG, Ishak HD, et al (2011) Ecology of microfungal communities in gardens of fungus-growing ants (Hymenoptera: Formicidae): A year-long survey of three species of attine ants in Central Texas. FEMS Microbiol Ecol 78:244–255. doi: 10.1111/j.1574- 6941.2011.01152.x
- Ronquist F, Teslenko M, van der Mark P, et al (2012) MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. Syst Biol 61:539– 542. doi: 10.1093/sysbio/sys029
- Seifert KA, Samson RA, Chapela IH, et al (1995) *Escovopsis aspergilloides* , a Rediscovered Hyphomycete from Leaf-Cutting Ant Nests. Mycological Society of America 87:407–413
- Slepecky RA, Starmer WT (2009) Phenotypic plasticity in fungi: a review with observations on *Aureobasidium pullulans*. Mycologia 101:823–832. doi: 10.3852/08-197
- Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30:1312–1313. doi: 10.1093/bioinformatics/btu033
- Sung GH, Poinar GO, Spatafora JW (2008) The oldest fossil evidence of animal parasitism by fungi supports a Cretaceous diversification of fungal-arthropod symbioses. Mol Phylogenet Evol 49:495–502. doi: 10.1016/j.ympev.2008.08.028
- Taerum SJ, Cafaro MJ, Little AE., et al (2007) Low host-pathogen specificity in the leaf-cutting ant-microbe symbiosis. Proc R Soc B Biol Sci 274:1971–1978. doi: 10.1098/rspb.2007.0431
- Therneau TM, Atkinson EJ (2019) An Introduction to Recursive Partitioning Using the RPART Routines. Mayo Clin Sect Biostat Tech Rep 61:33
- Williams G (2011) Decision Trees. Data Mining with Rattle and R: The Art of Excavating Data for Knowledge Discovery Use R. 205–244. doi: 10.1007/978-1-4419-98
- Wrzosek M, Ruszkiewicz-Michalska M, Sikora K, et al (2017) The plasticity of fungal interactions. Mycol Prog 16:101–108. doi: 10.1007/s11557-016-1257-x

Yek SH, Boomsma JJ, Poulsen M (2012) Towards a better understanding of the evolution of specialized parasites of fungus-growing ant crops. Psyche (Stuttg) 2012:. doi: 10.1155/2012/239392

### Fig. 1.

Colapsed phylogenetic tree (see the whole tree in Fig. S2) based on Bayesian Inference of the *tef*1, indicating the placement of all strains previously named as *Escovopsis*. The tree gathers all available *tef*1 sequences found in the literature with the data set used in this study (including the sequences of the nine *Escovopsis* ex-type strains evaluated here). The tree contains a total of 415 sequences which include: 281vesiculate-*Escovopsis* (Clade A), 70 non-vesiculate *Escovopsis* (Clades B, C, D, E) and 63 strains from five Hypocreaceae genera (*Escovopsioides*, *Hypomyces*, *Protocrea*, *Sphaerostilbella*, *Trichoderma*). *Lecanicillium antillanum* CBS 35085 is the outgroup of the tree. There is no information on literature about the morphological feature of the clades C and D.



#### Fig. 2.

Phylogenetic tree, based on Bayesian Inference, indicating the placement of *Escovopsis* (brown branches), *Sympodiorosea* (pink branches) and *Luteomyces* (yellow branches) within Hypocreales. Highlighted clades in different colours represent six different Hypocreales families (Clavicipitaceae, Cordycipietaceae, Hypocreaceae, Nectriaceae, and Ophiocordycipitaceae). The analysis was based on concatenated sequences of LSU, *tef*1, *rpb*1 and *rpb*2. The final alignment of 3305 characters consisted of sequences from 145 strains. Numbers on branches indicate BI posterior probabilities and ML bootstrap support values. The *Stachybotrys* clade (dark green) was used to root the tree. ET indicates ex-type isolates.



Fig. 3.

Phylogenetic placement of *Escovopsis*, *Sympodiorosea* and *Luteomyces* within *Hypocreaceae*. Phylogenies were inferred using BI analysis and are separated for each molecular marker: (A) ITS, B) LSU, C) *tef*1, D) *rpb*1, and E) *rpb*2). The remaining two trees are based on concatenated datasets of (F) all five markers, and (G) four of the five markers (LSU, *rpb*1, *rpb*2, and *tef*1). Numbers on branches indicate BI posterior probabilities and ML bootstrap support values. *Lecanicillium antillanum* CBS35085 was used as the outgroup. ET indicates ex-type isolates.



Fig. 4.

Phylogenetic placement of *Escovopsis* species. Phylogenies were inferred using BI analysis: A) Collapsed tree obtained from a combined dataset of LSU, *rpb*1, *rpb*2, and *tef*1 markers. B) Concatenated tree obtained combining ITS, LSU, *rpb*1, *rpb*2, and *tef*1. C) Conidiophores of each extype species. The numbers on branches indicate the BI posterior probabilities and ML bootstrap support. ET indicates ex-type isolates.



## Fig. 5.

Colony morphology of the seven *Escovopsis* type species (*Escovopsis senso stricto*), *E. trichodermoides* (*Luteomyces trichodermoides*) and *E. kreiselii* (*Sympodiorosea kreiselii*). All cultures were evaluated at 25 °C in the dark, after seven days for *Escovopsis* and 15 days for *L. trichodermoides* and *S. kreiselii*.



Fig. 6.

Illustration of the microscopic structures of the genus *Escovopsis*. A-B: Mono-vesiculate conidiophores. C-H: Poly-vesiculate conidiophores. F: Conidiophore with "swollen cell". I-U: Different shapes of vesicles (I: Globose, J: Sub-globose, K: Capitate, L: Obovoid, M: Prolate, N: Spatulate, O: Clavate, P: Cymbiform, Q: Oblanceolate, R: Subulate, S: Cylindric, T: Filiform, U: Clavate-septate, V: Cylindric-septate). W-Z: Different shapes of the phialides. Different shapes of conidia (a: Globose, b: Sub-globose, c: Ellipsoidal, d: Oblong, e: Oblong-ornamented).



Fig. 7. Morphological characters of *Escovopsis weberi*. A-C: Cultures on PDA, MEA and CMD, respectively, after 7 days of growth at 25 °C. D: Mono-vesiculate conidiophores on aerial mycelium. E. Poly-vesiculate conidiophores. F: Septate-cylindric vesicle. G: Cylindric vesicle. H: Clavate vesicle. I: Phialides. J: Conidia.



Morphological characters of *Escovopsis aspergilloides*. A-C: Cultures on PDA, MEA and CMD, respectively, after 7 days of growth at 25 °C. D. Mono-vesiculate conidiophore. E-F: Poly-vesiculate conidiophores. G: Globose vesicle with phialides. H: Phialides. I: Conidia. J: Chlamydospore.



Morphological characters of *Escovopsis clavata*. A-C: Cultures on PDA, MEA and CMD, respectively, after 7 days of growth at 25 °C. D: Mono-vesiculate conidiophores. E. Poly-vesiculate conidiophore. F: Conidiophore with infertile hypha at the apex. G: conidiophore with swollen cell. H: Clavate vesicle with phialides. I: Phialides. J: Conidia.



Fig 10.





Morphological characters of *Escovopsis moelleri*. A-C: Cultures on PDA, MEA and CMD, respectively, after 7 days of growth at 25 °C. D: Mono-vesiculate conidiophore. E: Poly-vesiculate conidiophore. F: Subulate vesicle. G: Oblanceolate vesicle. H: Clavate vesicle. I: Phialides with conidia. J: Ornamented conidia.



Morphological characters of *Escovopsis multiformis*. A-C: Cultures on PDA, MEA and CMD, respectively, after 7 days of growth at 25 °C. D: Mono-vesiculate conidiophore. E-F: Poly-vesiculate conidiophores. G. Conidiophores with swollen cell. H: Clavate vesicle with phialides. I: Phialides. J: Conidia.



Fig. 13.

Illustration of the microscopic structures of the genus *Sympodiorosea*. A: Conidiophore pattern on aerial mycelium. B. Conidiophore shape. C-H: Shapes of the sympodial conidiogenous cells. I: Conidia with denticle (coming from the conidiogenous cell), J: Conidia with a hole (when the denticle remains on the conidiogenous cell). K: Chlamydospores in chain.





Morphological characters of *Sympodiorosea kreiselii*. A-C: Cultures on PDA, MEA and CMD, respectively, after 7 days of growth at 25 °C. D-F. Conidiophores. G: Sympodial conidiogenous cell with conidia. H: Chlamydospores. I: Conidia.



Illustration of the microscopic structures of the genus *Luteomyces*. A: Conidiophore pattern on aerial mycelium. B. Conidiophore shape. C-F: Shapes of the syncronous conidiogenous cells. G: Conidia with ornamentation. H: Smooth conidia. I: Chlamydospores.



# Fig. 16.

Morphological characters of *Luteomyces trichodermoides*. A-C: Cultures on PDA, MEA, and CMD, respectively, after 7 days of growth at 25 °C. D-E. Conidiophores. F: Conidiogenous cells. G: Chlamydospores. H: Conidia.



# **Supporting information**

#### Fig. S1.

Phylogenetic placement of *Escovopsis* species described in Marfetán et al. (2019). The phylogenetic tree was reconstructed in order to include the 24 LSU sequences (in the green box on the tree) generated in Marfetán et al. (2019). The tree was reconstructed using Maximum Likelihood (ML) in RAxML v.8 (Stamatakis 2014) and Bayesian Inference (BI) in MrBayes v.3.2.2 (Ronquist et al. 2012) using the GTR model. For ML analyses, 1000 independent trees and 1000 bootstrap replicates were generated; one million generations of the Markov Chain Monte Carlo (MCMC) were enough to reach convergence. The numbers on branches indicate the BI posterior probabilities and ML bootstrap support*. Lecanicillium antillanum* CBS35085 was used as the outgroup. The five described species formed two clades (green box) within *Escovopsis* and close to *E*. *aspergilloides* and *E*. *lentecrescens*. *E*. *atlas*, *E*. *catenulate*. *E*. *longivesica*, *E*. *pseudoweberi*, were placed into the same clade. Some strains identified as *E*. *weberi* are in the same clade. The four strains of *E*. *primorosea* formed a monophyletic clade.



### Fig. S2

Extended phylogenetic tree, based on Bayesian Inference of the *tef*1, indicating the placement of all strains previously named as *Escovopsis*. The tree gathers all available *tef*1 sequences found in the literature with the data set used in this study (including the sequences of the nine *Escovopsis* ex-type strains evaluated here). The tree contains a total of 415 sequences which include: 281vesiculate-*Escovopsis* (Clade A), 70 non-vesiculate *Escovopsis* (Clades B, C, D, E) and 63 strains from five Hypocreaceae genera (*Escovopsioides*, *Hypomyces*, *Protocrea*, *Sphaerostilbella*, *Trichoderma*). *Lecanicillium antillanum* CBS35085 is the outgroup of the tree. There is no information on literature about the morphological feature of the clades C and D.



