



***Brunneodinemasporium jonesii* and *Tainosphaeria jonesii* spp. nov. (Chaetosphaeriaceae, Chaetosphaeriales) from southern China**

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Lu YZ, Liu JK, Hyde KD, Bhat DJ, Xiao YP, Tian Q, Wen TC, Boonmee S, Kang JC 2016 – *Brunneodinemasporium jonesii* and *Tainosphaeria jonesii* spp. nov. (Chaetosphaeriaceae, Chaetosphaeriales) from southern China. Mycosphere 7 (9), 1323–1332, Doi 10.5943/mycosphere/7/9/6

Abstract

A study of the fungi of Guangxi Province, China revealed two novel species, namely *Brunneodinemasporium jonesii* and *Tainosphaeria jonesii* which are introduced in this paper. Molecular analysis based on combined ITS and LSU sequence data showed that 1) *Brunneodinemasporium jonesii* formed a distinct clade with the type species *B. brasiliense* and is therefore introduced as the second species in this monotypic genus; 2) The isolates of *Tainosphaeria jonesii* clustered together with *T. crassiparvies* and *T. siamensis*, and showed a close relationship with *T. siamensis*, but is a phylogenetically distinct species. It is herein described as the third species of *Tainosphaeria*. Morphological examination showed that 1) *Brunneodinemasporium jonesii* differs from the generic type species as its conidia have mucilaginous balls at each end, which are aggregated in chains, arising from conidiogenous cells that are aggregated into conspicuous slimy, dome-shaped masses; 2) *Tainosphaeria jonesii* is characterized by its mononematous conidiophores, phialidic conidiogenous cells with funnel-shaped collarettes at the apices and conidia with single unbranched, flexuous, tubular appendages at each end. Descriptions, illustrations and molecular analyses are provided for these new species.

Keywords – New species – phylogeny – Sordariomycetes – taxonomy – woody fungi

Introduction

The order *Chaetosphaeriales* was introduced in *Sordariomycetidae* by Huhndorf et al. (2004) based on molecular phylogenetic analysis of LSU sequence data. *Chaetosphaeriales* comprises two families, *Chaetosphaeriaceae* and *Helminthosphaeriaceae* with 38 and seven genera respectively (Maharachchikumbura et al. 2015, 2016, Liu et al. 2016). The genera *Brunneodinemasporium* and

Tainosphaeria belong to the family *Chaetosphaeriaceae*.

The monotypic genus *Brunneodinemasporium* was introduced by Crous et al. (2012) with *B. brasiliense* Crous & R.F. Castañeda as the type species, to accommodate a dinemasporium-like species with tightly aggregated brown conidiogenous cells and pale brown conidia. According to Crous et al. (2012), *Brunneodinemasporium* differs from *Dinemasporium* in having randomly distributed setae throughout the basal stroma. *Dinemasporium* on the other hand, has a densely-aggregated layer of brown conidiogenous cells, with a prominent periclinal thickening and apically tapering conidia, that are pale brown, and have setae that are separated from the conidia by a septum (Crous et al. 2012, Liu et al. 2015). *Brunneodinemasporium* are saprobic on decaying leaves (Crous et al. 2012).

The genus *Tainosphaeria* was introduced by Fernández & Huhndorf (2005) based on the type species *T. crassiparves* F.A. Fernández & Huhndorf. It is characterized by subglobose to ovoid ascomata, simple, septate, hyaline paraphyses, unitunicate, cylindrical, pedicellate asci, with an apical ring, and hyaline, septate ascospores. Fernández & Huhndorf (2005) suggested that *Tainosphaeria* bears morphological similarities and is phylogenetically close to *Zignoëlla*. The asexual morph of *Tainosphaeria* resembles *Chloridium*, *Codinaea*, *Striatosphaeria* and *Zignoëlla* (Fernández et al. 2005). The asexual morph resembles *Chloridium matsushimae* W. Gams & Hol.-Jech. in the percurrent proliferations of the conidiogenous cell and the setulose conidia. It also resembles *Codinaea aristata* Maire in the terminal integrated conidiogenous cell, conspicuous funnel-shaped collarete and terminally setulate conidia. Liu et al. (2016) studied the family Chaetosphaeriaceae and described a second species named *T. siamensis* from freshwater in Thailand. *Tainosphaeria* species are reported as saprobic on decaying or submerged wood (Fernández & Huhndorf 2005, Liu et al. 2016).

