The Genera of Fungi: fixing the application of type species of generic names

Pedro W. Crous1,2,3, Alejandra Giraldo4, David L. Hawksworth5,6,7, Vincent Robert1, Paul M. Kirk7,8, Josep Guarro4, Barbara Robbertse9, Conrad L. Schoch9, Ulrike Damm10, Thippawan Trakunyingcharoen11, and Johannes Z. Groenewald1

1CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands; corresponding author e-mail: p.crous@CBS.knaw.nl
2Microbiology, Department of Biology, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands
3 Wageningen University and Research Centre (WUR), Laboratory of Phytopathology, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands
4Unitat de Micologia, Facultat de Medicina i Ciències de la Salut and ISPV, Universitat Rovira i Virgili, Sant Llorenç 21, 43201 Reus, Tarragona, Spain
5Departamento de Biologia Vegetal II, Facultad de Farmacia, Universidad Complutense de Madrid, Plaza Ramón y Cajal, Madrid 28040, Spain
6Department of Life Sciences, The Natural History Museum, Cromwell Road, London SW7 5BD, UK
7Mycology Section, Royal Botanic Gardens, Kew, Surrey TW9 3DS, UK
8State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China
9National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Maryland, USA
10Senckenberg Museum of Natural History Görlitz, PF 300 154, 02806 Görlitz, Germany
11Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand

Abstract: To ensure a stable platform for fungal taxonomy, it is of paramount importance that the genetic application of generic names be based on their DNA sequence data, and wherever possible, not morphology or ecology alone. To facilitate this process, a new database, accessible at www.GeneraofFungi.org (GoF) was established, which will allow deposition of metadata linked to holotype, lectotype, or epitype specimens, cultures and DNA sequence data of the type species of genera. Although there are presently more than 18,000 fungal genera described, we aim to initially focus on the subset of names that have been placed on the “Without-prejudice List of Protected Generic Names of Fungi” (see IMA Fungus 4(2): 381–443, 2013). To enable the global mycological community to keep track of typification events and avoid duplication, special MycoBank Typification identifiers (MBT) will be issued upon deposit of metadata in MycoBank. MycoBank is linked to GoF, thus deposited metadata of generic type species will be displayed in GoF (and vice versa), but will also be linked to Index Fungorum (IF) and the curated RefSeq Targeted Loci (RTL) database in GenBank at the National Center for Biotechnology Information (NCBI). This initial paper focuses on eight genera of appendaged coelomycetes, the type species of which are neo- or epitypified here: Bartaliniia (Bartaliniia robillardoides; Amphisphaeriaceae, Xylariales), Chaetospermum (Chaetospermum chaetosporum; incertae sedis, Sebacinales), Coniella (Coniella fragariae, Schizoparmaceae, Diaporthales), Crinitospora (Crinitospora pulchra, Melanconidaceae, Diaporthales), Eleutheromyces (Eleutheromyces subulatus, Helotiales), Kellermania (Kellermania yuccigena, Planistromataceae, Botryosphaeriales), Mastigiosporum (Mastigiosporum album, Helotiales), and Mycortribulus (Mycortribulus mirabilis, Agaricales). Authors interested in contributing accounts of individual genera to larger multi-authored papers to be published in IMA Fungus, should contact the associate editors listed below for the major groups of fungi on the List of Protected Generic Names for Fungi.

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INTRODUCTION

In The Genera of Fungi, Clements & Shear (1931) summarised the mycological information available at that time to provide a classification of all genera of fungi (kingdom Fungi, including lichen-forming fungi, and also Oomycota). In the process, they selected type species for many genera in which no type was designated, thus attempting to fix the application of all generic names. Since that historic publication, mycology as a discipline has advanced rapidly, with the first DNA sequence data becoming available in GenBank around 1991 (Hibbett et al. 2011). Taylor et al. (2000) proposed the Genealogical Concordance Phylogenetic Species Recognition concept to delimit fungal species by utilising characters from multiple
independent loci. This still provides the benchmark for phylogenetic species delimitation in mycology. However, less precise methods were needed in order to address the challenge to document all life on the planet in a reasonable time frame. The possibility for rapid specimen identification and species discovery by means of their DNA sequence data gained extra momentum when Hebert et al. (2003) introduced the concept of DNA Barcoding. This aims to use a single, variable stretch of DNA (DNA barcode) to identify all euukaryotic life on Earth. Although it soon became clear that the mitochondrial gene CO1 was unsuitable as a universal DNA barcode for fungi, the fungal community addressed the situation by adopting the widely used internal transcribed spacer (ITS) region of the nuclear ribosomal DNA as the Fungal DNA barcode (Schoch et al. 2012). This marker had a 73 % probability to correctly identify a fungal species screened, which was comparable to the two barcode markers in a more stable taxonomic system, it is thus of the utmost importance to combine DNA-sequence based comparative methods with the application of generic names. During the past 14 years (2000–2013) the mycological community has described 1 833 fungal genera, for which only 155 (8.4 %) currently have types linked to reliably annotated ITS DNA sequence data in the public databases. In other words, the problems related to the imprecise morphological application of names without DNA data continues to worsen. To alleviate and contain this issue, we herewith launch The Genera of Fungi project, which will aim to sequence, restudy and/or recollect the type species of genera envisaged to be given a protected status at the IBCXIX in 2017. Although there are presently approximately 18 000 generic names of fungi in MycoBank and Index Fungorum, this list will focus on the subset of names that are currently accepted (Kirk et al. 2013).

The aims of this project are to:

(1) Establish a new website, www.GeneraOfFungi.org, to host a database that will link metadata to other databases such as MycoBank, Index Fungorum, BOLD, UNITE, and associated DNA barcodes (ITS, LSU and other loci as needed) to GenBank and RTL (Schoch et al. 2014).

(2) Source type specimens and cultures of the type species of genera from fungaria and Biological Resource Centres (BRCs), and derive the metadata required as explained below.

(3) Recollect fresh material of the type species if not already available, and as far as possible derive DNA barcodes and cultures from this material.

(4) Designate type species, and type specimens of those species, for those genera where this has not been indicated in the original publications.

(5) Fix the genetic application of the type species of generic names by means of lecto-, neo-, or epitypification as appropriate, and at the same time deposit cultures in at least two Biological Resource Centres (BRCs) from which they would be widely available to the international research community.

(6) Publish modern descriptions of the type species and relevant typifications in appropriate mycological journals (supplemented by MBT or IF numbers for registration), and also deposit associated metadata in www.GeneraOfFungi.org, which will link metadata to other databases as indicated above.

