Mycol Progress (2014) 13:671–681
DOI 10.1007/s11557-013-0949-8

ORIGINAL ARTICLE

Sporoschismopsis angustata sp. nov., a new holomorph species in the Reticulascaceae (Glomerellales), and a reappraisal of *Sporoschismopsis*

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Received: 24 October 2013 / Revised: 26 November 2013 / Accepted: 1 December 2013 / Published online: 24 December 2013

Abstract A holomorph species, *Sporoschismopsis angustata,* is described. It represents the second known and experimentally proven teleomorph-anamorph link in the genus. In the multigene analysis, based on sequences of small and large subunits of nuclear ribosomal DNA (nc18S and nc28S rDNA) combined with the second largest subunit of RNA polymerase II (RPB2), *Sporoschismopsis* is positioned in the Reticulascaceae of the Glomerellales (Hypocreomycetidae). In keeping with the tenets of the new International Code of Nomenclature for algae, fungi and plants, the oldest generic name *Sporoschismopsis* is used for the holomorph. The teleomorph genus *Porosphaerellopsis* is formally transferred to the synonymy of *Sporoschismopsis*, and a new combination of *P. sporoschismophora* in *Sporoschismopsis* is proposed. *Porosphaerellopsis bipolaris* is not accepted in *Sporoschismopsis*. A key to the species accepted in *Sporoschismopsis* is provided. *Sporoschismopsis* is compared with the morphologically similar *Sporoschisma* of the Chaetosphaeriales (Sordariomycetidae). Their delimitation is re-evaluated in the light of changes to the genus concept suggested by Goh et al. (Mycol Res 101: 1295–1307, 1997). The characters of percurrently regenerating conidiophores and the shape of the phialide venter are not accepted as the main diagnostic criteria at the genus level. Instead, the original concepts of both genera are followed, and *Sporoschismopsis* is most readily distinguished from *Sporoschisma* by the absence of capitate setae and the anatomy of the conidia. *Sporoschismopsis australiensis* is transferred to *Sporoschisma*. The capitate setae are discussed and linked as a diagnostic character with members of the Chaetosphaeriales.

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Keywords Capitate setae · Genus concept · Multigene phylogeny · *Porosphaerellopsis* · *Sporoschisma* · Systematics

Introduction

The genus *Sporoschismopsis* Hol.-Jech. & Hennebert was described for saprobic, wood-inhabiting dematiaceous hyphomycetes (Holubová-Jechová and Hennebert 1972). It is characterized by robust conidiophores, often percurrently regenerating monophialides terminating in a funnel-shaped collarette, and brown, septate, clavate, cuneiform, obovate or pyriform conidia, bluntly rounded at the distal end and truncate at the basal end, developing in a basipetal succession in fragile chains. To date, the genus comprises five species, viz. *S. australiensis* Goh & K. D. Hyde, *S. caribensis* Hol.-Jech., *S. dingleyae* S. Hughes & Hennebert, *S. moravica* Hol.-Jech. & Hennebert (type species), and *S. simmonsii* (Morgan-Jones) Hol.-Jech. & Hennebert (Hughes 1978; Holubová-Jechová and Hennebert 1972; Goh et al. 1997; Holubová-Jechová 1973, 1982).

Porosphaerellopsis sporoschismophora Samuels & E. Müll. is the only known teleomorph linked experimentally with *Sporoschismopsis* (as *Sporoschisma*-like, Samuels and Müller 1978; Müller and Samuels 1982a). Goh et al. (1997) identified the anamorph as *S. caribensis*. The teleomorph is characterized by reticulate interthecial filaments, which are filiform, branching, anastomosing, and form a "network" structure. However, such centrum is unique among taxa accommodated in the Sordariomycetidae, where the fungus was placed (Samuels and Müller 1978; Réblová et al. 1999). Another species, *Porosphaerellopsis bipolaris* K. M. Tsui & K. D. Hyde, was described by Ranghoo et al. (2001) from freshwater habitat. It possesses different centrum of wider, apically free true paraphyses, and the anamorph remains unknown. Based on molecular DNA data of nuclear large subunit ribosomal DNA (nc28S rDNA), the placement of *Sporoschismopsis* in the

Hypocreomycetidae (as the teleomorph *P. sporoschismophora*) was confirmed, and a relationship with *Colletotrichum* Corda (as *Glomerella* Spauld. & H. Schrenk), though unsupported, was suggested by Huhndorf et al. (2004). In the phylogenetic analysis of three genes, two nuclear ribosomal genes combined with a protein-coding gene, *Sporoschismopsis* was confirmed a member of the Reticulascaceae of the Glomerellales (Réblová et al. 2011). Similar reticulate interthecial filaments in the centrum were described for teleomorphs of *Cylindrotrichum* Bonord. (as *Reticulascus* Réblová & W. Gams) of the same family (Réblová and Gams 1999; Réblová et al. 2011).

Remarkable morphological similarities in conidiophores, phialides and conidia exist between *Sporoschismopsis* and the genus *Sporoschisma* Berk. & Broome of the Chaetosphaeriales. Delimitations of the latter genus proposed by Hughes (1966) and Nag Raj and Kendrick (1975) were based on the presence of capitate setae, which arise with conidiophores in tufts from small basal stromata, and the anatomy of conidia. Goh et al. (1997) emended the generic concepts of *Sporoschismopsis* and *Sporoschisma,* suggesting that the percurrent proliferation of conidiophores and the shape of phialide, viz. the presence/absence of a swollen venter, would have greater taxonomic significance at the genus level.

A recent collection made on a decaying twig of *Tilia cordata* Mill. represents an undescribed species of *Sporoschismopsis*. The ascomata grow on decorticated wood and periderm partly peeled off in juxtaposition with conidiophores of the anamorph. The fungus is characterized by dark brown, glabrous, papillate ascomata with two-layered wall; and unitunicate asci with a distinct inamyloid apical ring containing eight three-septate, fusiform, brown ascospores with middle cells darker than the distal ones. The colony is effuse, hairy, consisting of robust, upright, brown conidiophores terminating in a monophialide with attached basipetal chain of clavate to subcylindrical-clavate, pale brown, three-septate conidia. The same conidiophores and conidia were also produced in vitro from isolated ascospores.

To study phylogenetic relationships of the undescribed species of *Sporoschismopsis* with other taxa of the Glomerellales, a multigene phylogenetic analysis was performed. Sequence data from members of the Hypocreomycetidae were utilized in two data sets, the internal transcribed spacer (ITS) region of the DNA operon (ITS1-5.8S-ITS2), and small and large subunits of nuclear ribosomal DNA (nc18S and nc28S rDNA) combined with the second largest subunit of RNA polymerase II (RPB2) in a multigene analysis. For each data set, maximum likelihood and Bayesian inference were performed.