In this paper, we introduce a novel *Brunneodinemasporium* species and one new *Tainosphaeria* species based on morphology and phylogenetic analysis.

Materials and Methods

Sample collection and specimen examination

Decaying wood samples were randomly collected from sampling sites in flowing freshwater streams of Guangxi Province, China. Samples were returned to the laboratory in Zip-lock plastic bags. The material was examined with a Motic SMZ 161 series stereo-microscope. Micro-morphological structures were photographed using a Nikon ECLIPSE Ni compound microscope fitted with a Canon EOS 600D digital camera and measurements made using Tarosoft (R) Image Frame Work program (Liu et al. 2010). Figures were processed with an Adobe Photoshop CS6 Extended version 10.0 software (Adobe Systems, USA).

Single spore isolations were obtained using the method described by Chomnunti et al. (2014). Germinating spores were aseptically transferred to fresh potato-dextrose agar (PDA) media and incubated at 25–30 °C. The type specimens and ex-type living cultures are deposited in the Herbarium of Guizhou Academy of Agricultural Sciences (Herb. GZAAS) and Guizhou Culture Collection (GZCC), Guiyang, China respectively. Facesoffungi and Index Fungorum numbers are provided (Jayasiri et al. 2015, Index Fungorum 2016).

DNA extraction, PCR amplification and sequencing

Genomic DNA was extracted from fungal mycelium grown on PDA at 28 °C for 30 days. Two genes were amplified with universal primers, namely the internal transcribed spacer region of ribosomal DNA (ITS: ITS5/ITS4) (White et al. 1990), large subunit nuclear ribosomal DNA (LSU: LROR/LR5) (Vilgalys & Hester 1990). The PCR products were purified and sequenced with the same primers. The amplification reactions were carried out with the following protocol refs: The final volume of the PCR reaction was 50 µl which contained 2 µl of DNA template, 2 µl of each forward and reverse primers, 25 µl of 2 × Bench Top™ Taq Master Mix (mixture of Taq DNA Polymerase, dNTPs, and MgCl₂; Solarbio life sciences, Beijing, P. R. China) and 19 µl of sterilized water. The

PCR thermal cycle program for ITS gene amplification was provided as: initially 95 °C for 3 min, followed by 34 cycles of denaturation at 95 °C for 30 s, annealing at 51 °C for 1 min, elongation at 72 °C for 45 s, and final extension at 72 °C for 10 min. The PCR thermal cycle program for LSU gene amplification were provided as: initially 95 °C for 3 min, followed by 30 cycles of denaturation at 94 °C for 30 s, annealing at 51 °C for 50 s, elongation at 72 °C for 1 min, and final extension at 72 °C for 7 min. The quality of PCR products were checked on 1 % agarose gel electrophoresis strained with ethidium bromide. The PCR products were send for sequencing at Sangon Biotech, Shanghai, China.

Table 1 Isolates used in this study and their ITS and LSU GenBank accession numbers