Generating DNA barcodes

Although the ITS region is the designated DNA barcode for fungal species identification (Schoch et al. 2012), the partial LSU (28S rDNA; spanning at least the first 850 bp – see Material & Methods below) is recommended for phylogenetic analyses to resolve and contextualise genera. Many loci can be employed in phylogenetic analyses but, we recommend that the ITS and LSU loci are generated on a routine basis for this project. To address the circumstances where DNA sequencing facilities are not freely available to
many mycologists, the International Mycological Association (IMA), in collaboration with the World Federation for Culture Collections (WFCC), plans to set up a global network of BRCs and fungaria, that will, in exchange for the deposit of cultures (and/or specimens), generate free barcodes for the depositor. These collaborating BRCs will be listed on the Genera of Fungi database website.

Publication strategy
Of primary concern is that metadata related to type species of genera be deposited in the Genera of Fungi database (www.GeneraOfFungi.org), and all new typification events are registered in MycoBank (MBT numbers) or Index Fungorum. Various publication options are possible, and genera could be published as individual articles (or several combined into a single article as done here) in mycological journals of choice. It is recommended that the following issues are addressed in such publications:

(1) Taxonomic history of the genus.
(2) Phylogenetic placement of the type species of the genus.
(3) New nomenclature merging asexual and sexual generic names based on stability.
(4) Generic and species description, with reference collection (e.g. fungarium), MycoBank or Index Fungorum, and INSDC sequence accession numbers.
(5) Eventual name changes that result from the new phylogenetic placement.
(6) Notes discussing the relevance and implications of the phylogeny of the genus.

Management
A team of associate editors will be appointed for major groups of fungi. It is recommended that mycologists in different countries form a national node, which could focus on trying to recollect the genera described from specific substrates in each country. In the meanwhile, MycoBank and Index Fungorum will try to elucidate which genera were described from different countries and on which substrates. This information is not currently present in our databases for most genera, and is the biggest impediment to this project. Mycologists could contact BRCs to get assistance to generate DNA barcodes of potential neo- or epitype material. The publication strategy followed will depend on the authors, but deposit of data in GoF will be facilitated via MycoBank (there is thus no duplication of work, as these databases are linked). Authors interested in contributing accounts of individual genera as part of larger multi-authored papers published in IMA Fungus, should submit materials to the following associate editors: Pedro Crous (p.crous@cbs.knaw.nl) and David Hawksworth (d.hawksworth@nhm.ac.uk) for ascomycetes and basidiomycetes, Thorsten Lumbsch (tlumbsch@fieldmuseum.org) for lichenized fungi, Kerstin Voigt (Kerstin.Voigt@hki-jena.de) for zygomycetes, and Roger Shivas (Roger.Shivas@daff.qld.gov.au) for rusts and smuts.

MATERIALS AND METHODS

Isolates
Several genera were re-described based on cultures obtained from the CBS-KNAW Fungal Biodiversity centre in Utrecht, The Netherlands (CBS-KNAW) and the working collection of P.W. Crous (CPC), housed at CBS. For fresh collections, leaves and twigs were placed in damp chambers, and incubated at room temperature for 1–2 d. Single conidial colonies were established from sporulating conidiomata in Petri dishes containing 2 % malt extract agar (MEA) as described earlier (Crous et al. 1991). Colonies were sub-cultured onto 2 % potato-dextrose agar (PDA), oatmeal agar (OA), MEA (Crous et al. 2009b), autoclaved pine needles on 2 % tap water agar (PNA) (Smith et al. 1996), and incubated at 25 °C under continuous near-ultraviolet light to promote sporulation. Reference strains and specimens are maintained at the CBS.

DNA isolation, amplification and analyses
Genomic DNA was extracted from fungal colonies growing on MEA using the UltraClean™ Microbial DNA Isolation Kit (MoBio Laboratories, Inc., Solana Beach, CA, USA) according to the manufacturer’s protocol. The primers V9G (de Hoog & Gerrits van den Ende 1998) and LR5 (Vilgalys & Hester 1990) were used to amplify part (ITS) of the nuclear rDNA operon spanning the 3’ end of the 18S nrRNA gene, the first internal transcribed spacer (ITS1), the 5.8S nrRNA gene, the second ITS region (ITS2) and approximately 900 bp of the 5’ end of the 28S nrRNA gene. The primers ITS4 (White et al. 1990) and LSU1Fd (Crous et al. 2009a) were used as internal sequence primers to ensure good quality sequences over the entire length of the amplicon. Amplification conditions followed Cheewangkoon et al. (2008). The program SeqMan v. 7.0.0 (DNASTAR, Madison, WI, USA) was used to obtain consensus sequences of each isolate. Blast searches using ITS and LSU sequences were performed for each isolate and the closest matches were retrieved and included in the phylogenetic analysis. The sequence alignment and subsequent phylogenetic analyses of the LSU data were carried out using methods described by Crous et al. (2006). Gaps were treated as “fifth state” data in the parsimony analysis. Sequence data were deposited in GenBank (Table 1) and the alignment and tree in TreeBASE (http://www.treebase.org). Remaining sequence data are discussed under the species notes below.

Morphology
Slide preparations were mounted in clear lactic acid, lactophenol cotton blue or Shear’s mounting fluid from colonies sporulating on MEA, PDA, PNA, or OA. Sections of conidiomata were made by hand for examination purposes. Observations were made with a Zeiss V20 Discovery stereo-microscope (Zeiss, Oberkochen, Germany), and with a Zeiss Axio Imager 2 light microscope using differential interference contrast (DIC) illumination and an AxioCam MRc5 camera and Zen software. Additional photomicrographs were done using a Nikon Eclipse Ni-U microscope (Nikon, Tokyo, Japan), a Nikon SMZ1500 stereo-microscope, Nikon DS-U3 digital camera and Nis Elements imaging software. Colony
Table 1. Collection details and GenBank accession numbers of isolates included in this study.