Fig. S3.

Cladogram and dichotomous key to identify *Escovopsis* species. A) Cladogram performed using a recursive partitioning algorithm in R 3.6.3 "rpart" library. The nodes numbered in red correspond to the steps (morphological features) needed to identify the species. B) dichotomous key reconstructed following the steps (nodes in red) of the cladogram.



<b>Previous</b> fungal species name	<b>Current fungal</b> species name	<b>Strain ID</b>	<b>Specimen</b> voucher	City, State, Country	Habitat	<b>GenBank</b> accession numbers tef1	<b>References</b>
Cladobotryum	Cladobotryum	<b>CBS</b>	---	---	---	FN868712	Poldmaa, K. (2011)
asterophorum	asterophorum	676.77					
Cladobotrvum cubitense	Cladobotrvum cubitense	<b>CBS</b> 416.85	$---$	---	---	FN868713	Poldmaa, K. (2011)
Cladobotrvum	Cladobotrvum	<b>CBS</b>	$---$			FN868716	Poldmaa, K. (2011)
heterosporum	heterosporum	719.88					
Cladobotryum multiseptatum	Cladobotryum multiseptatum	<b>CBS</b> 472.71	$---$	---	$---$	FN868723	Poldmaa, K. (2011)
Cladobotryum	Cladobotryum	TFC 97-23	$---$	$---$	$- - -$	FN868724	Poldmaa, K. (2011)
paravirescens	paravirescens						
Cladobotrvum penicillatum	Cladobotryum penicillatum	<b>CBS</b> 407.80	$---$	---		FN868725	Poldmaa, K. (2011)
Cladobotrvum protrusum	Cladobotrvum protrusum	<b>CBS</b> 118999	$---$	$---$	$---$	FN868726	Poldmaa, K. (2011)
Cladobotryum purpureum	Cladobotryum purpureum	<b>CBS</b> 154.78	$---$	---	$---$	FN868733	Poldmaa, K. (2011)
Cladobotryum rubrobrunnesce ns	Cladobotryum rubrobrunnesce ns	<b>CBS</b> 176.92				FN868734	Poldmaa, K. (2011)
Cladobotryum sp. KP-2010b	Cladobotryum sp. KP-2010b	<b>TFC</b> 201295	---	---	$- -$	FN868721	Poldmaa, K. (2011)
Cladobotryum tchimbelense	Cladobotryum tchimbelense	<b>TFC</b> 201146	$---$	---	$\overline{a}$	FN868737	Poldmaa, K. (2011)
Cladobotryum tenue	Cladobotryum tenue	G.A. 05/54.K	TFC:05-91	Germany	Russula sp.	HF911717	Poldmaa, K. (2011)
Escovopsioides nivea	Escovopsioides nivea	<b>CBS</b> 135749 <sup>ET</sup>	AUJ6	Viçosa, Minas Gerais, Brazil	Fungus garden of Acromyrmex subterraneus subterraneus	JO855713	Augustin et al. (2013)
Escovopsioides sp.	Escovopsioides nivea	LESF159	J08	Corumbataí, São Paulo, Brazil	Fungus garden of Atta sexdens rubropilosa	MF140949	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	LESF601	J09	Rio Claro - SP, <b>Brazil</b>	Fungus garden of Trachymyrmex sp.	MF140964	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 151</b>	J <sub>02</sub>	Corumbataí, São Paulo, Brazil	Fungus garden of Atta sexdens rubropilosa	MF140948	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 510</b>	J10	Botucatu, São Paulo, Brazil	Fungus garden of Atta sexdens rubropilosa	MF140950	Osti and Rodrigues (2018)

Table S1. Metadata used to know the phylogenetic placement of all strains previously named as *Escovopsis*.














































<b>Previous</b>	<b>Current fungal</b>	<b>Strain ID</b>	Specimen voucher	City, State, Country	<b>GPS</b>	Habitat	<b>GenBank accession numbers</b>					
fungal species name	species name						<b>ITS</b>	<b>LSU</b>	tef1	rpb1	rpb2	<b>References</b>
Escovopsioides nivea	Escovopsioides nivea	<b>CBS</b> 135749ET	AUJ6	Viçosa, Minas Gerais, Brazil	20°44'31.71"S, 42°52'43.83"W	Fungus garden of Acromyrmex subterraneus subterraneus	JO815078	JO855716	JO855713	MT305414#	MT305539#	Augustin et al. (2013)
Escovopsioides sp.	Escovopsioides nivea	LESF159	J08	Corumbataí, São Paulo, Brazil	22° 17' 21.7" S; 47° 39' 22.8" W	Fungus garden of Atta sexdens rubropilosa	MF116014	MF116034	MF140949	MT305444	MT305569	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	LESF601	J09	Rio Claro - SP, <b>Brazil</b>	$---$	Fungus garden of Trachymyrmex sp.	MF116029	MF116049	MF140964	MT305487 <sup>#</sup>	MT305612#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 151</b>	$J_{02}$	Corumbataí, São Paulo, Brazil	22° 17' 21.7" S; 47° 39' 22.8" W	Fungus garden of Atta sexdens rubropilosa	MF116013	MF116033	MF140948	MT305442 <sup>#</sup>	MT305567#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 510</b>	J10	Botucatu, São Paulo, Brazil	22° 54' 28.4" S: 48° 18' 55.7" W	Fungus garden of Atta sexdens rubropilosa	MF116015	MF116035	MF140950	MT305474#	MT305599#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 587</b>	J <sub>01</sub>	Camacan, Bahia, <b>Brazil</b>	15° 23' 18.2" S; 39° 33' 30.5" W	Fungus garden of Atta cephalotes	MF116016	MF116036	MF140951	MT305477#	MT305602#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 588</b>	J03	Camacan, Bahia, <b>Brazil</b>	15° 25′ 32.3″ S 39° 32' 48.1" W	Fungus garden of Atta cephalotes	MF116017	MF116037	MF140952	MT305478#	MT305603#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 589</b>	J05	Camacan, Bahia, <b>Brazil</b>	15° 23' 14.8" S: 39° 33' 28.4" W	Fungus garden of Atta cephalotes	MF116018	MF116038	MF140953	MT305479#	MT305604#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 590</b>	J06	Camacan, Bahia, <b>Brazil</b>	$15^{\circ} 23' 15.2$ " S; 39° 33' 28.0" W	Fungus garden of Atta cephalotes	MF116019	MF116039	MF140954	MT305480#	MT305605#	Osti and Rodrigues (2018)
Escovopsioides	Escovopsioides nivea	<b>LESF 591</b>	J04	Botucatu, São Paulo, Brazil	22° 54' 26.6" S: 48° 18' 29.2" W	Fungus garden of Atta capiguara	MF116020	MF116040	MF140955	MT305481	MT305606#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 592</b>	J12	Camacan, Bahia, <b>Brazil</b>	15° 22′ 50.3″ S: 39° 34′ 03.5" W	Fungus garden of Acromyrmex sp.	MF116021	MF116041	MF140956	MT305482#	MT305607#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 596</b>	J16	Chuvisca - RS, <b>Brazil</b>	30° 50' 10.2" S: 51° 55' 10.4" W	Fungus garden of Acromyrmex sp.	MF116025	MF116045	MF140960	MT305483 <sup>#</sup>	MT305608#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 597</b>	J17	Camacan, Bahia, <b>Brazil</b>	15° 23' 29.7" S: 39° 33' 31.3" W	Fungus garden of Atta cephalotes	MF116026	MF116046	MF140961	MT305484#	MT305609#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 598</b>	J18	Camacan, Bahia, <b>Brazil</b>	15° 23' 17.8" S; 39° 33' 22.3" W	Fungus garden of Atta cephalotes	MF116027	MF116047	MF140962	MT305485#	MT305610#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 599</b>	J19	Sentinela do Sul - RS, Brazil	$\hspace{0.05cm}---\hspace{0.05cm}$	Fungus garden of Acromyrmex heyeri	MF116028	MF116048	MF140963	MT305486 <sup>#</sup>	MT305611#	Osti and Rodrigues (2018)
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 1009</b>	QVM137	Camp 41, Manaus, Amazonas, Brazil	2° 26' 55.3" S: 59° 46' 10.9" W	Fungus garden of Apterostigma sp.	MT273483	MT273572	MT305392	MT305516	MT305641	This study
Escovopsioides sp.	Escovopsioides nivea	<b>LESF 1023</b>	QVM151	Camp 41, Manaus, Amazonas, Brazil	$2^{\circ}$ 26 '52.5" S; 59° 45' 53.4" W	Fungus garden of Trachymyrmex sp.	MT273485	MT273574	MT305394	MT305518	MT305643	This study

Table S2. *Escovopsis* strains used in the phylogenetic analyses and their associated metadata.

















 $E<sup>T</sup>$  Ex-type;  $*$  sequences obtained in this study.

Table S3. Molecular markers, primers and Polymerase Chain Reaction (PCR) conditions.