Materials and methods

Herbarium material and fungal strains

Dry ascomata were rehydrated with water; material was examined with an Olympus SZX12 dissecting microscope, and centrum material (including asci, ascospores and paraphyses) was mounted in Melzer's reagent, 90 % lactic acid, lactophenol with cotton blue or aqueous cotton blue (1 mg/ml). Hand sections of the ascomatal wall were studied in 3 % KOH. All measurements were made in Melzer's reagent. Means ± standard deviations (s.d.) based on 20–25 measurements are given for dimensions of asci, ascospores, conidia and conidiogenous cells. Images were captured by differential interference (DIC) or phase contrast (PC) microscopy using an Olympus DP70 Camera operated by Imaging Software Cell on an Olympus BX51 compound microscope.

Multi-ascospore isolates were obtained from fresh material with the aid of a spore isolator (Meopta, Prague, Czech Republic). Isolates were grown on potato-dextrose agar (PDA, Oxoid) and potato-carrot agar (PCA, Gams et al. 1998). Colonies were examined after incubation at 25 °C in the dark for 7, 21 and 30 days. A culture is maintained at CBS (CBS-KNAW Fungal Biodiversity Center, Utrecht, the Netherlands). Type material is deposited in PRM herbarium (National Museum in Prague).

DNA isolation, amplification and sequence alignment

These procedures were performed as described in Réblová et al. (2011). Accession numbers and isolate information for new ITS, nc28S, nc18S and RPB2 sequences derived from DNA extract of multiple-ascospore isolate of the new species of *Sporoschismopsis* are listed under the species treated. The new sequences were aligned with homologous sequences retrieved from GenBank. The selection of retrieved sequences was adjusted according to the BLAST top hits for each gene. The GenBank accession numbers of the sequences selected for phylogenetic analyses are given in the tree after the taxon names (Figs. 1, 2).

All sequences were manually aligned in BioEdit v. 7.0.9.0 (Hall 1999). The nc18S and nc28S alignments were enhanced by utilizing the homologous 2D structure of *Saccharomyces cerevisiae* Meyen ex E.C. Hansen (Gutell 1993; Gutell et al. 1993) in order to improve the decisions on homologous characters and introduction of gaps. These procedures and alignment of RPB2 sequences were performed as described in Réblová and Réblová (2013).

Two sequence alignments were constructed: (1) a three-gene alignment (nc18S-nc28S-RPB2) and (2) ITS alignment (ITS1-nc5.8S-ITS2). To combine sequences for a three-gene alignment, the individual alignments were concatenated into one. The given length of the alignment was assessed after

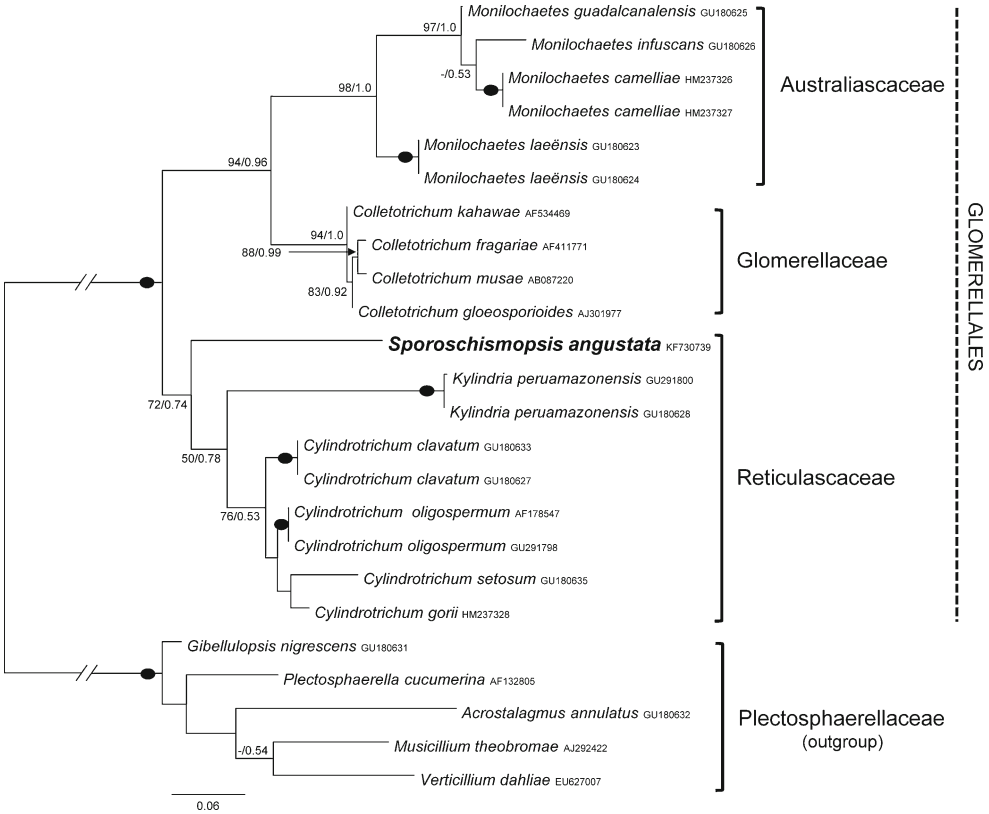


Fig. 1 Phylogenetic analysis of *Sporoschismopsis angustata* and members of the Glomerellales. Phylogram inferred from the ITS rDNA sequences with ML analysis using a GTRCAT model of evolution. Maximum likelihood bootstrap support (ML BS) and Bayesian posterior probability (PP) are indicated at the nodes. Branches with a black ellipse symbol indicate ML BS=100 %, PP values=1.0. The GenBank accession numbers are given after the names in the tree

introduction of gaps (see Results). The alignments and phylogenetic studies are deposited in TreeBase (Study no. 14816).

Phylogenetic analyses

All characters in the ITS alignment were included in the analysis. The first two-thirds of the 5′ half of the nc28S (D1 and D2 domains corresponding to the first 1,197 nucleotides of *Saccharomyces cerevisiae*), the almost entire nc18S, and the 5−7 segment of the RPB2 were analyzed. Bases 1−74 and 1−105 of the nc28S and nc18S alignments, respectively, and bases 1−60 of the RPB2 alignment were excluded from phylogenetic analysis because of the incompleteness of the 5′-end of the majority of the available sequences. Several outgroup taxa were used to root phylogenies, viz. five members of the Plectosphaerellaceae in the ITS phylogeny, and *S. cerevisiae* and *Vanderwaltozyma polyspora* (Van der Walt) Kurtzman (Saccharomycetes) in the three-gene phylogeny.