<table>
<thead>
<tr>
<th>Species</th>
<th>Culture collection no1</th>
<th>Substrate</th>
<th>Location</th>
<th>Collector</th>
<th>GenBank Accession no2</th>
</tr>
</thead>
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<td>Bartalinia robillardoides</td>
<td>CBS 122705 (ex-epitype)</td>
<td>Leaf of Cordia myxa</td>
<td>Italy</td>
<td>–</td>
<td>KJ710438 KJ710460</td>
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<td>Chaetospermum chaetosporum</td>
<td>CBS 154.59 (ex-neotype)</td>
<td>Soil of rain forest</td>
<td>Peru: Iquitos</td>
<td>M. Christensen</td>
<td>KJ710441 KJ710463</td>
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<td>Coniella cf. fragariae</td>
<td>CBS 612.75</td>
<td>Leaf of Alnus glutinosa</td>
<td>Pakistan: Lahore</td>
<td>S. Ahmed</td>
<td>KJ710440 KJ710462</td>
</tr>
<tr>
<td>Coniella fragariae</td>
<td>CBS 110394</td>
<td>Soil of epitype</td>
<td>CBS 154.59</td>
<td>Submerged dead leaf of Alnus glutinosa</td>
<td>KJ710439 KJ710461</td>
</tr>
<tr>
<td>CBS 167.84 = CPC 3934</td>
<td>CBS 172.49 = CPC 3930 (ex-neotype)</td>
<td>Leaf of Cordia myxa</td>
<td>Belgium: Lint</td>
<td>A. von Tiedemann</td>
<td>EU754149 AY339318</td>
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<tr>
<td>CBS 138.32 = CPC 22807 (ex-epitype)</td>
<td>CBS 183.52</td>
<td>Tamarix</td>
<td>–</td>
<td>S. de Boer</td>
<td>KJ710442 KJ710464</td>
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<td>France: Chancay</td>
<td>G. Bollen</td>
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<td>CBS 138015 = CPC 20827 (ex-epitype)</td>
<td>Branches of Mangifera indica</td>
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<td>T. Trakunyingcharoen</td>
<td>KJ710443 KJ710466</td>
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<td>Decaying Russulaeaceae</td>
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<td>L. Sigler</td>
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<td>Sweden</td>
<td>K.A. Seifert</td>
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<td>CBS 138014 = CPC 22807 (ex-epitype)</td>
<td>Agaric, blackened and mummified</td>
<td>France: Massif des Cèdres</td>
<td>H.A. van der Aa</td>
<td>KJ710445 KJ710469</td>
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<td>P.W. Crous</td>
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<td>CPC 20623</td>
<td>CPC 20623</td>
<td>Leaves of Yucca rostrata</td>
<td>USA: California</td>
<td>P.W. Crous</td>
<td>KJ710448 KJ710473</td>
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<tr>
<td>CPC 22946</td>
<td>CPC 22946</td>
<td>Alopecia pratensis</td>
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<td>U. Damm</td>
<td>KJ710452 KJ710477</td>
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<td>CBS 138016 = CPC 14167 (ex-epitype)</td>
<td>Eucalyptus pilbara x brassiana</td>
<td>Indonesia</td>
<td>M.J. Wingfield</td>
<td>KJ710458 KJ710483</td>
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<td>Leaves of Eucalyptus urophylla</td>
<td>China</td>
<td>Cheng Mai &amp; Xudong Zhao</td>
<td>KJ710456 KJ710481</td>
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<td>Mycotribulus mirabilis</td>
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<td>Leaves of Eucalyptus camaldulensis</td>
<td>Venezuela</td>
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<td>KJ710457 KJ710482</td>
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</table>


2 LSU: large subunit (28S) of the nrRNA gene; ITS: internal transcribed spacers and intervening 5.8S nrDNA.
characters and pigment production were noted after 1 mo of growth on MEA and OA (Crous et al. 2009b) incubated at 25 °C. Colony colours (surface and reverse) were rated according to the colour charts of Rayner (1970).

RESULTS

Phylogeny

For the type species treated here, amplicons of approximately 1 700 bases were obtained of the partial 18S rRNA, full length ITS and partial 28S rRNA (LSU) genes of the isolates listed in Table 1. The LSU alignment was used to resolve the generic placement of strains (Fig. 1) and the ITS (not shown) for species identification. The manually adjusted LSU alignment contained 86 sequences (including the outgroup sequence) and 798 characters including alignment gaps were used in the phylogenetic analysis; 349 of these were parsimony informative, 42 were variable and parsimony-uninformative, and 407 were constant. The parsimony analysis yielded the maximum setting of 1000 equally most parsimonious trees (TL = 1290 steps; CI = 0.493; RI = 0.928; RC = 0.458), which allowed the genera treated here to be assigned to at least order level (Fig. 1; discussed below in the Taxonomy section). Neighbour-joining analyses using three substitution models on the sequence alignment yielded tree topologies delimiting similar terminal clades to those of the parsimony analysis (data not shown), but with some rearrangements at the deeper nodes.

THE GENERA


Current generic circumscription: Conidiomata stromatic, varying from pycnidio to indeterminate, subdermal, intracortical or subepidermal in origin, immersed, unি- to plurilocular, locules occasionally convoluted, dark brown to brown, glabrous, wall of textura angularis or textura globulosa, sometimes of textura prismatic, cells thick-walled and dark brown to brown in the outer layers, becoming thin-walled and paler toward the conidial hymenium. Conidiophores arising from the inner layers lining the conidioma, or at the base and extending part way up the side walls, sparsely septate and irregularly branched, often reduced to conidigenous cells, hyaline, thin-walled, smooth, with percurrent proliferations, and apical periclinal thickenings (collarettes and regeneration of conidigenous cells absent). Conidia cyindrical to fusiform with an acute or blunt apex and a truncate base, straight or slightly curved, 3–4-euseptate, apical cell hyaline and devoid of contents, other cells hyaline to pale brown, wall smooth, with or without constrictions at septa, suprabasal cell longer than the rest, apical appendage single, arising as a tubular extension of the apical cell and not separated from it by a septum, invariably trifid with 2–4, narrow, attenuated, flexuous, divergent branches; basal appendage tubular, single, unbranched, exogenous, filiform, flexuous.

Type species: Bartalinia robillardoides Tassi 1900.


(Fig. 2)

Folicolous. Conidiomata stromatic, pycnidoid to indeterminate or variable, amphiogenous, scattered to gregarious, sub-epidermal, initially immersed, becoming erumpent, globose or depressed globose to angular, 180–240 µm diam, 80–200 µm high, unilocular, glabrous brown to black, lacking an ostiole; wall to 40 µm thick, of textura angularis, cells thick-walled and brown in the outer layers, becoming thin-walled and paler toward the conidial hymenium. Conidiophores arising all around the cavity of the conidioma from the innermost wall layer, reduced to conidigenous cells, invested in mucus. Conidiogenous cells ampulliform, hyaline, thin-walled, smooth, 4–8 × 3–4.5 µm. Conidia subcyindrical, 4-septate, smooth, slightly constricted at the septa, (19–)21–24–(27) × 3–4 µm, bearing appendages; basal cell obconic with a truncate base, hyaline; apical cell conical, hyaline, devoid of contents, forming a tubular, branched appendage; apical appendage branches into three unbranched, attenuated, flexuous, divergent branches, (15–)16–20–(22) µm long; basal appendage single, unbranched, filiform, flexuous, excentric, 4–7 µm long.