Taxon	Culture No.	GenBank Accession No.	
		LSU	ITS
<i>Brunneodinemasporium brasiliense</i>	CBS 112007	JQ889288	JQ889272
<i>Brunneodinemasporium jonesii</i>	GZCC 16-0050	KY026055	KY026058
<i>Chaetosphaeria preussii</i>	CBS 262.76	AF178561	– ^a
<i>Chloridium lignicola</i>	CBS 143.54	AF178544	AF178544
<i>Codinaeopsis gonytrichoides</i>	CBS 593.93	AF178556	AF178556
<i>Dendrophoma cytisporoides</i>	CBS 223.95	JQ889289	JQ889273
<i>Dictyochaeta siamensis</i>	MFLUCC 15-0614	KX609952	KX609955
<i>Dinemasporium decipiens</i>	CBS 592.73	JQ889291	JQ889275
<i>Dinemasporium morbidum</i>	CBS 129.66	JQ889296	JQ889280
<i>Dinemasporium morbidum</i>	CBS 995.97	JQ889297	JQ889281
<i>Dinemasporium strigosum</i>	CBS 828.84	JQ889299	JQ889283
<i>Ellisembia brachypus</i>	HKUCC 10555	DQ408563	–
<i>Exserticlava vasiformis</i>	TAMA 450	AB753846	–
<i>Infundibulomyces cupulata</i>	BCC11929	EF113979	–
<i>Infundibulomyces oblongisporus</i>	BCC13400	EF113980	–
<i>Lasiosphaeria ovina</i>	SMH4605	AY436413	–
<i>Lecythothecium duriligni</i>	CBS 101317	AF261071	–
<i>Melanochaeta aotearoae</i>	SMH 3551	AF466082	–
<i>Melanochaeta hemipsila</i>	SMH 2125	AY346292	–
<i>Melanochaeta taitensis</i>	GKM156N	EU583220	–
<i>Melanochaeta taitensis</i>	GKM150N	EU583219	–
<i>Melanopsammella gonytrichii</i>	SMH 3785	AF466085	–
<i>Melanopsammella vermicularioides</i>	FC 404	AF466087	–
<i>Menispora tortuosa</i>	DAOM 231154	AY544682	KT225527
<i>Menispora tortuosa</i>	CBS 214.56	AF178558	AF178558
<i>Menisporopsis theobromae</i>	MFLUCC 15-0055	KX609954	KX609957
<i>Neopseudolachnella acutispora</i>	MAFF 244358	AB934041	AB934065
<i>Neopseudolachnella magnispora</i>	MAFF 244359	AB934042	AB934066
<i>Neopseudolachnella uniseptata</i>	MAFF 244360	AB934043	AB934067
<i>Pseudodinemasporium fabiforme</i>	MAFF 244361	AB934044	AB934068
<i>Pseudolachnea hispidula</i>	MAFF 244364	AB934047	AB934071
<i>Pseudolachnea fraxini</i>	CBS 113701	JQ889301	JQ889287
<i>Pseudolachnella botulispora</i>	MAFF 244367	AB934050	AB934074
<i>Pseudolachnella scolecospora</i>	MAFF 244379	AB934062	AB934086
<i>Pyrigemmula aurantiaca</i>	CBS 126743	HM241692	HM241692
<i>Pyrigemmula aurantiaca</i>	CBS 126744	HM241693	HM241693
<i>Rattania setulifera</i>	GUFCC 15501	HM171322	GU191794
<i>Tainosphaeria crassiparies</i>	SMH 1934	AF466089	–
<i>Tainosphaeria siamensis</i>	MFLUCC15-0607	KX609953	KX609956
<i>Tainosphaeria jonesii</i>	GZCC 16-0053	KY026056	KY026059
<i>Tainosphaeria jonesii</i>	GZCC 16-0065	KY026057	KY026060
<i>Thozetella nivea</i>	–	EU825200	EU825201
<i>Umbrinosphaeria caesariata</i>	CBS 102664	AF261069	–
<i>Zignoëlla pulviscula</i>	MUCL 15710	AF466090	–
<i>Zignoëlla pulviscula</i>	SMH 3289	AF466091	–

Notes – New isolates are in bold. ^a No data in GenBank.

Phylogenetic analysis

The sequenced taxa were determined using nucleotide BLAST searches online in GenBank (<http://www.ncbi.nlm.nih.gov/>) and those in recent papers on the family and genera studied herein (Crous et al. 2012, Ariyawansa et al. 2015, Liu et al. 2015, 2016, Maharachchikumbura et al. 2015, 2016). The combined alignments of ITS and LSU sequence data from the closest relatives in *Chaetosphaeriaceae* were used to generate phylogenetic placements. *Lasiosphaeria ovina* (strain SMH 4605) was used as the outgroup taxon. The sequence accessions in the analysis are provided in Table 1. The sequence data were aligned using MAFFT v.7.110 online program (<http://mafft.cbrc.jp/alignment/server/>) (Katoh & Standley 2013), and manually adjustment in BioEdit 7.2.3 (Hall 1999). Maximum likelihood (ML) and Bayesian inference (BI) were used in analyses with individual data from each partition in addition to the combined aligned dataset.