	<b>Specimen</b>		<b>GeneBank accession number</b>					
<b>Taxon</b>	voucher	Host/substratum	<b>LSU</b>	tef1 rpb1		rpb2		
Aphysiostroma stercorarium	ATCC 62321	on cow dung	AF543792	AF543782	AY489633	EF469103		
Aschersonia badia	<b>BCC 8105</b>	scale insect (Hemiptera)	DO518752	DO522317	DO522363	DO522411		
Aschersonia placenta	<b>BCC 7869</b>	scale insect (Hemiptera)	EF469074	EF469056	EF469085	EF469104		
Balansia henningsiana	GAM 16112	Panicum sp. (Poaceae)	AY545727	AY489610	AY489643	DQ522413		
Balansia pilulaeformis	AEG 94-2	Poaceae	AF543788	DQ522319	DQ522365	DQ522414		
Claviceps paspali	<b>ATCC 13892</b>	Poaceae	U47826	DQ522321	DQ522367	DQ522416		
Claviceps purpurea	GAM 12885	Dactylis glomerata (Poaceae)	AF543789	AF543778	AY489648	DO522417		
Cordyceps bifusispora	<b>EFCC 5690</b>	lepidopteran pupa	EF468806	EF468746	EF468854	EF468909		
Cordyceps cardinalis	<b>OSC 93609</b>	lepidopteran larva	AY184962	DO522325	DQ522370	DQ522422		
Cordyceps kyusyuënsis	<b>EFCC 5886</b>	lepidopteran pupa	EF468813	EF468754	EF468863	EF468917		
Cordyceps militaris	<b>OSC 93623</b>	lepidopteran pupa	AY184966	DQ522332	DQ522377	AY545732		
Cordyceps cf.	<b>ARSEF 5691</b>	Lepidoptera	EF468819	EF468759	EF468867	EF468921		
ochraceostromata								
Cordyceps scarabaeicola	<b>ARSEF 5689</b>	scarabaeid adult (Coleoptera)	AF339524	DO522335	DO522380	DO522431		
Cordyceps cf. takaomontana	NHJ 12623	Lepidoptera	EF468838	EF468778	EF468884	EF468932		
Cordyceps tuberculata	<b>OSC 111002</b>	Lepidoptera	DQ518767	DQ522338	DQ522384	DQ522435		
Cosmospora coccinea	CBS 114050 AR2741	Inonotus nodulosus (Hymenomycetes)	AY489734	AY489629	AY489667	DO522438		
Elaphocordyceps capitata	<b>OSC 71233</b>	Elaphomyces sp. (Euascomycetes)	AY489721	AY489615	AY489649	DO522421		
Elaphocordyceps fracta	<b>OSC 110990</b>	Elaphonyces sp. (Euascomycetes)	DO518759	DO522328	DO522373	DO522425		
Elaphocordyceps japonica	<b>OSC 110991</b>	Elaphomyces sp. (Euascomycetes)	DO518761	DQ522330	DQ522375	DO522428		
Elaphocordyceps longisegmentis	<b>OSC 110992</b>	Elaphomyces sp. (Euascomycetes)	EF468816		EF468864	EF468919		
Elaphocordyceps ophioglossoides	OSC 106405	Elaphomyces sp. (Euascomycetes)	AY489723	AY489618	AY489652	DQ522429		
Elaphocordyceps subsessilis	<b>OSC 71235</b>	scarabaeid larva (Coleoptera)	EF469077	EF469061	EF469090	EF469108		
Engyodontium aranearum	CBS 309.85	spider (Arachnida)	AF339526	DO522341	DO522387	DO522439		
Epichloë typhina	<b>ATCC</b> 56429	Festuca rubra (Poaceae)	U17396	AF543777	AY489653	DO522440		
Haptocillium balanoides	CBS 250.82	nematode	AF339539	DQ522342	DO522388	DO522442		
Haptocillium sinense	CBS 567.95	nematode	AF339545	DQ522343	DQ522389	DQ522443		
Haptocillium zeosporum	CBS 335.80	nematode	AF339540	EF469062	EF469091	EF469109		
Hirsutella sp.	<b>OSC 128575</b>	hemipteran adult	EF469079	EF469064	EF469093	EF469110		
Hydropisphaera erubescens	ATCC 36093	Cordyline banksii (Laxmanniaceae)	AY545726	DQ522344	DQ522390	AY545731		
Hydropisphaera peziza	CBS 102038 GJS 92-101	on bark	AY489730	AY489625	AY489661	DQ522444		
Hypocrea lutea	ATCC 208838	on decorticated conifer wood	AF543791	AF543781	AY489662	DO522446		
Hypocrea rufa	CBS 114374	on bark	AY489726	AY489621	AY489656	EF692510 c		
Hypocrella schizostachyi	<b>BCC 14123</b>	scale insect (Hemiptera)	DQ518771	DQ522346	DQ522392	DO522447		
Hypocrella nectrioides	GJS 89-104	scale insect (Hemiptera)	U47832	DQ522347	DQ522393	DQ522448		
Isaria cf. farinosa	<b>OSC 111004</b>	lepidopteran pupa	EF468840	EF468780	EF468886			
Isaria tenuipes	<b>OSC 111007</b>	lepidopteran pupa	DQ518773	DQ522349	DQ522395	DQ522449		

Table S4. *Hypocreales* strains used in the phylogenetic analyses and their associated metadata.







Table S5. Culture media used in previous studies to evaluate the morphological characters of *Escovopsis* species.

	<b>Morphological characters</b>	E. aspergiloides	E. clavata	E.lentecrescens	E. microspora	E. moelleri	E. multiformis	E. weberi	Luteomyces	Sympodiorosea
$\mathbf{1}$	Colonies growing at 10°C	no	no	no	yes	yes	yes	yes	yes	yes
$\overline{2}$	Colonies growing 30 °C	no	no	no	yes	no	yes	yes	yes	yes
3	Brown colour on Colonies at seven days	yes	yes	yes	yes	yes	yes	yes	no	no
4	Pink colour on Colonies at 14 days	no	no	no	no	no	no	no	no	yes
5	Yellow colour on Colonies at 14 days	no	no	no	no	no	no	no	yes	no
6	Pink to pinkish-Brown colour on Colonies at seven days on MEA and PDA Light-yellow to yellowish-	no	no	no	yes	no	no	yes	no	no
7	brown colour on Colonies at seven days on PDA	yes	no	no	no	no	no	no	no	no
8	<b>Pustules formation</b>	no	no	no	yes	no	yes	yes	no	no
9	Pyramidal and irregular conidiophore	no	no	no	yes	yes	no	yes	yes	no
10	Only irregular conidiophores	yes	yes	yes	no	no	yes	no	no	no
11	Conidiophore with swollen cell	no	yes	no	no	no	yes	no	no	no
12	Conidiophore axis ending in an infertile hypha	no	yes	no	no	no	no	no	no	no
13	Conidiophore branch as long as conidiofore axis	no	yes	no	no	no	yes	no	no	no
14	Vesicle	yes	yes	yes	yes	yes	yes	yes	no	no
15	Vesicle globose	yes	yes	yes	no	no	yes	no	no	no
16	Vesicle capitate	yes	yes	yes	no	no	yes	no	no	no
17	Vesicle obovoid	yes	yes	yes	no	no	yes	no	no	no
18	Vesicle prolate	yes	yes	no	no	no	yes	no	no	no
19	Vesicle spatulate	yes	yes	no	no	no	yes	no	no	no
20	Vesicle clavate	yes	yes	no	yes	yes	yes	yes	no	no
21	Vesicle cymbiform	no	yes	no	yes	yes	yes	yes	no	no
22	Vesicle oblanceolate	no	no	no	yes	yes	no	yes	no	no
23	Vesicle Subulate	no	no	no	yes	yes	no	yes	no	no
24	Vesicle cilindric	no	yes	no	yes	yes	yes	yes	no	no
25	Vesicle filiform	no	no	no	yes	no	no	yes	no	no
26	Vesicle clavate-septate	no	no	no	yes	yes	no	yes	no	no
27	Vesicle cilindric-septate	no	no	no	yes	no	no	yes	no	no
28	Phialide	yes	yes	yes	yes	yes	yes	yes	no	no
29	phialides on aerial mycelia	no	no	no	yes	no	no	ves	no	no

Table S6. Morphological features used to construct the dichotomous key of *Escovopsis*, *Luteomyces*, and *Sympodiorosea* spp.



#### **References**

Augustin JO, Groenewald JZ, Nascimento RJ, Mizubuti ESG, Barreto RW, Elliot SL, Evans HC (2013). Yet more "weeds" in the garden: Fungal novelties from nests of leaf-cutting ants. PLoS One 8: e82265. doi: 10.1371/journal.pone.0082265

Chaverri P, Castlebury LA, Samuels GJ, Geiser DM (2003). Multilocus phylogenetic structure within the *Trichoderma harzianum* / *Hypocrea lixii* complex. Molecular Phylogenetics and Evolution 27: 302–313. doi: 10.1016/S1055-7903(02)00400-1

Currie CR, Wong B, Stuart AE, Schultz TR, Rehner SA, Mueller UG, Sung GH, Spatafora JW, Straus NA (2003). Ancient tripartite coevolution in the attine ant-microbe symbiosis. Science 299: 386–388. doi:10.1126/science.1078155

Haugland RL, Heckman JL (1998). Identification of putative sequence specific PCR primers for detection of the toxigenic fungal species *Stachybotrys chartarum*. Molecular and Cellular Probes 12: 387–396. doi: 10.1006/mcpr.1998.0197

Jaklitsch WM, Põldmaa K, Samuels GJ (2011). Reconsideration of *Protocrea* ( *Hypocreales*, *Hypocreaceae* ). *Mycologia* 100: 962- 984.

Liu YJ, Whelen S, Hall BD (1999). Phylogenetic Relationships Among *Ascomycetes*: Evidence from an RNA Polymerse II Subunit. Molecular Biology and Evolution 16: 1799–1808.

Masiulionis VE, Cabello MN, Seifert KA, Rodrigues A, Pagnocca FC (2015). *Escovopsis trichodermoides sp. nov*., isolated from a Fungus garden of the lower attine ant *Mycocepurus goeldii*. Antonie van Leeuwenhoek 107: 731–40. doi: 10.1007/s10482-014-0367-1 Meirelles LA, Montoya QV, Solomon SE, Rodrigues A (2015a). New light on the systematics of fungi associated with attine ant gardens and the description of *Escovopsis kreiselii* sp. nov. PLoS One 10: e0112067. doi: 10.1371/journal.pone.0112067

Meirelles LA, Solomon SE, Bacci M, Wright AM, Mueller UG, Rodrigues A (2015b). Shared *Escovopsis* parasites between leafcutting and non-leaf-cutting ants in the higher attine fungus-growing ant symbiosis. Royal Society Open Science 2: 150257. doi:10.1098/rsos.150257

Montoya QV, Martiarena MJS, Polezel DA, et al (2019). More pieces to a huge puzzle: Two new Escovopsis species from fungus gardens of attine ants. MycoKeys 46: 97–118. doi: 10.3897/mycokeys.46.30951

Osti JF, Rodrigues A (2018). *Escovopsioides* as a fungal antagonist of the fungus cultivated by leafcutter ants. BMC Microbiology 18: 130. doi:10.1186/s12866-018-1265-x.

Põldmaa K (2011). Tropical species of *Cladobotryum* and *Hypomyces* producing red pigments. Studies in Mycology 68: 1–34. doi: 10.3114/sim.2011.68.01

Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Fungal Barcoding Consortium (2012). Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proceedings of the National Academy of Sciences of The United States of America 109: 6241–6246. doi:10.1073/pnas.1117018109

Spatafora JW, Sung GH, Sung JM, Hywel-Jones NL, White JF Jr (2007). Phylogenetic evidence for an animal pathogen origin of ergot and the grass endophytes. Molecular Ecology 16: 1701–1711. doi: 10.1111/j.1365-294X.2007.03225.x

Taerum SJ, Cafaro MJ, Little AE, Schultz TR, Currie CR (2007). Low host-pathogen specificity in the leaf-cutting ant-microbe symbiosis. Proceedings of the Royal Society B: Biological Sciences 274:1971–1978. doi: 10.1098/rspb.2007.0431

White TJ, Bruns T, Lee SH, Taylor JW (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: PCR protocols: a guide to methods and applications (Innis MA, Gelfand DH, Sninsky JJ, White TJ). Academic Press, London: 315−322. doi: 10.1016/b978-0-12-372180-8.50042-1

# **Chapter III**

### **Digging into the past of a fungus-growing ant guest: origin and evolution of** *Escovopsis*

Quimi Vidaurre Montoya<sup>1,2\*</sup>, Maria Jesus Sutta Martiarena<sup>1,2</sup>, Claudia Solis<sup>3</sup>, Ricardo Kriebel<sup>4</sup>, Nicole Marie Gerardo<sup>5</sup>, Andre Rodrigues<sup>1,2\*</sup>

<sup>1</sup> Department of General and Applied Biology, São Paulo State University (UNESP), Rio Claro, SP, Brazil.