Culture characteristics: Colonies covering the dish in 2 wk at 25 °C, flat, spreading, with moderate aerial mycelium, and even, lobate margins. On PDA surface greyish at centre and olivaceous black toward the periphery; reverse olivaceous black. On MEA attaining 60 mm diam after 1 mo, surface dirty white to honey, with patches of pale olivaceous grey, reverse olivaceous grey with patches of dirty white. On OA surface umber with patches of pale olivaceous grey and buff, reverse dark brown at centre and sepia toward the periphery.


Notes: The genus Bartalinia (Amphisphaeriacaeae, Xylariales), has no known sexual morph, and presently contains around 22 names representing about 18 taxa, six of which were treated by Nag Raj (1993). Although von Arx (1981) regarded Bartalinia as synonym of Seimatosporium, this was not accepted by Nag Raj (1993) because of differences in their conidial appendages. Both are now recognised as genera in their own right (Tanaka et al. 2011). Nag Raj (1979) and Sutton (1993) transferred Bartalinia nolinae and B. themedae to the genera Libartania and Kellermannia, respectively. Later Nag Raj (1993) included in Bartalinia some species of
Fig. 1. The first of 1000 equally most parsimonious trees resulting from a parsimony analysis of the LSU sequence alignment. The bootstrap support values are indicated at the nodes and the scale bar represents the number of changes. Thickened branches reflect those branches present in the strict consensus tree. Orders are indicated in coloured blocks and species names in black text. GenBank accession numbers for downloaded sequences are shown before species names and culture collection numbers after species names. The tree was rooted to *Saccharomyces cerevisiae* (GenBank Z73326).
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Fig. 1. (Continued).
Pestalotia and Hyalotila, accepting six species in Bartalinia and questioned the status of four of them i.e. B. bella, B. terricola, B. begoniae and B. bombacicola. More recently, six new species have been added to the genus. Andrianova & Minter (2007) introduced the new species B. goniolimonis from leaf spots of Goniolimon speciosum and provided a taxonomic key to the genus. The most recent species is B. pondoensis, isolated from leaves of Maytenus abbottii in South Africa; which is similar on ITS to B. laurina, but morphologically different (Marincowitz et al. 2010). In spite of Bartalinia being a relatively unknown genus, cultures of B. robillardoides were reported to produce the anticancer drug taxol (Gangadevi & Muthumary 2008).

There are currently four ITS sequences listed as “Bartalinia robillardoides” in the NCBI GenBank nucleotide database. Of these, one (GenBank EU552102 derived from CBS 122686; from Leucadendron sp., South Africa) differs with 1 nucleotide from our ex-epitype strain, and the second (GenBank KF656706 derived from TCM-50; host and country not clearly specified) has some mismatches at the beginning and end of the sequences that could be the result of sequence annotation. The remaining two sequences (GenBank HM802301 derived from SKJM1096; host and country not specified; and GenBank AF405301 derived from BRIP 14180; from Macrotyloma daltonii, Australia) also differs in two nucleotides from our sequence. Although GenBank AF382366 is from the same strain that could be Bartalinia pondoensis, a blast search only confirmed the affiliation of the sequence to the genus but not to the species.

Authors: D.A. Giraldo López and P.W. Crous


Current generic circumscription: Conidiomata stromatic, pycnidial, innate-erumpent, initially closed, ultimately opening by an irregular split in the apical wall, gelatinous, off white or pearl white when moist, unilocular, with the locule occasionally irregularly divided or convoluted, glabrous; wall heavily gelatinised, of textura intricata to textura obliqua. Conidiophores lining the base and part way up the side walls and arising from the innermost elements of the wall, loosely aggregated, sparingly branched and septate at the base, hyaline, smooth, invested in mucus. Conidiogenous cells discrete, cylindrical to subcylindrical or irregular, hyaline, smooth, bearing a single terminal conidium or an apical cluster of up to four conidia; conidiogenous cell with several percurrent annellations with periclinal thickening, but collarettes absent. Conidia broadly ellipsoidal to cylindrical with obtuse ends, unicellular, hyaline, smooth; appendages tubular, not separated from the conidium body by septa, polar

Fig. 2. Bartalinia robillardoides (CBS 122705). A. Colony sporulating on PDA. B–D. Section through conidiomatal wall, showing conidiogenous cells. E–G. Conidia. Bars: A = 250 µm, all others = 10 µm.
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or subpolar, occasionally lateral as well, unbranched, filiform
or narrow and attenuated, flexuous, often collapsing and
ribbon-like with age.

Type species: Chaetospermum chaetosporum (Pat.) A.L.
Sm. & Ramsb. 1914.

Chaetospermum chaetosporum (Pat.) A.L. Sm. &
Fr. 4: 39 (1888).
Synonym: Chaetospermum chaetosporum (Pat.) Höhn.,
(Fig. 3)

Caulicolous or foliicolous. Conidiomata stromatic, pycnidiod,
scattered to gregarious and confluent, subepidermal
or subperidermal in origin, innate erumpent, globose to
subglobose or hemispherical in sectional view, 400–500 µm
diam, closed but dehiscing by an irregular split in the apical
wall, pearl white and gelatinous when moist, yellowish brown
and waxy when dry, glabrous; wall to 50 µm thick, of textura
intricata to textura obliterata. Conidiophores arising from the inner
layer of the cavity, loosely aggregated, sparingly branched
and septate at the base, hyaline, smooth, invested in mucus. Conidiogenous
cells discrete, cylindrical to subcylindrical or irregular, hyaline, smooth, bearing a single terminal conidium,
(10–)12–21(–27) × 2–4 µm, without holoblastic-sympodial
proliferations. Conidia broadly ellipsoidal to cylindrical with
obtuse ends, hyaline, smooth, (24–)28–34(–36) × (5–)
6–9(–10) µm; appendages 5–10 at each end, tubular, not
separated from the conidium body by septa, circumpolar to
subpolar, unbranched, filiform, flexuous, often collapsing and
ribbon-like with age, (20–)28–43(–53) µm long.

Culture characteristics: Colonies spreading, flat, covering
the dish in 2 wk at 25 ºC, with sparse aerial mycelium, and
even, smooth margins. On MEA and PDA surface dirty white
with pale vinaceous pycnidia. On OA surface whitish or pale
luteus covered with rosy buff pycnidia; reverse pale luteus.