The combined multigene data set was partitioned into four subsets of nucleotide sites; (i) nc28S, (ii) nc18S genes, (iii) first and second codon positions of RPB2, (iv) third codon position of RPB2. Maximum likelihood analysis (ML) was performed with RAxML-HPC v. 7.0.3 (Stamatakis et al. 2005; Stamatakis 2006) using a GTRCAT model of evolution, which is a combination of GTRGAMMA and GTRCAT. The GTRCAT model (a RAxML-specific alternative model, in which the alignment sites are pooled into a pre-specified number of rate categories) was used for the heuristic search, and the best tree was then optimized and the likelihood values were calculated under the GTRGAMMA model. The nodal support was verified by nonparametric bootstrapping (BS) with 1,000 replicates.

Bayesian inference was performed in a likelihood framework, as implemented by MrBayes v. 3.0b4 software package to reconstruct phylogenetic trees (Huelsenbeck and Ronquist 2001). The program MrModeltest2 v. 2.3 (Nylander 2008) was used to infer the appropriate substitution model that would best fit the model of DNA evolution for our sequence data sets. Multiple Bayesian searches using Metropolis-coupled Markov chain Monte Carlo sampling were conducted. One cold and three heated Markov chains were used in the analysis. Bayesian analysis was run for 5 million generations, with trees sampled every 1,000 generations. The first 20,000 trees, which represented the burn-in phase of the analysis, were discarded. To estimate posterior probabilities (PP) of recovered branches, 50 % majority rule consensus trees were created from the remaining trees using PAUP (Larget and Simon 1999).

Phylogenetic results

The ITS data set for 19 species consisted of 24 sequences, each with 577 characters. The ML tree is shown in Fig. 1. The Glomerellales was resolved as a robust clade (ML BS

100 % / PP 1.0), comprising three major lineages: the Australiascaceae (98/1.0), Glomerellaceae (94/1.0), and Reticulascaceae (72/0.74). The latter family contains *Sporoschismopsis angustata* at the basal position, as sister taxon to *Kylindria* and *Cylindrotrichum*.

In the second analysis, the combined nc18S, nc28S and RPB2 sequences were assessed for 57 species of the Hypocreomycetidae. This multiple alignment consisted of 4231 characters. The ML tree is shown in Fig. 2. In this phylogeny, the Glomerellales is shown as a well-supported monophyletic clade (79/1.0), which together with the Plectosphaerellaceae (100/1.0) forms a robust clade (100/1.0) within the Hypocreomycetidae. The Glomerellales comprises three major subclades; the Australiascaceae (94/1.0), Glomerellaceae (100/1.0) and Reticulascaceae (100/1.0). *Sporoschismopsis angustata* and *S. sporoschismophora* form a strongly supported clade (95/1.0) within the Reticulascaceae.

Taxonomy

Sporoschismopsis Holubová-Jechová & Hennebert, Bull. Jard. Bot. Nat. Belg. 42: 385. 1972.

= *Porosphaerellopsis* Samuels & E. Müll., Sydowia 35: 143. 1982a.

≡ *Porosphaeria* Samuels & E. Müll., Sydowia 31: 127. 1978, non *Porosphaera* Dumort., Commentaries Botaniques p. 31. 1822.

Ascomata superficial to semi-immersed, sometimes with a small basal stroma, subglobose, conical or ovate, with a minute papilla or non-papillate, dark brown, glabrous. *Ascomatal wall* fragile, two-layered to three-layered; the third layer when present comprising pale brown to hyaline disintegrating cells. *Interthecial filaments* hyaline, septate, filiform, branching, anastomosing, forming a "network". *Asci* unitunicate, eight-spored, with a pronounced inamyloid, apical ring. *Ascospores* ellipsoidal with narrow ends to fusiform, transversely septate, uniformly brown or middle cells darker than the distal ones, contain a pore in the middle of each septum and at each end, pores distinct or indistinct.

Colonies effuse, hairy, brown or black. *Conidiophores* erect, straight to slightly flexuous, unbranched, brown, septate, thick-walled, terminating in a cylindrical to slightly flask-shaped monophialide with a deep funnel-shaped collarette that does not enclose more than one mature conidium. *Phialides* often regenerate percurrently after formation of the first chain of conidia, producing successively a series of functional phialides. *Conidia* clavate, cuneiform, obovate, pyriform to subcylindrical-clavate, with bluntly rounded distal end and truncate basal end, septate, uniformly brown or with paler distal and/or basal cells, septa in some cases obscured by a darker band, without or with conspicuous pores at the septa. Conidia developing subendogenously or endogenously at the apex of the phialide, maturing within the collarette and forming long fragile chains.

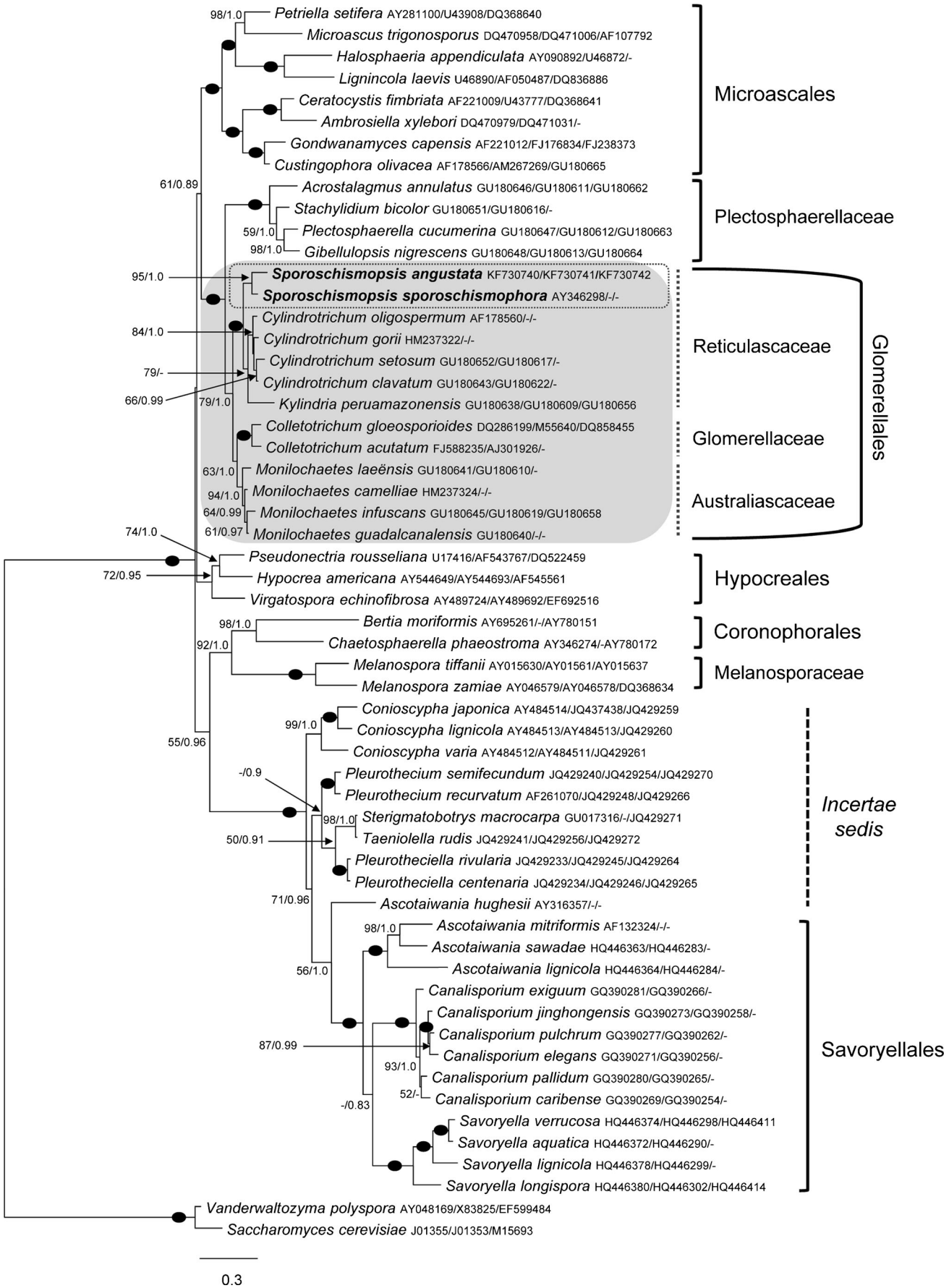
Fig. 2 Phylogenetic analysis of *Sporoschismopsis angustata* and members of the Hypocreomycetidae. Phylogram inferred from the combined nc28S-nc18S-RPB2 sequences. Model of evolution, support at the nodes and symbol explanation are identical to those mentioned in Fig. 1. The GenBank accession numbers given in the tree after the names are those of nc28S/nc18S/RPB2 genes. Missing sequences are indicated by "-" ▶