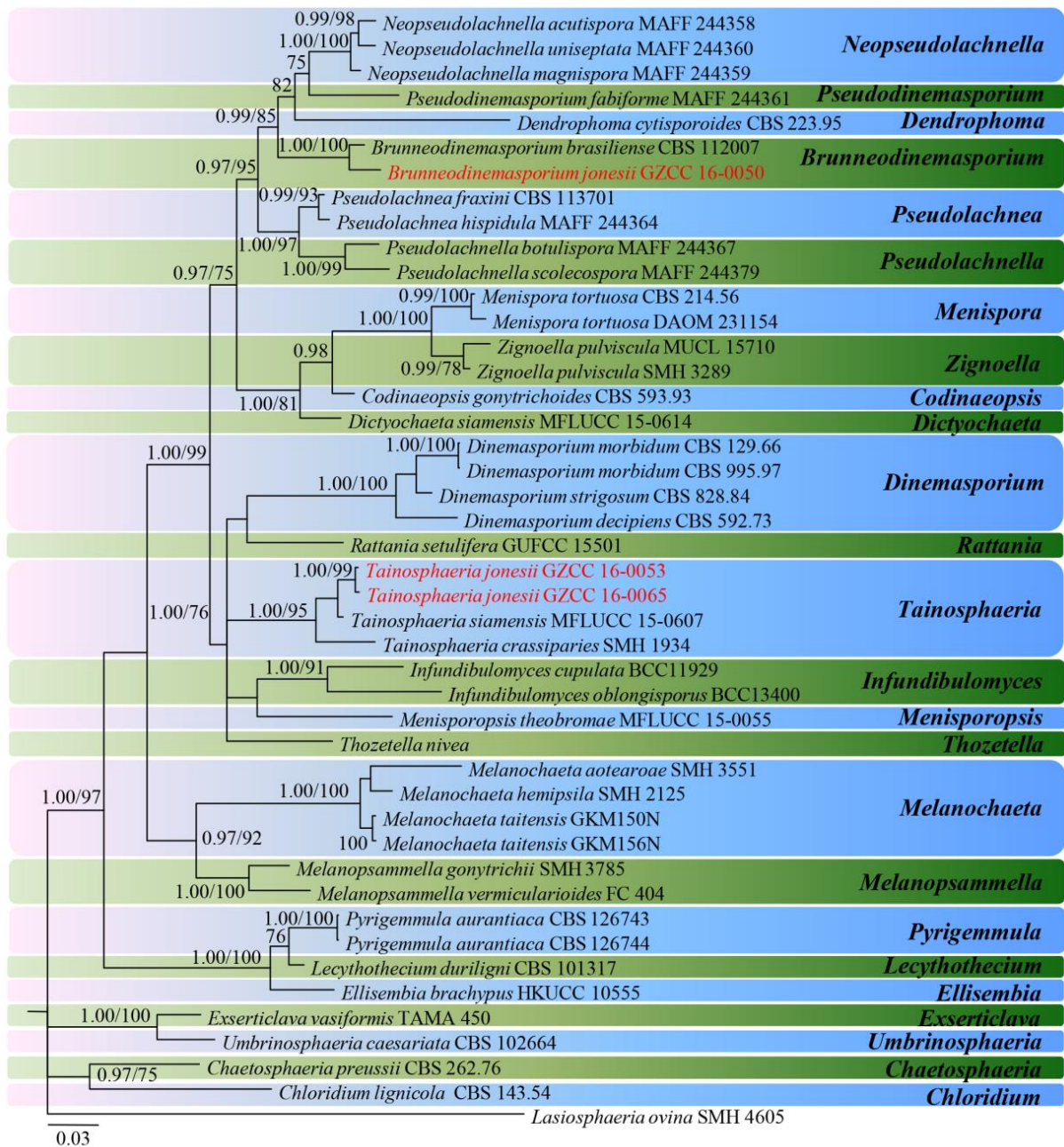


Fig. 1 – Consensus phylogram (50%) majority rule resulting from a Bayesian analysis of a combined ITS and LSU sequence alignment. Bayesian posterior probabilities greater than 0.95 (PP) and RAxML bootstrap support values greater than 75% (BS) are shown at the nodes. The tree is rooted with *Lasiosphaeria ovina* SMH 4605 (*Lasiosphaeriaceae*). New isolates are in red.