Specimens examined: France: Lons-ie-Saulnier (Jura), on roots of
Poaceae, 1888?, holotype presumed lost. – Switzerland: Ticino,
affluent to Lago di Origlio, from submerged dead leaf of
Alnus glutinosa, July 1958, A. L. van Beverwijk (CBS H-10131, – neotype
designated here, MBT178269; culture ex-neotype CBS 154.59).
– Pakistan: Lahore, from leaf of Cordia myxa, S. Ahmed (CBS
H-10132, culture CBS 612.75).

Fig. 3. Chaetospermum chaetosporum (CBS 154.59). A. Colony sporulating on SNA. B–F. Sections through conidiomata, showing conidiogenous
Notes: Chaetospermum was introduced by Saccardo (1892) to accommodate Tubercularia chaetospora, a species described previously by Patouillard (1888) from decaying grass, using the name C. tubercularioïdes, which was changed to C. chaetosporum by Smith & Ramsbottom (1914) following the International rules of nomenclature, which is currently used for the type species of the genus. Pestalozziella ambiguа from stems of Artemisa was described by von Höhnel (1907), with similar conidia to those of Tubercularia chaetospora. Later the same author considered both species as co-generic (von Höhnel 1924). Nag Raj (1993) reviewed the genus considering C. gelatinosum a synonym of Mastigoglena gelatinosum and C. carneum a nomen dubium. Rajeshkumar et al. (2010) proposed the new species Chaetospermum setosum, isolated from leaves of Mangifera indica in India, and considered C. indicum as a synonym of C. chaetospermum. They also provided a taxonomy key for the genus. The genus Chaetospermum (incertae sedis, Sebacinales) presently contains eight species. Other than Chaetospermum chaetosporum frequently being isolated from leaf litter of diverse substrate, not much is known of the genus. A conidiomatal developmental study of C. chaetospermum was published by Fonseka (1960), while Sutton (1977) treated several generic synonyms, and Nag Raj (1993) provided a key to four species.

The phylogeny of Chaetospermum is poorly known. Rungjindamaи et al. (2008) based on LSU and SSU sequences suggested that Chaetospermum could be located in basidiomycetes, since two species of the genus, C. camelliae and C. artocarpi, were phylogenetically related with members of Sebacinaeae (Sebacinales, Agaricomycetes). Unfortunately, the type species of Chaetospermum was not included in that study. Our study revealed that the type species of the genus is a member of Sebacinales, which agrees with Rungjindamaи et al. (2008), Wells & Bandoni (2001) and Kirschner & Oberwinkler (2009). Further evidences are the presence of a Chaetospermum morph in cultures of the basidiomycete Efibulobasidium albescens (Wells & Bandoni 2001), and of conidia of Chaetospermum gossypinum together with basidiospores of Efibulobasidium albescens in the same specimens (Kirschner & Oberwinkler 2009). Additionally, they observed morphological characteristics typical of Sebacinales such as dolipore septa with continuous parenthesomes in specimens of C. chaetosporum.

The ITS sequence data of E. albescens (type species of the genus Efibulobasidium, AF384860) shows 98.9 % similarity with CBS 154.59 (neotype of C. chaetosporum), suggesting that they are congeneric, and that Chaetospermum (1892) should have preference over Efibulobasidium (1975) (Wells 1975).

Authors: D.A. Giraldo López and P.W. Crous


Current generic circumscription: Conidiomata pycnidial, immersed to semi-immersed, unilocular, glabrous, ostiolate, brown to dark brown or black wall of thin, pale brown textura angularis on the exterior, and hyaline, thin-walled, textura prismatica in the inner layers except at the base which has a convex, pulvinate tissue of hyaline textura angularis giving rise to conidiophores or conidigenous cells; ostiole central, circular or oval, often situated in a conical or rostrate neck. Conidiophores mostly reduced to conidigenous cells, occasionally septate and branched at the base, invested in mucus. Conidigenous cells discrete, cylindrical, subcylindrical, obclavate or lageniform, hyaline, smooth-walled, proliferating percurrenty, or with visible perincidal thickening. Conidia ellipsoid, globose, napiform, fusiform or navicular with a truncate base and an obtuse to apiculate apex, unicellular, thin- or thick-walled, smooth, olivaceous brown to brown, sometimes with a longitudinal germ-slit, with or without a mucoid appendage extending from the apex to base on one side of the conidium. Spermaphores formed in same conidioma, hyaline, smooth, 1-septate with several apical conidigenous cells, or reduced to conidigenous cells. Spermogenous cells cells hyaline, smooth, lageniform to subcylindrical, with visible apical perincidal thickening. Spermata hyaline, smooth, red-shaped with rounded ends.

Type species: Coniella fragariae (Oudem.) B. Sutton 1977 (syn. Coniella pulchella Höhn. 1918).


(Fig. 4)
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Culture characteristics: Colonies on MEA flat, white on the surface, and pale luteous in reverse, reaching 60 mm after 2 wk at 25 °C, with black conidiomata evenly distributed on surface on the plate, same on PDA and OA.


Notes: We have been unable to trace any original material of Coniothyrium fragariae (The Netherlands, on Fragaria vesca, 1883, C.A.J. Oudemans), and hence a neotype is designated here to fix the application of the name. The concept of C. fragariae has not changed since the first molecular phylogeny was published on the genus (van Niekerk et al. 2004).

The genus Coniella currently includes about 30 species (Schizoparmaceae, Diaporthales), many of which are soil-borne, and well-known as leaf, stem, and root pathogens of a diverse range of hosts such as Fragaria spp., Ananas comosus, Pinus patula, Rosa spp., Pismum spp. (Sutton 1980, van Niekerk et al. 2004, Miranda et al. 2012). The genus was proposed by von Höhnel (1918) with a single species, C. pulchella, described from Paeonia officinalis. Petrak & Sydow (1927) split Coniella into two subgenera: Euconiella and Pseudoconiella. The former included C. pulchella and C. diploidiella and the latter comprised C. granati (Sutton 1969). The genera Anthasthoopa and Cyclodomella were proposed for A. simba and C. nigra, respectively; the first species occurring on pods of Caesalpinia pulcherrima and the second one isolated from soil (Subramanian & Ramakrishnan 1956, Mathur & Thirumalachar 1959). Petrak (1960) did not agree with this proposal, and concluded that Cyclodomella nigra is a cultural variant of Coniella diploidiella. Later, Sutton (1969) considered both genera, Anthasthoopa and Cyclodomella, as synonyms of Coniella. Coniella pulchella was considered a synonym of C. fragariae by Sutton (1980), who as well as Nag Raj (1993), who treated the genus Pilidiella as a synonym of Coniella. However, van der Aa (in von Arx 1973) and von Arx (1981) treated Coniella and Pilidiella as separate genera, the former characterised by dark brown conidia and Pilidiella by hyaline conidia becoming pale brown with age. Molecular studies have confirmed the criteria of van der Aa (in von Arx 1973) and von Arx (1981) demonstrating that both genera are different. Pilidiella presently contains species with pigmented, as well as hyaline conidia, and Schizoparmae sexual morphs, while Coniella comprises species with dark brown conidia. Rossman et al. (2007) introduced the family name Schizoparmaceae (Diaporthales) to accommodate these genera.