Sporoschismopsis angustata Réblová, *sp. nov*. Figs. 3, 4, 5. **MycoBank** MB805803

Etymology: *Angustatus* (L, *angustus* = narrow) refers to the width of conidia, which is the narrowest among the known *Sporoschismopsis* species.

Ascomata solitary or aggregated on wood that is decorticated or with periderm partly peeled off, superficial to semi-immersed, non-stromatic, (150–)200–300 μm diam, 220–320 μm high, subglobose to conical, black, glabrous, with sparse, septate, brown, 2.0–3.0 μm wide hyphae growing from the base, with a minute papilla pierced by the ostiolum; ostiolum lined with vertically arranged hyaline periphyses. *Ascomatal wall* 18–23 μm thick, fragile, two-layered. Outer layer consisting of thick-walled, brown, elongated or brick-like cells of *textura prismatica* with opaque walls, towards the interior grading into several layers of thin-walled subhyaline to hyaline, flattened cells. *Interthecial filaments* hyaline, septate, filiform, branching, anastomosing, forming a "network", not constricted at the septa, (0.7–)1.0–1.8(−2.0) μm wide, attached to the hymenium and to the top of the inner ascomatal wall. *Asci* (105–)110–130(−156)×(8.0–)8.5–9.5 μm (m ± s.d. = 120.8 ± 12.4×9.0 ± 0.6 μm), cylindrical, short-stipitate, apex broadly truncate with a minute inamyloid apical annulus, 2.8–3.0 μm wide, *ca*. 1.8 μm high; eight-spored. *Ascospores* (14.5–)15–17.5(−19)×(5.2–)5.5–6.0 μm (m ± s.d. = 16.4 ± 1.4×5.5 ± 0.4 μm), l/w 2.5–3.0, fusiform, three-septate, uniformly pale brown or with the two middle cells darker, the end ones paler brown to subhyaline, without pores at the septa or in the end cells, smooth-walled, obliquely uniseriate within the ascus, mature ascospores becoming minutely verrucose.