<sup>2</sup> Centre for the Studies of Social Insects, São Paulo State University (UNESP), Rio Claro, SP, Brazil.

<sup>3</sup> Department of Statistics, University of Wisconsin, Madison, Madison, WI, 53706 USA.

<sup>4</sup> Department of Botany, University of Wisconsin-Madison, Madison, WI 53706 USA.

<sup>5</sup> Emory University, Department of Biology, O. Wayne Rollins Research Center, Atlanta, USA.

\* Corresponding author:

Andre Rodrigues (andre.rodrigues@unesp.br)

Universidade Estadual Paulista (UNESP), Departamento de Biologia Geral e Aplicada Avenida 24-A, n. 1515, Bela Vista, Rio Claro, SP, Zip code: 13.506-900 Phone #: 55 19 3526-4364

## **Abstract**

Host-parasite relationships shape the evolution of organisms. Fungi in the genus *Escovopsis* are thought to have co-evolved with fungus-growing ants parasitizing their fungal cultivars. However, the origin of *Escovopsis*, how and when the genus reached attine colonies, and its geographical distribution were never addressed so far. Here we investigate the origin and trait evolution of *Escovopsis* to shed light on the evolutionary history of the genus, its relationship with the attine ants and the adaptations it experienced throughout its lifetime. Our results showed that *Escovopsis*: i) is distributed across America and has originated approximately 56.9 Mya, ii) lived outside attine colonies for almost 20 Mya before gaining access to this environment, iii) co-evolved only with few attine ant genera, and iv) has experienced several trait adaptations likely related to overcome the barriers of the attine colonies and establish within this environment. Hypotheses on the ecology of the *Escovopsis* ancestor, the possible scenarios of how it reached the colonies, its evolution, and its current ecology are also discussed.

**Keywords**: Parasite, Fungus-growing ants, Symbiosis, Evolution, trait evolution

## **Introduction**

Host-parasite relationships are one of the major drivers of the evolution of organisms  $1-5$ . Exploring the origin of host-parasite relationships is a difficult task  $6$ , but it help us to understand the trait adaptations of the organisms involved<sup>7</sup>. *Escovopsis* (Ascomycota: Hypocreales, Hypocreaceae) is a common resident of fungus-growing ant colonies (subfamily Myrmicinae, Attina subtribe, "the attines"), which was suggested to have coevolved with these ants parasitizing their fungal cultivars  $8-14$ . Parasites associated with social insect environments are extremely important to the evolutionary success of these organisms because they affect both the host which they rely on and the colony to which they belong  $15-$ <sup>17</sup>. Therefore, the discovery of a specialized parasite within attine ant colonies  $10,18$  was of great importance for the study of the evolution of these insects. Nonetheless, while it is known that attines originated approximately 65 million years ago  $19-21$ , the origin of *Escovopsis* is still a mystery. Accordingly, the evolutionary history of this genus, when it gained access to attine colonies, and when it adopted a parasitic lifestyle remain poorly understood.

The current *Escovopsis* - attine ant co-evolution hypothesis is based on the assumption that *Escovopsis* parasitizes the fungal cultivars and on the co-cladogenesis patterns between *Escovopsis* and attine ants  $9-13,22,23$ . Nevertheless, besides the unknown origin of *Escovopsis*, taxonomic studies evidenced that the genus is paraphyletic  $24-27$ . Recently, *Escovopsis* was re-assessed using a detailed taxonomic and phylogenetic approach and the evidence showed more than one genus within *Escovopsis* (Montoya et al. 2020 submitted). Accordingly, the same study showed that *Escovopsis* could not be related to the entire Attina subtribe but only with few genera. Notwithstanding, to which attine genera and fungal cultivars *Escovopsis* is related to, is still not fully understood. Although the taxonomy and phylogeny of *Escovopsis* moved forward, other important questions still remain open such as: what is the extent of *Escovopsis* diversity? And how is the genus phylogeographically distributed? To answer those and other similar questions, a large collection of *Escovopsis* from all attine ant genera and from different locations across America is necessary.

Parasites develop different mechanisms to overcome the barriers of their hosts in search for nutrients  $28-31$ . However, hosts are not passive agents but they react to kill or avoid parasites <sup>32</sup>. The reciprocal adaptations of hosts and parasites to the pressures generated by their interactions and the environment promote the evolution of behavioural, physiological, and morphological traits in both organisms  $33-36$ . Attine ant colonies are extremely complex superorganisms which present many barriers to avoid the entrance of alien microorganisms within their fungus gardens<sup>37</sup>. Consequently, it is expected that *Escovopsis* had undergone different trait adaptations during the process of establishment within the colonies, and to cope to the pressures generated by the immune system of the colonies and the mutualistic fungus responses (which are still unexplored $37$ ). Nonetheless, evolutionary adaptations of *Escovopsis* whether behavioural, physiological, or morphological are completely unknown.

In this study, we shed light on the origin and evolutionary history of *Escovopsis*. By assessing a large collection of *Escovopsis* strains from several attine species from many countries across America we determined: i) the origin and the time during the evolutionary process when the genus entered attine ant colonies, ii) its geographical distribution, iii) its phylogenetic correlation with the attine ants and iv) several trait adaptations experienced by

the genus throughout its evolution. Our results are not only answering key-questions on the ecology and evolution of *Escovopsis* but it will allow scientists to better understand the evolutionary history of the attine ants' system.

#### **Results**

#### *Escovopsis* **is not associated to all fungus-growing ants, but only to some genera**

Our results evidence that *Escovopsis* is only associated with higher attine ants *Atta, Acromyrmex, Sericomyrmex*, and *Trachymyrmex*, and with the lower attine genus *Apterostigma* (Fig. 1A-B). There are no exclusive co-cladogenesis patterns between the *Escovopsis* and ant clades (Fig. 1A-B). However, the most derived *Escovopsis* clade (clade I) are more related to the most derived attines clades, the leaf-cutting ant genera *Atta* and *Acromyrmex* (Fig. 1A-B). *Escovopsis moelleri*, *E. lentecrescens*, and *E. aspergilloides* clades (Clade II and III) are more related to *Trachymyrmex* (Fig. 1A-B) and the most basal *Escovopsis* clade (*E*. *multiformis* and *E*. *clavata* - Clade IV) is more related to *Apterostigma* (Fig. 1A-B). Interestingly, the ant genera *Atta, Acromyrmex* and *Trachymyrmex* harbour the greatest diversity of *Escovopsis*. Moreover, while no *Escovopsis* from the most basal clade were found in *Atta* and *Acromyrmex*, some strains isolated from fungus gardens of *Apterostigma* spp. (NGL075, 080, 081, 083 and LESF 878) are placed in the most derived clade of the genus (Fig. 1A-B).

#### *Escovopsis* **is distributed across America**

Our findings revealed that *Escovopsis* is distributed throughout the American continent (Fig. 1B-C). Our results do not evidence a geographic pattern of distribution of the genus, likely influenced by the difference between the attines sampling efforts. For instance,

most of the *Escovopsis* strains where isolated from Panamá and Brazil. However, there are still many countries (Argentina, Paraguay, Uruguay, Bolivia, Chile, Peru, Colombia, Ecuador, Venezuela, Guyana, Surinam, Costa Rica, Nicaragua, Honduras, El Salvador, Guatemala, Belize, Mexico, and United States) from where few samples were obtained or there are no samples at all. This sample gap generates fragmentary information about the phylogeographic distribution of the genus. Despite this, it is important to highlight that samples from a small region in Panama harbours a great diversity of *Escovopsis* placed throughout the genus phylogeny and the most derived *Escovopsis* clade was only found in this country so far. On the other hand, while Brazil also presents a great *Escovopsis* diversity, the genus is spread across the country, in an area much larger than that observed in Panama, but without a specific prevalence. However, these results could be also being influenced by the difference between the attines sampling efforts in both Panama and Brazil. Future studies that fill this gap will shed light on where *Escovopsis* has originated and how was the genus diversification since there.

# *Escovopsis* **originated in the same period as fungus-growing ants but entered their colonies 18 Mya later**

Divergence time analysis revealed that *Escovopsis* originated 56.9 Mya ago (clade 12  $-$  Fig. 2), a one-time close to the origin of the attine ants and the fungus domestication  $2^1$ . *Escovopsis* diversified into four major clades (clades 13, 15, 17, 18 – Fig. 2). The most basal clade (clade 13) originated approximately 39.1 Mya ago, while the most derived clade (clade 18) originated 17.2 Mya ago. These results point that *Escovopsis* had an independent evolutionary history from the attine before these ants introduce it to their colonies at least 18 Mya later of its origin (Fig. 2).
# *Escovopsis* **has experienced different trait adaptations since its arrival to the attine ants' colonies**

Morphometric, growth rate and character state reconstruction analysis in *Escovopsis*  (Fig. 3) revealed that: i) conidiophores of the basal clades in *Escovopsis* usually form terminal swollen cells at the apex (from where the branches are formed – Fig. 3C). However, these structures are absent in the most derived clades (Fig. 3B); ii) vesicles of the conidiophores have been gradually changing from globose to cylindrical as the genus was diversifying, and the most derived clades are losing these structures (Fig. 3A); iii) the number of vesicles per conidiophore has dramatically increased (from 1-2 in the more basal clades to 53 in the more derived once) throughout the genus diversification (Fig. 3L); iv) Despite the modification of the vesicles, the number of phialides per vesicle has remained over the evolution (Fig. 3M); v) the production of phialides on the basal clades of the genus is restricted to the vesicles (Fig. 3F-I), while the most derived strains are also producing them on the aerial mycelia (Fig. 3D-E); vi) the colony growth rate on artificial media has gradually increased as the genus diversified (Fig. 3J-K).

# **Discussion**

This study provides evidence on the evolutionary history of *Escovopsis*, as well as on the association of the genus with fungus-growing ants, its geographical distribution and the trait adaptations it experienced across its existence. Our results supported that *Escovopsis* is widely distributed across America, and while its origin corresponds in time with the origin of the fungus-growing ants, the genus did not co-evolve with all attines, but just with few

genera. Besides, the ancestor of *Escovopsis* lived outside the attine colonies and once it was introduced to this environment it experienced several trait adaptations likely related to overcome the barriers of the ant environment and to thrive within the fungus gardens. These results fill important gaps on the ecology and evolution of *Escovopsis* and give new directions to understand the evolution of the attine ants' system.