One strain that was previously identified as Coniella fragariae (CBS 110394), was revealed to belong to a different species based on the LSU sequence (Fig. 1).

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Fig. 4. Coniella fragariae (CBS 172.49). A. Colony sporulating on PDA. B–C. Sections through conidiomata. D–E. Conidiogenous cells. F. Conidia. Bars: A–B = 500 µm, all others = 10 µm.
Crouset al.


Current generic circumscription: *Conidiomata* stromatic, acervuloid, epidermal, immersed to semi-immersed, brown; basal stroma of *textura angularis* to *textura globulosa*. *Conidiophores* arising from the uppermost cells of basal and parietal tissue, unbranched, septate at only the base, hyaline, smooth, invested in mucus. *Conidiogenous cells* discrete or integrated, cylindrical to lageniform, hyaline, smooth-walled; proliferating several times percurrently at apex. *Conidia* ellipsoid with an obtuse apex and broad truncate base, euseptate, hyaline, thick-walled, smooth, with several appendages that are tubular, unbranched, filiform, flexuous, arising from the apex.

**Type species**: *Crinitospora pulchra* B. Sutton & Alcorn 1985.


(Fig. 5)

Caulicolous. *Conidiomata* stromatic, acervuloid separate, immersed to erumpent, 200–300 µm high, 300–500 µm wide, brown, opening by irregular rupture with yellow conidial cirrus, that turns brown with age; wall of several layers of pale brown *textura angularis* to *globulosa*. *Conidiophores* lining the inner cavity, hyaline, smooth, 1–2-septate, unbranched, subcylindrical, to 50 µm long. *Conidiogenous cells* subcylindrical to lageniform, hyaline, smooth, 8–25 × 3–6 µm. *Conidia* hyaline, smooth, guttulate, ellipsoid, with obtuse apex and broadly truncate base (3–5 µm diam), medially 1–septate, rarely 0–2-septate, (20–)30–35(–40) × (10–)15–17(–20) µm, with 4–10 apical appendages, tubular, unbranched, filiform, divergent, flexuous, to 50 µm long; conidia turn brown at germination in culture.

Culture characteristics: Colonies reaching 40 mm diam after 2 wk at 25 ºC, flat, spreading, with sparse aerial mycelium, and lobate, feathery margins. On MEA surface olivaceous grey, with patches of buff, reverse reverse olivaceous grey in centre, dirty white in outer region. On OA surface olivaceous grey. On PDA surface dirty white, mostly with submerged mycelium, developing yellow concentric rings in older cultures.


Notes: The genus *Crinitospora* (*Melanconidaceae, Diaporthales*) is monotypic and no sexual morph has thus far been linked to it. The fungus was initially collected from twigs of *Mangifera indica* in Australia (Sutton & Alcorn 1985); the collection from Thailand studied here, also on *M. indica*, represents the second report of this fungus. Although it is caulicolous on *M. indica*, not much is known about its ecology or pathology.

Authors: P.W. Crous and T. Trakunyingcharoen


Synonymy: Unconfirmed generic synonyms include *Eleutheromyces* Höhn. 1908, and *Eleutheris* Clem. & Shear 1931 (Nag Raj 1993).
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Current generic circumscription: Conidiomata pycnidial, conical to cornute, gelatinous, translucent yellowish or yellowish brown to dark brown, unilocular, glabrous, ostiolate, wall of textura angularis; ostiole central, circular. Conidiophores arising all around the cavity of the conidioma, cylindrical, branched mostly at the base, septate, hyaline, smooth, invested in mucus. Conidiogenous cells integrated with the conidiogenous loci immediately below the septa, hyaline, smooth-walled, with visible periclinal thickening at apex. Conidia aseptate, lenticular to fusiform, hyaline, smooth-walled; apical and basal appendages cellular, delimited from the conidium body by septa; basal appendage developing before the conidium body.

Type species: Eleutheromyces subulatus (Tode) Fuckel 1870.

Eleutheromyces subulatus (Tode) Fuckel, Jahrb. Nassauischen Vereins Naturk. 23–24: 183 (1870) [*1869*].

Fig. 6. Eleutheromyces subulatus (CBS 113.86). A. Colony sporulating on OA. B–F. Conidiophores giving rise to conidia. G. Smaller conidia of unidentified Eleutheromyces sp. (CBS 139.90). Bars: A = 250 µm, all others = 10 µm.

Fungicolous. Conidiomata pycnidial, scattered to densely gregarious, seemingly superficial but innate erumpent, oval, long conical or cornute, 100–250 µm diam, 150–500 µm high, unilocular, glabrous, gelatinous, translucent, yellowish brown when dry, paler coloured when moist; wall up to 45 µm thick, of textura angularis, cells thick-walled, pale brown to pale yellow; ostiole central, circular. Conidiophores lining the cavity of the conidioma, cylindrical, branched mostly at the base, septate, often variously curved, hyaline, smooth, to 60 µm long, invested in mucus. Conidiogenous cells cylindrical, integrated, hyaline, smooth, 5.5–13 × 2.5–4 µm. Conidia ellipsoidal or lenticular, aseptate, hyaline, 4.5–7 × 2–4 µm (av. 6 × 2 µm), one appendage at each end delimited by a septum; appendages tubular, attenuated; apical appendage 2–5 µm long; basal appendage 1–3 µm long.

Culture characteristics: Colonies flat, spreading, reaching 40 mm diam after 2 wk at 25 ºC, with sparse aerial mycelium, and smooth margins. On MEA reaching 11–33 mm after 1 mo, surface and reverse dirty white to peach or coral with honey regions. On OA attaining 40–45 mm after 1 mo; surface buff, ochraceous or flesh, pycnidia with spores beige in mass.