Colonies effuse, hairy, dark brown, irregular. *Conidiophores* arising singly or in tufts of 2–3, robust, upright, straight or slightly flexuous, unbranched, with immersed bulbose base and sparse basal hyphae, septate, 100–250 μm long, 6.0–7.5(−8.0) μm wide, brown to dark brown, thick-walled, smooth-walled, terminating in a monophialide. *Phialides* 45–55 μm long, 8.0–9.0(−10.0) μm wide at the broadest point (m ± s.d. = 50.2 ± 3.3×8.6 ± 0.6 μm), tapering to 4.5–5.0 μm, brown, terminated by a funnel-shaped, pale brown *collarette*, (12–)15–19 μm deep, (4.5–)5.0–6.0(−7.0) μm wide. Phialides regenerating percurrently after formation of the first chain of conidia, producing successively a series of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Lignincola laevis U46890/AF050487/DQ836886
Ceratocystis fimbriata AF221009/U43777/DQ368641
Ambrosiella xylebori DQ470979/DQ471031/-
Gondwanamyces capensis AF221012/FJ176834/FJ238373
Custingophora olivacea AF178566/AM267269/GU180665
Microascales
Acrostalagmus annulatus GU180646/GU180611/GU180662
Stachylidium bicolor GU180651/GU180616/-
Plectosphaerella cucumerina GU180647/GU180612/GU180663
Gibellulopsis nigrescens GU180648/GU180613/GU180664
Plectosphaerellaceae
Sporoschismopsis angustata KF730740/KF730741/KF730742
Sporoschismopsis sporoschismophora AY346298/-/-
Cylindrotrichum oligospermum AF178560/-/-
Cylindrotrichum gorii HM237322/-/-
Cylindrotrichum setosum GU180652/GU180617/-
Cylindrotrichum clavatum GU180643/GU180622/-
Kylindria peruamazonensis GU180638/GU180609/GU180656
Reticulascaceae
Colletotrichum gloeosporioides DQ286199/M55640/DQ858455
Colletotrichum acutatum FJ588235/AJ301926/-
Glomerellaceae
Monilochaetes laeënsis GU180641/GU180610/-
Monilochaetes camelliae HM237324/-/-
Monilochaetes infuscans GU180645/GU180619/GU180658
Monilochaetes guadalcanalensis GU180640/-/-
Australiascaceae
Glomerellales
Pseudonectria rousseliana U17416/AF543767/DQ522459
Hypocrea americana AY544649/AY544693/AF545561
Virgatospora echinofibrosa AY489724/AY489692/EF692516
Hypocreales
Bertia moriformis AY695261/-/AY780151
Chaetosphaerella phaeostroma AY346274/-AY780172
Coronophorales
Melanospora tiffanii AY015630/AY01561/AY015637
Melanospora zamiae AY046579/AY046578/DQ368634
Melanosporaceae
Conioscypha japonica AY484514/JQ437438/JQ429259
Conioscypha lignicola AY484513/AY484513/JQ429260
Conioscypha varia AY484512/AY484511/JQ429261
Pleurothecium semifecundum JQ429240/JQ429254/JQ429270
Pleurothecium recurvatum AF261070/JQ429248/JQ429266
Sterigmatobotrys macrocarpa GU017316/-/JQ429271
Taeniolella rudis JQ429241/JQ429256/JQ429272
Pleurotheciella rivularia JQ429233/JQ429245/JQ429264
Pleurotheciella centenaria JQ429234/JQ429246/JQ429265
Ascotaiwania hughesii AY316357/-/-
Incertae sedis
Ascotaiwania mitriformis AF132324/-/-
Ascotaiwania sawadae HQ446363/HQ446283/-
Ascotaiwania lignicola HQ446364/HQ446284/-
Canalisporium exiguum GQ390281/GQ390266/-
Canalisporium jinghongensis GQ390273/GQ390258/-
Canalisporium pulchrum GQ390277/GQ390262/-
Canalisporium elegans GQ390271/GQ390256/-
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Canalisporium caribense GQ390269/GQ390254/-
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Savoryella aquatica HQ446372/HQ446290/-
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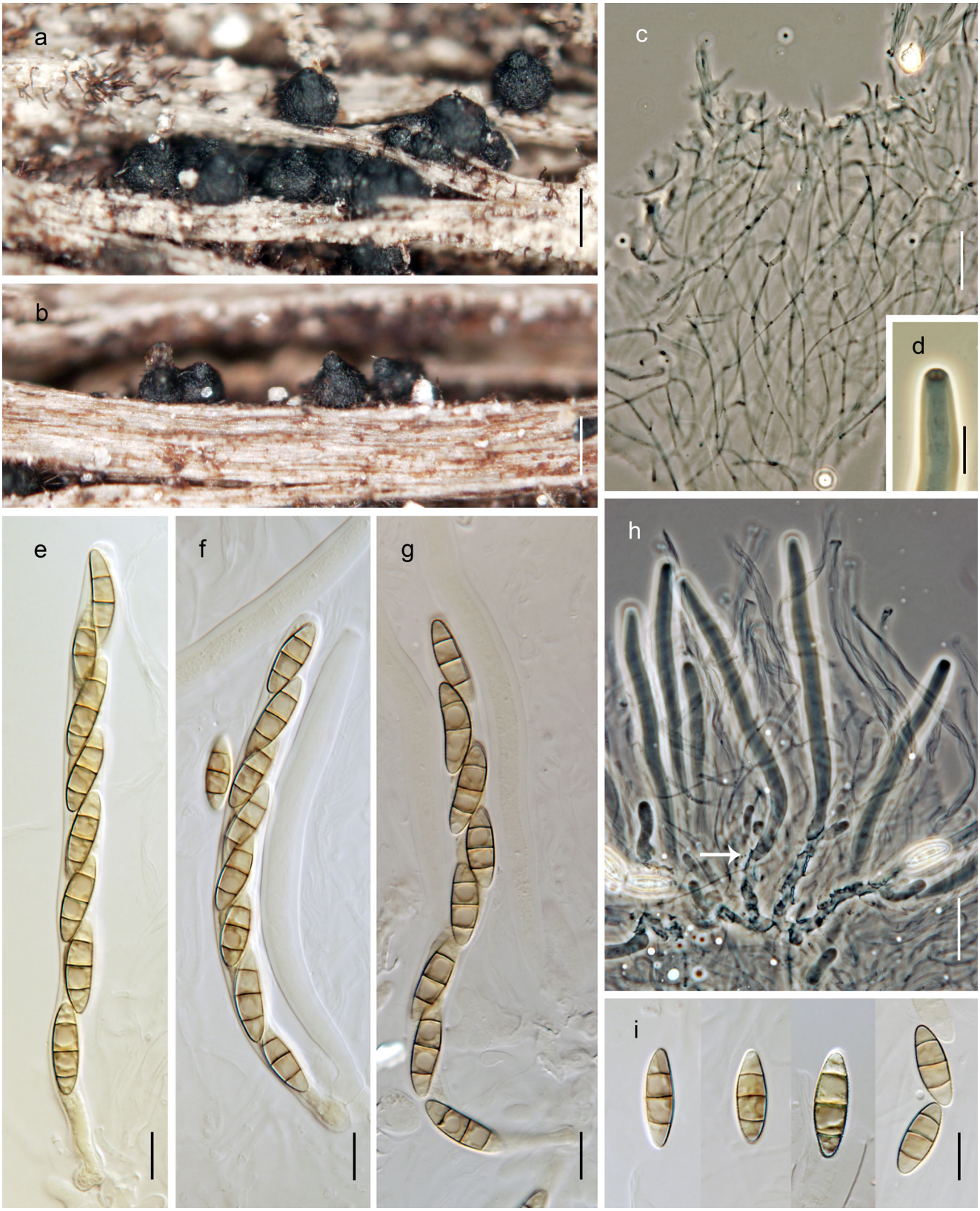

Fig. 3 *Sporoschismopsis angustata* on natural substrate. **a**, **b** Ascomata on decorticated wood, in a juxtaposition with conidiophores of the anamorph. **c** Interthecial filaments, branching, anastomosing, forming a "network" in the centrum. d Ascal apex with an apical ring. **e**–**g** Asci with ascospores arranged obliquely uniseriate. **h** Young asci attached to the ascogenous hyphae. **i** Ascospores. **a**-**i** (PRM 922622, holotype); **c**, **d**, **h** (PC), **e**–**g**, **i** (DIC); Bars: **a**, **b** = 300 μm, **c**, **h** = 20 μm, **d**–**g**, **i** = 10 μm