Combining the evidence on the origin of *Escovopsis* (Fig. 2), the *Escovopsis*-ant interaction (Fig. 1), the origin of attines<sup>19,21</sup>, and the ants' collecting behaviour<sup>37,38</sup> there are four possible scenarios to explain the evolution of *Escovopsis*, its arrival in the attine ant colonies, and the ecological role of its ancestor. First, the ancestor of *Escovopsis* was living outside the attine colonies at least 18 Mya. This scenario is possible if we consider that: i) *Escovopsis* originated  $\cong$  56.9 Mya ago, its most basal clade has  $\cong$  39.1 Mya, and the most derived clade ≅ 17.2 Mya, ii) *Escovopsis* is only associated to *Atta*, *Acromyrmex, Trachymyrmex*, *Sericomyrmex* and *Apterostigma* (Fig. 1A-B), iii) *Apterostigma* originated approximately 38 Mya ago, *Trachymyrmex* and *Sericomyrmex* 28 Mya ago, and *Atta*, Acromyrmex 18 Mya ago<sup>21</sup>. Therefore, *Escovopsis* might have been living, at least, 18 Mya outside the attine's colonies, and reached this environment at most the last 38 Mya. Thus, *Escovopsis* would have reached first the *Apterostigma* colonies ( $\cong$  38 Mya ago), then the *Trachymyrmex* and *Sericomyrmex* colonies (≅ 28 Mya ago), and last the *Atta* and *Acromyrmex* colonies ( $\cong$  18 Mya ago). Second, the *Escovopsis* ancestor had a saprotrophic lifestyle, living in association with dead plant material, dry seeds, insect frass and carcasses. Thus, the ancestor might have been introduced within the attines' colonies along with the substrate collected by the ants. Three facts support this scenario: i) *Escovopsis* clades related to *Apterostigma*, *Trachymyrmex*, and *Sericomyrmex* originated before the *Escovopsis* clades associated with *Atta* and *Acromyrmex* <sup>21</sup>; ii) The genera *Apterostigma*, *Trachymyrmex*, and *Sericomyrmex* collect dead plant material to feed their mutualists <sup>38</sup>; iii) *Apterostigma* has a preference for collecting insect frass and carcasses. Third, the *Escovopsis* ancestor had an endophytic lifestyle, living mainly in the leaf's mesophyll, and was introduced within the attines' colonies along with the fresh plant material collected by the ants. Three facts support this hypothesis: i) the most derived *Escovopsis* clade (Fig. 2) originated at the same period of time as *Atta*, and  $Acromv$ rmex<sup>21</sup> and it is mostly related to these ant genera (Fig. 1A-B), ii) the most remarkable collecting behaviour that differs *Atta* and *Acromyrmex* to the other attine genera is the preference for fresh plant material to feed their mutualist  $37,38$  and, iii) different from the other attine genera these ants evolved complex and careful behaviours to clean the surface of the collected material, before adding them in the fungus gardens  $37,39$ . Accordingly, it is less likely that fungi that colonize the surface of the collected substrate can reach the gardens of *Atta* and *Acromyrmex*. Meaning that, *Escovopsis* must have been living in the leaf's mesophyll as an endophyte. Fourth, the *Escovopsis* ancestor had symbiotic relationships with other fungi. This scenario could be possible if we consider that attines from the genus *Acromyrmex* can also collect basidiomatas in nature <sup>40</sup>. This behaviour is still not well studied for the other attines; however, future studies should confirm if this scenario is likely.

The current ecological role of *Escovopsis* is of great interest for scientists that study the attine ant-fungal mutualism  $10,13,23,41-46$ . The life-cycle of the genus is a cornerstone to unravel this issue, yet it is completely unknown. However, there are two important pieces of information that can help us to have a glimpse about how this big puzzle looks like. First, although the ants share some *Escovopsis* strains, the most derived clades of *Escovopsis* are more related with *Atta* and *Acromyrmex* (which harbour the greatest diversity of *Escovopsis*),

the most basal clades of *Escovopsis* are more related with *Apterostigma* and the clades in transition of the genus are more related with *Trachymyrmex* (Fig. 1A-B). Second, while *Atta* and *Acromyrmex* (leaf-cutting ants) collect preferentially fresh plant material <sup>38</sup>, and *Sericomyrmex* and *Trachymyrmex* prefer to collect dry plant material, fruits and seeds <sup>38</sup>, the preference for those substrates are not exclusive to none of the groups. Sporadically leafcutting ants also collect dry plant material, fruits and seeds, and *Sericomyrmex* and *Trachymyrmex* can also collect fresh plant material <sup>38</sup>. On the other hand, *Apterostigma* collects preferentially insects' frass, but they can also collect dry plant material, fruits and seeds <sup>38</sup>. Therefore, it is very likely that *Escovopsis* is still entering the colonies together with the material collected by the ants (as saprotrophs or endophytes). Then, once the genus reaches the fungus gardens it would be using its saprotrophic ability to take advantage of nutrients of that environment<sup>47</sup>, competing with other organisms (including the fungal cultivars) and probably using parasitic mechanisms to take advantage of their competitors. Furthermore, considering that *Escovopsis* that forms globose vesicles are mostly associated to *Apterostigma*; those that form sub-globose to clavate vesicles are more related *Trachymyrmex* and *Sericomyrmex*; and those that form cylindric vesicles to filiform (nonvesicles) are mostly associated to *Atta* and *Acromyrmex*; *Escovopsis* strains with globose vesicles could be more related with a saprotrophic lifestyle, while strains that present subglobose - clavate and cylindrical - non-vesicles could present both saprotrophic and endophytic lifestyles.

Fungi in the Hypocreaceae are widely known as mycoparasites, however, only few species in this family present a true parasitic lifestyle <sup>48,49</sup>. Conversely, the vast majority of members in this family are somehow associated with plants, either as endophytes or as

saprotrophs  $50-54$ . Furthermore, parasites in this family are not obligate parasites (like biotrophs), but they can also live as endophytes or saprotrophs  $53-55$ . Because phylogenetic closely related species can exhibit similar traits or behaviours  $^{56}$ , it is expected that some strains in *Escovopsis* could also present a mycoparasitic lifestyle. Indeed, just one strain from one out of 26 clades of *Escovopsis* (Montoya et al. 2020 submitted) was reported as a virulent parasite<sup>9</sup>, and most of the strains of the genus only affect fungal cultivars *in vitro* or in dysfunctional colonies in the laboratory but not in natural conditions.

Parasites develop specialized organs, chemical compounds and other mechanisms to adhere, penetrate and avoid host immune systems  $57-59$ . Our results evidenced that as *Escovopsis* diversified, it lost the swollen cells of their conidiophores, changed the shape of their vesicles, increased the number of the vesicles per conidiophore, start producing phialides on the aerial mycelia and gradually increased its growth rate. By avoiding swollen cells, the fungus was able to produce more branches per conidiophore which in turn increased the number of vesicles per conidiophore. Because phialides (cells responsible for the conidia production) are produced on vesicles, the number of vesicles is directly related to the number conidia produced. Thus, the larger the vesicles, the greater the number of phialides and the greater the amount of conidia produced. If we add the fact that the growth velocity of the species has also increased as the genus derived (Fig.4J-K), then we can conclude that *Escovopsis* is evolving to increase its reproduction efficiency. Considering what was discussed about the ecology of *Escovopsis* it is more likely that the ecosystem of the attine ant colonies is the main factor that influenced trait evolution in *Escovopsis*.

On the other hand, hosts react against parasites by: i) behavioural avoidance  $^{60,61}$ , ii) physical or physiological barriers  $^{62}$ , iii) fighting against within-host development  $^{17,63}$  and iv) adjusting their immune systems  $28,64$ . Nonetheless, the adaptation of both the fungal cultivar and the ecosystem of the attines to avoid or kill *Escovopsis* are completely unknown. Moreover, considering: i) that more than half of the organisms on our planet have a parasitic lifestyle  $17,65$ , ii) the huge diversity of microorganisms introduced by attines into their gardens for tens of millions of years  $^{19}$ , iii) that the presence of different parasites living on the same host at the same time is a fairly common event in nature <sup>66</sup>, and iv) that other Hypocreaceae genera like *Trichoderma* and *Cladobotryum* also have the potential to act as mycoparasites  $49,54,67$ ; then, the possibility that other fungi could be also taking advantage of both the fungal cultivar and the ecosystem of the attines is highly expected. Consequently, trait adaptations of both the mutualistic fungus and the attines' ecosystem (whatever they are) must have arisen in response to the combination of the pressures generated by all these organisms instead of just one of them. Future studies should consider to evaluate the trait evolution of the attines colonies and of their fungal cultivar to understand the parasitic dynamics of this ecosystem.

#### **Material and Methods**

#### **Isolates**

This study amassed a total of 400 colonies from 11 out of 17 attine genera (*Atta, Acromyrmex*, *Apterostigma*, *Cyphomyrmex*, *Myrmecocrypta, Mycetarotes*, *Mycetophylax*, *Mycetoritis*, *Myrmicocrypta*, *Sericomyrmex*, and *Trachymyrmex*). The ants' colonies were collected in six different countries (Argentina, Brazil, Costa Rica, Ecuador, Panama, and United States). A total of 286 *Escovopsis* strains where isolated from these colonies (Table

S1). A total of 64 out of the 286 strains were isolated in this study and the remaining were obtained from the Gerardo Laboratory (Emory University, Atlanta, USA) and the Laboratory of Fungal Ecology and Systematics (LESF - São Paulo State University, Rio Claro, SP, Brazil).

For *Escovopsis* isolation, we followed the methods performed by Montoya et al.  $(2019)^{68}$ . Briefly, seven fungus-garden fragments (varying  $0.5-1$  mm<sup>3</sup>) were inoculated on plates containing potato dextrose agar (PDA, Neogen Culture Media, Neogen®) supplemented with 150  $\mu$ g mL<sup>-1</sup> chloramphenicol (Sigma). Three plates were inoculated per each ant colony. Once *Escovopsis* was isolated from garden fragments, axenic cultures were prepared and stored in sterile distilled water (Castellani 1963) at  $8 - 10$  °C, and in 10% glycerol at -80 °C. All strains were deposited at LESF and at the Microbial Resources Center (CRM-UNESP).

# **DNA extraction, PCR and sequencing**

The genomic DNA of the 286 strains was extracted using a modified CTAB method (Möller et al. 1992). Briefly, fungal aerial mycelia, grown for seven days at 25 °C on PDA, was crushed with the aid of glass beads (Sigma) in lysis solution and incubated at 65 °C for 30 minutes. The organic phase was separated using a solution of chloroform-isoamyl alcohol  $(24:1)$ . Then, the material was centrifuged  $(10,000 \text{ g}$  for 10 minutes), and the supernatant with the genomic DNA was collected. This extract was precipitated with 3M sodium acetate and isopropanol and purified with two successive washes of 70% ethanol. The DNA was suspended in 30 µL of Tris-EDTA solution and stored at -20 °C.