Notes: The genus Eleutheromyces (incertae sedis, Helotiales) presently contains two species that are fungicolous, growing on agarics. The genus has been reported from North America and Europe. A Hyphozyma synasexual morph was reported for E. subulatus by Sigler (1990), while Tsuneda et al. (1997) again linked this morph to black spot disease of Lentinula edodes. Two cultures listed in the CBS collection as E. subulatus (CBS 458.88 and CBS 139.90) were found to be
phylogenetically and morphologically distinct (Figs 1 & 6, respectively) and represent different taxa. Highest similarity of the LSU sequences was found with "Mollisia incrustata" GenBank GU727556; however, this sequence does not appear to be congeneric with other Mollisia sequences on GenBank (data not shown) and thus the application of the supposed taxonomic lineage of Mollisia (Leotiomycetes; Helotiales; Dermatocarpaceae) would not be confirmed here. Examination of the blast results also did not result in a clear affinity to any of the classes, with a more or less equal similarity to both Leotiomycetes and Sordariomycetes and therefore this genus is treated here as incertae sedis. It is quite possible that the genus belongs to a class that is currently not represented in the NCBI GenBank nucleotide database.

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Kellermania Ellis & Everh., J. Mycol. 1: 153 (1885).

Current generic circumscription: Conidiomata pycnidial, immersed, glabrous, ostiolate; wall thick, of textura angularis, cells thick-walled, dark brown to brown in the outer layers, and of textura prismatica, cells thin-walled, hyaline in the inners layers, with columnar, thin-walled, colourless cells surrounding the ostiole; ostiole circular or oval, non-papillate. Conidiophores lining the cavity of the conidioma, reduced to conidiogenous cells, invested in mucus. Conidiogenous cells discrete, often of two kinds: those producing macroconidia, lining most of the conidiomatal cavity, cylindrical to subcylindrical, hyaline, smooth; those producing microconidia confined to the area of inner wall around the ostiole, ampulliform to broadly ampulliform, hyaline, smooth. Conidiogenesis ontogeny holoblastic by apical wall-building in the first conidium and by replacement wall-building in subsequent conidia; maturation by moderate diffuse wall-building synchronous with conidium ontogeny; delimitation by a transverse septum; secession schizolytic; proliferation usually absent, when present enteroblastic-pericentric to produce an additional conidium at a higher level; periclinal thickenings absent, but occasional annellations may be present; regeneration of conidiogenous cells absent. Macroconidia cylindrical to narrowly clavate with a truncate base, unicellular or euseptate, hyaline, thick-walled, smooth; appendages arising initially as tubular extensions of the conidium body, single, stout and unbranched, or up to six, attenuated, flexuous. Microconidia cylindrical to ellipsoidal or irregular with a rounded or blunt apex and a truncate base bearing minute marginal frills, unicellular, hyaline, smooth.

Type species: Kellermania yuccigena Ellis & Everh. 1885.

Kellermania yuccigena Ellis & Everh., J. Mycol. 1(12): 154 (1885); as ‘yuccaegena’.
(Fig. 7)

Foliicolous. Description based on colonies sporulating on OA. Conidiomata pycnidial, black, solitary, immersed, globose, unilocular, to 300 µm diam; wall of 8–10 cells of brown textura angularis; ostiole central, non-papillate, to 20 µm diam, exuding a hyaline conidial mass. Conidiophores lining the inner cavity, reduced to conidiogenous cells, hyaline, smooth, subcylindrical to ampulliform, (10–15 (–25) × 5–7(–25) µm (shorter on host material, to 12 µm in length, and 6 µm in width), proliferating percurrently at apex (much more prominent in culture), invested in mucus. Conidia hyaline, smooth, gulletate, cylindrical, 1-septate (submedian), (35–)40–50(–62) × (9–)10–12(–14) µm (slightly wider on OA than on host tissue); apex giving rise to a simple setulate, unbranched appendage (but on OA at times bifurcate), 22–32 µm long; conidial base truncate, with a minute marginal frill, 1 µm long. Microconidia observed in culture, forming in same conidioma, hyaline, smooth, gulletate, subcylindrical, aseptate, apex obtuse, base truncate, 6–20 × 4–6 µm.

Culture characteristics: Colonies spreading, flat, reaching 50 mm diam after 2 wk at 25 ºC, with moderate, fluffy aerial mycelium and feathery, lobate margins. On MEA surface dirty white, reverse buff. OA surface dirty white to cream; on PDA surface and reverse dirty white.


Notes: The genus Kellermania (Planistromataceae, Botryosphaeriales; Slippers et al. 2013) presently includes around 40 species, many of which were recently included in phylogenetic studies (Minnis et al. 2012, Crous et al. 2013). Although Sutton (1980) retained Alpakesa, Kellermania, and Piptarthron as separate genera, Nag Raj (1993) reduced Alpakesa to synonymy under Kellermania. Minnis et al. (2012) published the first phylogenetic revision of the group, and reduced all these genera to synonymy under Kellermania, supporting the view of Crous et al. (2012) that conidial appendages as single characters have insufficient value to separate genera in coelomycetes, and should rather be seen as species-specific characters. Names formerly described in genera typified by sexual morphs (Planistroma, Mycotaxon 753 – holotype of Y. angustifolia; BPI 374463 – isotype; New Mexico: Socorro County, west side of US Highway 25, mile 105.4, on leaves of Yucca elata, 12 Apr. 1992, A.W. Ramaley 9217 (UC 1475102 – holotype of P. uniseptata); California: Walnut Creek, Ruth Bancroft Garden, 1552 Bancroft Road, on leaves of Yucca rostrata, 20 Mar. 2012, P.W. Crous (CBS H-21730 – epitype designated here of K. yuccigena, MBT178281; cultures ex-epitype CPC 20627 = CBS 138015, CPC 20623).

Notes: The genus Kellermania (Planistromataceae, Botryosphaeriales; Slippers et al. 2013) presently includes around 40 species, many of which were recently included in phylogenetic studies (Minnis et al. 2012, Crous et al. 2013). Although Sutton (1980) retained Alpakesa, Kellermania, and Piptarthron as separate genera, Nag Raj (1993) reduced Alpakesa to synonymy under Kellermania. Minnis et al. (2012) published the first phylogenetic revision of the group, and reduced all these genera to synonymy under Kellermania, supporting the view of Crous et al. (2012) that conidial appendages as single characters have insufficient value to separate genera in coelomycetes, and should rather be seen as species-specific characters. Names formerly described in genera typified by sexual morphs (Planistroma,
Planistromella), were combined into Kellermania by Minnis et al. (2012).

Authors: P.W. Crous and D.A. Giraldo López


Synonymy: Unconfirmed generic synonyms include *Amastigosporium* Bond.-Mont. and *Amastigis* Clem. & Shear 1931 (Braun 1995).