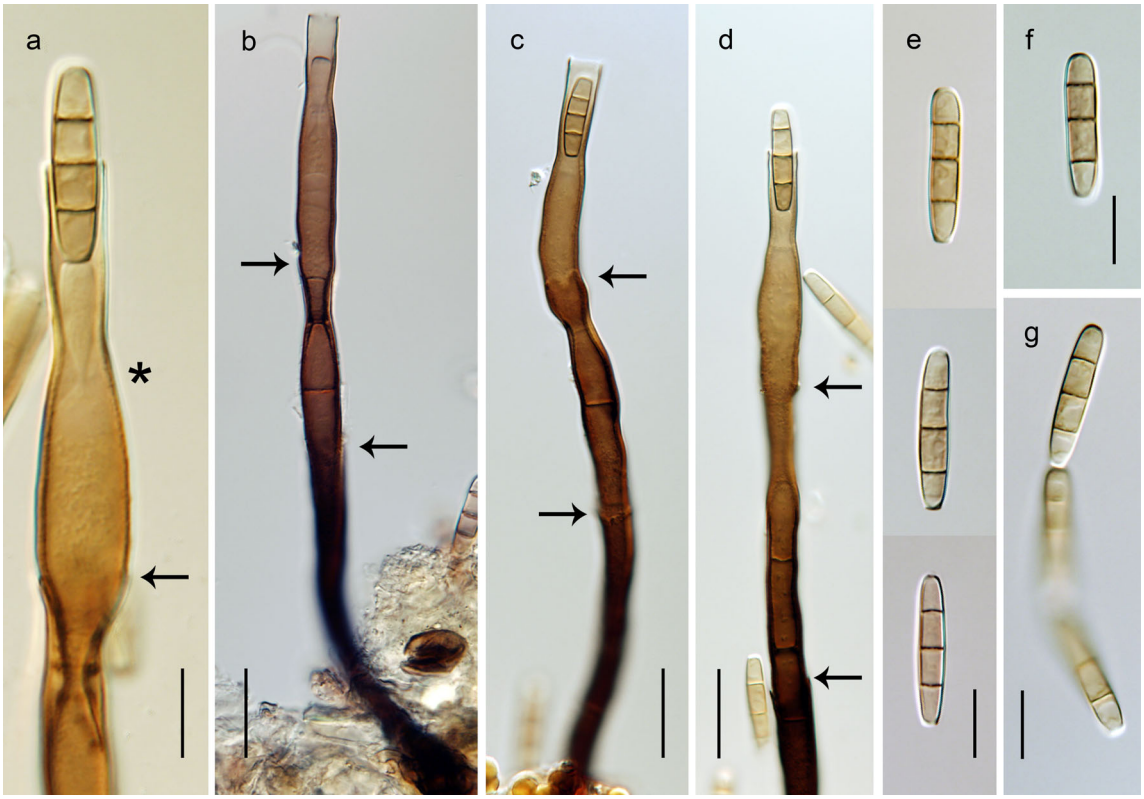

Fig. 4 *Sporoschismopsis angustata* on natural substrate. **a** Detail of the phialide and deep, hardly flaring, funnel-shaped collarette. **b**–**d** Conidiophores. **e**, **f** Conidia. **g** A chain of three conidia. Arrows indicate percurrent regeneration of the phialide. Asterisk indicates the point, where the venter merges into the collarette and a new conidium is borne at the apex of a phialide. Conidia maturing within the collarette in **a**, **c**, **d**; **a**–**g** (PRM 922622, holotype); **a**–**g** (DIC); Bars: **a**, **e**-**g** = 10 μm, **b**-**d** = 20 μm

two to four functional phialides. *Conidia* (17–)18–23(−26.5)×4.0–4.5(−5.0) μm (m ± s.d. = 20.5 ± 2.4×4.5 ± 0.4 μm), l/w 3.5–5.0(−6.0), clavate to subcylindrical-clavate, bluntly rounded at the apex, truncate at the base, 2.0–2.5 μm wide at the base, three-septate, pale brown, middle cells slightly darker than the end cells, septa not obscured by a darker band, without pores, smooth-walled. Conidia developing endogenously at the apex of the phialide, mature within the collarette, forming long fragile chains or collapsing in water droplets to conidial heads.

Characteristics in culture: Ascospores germinating after 48 h on PDA. Growth slow: colonies on PDA reaching 20–30 mm diam after 30 d at 25C in darkness, whitish; aerial hyphae abundant with a moist appearance; sterile, margin uneven; pale brown pigment diffusing into the agar. Colonies on PCA reaching 25–33 mm diam after 30 d at 25C in darkness, effuse, brown; aerial hyphae sparse or lacking; sporulating conidiophores growing throughout the colony; margin uneven; pale brown pigment diffusing into the agar. *Conidiophores* identical to those described on the natural substratum, 40–100 μm long, 5.0–6.5(−7.5) μm wide. *Phialides* 30–48 μm long, 7.0–9.0(−11.0) μm wide at the broadest point (m ± s.d. = 40.6 ± 5.3×8.6 ± 1.1 μm), tapering to (3.6–)4.5–5.0(−6.0) μm, brown, often regenerating percurrently after formation of a few conidia. *Collarette* (9.0–)11.5–15(−17) μm deep, 5.0–6.5 μm wide, funnel-shaped, pale brown to subhyaline. *Conidia* (14–)15–17(−17.5)×4.0–5.0(−5.5) μm (m ± s.d. = 16.1 ± 0.9×4.6 ± 0.4 μm), l/w 2.0–2.5, clavate, bluntly rounded at the apex, truncate at the base, 1.7–2.5 μm wide at the base, three-septate, uniformly pale brown or the middle cells slightly darker than the end cells, septa not obscured by a darker band, without pores, smooth-walled. No ascomata have developed in culture within 120 days.

Specimen examined: CZECH REPUBLIC. Southern Moravia, Mikulov district, Klentnice, Děvín-Kotel-Soutěska National Natural Reserve, on decaying wood and peeled off periderm of a twig of *Tilia cordata*, 31 Oct. 2011, *M. Réblová* (HOLOTYPE PRM 922622; living culture CBS 136360, ex-type).

Sequences: ITS: KF730739, nc28S: KF730740, nc18S: KF730741, RPB2: KF730742.

Comments: Among the known *Sporoschismopsis* species, *S. angustata* is readily distinguished by having the narrowest three-septate conidia, uniformly pale brown or with middle cells slightly darker than the distal ones, and with septa that are not obscured by a darker band. Similar uniformly brown, three-septate conidia also occur in *S. dingleyae* (Hughes 1978)