Five molecular markers were amplified for *Escovopsis* strains isolated in this study: the internal transcribed spacer (ITS4 - 5'TCCTCCGCTTATTGATATGC3', ITS5 - 5'GGAAGTAAAAGTCGTAACAAGG3')<sup>69,70</sup>, the large subunit ribosomal RNA (CLA-F -5'GCATATCAATAAGCGGAGGA3', CLA-R - 5'GACTCCTTGGTCCGTGTTTCA3')<sup>10</sup>, the translation elongation factor 1-alpha (EF6–20F 5'AAGAACATGATCACTGGTACCT3', EF6-1000R  $5'CGCATGTCRCGGACGGC3')$ <sup>71</sup>, the RNA polymerase II protein-coding gene *rpb*1 (RPB1-Af, RPB1Ac - 5'GARTGYCCDGGDCAYTTYGG3', RPB1-Cr -  $5'CCNGCDATNTCRTTRTCCATRTA3')<sup>72</sup>$ , and the RNA polymerase II protein-coding gene rpb2 (fRPB2-5F (F) - 5'GA(T/C)GA(T/C)(A/C)G(A/T)GATCA(T/C)TT(T/C)GG-3'),  $fRPB2-7cR$  (R) - 5'CCCAT(A/G)GCTTG(T/C)TT(A/G)CCCAT3')<sup>72</sup>. From the strains obtained from Gerardo Laboratory and LESF we used previously published ITS, LSU and *tef*1 sequences, when available, and generated the missing sequences.

PCR reactions for ITS, LSU and *tef*1 were performed in a final volume of 25  $\mu$ L (4)  $\mu$ L of dNTPs [1.25 mM each]; 5  $\mu$ L of 5X buffer; 1  $\mu$ L of BSA [1 mg mL<sup>-1</sup>]; 2  $\mu$ L of MgCl<sub>2</sub> [25 mM]; 1  $\mu$ L of each primer [10  $\mu$ M]; 0.5  $\mu$ L of Taq polymerase [5 U  $\mu$ L<sup>-1</sup>], 2  $\mu$ L of diluted genomic DNA [1:100] and 8.5 µL of sterile ultrapure water); and in the case of *rpb*1 and *rpb*2, we added 1.5 µL of dimethyl sulfoxide (DMSO) and decreased the volume of sterile ultrapure water to 7.0  $\mu$ L. PCR condition for ITS and LSU was: 96 °C for 3 min, 35 cycles at 94 °C for 1 min, 55 °C for 1 min and a final extension step at 72 °C for 2 min  $10,69,70$ . For *tef*1 the conditions were: 96 °C for 3 min, 35 cycles at 96 °C for 30 s, 61 °C for 45 s and a final extension step at 72 °C for 1 min <sup>42</sup>. For *rpb*1 and *rpb*2 a touchdown PCR was used (96) °C for 5 min; 15 cycles of 94 °C for 30s, 65 °C for 1.5 min for *rpb*1 and for 1 min for *rpb*2 (the annealing temperature gradually decreased 1  $^{\circ}$ C per cycle) and 72  $^{\circ}$ C for 1.5 min for

*rpb*1 and for 1 min for *rpb*2; and then 35 cycles of 94 °C for 30s, 50 °C for 1 min and 72 °C for 1 min (Montoya et al. 2020 submitted).

Final amplicons were purified with the Wizard SV Gel and PCR Clean-up System (Promega) following the manufacturer's protocol. Sequences (forward and reverse) were generated on an ABI3500 (Life Technologies), and the consensus sequences were assembled in BioEdit v. 7.1.3<sup>73</sup> and Geneious<sup>74</sup>. All sequences will be deposited in GenBank (Table S2).

#### **Phylogenetic analysis**

We reconstructed the *Escovopsis* phylogeny to evaluate the *Escovopsis –* ants cocladogenesis and geographic distribution of the genus. A multilocus analysis was carried out for this purpose. The final dataset contained 286 sequences of 3709 bp in length [ITS (587 bp in length), LSU (591 bp), *tef*1 (758 bp), *rpb*1 (607 bp), and *rpb*2 (1045 bp)], and *Sympodiorosea kreiselii* CBS 139320<sup>ET</sup> (Ex-type strain) was used as the outgroup.

Each file was aligned separately in MAFFT (KATOH; STANDLEY, 2013) and the nucleotide substitution model of each alignment was calculated in jModeltest  $2^{75}$ . Then, all files were concatenated using Winclada v.1.00.08<sup>76</sup> and the phylogenetic tree was inferred using a Bayesian approach in MrBayes v. 3.2.1  $^{77}$ . The analysis was carried out with twelve separate runs (each consisting of eleven hot chains and one cold chain) in CIPRES [\(http://www.phylo.org/\)](http://www.phylo.org/). We used GTR+I+G model for ITS, LSU and *tef*1, and GTR for the genes *rpb*1 and *rpb*2. Ten million generations of the Markov Chain Monte Carlo (MCMC) were necessary to reach convergence [standard deviation of split frequencies fell below 0.01]. The first 50% of the generations of MCMC sampling were discarded as burn-in to generate

a consensus tree, and the final tree was edited in FigTree v.1.4 [\(http://tree.bio.ed.ac.uk/software/figtree/\)](http://tree.bio.ed.ac.uk/software/figtree/) and Adobe Illustrator CC v.17.1.

#### **Divergence time analysis**

To estimate the origin of the genus *Escovopsis* we reconstructed a phylogenetic tree combining the sequences of the representative strains of each clade in *Escovopsis* (n=35), *Escovopsioides* (n=10), *Luteomyces* (n=10), and *Sympodiorosea* (n=12) with the sequences of the Hypocreales provided by Sung et al. (2008). Thus, 172 sequences of LSU (594 bp), *tef*1 (776 bp), *rpb*1 (820 bp), and *rpb*2 (998 bp) were aligned separately in MAFFT  $^{78}$  and concatenated in Winclada v.1.00.08<sup>76</sup>. The final phylogenetic tree was inferred using the GTR model (calculated in jModeltest 2)<sup>75</sup> under a Bayesian approach<sup>77</sup>.

Then, we carried out a divergence time analysis based on the calibration of the Hypocreales tree made by Sung et al.  $(2008)^{79}$ . To do so, we uploaded the alignments of LSU, *tef*<sub>1</sub>, *rpb*<sub>1</sub>, and *rpb*<sup>2</sup> separately into BEAUti<sup>74</sup> to create the xml file with the partitions, the clock model and the priors. We use the nodes of the previous inferred tree as priors of monophyletic clades and the calibration of the tree was based on seven nodes previously calibrated by Sung et al.  $(2008)^{79}$  [node 1 (193 Mya), node 2 (176 Mya), node 3 (178 Mya), node 4 (170 Mya), node 5 (173 Mya), node 6 (165Mya) and node 7 (158 Mya)]. The analysis was performed in BEAST 2.5  $80$ . We used the uncorrelated relaxed clock site model  $81$  with a GTR substitution model to accommodate the rate heterogeneity across the branches of the tree. The clock model was the relaxed clock log normal with the priors specifying a Birth Death model processes, with the origin height of 193 (158, 232) Mya. We conducted four independent analyses with an MCMC length of 50.000.000 generations each, with sampling of every  $100<sup>th</sup>$  generation and removing 300.000 of generations as burn in. Finally, 750.000 trees where summarised using TreeAnotator 2.6 in  $BEAST<sup>74</sup>$ , and the final tree was manually edited using FigTree v.1.4 and Adobe Illustrator CC v.17.1.

#### **Morphometric analysis of vesicles**

A total of 22 strains representing all clades of the *Escovopsis* phylogeny were selected to evaluate the morphometry of the vesicles. Therefore, we carried out slide culture preparations to assess these microscopic structures (Montoya et al. 2020 submitted). To achieve this, each strain was inoculated on a  $0.5 \text{ mm}^3$  block piece of PDA medium, covered with a coverslip and incubated at  $25 \text{ °C}$  for 5 days in darkness. Then, the coverslips were removed and placed on slides with a drop of lactophenol. The slides were examined under a light microscope (DM750, Leica, Germany) and the vesicles were photographed using LAS EZ v.4.0 (Leica Application Suite).

The images of each of 22 strains (30 vesicles per strain) were then used to extract vesicles (660 vesicles in total) that were converted into black silhouettes, placed on white backgrounds and saved as jpeg files using GIMP 2.8  $^{82}$ . The outlines were then imported into R as a list of coordinates and four landmarks placed on the widest points of each vesicle (top, bottom and sides), to avoid unexpected twisting of specimens and improve their alignment. We estimated in Momocs that 32 harmonics were more than enough to achieve 99% of harmonic power<sup>83</sup>.

To extract shape information from *Escovopsis* vesicles we used the morphometric technique of Elliptic Fourier analysis (eFa) as implemented in the library Momocs v1.3.2  $^{83}$ for the R statistical environment  $^{84}$ . eFa is widely used by morphologists to quantify variation in shapes from outline data and has been used with all kinds of structures, including leaves  $85$ , fossil bivalves  $86$ , and fish  $87$ . The coefficients were summarized using principal components analysis (PCA) and morphospaces were drawn to visualize and interpret the results.

#### **Ancestral state reconstruction**

To better understand the evolution of vesicle shape in *Escovopsis*, we conducted an ancestral state reconstruction of this structure as a continuous variable. We exported the first principal component from the eFa, calculated a mean value for each strain, matched the strains to the chronogram and used the function contMap of the library phytools v0.7-70  $^{88}$ to reconstruct overall vesicle shape. This approach takes as input the phylogenetic tree and data for each tip and estimates the ancestral states at internal nodes using Maximum Likelihood and then interpolates the states along each edge  $89,90$ .

## **Colony growth rate analysis**

The same strains used in the morphometric and the ancestral state reconstruction analyses were also evaluated for the growth rate variation across the *Escovopsis* phylogeny. We followed the growth method described in Montoya et al. (2020 submitted). Briefly, 200 μL of 10<sup>6</sup> conidia per 1 uL were surface spread on Petri dishes (90 x 15 mm) containing water-agar (WA) and incubated for seven days at  $25 \text{ °C}$  in darkness. Then, we obtained fragments of 0.5 cm diameter of WA with mycelia and inoculated (four replicates to each strain) at the center of Petri dishes (90 x 15 mm) containing cornmeal agar (CMD - Neogen Culture Media) and malt extract agar 2% [MEA - 30 g L-1 of malt extract (Neogen Culture Media), 5 g  $L^{-1}$  of bacteriological peptone (Neogen Culture Media), 20 g  $L^{-1}$  of glucose (Labsynth®), and 15 g  $L^{-1}$  of Agar (Neogen Culture Media)]. This experiment was performed using four replicates of each media and for each strain, in three different weeks. The plates

were incubated at 25 ºC for four days in darkness and then we measured the colonies radius. Statistical analysis was performed in R Studio using one-way ANOVA, followed by Duncan's multiple range test, differences were considered significant when  $P \le 0.05$ .