Current generic circumscription: Graminicolous, causing leaf spots. Colonies amphigenous, whitish, subellipsoide to dense. Mycelium internal, hyphae inter- and intracellular, hyaline, septate, sparsely branched, narrow. Conidiophores usually reduced to a single conidiogenous cell, solitary or loosely grouped, occasionally subfuscoide, arising from internal hyphae by the formation of a narrow penetration hypha which perforates the outer epidermal wall and cuticle and develops into a more or less cylindrical, colourless superficial conidiogenous cell. Conidiogenesis monoblastic, determinate to polyblastic, proliferation percurrent, inconspicuously annellated; conidial scars unthickened, not darkened, more or less flat, truncate to somewhat convex. Conidia solitary, subcylindric, broadly ellipsoid-fusiform, euseptate, hyaline, smooth, without or with filament appendages, hila unthickened, not darkened, but conidia sometimes with a small cingulum-like ring at the base; conidial secession schizolytic.

Sexual morph: unknown

Type species: *Mastigosporium album* Riess 1852.


(Fig. 8)

Leaf spots amphigenous, pale brown, subcircular, up to 5 mm diam, containing creamy sporodochia. Mycelium consisting of hyaline, smooth, thin-walled, branched, septate, 2–3 µm diam hyphae. Conidiophores smooth, hyaline, subcylindric, 1–3-septate, mostly unbranched, flexuous, arising from a brown stroma, 20–70 × 5–7 µm. Conidiogenous cells terminal, integrated, subcylindric, smooth, hyaline, proliferating sympodially and percurrently at apex, 15–25 × 5–7 µm. Conidia solitary, obclavate to fusoid-ellipsoid, hyaline, guttulate, straight, 3–5 transversely euseptate, constricted at septa, hyaline but...
appearing olivaceous with age, widest in second cell from base, hilum truncate, 3–7 µm diam, with minute marginal frill, (48–) 55–65(–70) × (10–)12–15(–17) µm. Conidia containing several cellular appendages that are hyaline, smooth, subcylindrical, branched or not, septate. Apical appendage arising from terminal end, 20–120 × 2–3 µm, with 1–3 lateral branches, or branching dichotomously, flexuous, or apex giving rise to two appendages; apical appendage bluntly rounded, rarely with clavate apex. Lateral appendages (1–2) arising from apical cell or second or even third cell from apex, 40–100 µm long, 0–3-septate.

Culture characteristics: Colonies slow-growing, reaching 10 mm diam after 2 wk at 25 ºC, erumpent, with sparse aerial mycelium, and uneven, lobate margins. On MEA and PDA surface dirty white to buff. On OA surface umber with ochreous, diffuse pigment.


Notes: The genus Mastigosporium (Helotiales) has around 10 species and five varieties, and is known to have a high degree of host specialisation. Species of the genus are commonly associated with leaf spot diseases of Poaceae. The type species, M. album, is known from several grass species, occurring commonly in temperate regions, but also known from the Arctic. It is especially common on species of Alopecurus (Braun 1995).

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Current generic circumscription: Conidiomata pycnidoid, immersed at first and then becoming partly erumpent, unilocular, glabrous, brown, lacking an ostiole but dehiscing by an irregular rupture in the apical wall and overlying host tissue; wall of textura angularis, cells thick-walled and brown in the outer layers, thin walled and colourless in the inner layers. Conidiophores intermingled with paraphyses, arising from the inner layer of cells of the wall all around the cavity of the conidioma, branched or unbranched and septeate at the base, colourless, smooth, invested in mucus. Paraphyses filamentous, branched or unbranched, septeate, colourless, smooth, narrow at the base, broad and deeply lobed or irregular at the apex. Conidiogenous cells discrete, subcylindrical to obclavate, colourless, smooth. Conidiogenesis holoblastic, maturation by diffuse wall-building synchronous with conidium ontogeny; delimitation by a transverse septum; secession schizolytic, annellations, periclinal thickenings and regeneration of conidiogenous cells absent. Conidia naviculate to fusiform with a truncate base and an acute apex, unicellular, colourless, guttulate; bearing appendages at both ends; appendages tubular, filiform, flexuous, unbranched, apical appendage single; basal appendages 2–4; inserted laterally, slightly above conidium base.


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Associated with leaf litter of Eucalyptus spp. Conidiomata pycnidoid, separate, subepidermal, exuding a pale yellow conidial cirrus; subglobose, to 250 µm wide, and 300 µm high, unilocular, often irregularly lobed, opening by irregular rupture of apical wall, 20–30 µm thick, of brown textura angularis, becoming hyaline towards centrum. Paraphyses hyaline, smooth, branched or not, septate, 15–100 × 1–3 µm; apex irregularly curved to lobed. Conidiophores 0–2-septate, unbranched or branched below, 10–20 × 3–4 µm, hyaline, smooth, subcylindrical. Conidiogenous cells subcylindrical, terminal and lateral, hyaline, smooth, 1.5–2.5 µm; Conidia naviculate to fusiform, tapering to acutely rounded apex, and truncate base, aseptate, smooth, guttulate, (9–) 13–15(–18) × (2.5–)3(–3.5) µm, bearing a single tubular, filiform, flexuous apical appendage, 7–12 µm long; basal appendages (2–5) lateral, slightly above truncate base, unbranched, divergent, straight to flexuous, 8–12 µm long.

Culture characteristics: Colonies spreading, flat, reaching 55 mm diam after 2 wk at 25 ºC, with sparse aerial mycelium and feathery margins. On OA, MEA and PDA surface and reverse buff to dirty white.


Notes: The genus Mycotribulus is one of the few coelomycete genera confirmed within the Basidiomycota (Physalacriaceae, Agaricales according to Rungjindamai et al. 2008) and is presently monotypic. Isolates are commonly associated with Eucalyptus, but the species can also occur on other hosts such as Apodytes abbotii, Mangifera indica and Syzygium cordatum (Crous 1993, Marincowitz et al. 2010). The LSU sequence of two strains of Mycotribulus from Eucalyptus pellita × brassiana in Indonesia (this study) and E. camaldulensis in Thailand (BCC13341, GenBank accession EF589740, Rungjindamai et al. 2008), respectively, differed in their LSU sequence from M. mirabilis (Fig. 1) and might represent a second Mycotribulus species. Unfortunately no ITS sequence of BCC13341 was available for comparison.

Authors: P.W Crous and D.A. Giraldo López

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Fig. 9. Mycotribulus mirabilis (CBS 138016). A. Conidiomata on Eucalyptus leaf in vivo. B. Conidiomata forming on PDA. C–D. Conidiogenous cells giving rise to conidia. E–G. Conidia. Bars: A = 300 µm, B = 250 µm, all others = 10 µm.
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Eucalyptus

283–303.

Thyrsidiana

Cymbothyrium, Melanostroma, Phialophorophoma

Amphiciliella, Choanatiara


Pilidiella
tibouchinae