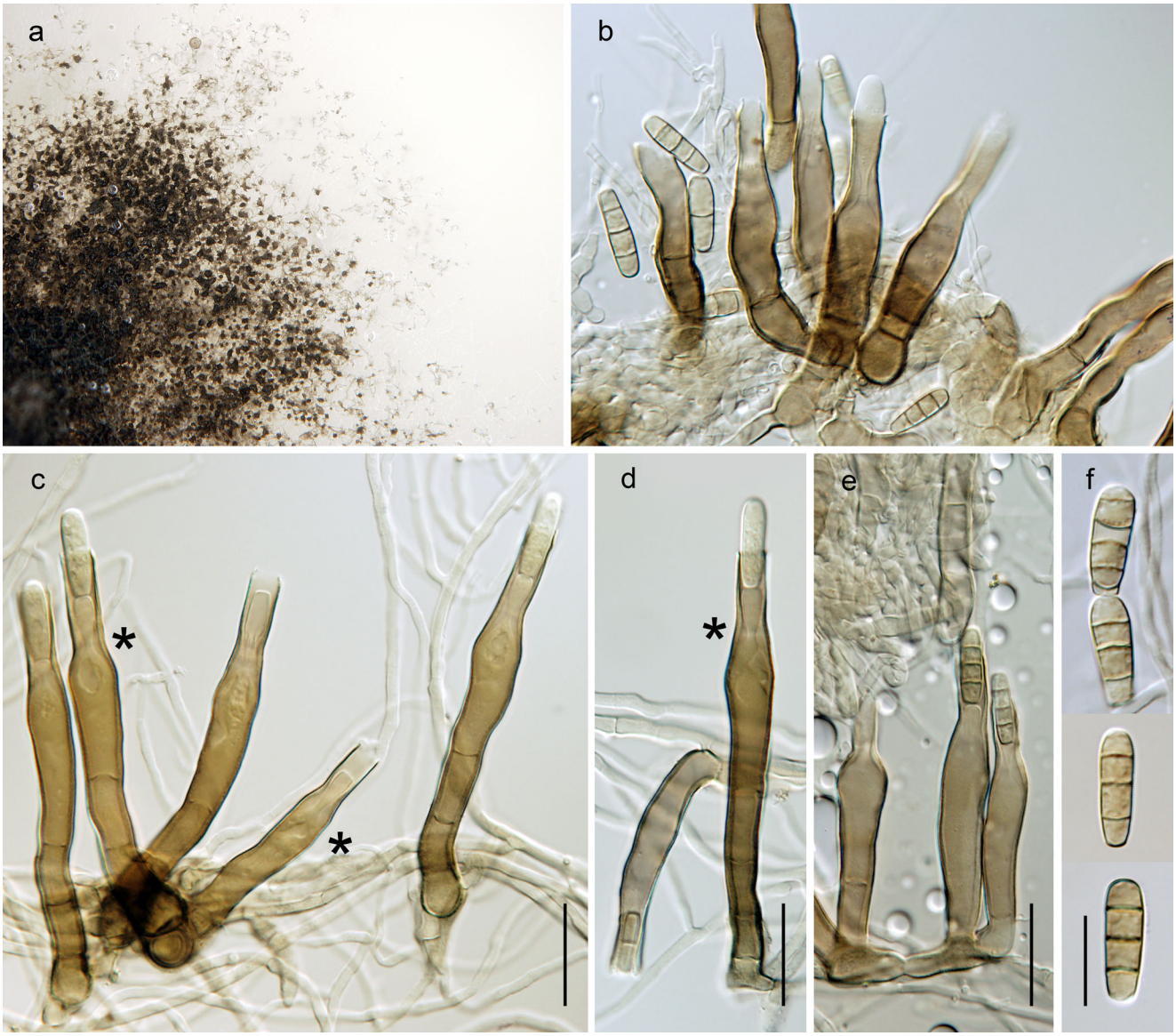

Fig. 5 *Sporoschismopsis angustata* in culture. **a** Colony sporulating on PCA. **b**–**e** Conidiophores with monophialides, conidia formed endogenously at the apex of the phialide and maturing within the collarette. **f** Conidia. Asterisk denoting wall thickening at the top of the venter where it merges into the collarette and a new conidium is borne at the apex of a phialide. **a**–**f** (CBS 136360, ex-type strain); **b**–**f** (DIC); Bars: **b**-**e** =20 μm; **f** =10 μm

and *S. simmonsii* (Morgan-Jones 1972). Both species differ from *S. angustata* by wider conidia and a darker band that obscures the conidial septa.

In the protologue of *S. simmonsii*, capitate setae are described. However, on the original photograph, only tufts of conidiophores are shown growing from the substratum. Repeated revisions of the type collection did not confirm the presence of capitate setae (Holubová-Jechová and Hennebert 1972; Ellis 1976; Hughes 1978).

The teleomorph of *S. sporoschismophora* (Samuels and Müller 1978) is well distinguishable from the teleomorph of *S. angustata* by shorter asci (85–120×8–10 μm) and longer three-septate ascospores (16–24×4–6 μm) that contain a conspicuous pore in the middle of each septum and one in each end; septa are slightly darker. It is a curious situation when one teleomorph of a species possesses pores at the septa, while the other does not. It is probable that the pores are present in the ascospores of in *S. angustata*, but are inconspicuous.

Sporoschismopsis sporoschismophora (Samuels & E. Müll.) Réblová, *comb. nov*. **MycoBank** MB805804

Basionym: *Porosphaerellopsis sproroschismophora* (Samuels & E. Müll.) Samuels & E. Müll., Sydowia 35: 143. 1982a

≡ *Porosphaeria sporoschismophora* Samuels & E. Müll., Sydowia 31: 127. 1978, nom. illegit. Art. 53.1 ICN.

Illustrations: Samuels and Müller (1978)

Habitat: Saprobic, on decorticated decaying wood in Brazil. Known only from the type locality.

Comments: The fungus was originally described as teleomorph species *P. sporoschismophora* with a *Sporoschisma*-like anamorph (Samuels and Müller 1978). Goh et al. (1997) identified the anamorph as *Sporoschismopsis caribensis*. The comparison of both taxa can be hampered by the fact that *S. caribensis* is known from the natural substratum, while *S. sporoschismophora* in axenic culture only. The in vitro conditions and different media may slightly change the colour, size and shape of conidia and conidiophores. The conidia of *S. caribensis* (Holubová-Jechová 1982) are longer and wider, septa are obscured by a darker band; two distal cells are paler than the central ones, and the basal cell is the palest. The collarette is verrucose and its wall is ornamented with minute low ridges. The conidia of *S. sporoschismophora* have only a paler basal cell, other cells are uniformly brown, and darker bands obscuring the septa are absent. Moreover, in each septum, a pore is visible and a central pore is also present in the basal cell. The morphological differences in the conidia are significant and warrant distinction of two different species.

Sporoschisma australiense (Goh & K.D. Hyde) Réblová, *comb. nov*. **MycoBank** MB805805

Basionym: *Sporoschismopsis australiensis* Goh & K.D. Hyde, Mycol. Res. 101: 1302. 1997.

Illustrations: Goh et al. (1997).

Habitat: On submerged wood in a freshwater stream, Australia. Known only from the type locality.

Comments: Based on the characters of cylindrical conidia with subtruncate ends, cylindrical and not flared collarette and presence of capitate setae growing in tufts with conidiophores from a basal stroma, the species is transferred to *Sporoschisma*, following the delimitation of the genus by Hughes (1966) and Nag Raj and Kendrick (1975). See also Discussion in this study.