## **Acknowledgments**

We are grateful to Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) for financial support (grants # 2014/24298-1, # 2017/12689-4 and #2019/03746-0) of AR and for scholarships (# 2016/04955-3 and # 2018/07931-3) to QVM. We are also grateful to the National Science Foundation for financial support of NMG (NSF DEB-1754595 and DEB-1927161). AR also thanks Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq for a fellowship (grant # 305269/2018-6). Likewise, we would like to thank the Laboratory of Fungal Ecology and Systematics (LESF - São Paulo State University, Rio Claro, SP, Brazil) and Gerardo Laboratory (Emory University, Atlanta, USA) research teams, especially Dr. Aileen Berasategui Lopez, and Dr. Caitlin Conn for valuable comments and discussions on this study.

#### **Author Contributions**

QVM, MJSM, NMG and AR designed the study. QVM carried out Phylogenetic Analysis. QVM and MJSM carried out the Growth rate and Microscopic experiments. QVM, CLS, RK carried out the morphometric and Ancestral state reconstruction analysis. QVM, AR, MSJM, NMG and AR wrote the manuscript.

# **References**

- 1. Poulin, R. Evolution of Parasite Life History Traits : Myths and Reality. *Parasitol Today.* **11,** 342-5 (1994).
- 2. Poulin, R., Thomas, F., Renaud, F. & Meeu, T. De. Manipulation of host behaviour by parasites : ecosystem engineering in the intertidal zone ?. *Proc Biol Sci*. **265,** 1091–1096 (1998).
- 3. Thomas, F. *et al.* Parasites and ecosystem what roles could they engineering. *Oikos* **84,** 167–171 (2014).
- 4. Feis, M. E., Goedknegt, M. A., Thieltges, D. W., Buschbaum, C. & Wegner, K. M. Biological invasions and host – parasite coevolution : different coevolutionary trajectories along separate parasite invasion fronts. *Zoology* **119**, 366–374 (2016).
- 5. Papkou, A., Gokhale, C. S., Traulsen, A. & Schulenburg, H. Host parasite coevolution : why changing population size matters. *Zoology* **119**, 330–338 (2016).
- 6. Filipiak, A., Zając, K., Kübler, D. & Kramarz, P. Coevolution of host-parasite associations and methods for studying their cophylogeny. *Invertebr. Surviv. J.* **13**, 56–65 (2016).
- 7. Aleuy, O. A. & Kutz, S. Adaptations , life-history traits and ecological mechanisms of parasites to survive extremes and environmental unpredictability in the face of climate change. *Int. J. Parasitol. Parasites Wildl.* **12**, 308–317 (2020).
- 8. Currie, C. R., Scott, J. a., Summerbell, R. C. & Malloch, D. Fungus-growing ants use antibiotic-producing bacteria to control garden parasites. *Nature* **398**, 701–704 (1999).
- 9. Currie, C. R. Prevalence and impact of a virulent parasite on a tripartite mutualism. *Oecologia* **128**, 99–106 (2001).
- 10. Currie, C. R. Ancient tripartite coevolution in the attine ant-microbe symbiosis. *Science* **299**, 386–388 (2003).
- 11. Reynolds, H. T. & Currie, C. R. Pathogenicity of *Escovopsis weberi*: The parasite of the attine ant-microbe symbiosis directly consumes the ant-cultivated fungus. *Mycologia* **96**, 955–959 (2004).
- 12. Gerardo, N. M., Mueller, U. G., Price, S. L. & Currie, C. R. Exploiting a mutualism: parasite specialization on cultivars within the fungus-growing ant symbiosis. *Proc. Biol. Sci.* **271**, 1791–1798 (2004).
- 13. Gerardo, N. M., Mueller, U. G. & Currie, C. R. Complex host-pathogen coevolution in the *Apterostigma* fungus-growing ant-microbe symbiosis. *BMC Evol. Biol.* **6**, 88 (2006).
- 14. Taerum, S. J., Cafaro, M. J. & Currie, C. R. Presence of multiparasite infections within individual colonies of leaf-cutter ants. *Environ. Entomol.* **39**, 105–113 (2010).
- 15. Boomsma, J. J., Schmid-Hempel, P. & Hughes, W. O. H. Life histories and parasite pressure across the major groups of social insects. *Insect Evol. Ecol.* **211**, 139–175 (2005).
- 16. Schmid-Hempel, P. Parasitism and life history in social insects. *Life Cycles Soc. Insects Behav. Ecol. Evol.* 37–48 (2006).
- 17. Fréderic, T., Jean-François, G. & François, R. *Ecology and evolution of parasitism*. (Oxford University Press, 2009).
- 18. Currie, C. R., Mueller, U. G. & Malloch, D. The agricultural pathology of ant fungus gardens. *Proc. Natl. Acad. Sci. U. S. A.* **96**, 7998–8002 (1999).
- 19. Schultz, T. R. & Brady, S. G. Major evolutionary transitions in ant agriculture. *Proc. Natl. Acad. Sci. U. S. A.* **105**, 5435–5440 (2008).
- 20. Ward, P. S., Brady, S. G., Fisher, B. L., Schultz, T. S. The evolution of myrmicine ants : phylogeny and biogeography of a hyperdiverse ant clade ( Hymenoptera : Formicidae ). *Syst. Entomol*. **40**, 61–81 (2015).
- 21. Branstetter, M. G. *et al.* Dry habitats were crucibles of domestication in the evolution of agriculture in ants. *Proc. Biol. Sci.* **284**, 20170095 (2017).
- 22. Cafaro, M. J. *et al.* Specificity in the symbiotic association between fungus-growing ants and protective *Pseudonocardia* bacteria. *Proc. Biol. Sci.* **278**, 1814–1822 (2011).
- 23. Birnbaum, S. S. L. & Gerardo, N. M. Patterns of specificity of the pathogen *Escovopsis* across the fungus-growing ant symbiosis. *Am. Nat.* **188**, 52–65 (2016).
- 24. Augustin, J. O. *et al.* Yet more 'weeds' in the garden: Fungal novelties from nests of leaf-cutting ants. *PLoS One* **8**, (2013).
- 25. Meirelles, L. A., Montoya, Q. V., Solomon, S. E. & Rodrigues, A. New light on the systematics of fungi associated with attine ant gardens and the description of *Escovopsis kreiselii* sp. nov. *PLoS One* **10**, (2015).
- 26. Meirelles, L. A. *et al.* Shared *Escovopsis* parasites between leaf-cutting and non-leafcutting ants in the higher attine fungus-growing ant symbiosis. *R. Soc. Open Sci.* **2**, (2015).
- 27. Montoya, Q. V., Martiarena, M. J. S., Polezel, D. A., Kakazu, S. & Rodrigues, A. More pieces to a huge puzzle: Two new *Escovopsis* species from fungus gardens of attine ants. *MycoKeys* **46**, (2019).
- 28. Camus, D., Zalis, M. G., Vannier-Santos, M. A. & Banic, D. M. The art of parasite survival. *Braz. J. Med. Biol. Res.* **28**, 399–413 (1995).
- 29. Libersat, F., Kaiser, M. & Emanuel, S. Mind control: How parasites manipulate

cognitive functions in their insect hosts. *Front. Psychol.* **9**, 1–6 (2018).

- 30. Schmid-Hempel, P. Immune defence, parasite evasion strategies and their relevance for 'macroscopic phenomena' such as virulence. *Philos. Trans. R. Soc. B Biol. Sci.* **364**, 85–98 (2009).
- 31. Aleuy, O. A. & Kutz, S. Adaptations, life-history traits and ecological mechanisms of parasites to survive extremes and environmental unpredictability in the face of climate change. *Int. J. Parasitol. Parasites Wildl.* **12**, 308–317 (2020).
- 32. Hughes, D. P., Brodeur, J. & Eric, F. T. *Host manipulation by parasites*. (Oxford University Press, 2015).
- 33. Gandon, S., Agnew, P. & Michalakis, Y. Coevolution between parasite virulence and host life‐history traits. *Am. Soc. Nat.* **160**, 374–388 (2002).
- 34. Arriero, E. & Møller, A. Host ecology and life‐history traits associated with blood parasite species richness in birds. *J. Evol. Biol.* **21**, 1504–13 (2008).
- 35. Martinsen, E. S., Perkins, S. L. & Schall, J. J. A three-genome phylogeny of malaria parasites (Plasmodium and closely related genera): Evolution of life-history traits and host switches. *Mol. Phylogenet. Evol.* **47**, 261–273 (2008).
- 36. Andersen, S. B. *et al.* Disease dynamics in a specialized parasite of ant societies. *PLoS One* **7**, (2012).
- 37. Goes, A. C., Barcoto, M. O., Kooij, P. W. & Bueno, O. C. How do leaf-cutting ants recognize antagonistic microbes in their fungal crops ? **8**, 1–12 (2020).
- 38. De Fine Licht, H. H. & Boomsma, J. J. Forage collection, substrate preparation, and diet composition in fungus‐growing ants. *Ecol. Entomol.* **35**, 259–269 (2010).
- 39. Rocha, S. L. *et al.* Recognition of endophytic *Trichoderma* species by leaf-cutting ants and their potential in a Trojan-horse management strategy. *R. Soc. Open Sci.* **4**,

160628 (2017).