Key to the species accepted in *Sporoschismopsis*

1. Conidia 3-septate 2
1. Conidia 3−7-septate, mostly 5-septate, [(24−)25−38(−43)×(6.5−)8.5−11.2 μm, (3.0−)4.0−6.0 μm wide at the base, clavate, central cells darker than the distal ones, septa of central cells obscured by a darker band] ..... *S. moravica*
2. Conidia up to 7.0 μm wide at the broadest point, uniformly brown 3
2. Conidia wider than 7.0 μm at the broadest point, uniformly brown or versicoloured 4
3. Conidia 4.0−4.5(5.0) μm wide ..... *S. angustata*
3. Conidia 6.0−7.0(−8.0) μm wide (16−20 μm long, cuneiform) ..... *S. simmonsii*
4. Conidia uniformly brown (18−27×9−11 μm, clavate) ..... *S. dingleyae*
4. Conidia with distal cells paler than the central ones and/or the basal cell is the palest....5
5. Conidial septa obscured by a darker band; conidia 21−30×8.5−16 μm, 4.0−7.0 μm wide at the base, clavate ..... *S. caribensis*
5. Conidial septa without a darker band, with a conspicuous pore at each septum and a central pore at the basal cell; conidia 18−22×10 μm, 6.5−8.0 μm wide at the base, obovate to cylindrical ..... *S. sporoschismoides*

Discussion

Species of *Sporoschismopsis* and *Sporoschisma* are morphologically remarkably similar. The genera share massive conidiophores, or stalked phialides, and brown, septate conidia that develop basipetally and successively, forming long fragile chains. Their teleomorphs are clearly distinguishable by different types of interthecial filaments. In *Sporoschismopsis*, the centrum consists of filiform reticulate filaments, frequently branching, anastomosing, and attached to the hymenium and to the top of the inner ascomatal wall (Samuels and Müller 1978; Müller and Samuels 1982b; this study) vs. true, generally wider paraphyses with free tapering apical ends in *Sporoschisma* (teleomorph *Melanochaeta* E. Müll., Harr & Sulmont; Müller et al. 1969). *Sporoschismopsis* is placed in the Reticulascaceae of the Glomerellales, together with the holomorph genus *Cylindrotrichum* and the anamorphic *Kylindria* (Réblová et al. 2011). *Sporoschisma*, on the other hand, is a member of the Chaetosphaeriaceae of the Chaetosphaeriales (Réblová et al. 1999; Huhndorf et al. 2004).

Sporoschismopsis accommodates taxa with robust, dark brown, septate conidiophores terminating in a monophialide with a deep funnel-shaped, hardly flaring collarette that does not enclose more than one mature conidium; the capitate setae are absent and stromata are not developed or may be rudimentary (Holubová-Jechová and Hennebert 1972; Holubová-Jechová 1982). The conidia are usually clavate, cuneiform, pyriform, obovate or subcylindrical-clavate, bluntly rounded at the distal end and truncate at the basal end. The phialides are cylindrical to flask-shaped, and often regenerate percurrently after production of several conidia. Based on the structure and function of the phialide, a close relationship with *Catenularia* was suggested by Holubová-Jechová and Hennebert (1972). The teleomorph-anamorph connection of *S. angustata* is the second known and experimentally proven link in *Sporoschismopsis*. *Porosphaerellopsis bipolaris* is another species accommodated in the former teleomorph genus (Ranghoo et al. 2001). It originates from freshwater habitat; the anamorph is unknown. It differs from the other two

teleomorphs of *Sporoschismopsis* by the centrum morphology; it comprises true paraphyses that are septate, tapering, apically free and longer than the asci, and ascospores possess bipolar mucilaginous pads. *Porosphaerellopsis bipolaris* is not accepted in *Sporoschismopsis,* and would be better placed among taxa of the Sordariomycetidae.

In contrast, the conidia of *Sporoschisma* are cylindrical, septate, and capitate setae are present and mixed in tufts with stalked phialides, borne on small superficial or semi-immersed stromata (Hughes 1966; Nag-Raj and Kendrick 1975; Ellis 1976). The stalked phialides are cylindrical or often have a slightly swollen venter, which narrows and expands gradually into a tubular collarette that is long enough to enclose more than one mature conidium. A chalara-like synanamorph was observed only in vitro (Müller and Samuels 1982c; Réblová unpubl.). Species of *Sporoschisma* are linked with teleomorphs in *Melanochaeta* (Müller et al. 1969; Hughes 1966; Müller and Samuels 1982c; Sivichai et al. 2000). The presence of capitate setae is closely associated with members of the Chaetosphaeriales. These upright setae are sterile, septate, brown, becoming paler to subhyaline towards the swollen apex, and bear a mucilaginous colourless cap or pale coloured exudate droplets that persist after drying. They accompany conidiophores of *Catenularia* and *Sporoschisma*, can often grow on ascomata of their respective teleomorphs, or can be present as capitate setae on ascomata of other members of *Chaetosphaeria* with hitherto unknown anamorphs, e.g. *C. capitata* Sivan. & H. S. Chang, and *C. conirostris* F. A. Fernández & Huhndorf (Fernández and Huhndorf 2005; Sivanesan and Chang 1995).

Sporoschismopsis is most readily distinguished from *Sporoschisma* by the absence of capitate setae and the anatomy of the conidia. Another important character that distinguishes members of these genera is the shape of the collarette. Although both genera were clearly delimited, some taxa may possess a mixture of morphological characters that may cause difficulties to place them unequivocally in either genus. Goh et al. (1997) considered percurrently proliferating conidiophores and presence/absence of a swollen venter of phialides to have greater taxonomic significance than characters listed above, and emended the generic concepts. In the light of these changes, *Sporoschismopsis australiensis* was placed in this genus (Goh et al. 1997). Although the species is characterized by cylindrical conidia with subtruncate ends, not flaring collarette and the presence of capitate setae arising in tufts with stalked phialides from a stromatic base, the percurrent regeneration of phialides and absence of a swollen venter were given preference. However, the percurrent regeneration of phialides, after having produced a certain number of conidia (or a first chain of conidia) from a fixed point, has little taxonomic significance. This may be often a matter of age, nutrient reserves, used medium and other factors. Also, the presence of a swollen venter is not a fixed morphological character of *Sporoschisma*. In *Sporoschisma nigroseptatum* D. Rao & P. Rag. Rao, the swelling of the phialide venter is variable and may be absent. The whole conidiophore, comprising the septate stalk and terminal monophialide, then tapers evenly from the base to the apex (Rao and Rao 1964; Hughes 1966). Variation in the shape of phialide was also observed in the new species *Sporoschismopsis angustata*. On the natural substrate, the phialides are cylindrical to slightly flask-shaped, while in the axenic culture, the conidiophore is reduced to few cells and swelling of the phialide venter is more pronounced.

Because percurrent regeneration of phialide and the presence or absence of a swollen venter are not considered characters delimiting both genera, the original concepts of *Sporoschisma* (Berkeley and Broome 1871; Hughes 1966) and *Sporoschismopsis* (Holubová-Jechová and Hennebert 1972) are followed in the present study, and *S. australiensis* is transferred to *Sporoschisma*.

Acknowledgments This study was supported by the Project of the National Foundation of the Czech Republic (GAP 506/12/0038) and as a long-term research development project of the Institute of Botany, Academy of Sciences No. RVO 67985939. I wish to thank Walter Gams for his helpful editorial suggestions. Václav Štěpánek is thanked for generating sequences used in this study.

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