- 40. Masiulionis, V. E., Weber, R. W. S. & Pagnocca, F. C. Foraging of *Psilocybe* basidiocarps by the leaf-cutting ant *Acromyrmex lobicornis* in Santa Fé, Argentina. **2,** 254 (2013).
- 41. Gerardo, N. M., Jacobs, S. R., Currie, C. R. & Mueller, U. G. Ancient host-pathogen associations maintained by specificity of chemotaxis and antibiosis. *PLoS Biol.* **4**, 1358–1363 (2006).
- 42. Taerum, S. J., Cafaro, M. J., Little, A. E. ., Schultz, T. R. & Currie, C. R. Low hostpathogen specificity in the leaf-cutting ant-microbe symbiosis. *Proc. Biol. Sci.* **274**, 1971–1978 (2007).
- 43. Folgarait, P., Gorosito, N., Poulsen, M. & Currie, C. R. Preliminary in vitro insights into the use of natural fungal pathogens of leaf-cutting ants as biocontrol agents. *Curr. Microbiol.* **63**, 250–258 (2011).
- 44. Elizondo Wallace, D. E., Vargas Asensio, J. G. & Pinto Tomás, A. A. Correlation between virulence and genetic structure of *Escovopsis* strains from leaf-cutting ant colonies in Costa Rica. *Microbiol.* **160**, 1727–1736 (2014).
- 45. Marfetán, J. A., Romero, A. I. & Folgarait, P. J. Pathogenic interaction between *Escovopsis weberi* and *Leucoagaricus* sp.: Mechanisms involved and virulence levels. *Fungal Ecol.* **17**, 52–61 (2015).
- 46. Heine, D. *et al.* Chemical warfare between leafcutter ant symbionts and a co-evolved pathogen. *Nat. Commun.* **9:2208**, 1–11 (2018).
- 47. Shik, J. Z, Rytter, W., Arnan, X. & Michelsen, A. Disentangling nutritional pathways linking leafcutter ants and their co‐evolved fungal symbionts using stable isotopes. *Ecology* **99**, 1999–2009 (2018).
- 48. Mukherjee, M. *et al. Trichoderma*-Plant-Pathogen Interactions: Advances in Genetics of Biological Control. *Indian J. Microbiol.* **52**, 522–529 (2012).
- 49. Carrasco, J., Navarro, M. J. & Gea, F. J. Cobweb, a serious pathology in mushroom crops: A review. *Spanish J. Agric. Res.* **15**, (2017).
- 50. Jaklitsch, W. M. European species of Hypocrea Part I. The green-spored species. *Stud. Mycol.* **63**, 1–91 (2009).
- 51. Jaklitsch, W. M. & Samuels, G. J. Europe PMC Funders Group Reconsideration of *Protocrea* ( Hypocreales , Hypocreaceae ). **100**, 962–984 (2011).
- 52. Rossman, A. & Seifert, K. Phylogenetic revision of taxonomic concepts in the Hypocreales and other Ascomycota - A tribute to Gary J . Samuels. *Stud. Mycol.* **68**, 1-256 (2011).
- 53. Põldmaa, K. Tropical species of *Cladobotryum* and *Hypomyces* producing red pigments. *Stud. Mycol.* **68**, 1–34 (2011).
- 54. Chaverri, P. *et al.* Systematics of the *Trichoderma harzianum* species complex and the re-identification of commercial biocontrol strains. *Mycologia* **107**, 558–590 (2015).
- 55. Bailey, B. A. & Melnick, R. L. The endophytic *Trichoderma*. 152–172 (2013).
- 56. Mitchell, E. *et al.* Behavioural traits propagate across generations via segregated iterative-somatic and gametic epigenetic mechanisms. *Nat. Commun.* **7,** 1–16 (2016).
- 57. Szabo, L. J. & Bushnell, W. R. Hidden robbers: The role of fungal haustoria in parasitism of plants. *Proc. Natl. Acad. Sci. U. S. A.* **98**, 7654–7655 (2001).
- 58. Howell, C. R. Mechanisms employed by *Trichoderma* species in the biological control of plant diseases: The history and evolution of current concepts. *Plant Dis.* **87**, 4–10 (2003).
- 59. Shimizu, K. & Aoki, K. Development of parasitic organs of a stem holoparasitic plant in genus *Cuscuta*. *Front. Plant Sci.* **10**, 1–11 (2019).
- 60. Behringer, D. C., Karvonen, A. & Bojko, J. Parasite avoidance behaviours in aquatic environments. *Philos. Trans. R. Soc. B Biol. Sci.* **373**, (2018).
- 61. Sarabian, C., Curtis, V. & McMullan, R. Evolution of pathogen and parasite avoidance behaviours. *Philos. Trans. R. Soc. B Biol. Sci.* **373**, 1–7 (2018).
- 62. Doran, K. S., Banerjee, A., Disson, O. & Lecuit, M. Concepts and mechanisms: Crossing host barriers. *Cold Spring Harb. Perspect. Med.* **3**, 1–20 (2013).
- 63. Sofonea, M. T., Alizon, S. & Michalakis, Y. From within-host interactions to epidemiological competition: A general model for multiple infections. *Philos. Trans. R. Soc. B Biol. Sci.* **370**, (2015).
- 64. Ryu, W.-S. Host immune response. *Mol. Virol. Hum. Pathog. Viruses* 63–82 (2017).
- 65. Meeûs, T. & François, R. Parasites within the new phylogeny of eukaryotes. *Parasites Trends*. **18**, 247–251 (2002).
- 66. Bordes, F. & Morand, S. The impact of multiple infections on wild animal hosts: a review. *Infect. Ecol. Epidemiol.* **1**, 7346 (2011).
- 67. Karlsson, M., Atanasova, L., Jensen, D. F. & Zeilinger, S. Necrotrophic Mycoparasites and Their Genomes. *Microbiol. Spectr.* **5**, (2017).
- 68. Montoya, Q. V., Martiarena, M. J. S., Polezel, D. A., Kakazu, S. & Rodrigues, A. More pieces to a huge puzzle: Two new *Escovopsis* species from fungus gardens of attine ants. *MycoKeys* **46**, 97–118 (2019).
- 69. TJ, W., T, B., SH, L. & JW, T. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: PCR protocols: a guide to methods and applications. (Academic Press, 1990).
- 70. Schoch, C. L. *et al.* Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proc. Natl. Acad. Sci.* **109**, 6241–6246 (2012).
- 71. Meirelles, L. A., Montoya, Q. V., Solomon, S. E. & Rodrigues, A. New light on the systematics of fungi associated with attine ant gardens and the description of *Escovopsis kreiselii* sp. nov. *PLoS One* **10**, 1–14 (2015).
- 72. Liu, Y. J., Whelen, S. & Hall, B. D. Phylogenetic relationships among ascomycetes: evidence from an RNA polymerse II subunit. *Mol. Biol. Evol.* **16**, 1799–1808 (1999).
- 73. Hall. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symp. Ser.* **41**, (1999).
- 74. Kearse, M. *et al.* Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28**, 1647–1649 (2012).
- 75. Darriba, D., Taboada, G. L., Doallo, R. & Posada, D. jModelTest 2: more models, new heuristics and parallel computing. *Nat. Methods* **9**, 772–772 (2012).
- 76. Nixon, K. C. WinClada ver. 1.0000. *Publ. by author, Ithaca, New York, USA* (2002).
- 77. Ronquist, F. *et al.* MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. *Syst. Biol.* **61**, 539–542 (2012).
- 78. Katoh, K. & Standley, D. M. MAFFT multiple sequence alignment software Version 7: Improvements in performance and usability. *Mol. Biol. Evol.* **30**, 772–780 (2013).
- 79. Sung, G. H., Poinar, G. O. & Spatafora, J. W. The oldest fossil evidence of animal parasitism by fungi supports a Cretaceous diversification of fungal-arthropod symbioses. *Mol. Phylogenet. Evol.* **49**, 495–502 (2008).
- 80. Drummond, A. J. & Rambaut, A. BEAST: Bayesian evolutionary analysis by

sampling trees. *BMC Evol. Biol.* **7**, 1–8 (2007).

- 81. Drummond, A. J., Ho, S. Y. W., Phillips, M. J. & Rambaut, A. Relaxed phylogenetics and dating with confidence. *PLoS Biol.* **4**, 699–710 (2006).
- 82. Solomon, R. W. Free and open source software for the manipulation of digital images. *Am. J. Roentgenol.* **192**, 330–334 (2009).
- 83. Bonhomme, V., Picq, S., Gaucherel, C. & Claude, J. Momocs: Outline analysis using R. *J. Stat. Softw.* **56**, 1–24 (2014).
- 84. R Core, T. *R: a Language and Environment for Statistical Computing. http://www.Rproject.org/* **2**, (2004).
- 85. Kincaid, D. T. & Schneider, R. B. Quantification of leaf shape with a microcomputer and Fourier transform. *Can. J. Bot.* **61**, 2333–2342 (1983).
- 86. Campton, J. S. Elliptic Fourier shape analysis of fossil bivalves: some practical considerations. *Lethaia* **28**, 179–186 (1995).
- 87. Caillon, F., Bonhomme, V., Möllmann, C. & Frelat, R. A morphometric dive into fish diversity. *Ecosphere* **9**, (2018).
- 88. Revell, L. J. phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.* **3**, 217–223 (2012).
- 89. Felsenstein, J. Phylogenies and the Comparative Method. *Am. Nat*. **125,** 1-15 (1985).
- 90. Revell, L. J. Two new graphical methods for mapping trait evolution on phylogenies. *Methods Ecol. Evol.* **4**, 754–759 (2013).

# **Figure legends**

# Fig. 1.

*Escovopsis* - attine ants co-cladogenesis and phylogeographic distribution. A-B) *Escovopsis*  - attine ants co-cladogenesis. Lines indicate the *Escovopsis* strains associated to *Atta* (green), *Acromyrmex* (blue), *Trachymyrmex* (purple), *Sericomyrmex* (orange) and *Apterostigma*  (red). C-D) Phylogeographic distribution of *Escovopsis* in the American continent. Lines plotted in the map indicate the origin of the ants from where *Escovopsis* strains were isolated.



Fig. 2.

Divergence age estimates of *Escovopsis*. Chronogram was constructed based on the tree obtained in the maximum likelihood analyses. A) Calibration was based on seven nodes from Hypocreales previously calibrated by Sung et al. (2008). B) Extended region of the Hypocreales. Calibrated nodes in Hypocreaceae are shown in blue. C) Ages in millions of years (Mya) of each calibrated node. Scales of each Chronogram in Mya.



# Fig. 3.

*Escovopsis* trait adaptations over the evolutionary time. A) Ancestral state reconstruction of the vesicles. Strains in the basal clades have globose vesicles that change into cylindric and no-vesicles in strains of the more derived clades. B-C) Types of conidiophores. Strains in the basal clades present conidiophores with swollen cells which appear to be lost in the most derived clades. D-I) Phialides formation. Strains in the basal and in the transitional clades form phialides only on vesicles (F-I – that correspond with the clades in red to light-blue on the ancestral state reconstruction tree) and strains in the most derived clades forms phialides on both vesicles (D) and aerial mycelia (E). J-K) Colony growth rates of the strains from (A). Increased growth rates correlate with the genus diversification. L) Number of vesicles per conidiophore. Increased number of vesicles also correlate with genus diversification. M) Number of phialides per vesicles. *Escovopsis* maintained the number of phialides over the evolution.



 $-0.222$  trait value  $0.16$ 







M

 $\overline{4}$ 



Number of vesicles per conidiophore



# **Overall thesis conclusion**

Fungiculture by attine ants have fascinated scientists since its discovery about 150 years ago. In addition to the economic importance of some attine species, colonies of these social insects are models to study evolution and symbiosis. Parasites directly influence the evolution of ecosystems, so that the discovery of *Escovopsis* was of great importance to understand the evolution of the fungus-growing ants' environment. The lack of a standardized taxonomy as well as an unresolved phylogeny of *Escovopsis*, studies on its origin, evolution, and ecology (lifestyle) have clouded our understanding of the impact of this fungus in the evolution of fungus-growing ants. By providing grounds for the systematics of *Escovopsis*, inferring its origin and raising hypothesis on its evolution, this study not only provides a stable foundation from which to build future research on the taxonomic diversity, ecology and the evolutionary history of the genus, but raises a different point of view on the evolution of the *Escovopsis*-attine ant symbiosis. We hope to open new windows for discussion to understand the evolution of both *Escovopsis* and the attine ants' ecosystem.