The phylogeny website tools “ALTER” (Glez-Peña et al. 2010) were used to transfer the alignment file from Nexus to Phy file for RAxML analysis. Maximum likelihood (ML) analysis was performed at the CIPRES Science Gateway v. 3.3 (<http://www.phylo.org/portal2/>, Miller et al. 2010) using RAxML v.8.2.8 as part of the “RAxML-HPC BlackBox” tool (Stamatakis 2006; Stamatakis et al. 2008). All free model parameters will be estimated by RAxML and ML estimate of 25 per site rate categories. Final ML search were conducted use the GTRGAMMA + I model. Bootstrap support values (BS) equal or greater than 75% are given above each node (Fig. 1).

Bayesian analysis was carried out using MrBayes v.3.1.2 (Ronquist & Huelsenbeck 2003). The best-fit model of sequences evolution was estimated by using MrModeltest 2.2 (Nylander 2004). Markov Chain Monte Carlo sampling (BMCMC) in MrBayes v.3.0b4 (Huelsenbeck & Ronquist 2001) were used to determine the Posterior probabilities (PP) (Rannala & Yang 1996; Zhaxybayeva & Gogarten 2002). Phylogenetic trees were sampled every 100th generation (resulting in 10,000 total trees) in 1,000,000 generations from the running of six simultaneous Markov chains. The first 2,000 trees which contained the burn-in phase of the analyses were discarded. The remaining 8,000 trees were used to calculate the posterior probabilities (PP) in the majority rule consensus tree. Bayesian posterior probabilities with those equal or greater than 0.95 are given below each node (Fig. 1). Phylogenetic trees were visualized using FigTree v1.4.0 (<http://tree.bio.ed.ac.uk/software/figtree/>, Rambaut 2012). The sequences are deposited in GenBank (Table 1). The alignment was deposited in TreeBASE (<http://www.treebase.org>, submission number 20263).

Results and Discussion

Phylogenetic analysis of combined LSU and ITS sequence data

Three isolates of hyphomycetes obtained from the incubated specimens of decaying wood were identified in the family *Chaetosphaeriaceae*. ITS and LSU sequence data and morphological characters were used to assign the species and to describe novel taxa with a comparison with similar taxa (Crous et al. 2012, Liu et al. 2016).

The combined sequence dataset of ITS and LSU was analyzed by using ML and Bayesian analyses (Fig. 1). All trees were similar in topology and did not differ significantly (data not shown). The combined sequence alignment comprised 45 taxa, including our new strains. Bootstrap support values of RAxML ($\geq 75\%$) are shown on the upper branches (Fig. 1). Values of the Bayesian PP (≥ 0.95) from MCMC analyses are shown below the branches.

One of our three isolates clustered with *Brunneodinemasporium brasiliense* in a well-supported clade, but is phylogenetically and morphologically distinct and is introduced as *B. jonesii* sp. nov. in this paper. Two morphologically similar, but phylogenetically different isolates to *Tainosphaeria siamensis* are identified as *T. jonesii* sp. nov.

Taxonomy

Brunneodinemasporium jonesii Y.Z. Lu, J.K. Liu & K.D. Hyde, sp. nov. Fig. 2

Index Fungorum number: IF 552516

Facesoffungi number: FoF 02638

Holotype – GZAAS 16–0062

Etymology – Named in honour of Professor E.B. Gareth Jones for his contributions to tropical mycology.

Saprobic on decaying wood in freshwater stream. Asexual morph: *Conidiomata* on woody substrate, mostly scattered or sometimes in groups of 2–3, superficial, globose to subglobose, becoming cupulate when dry, sporodochial, unilocular, dark brown to black, with a white to buff slimy conidial mass in center, setose. *Basal stroma* with cells of *textura angularis*. *Setae* abundant, brown to black, simple, straight, septate, wide at base, acute at apex, unbranched, smooth, thick-

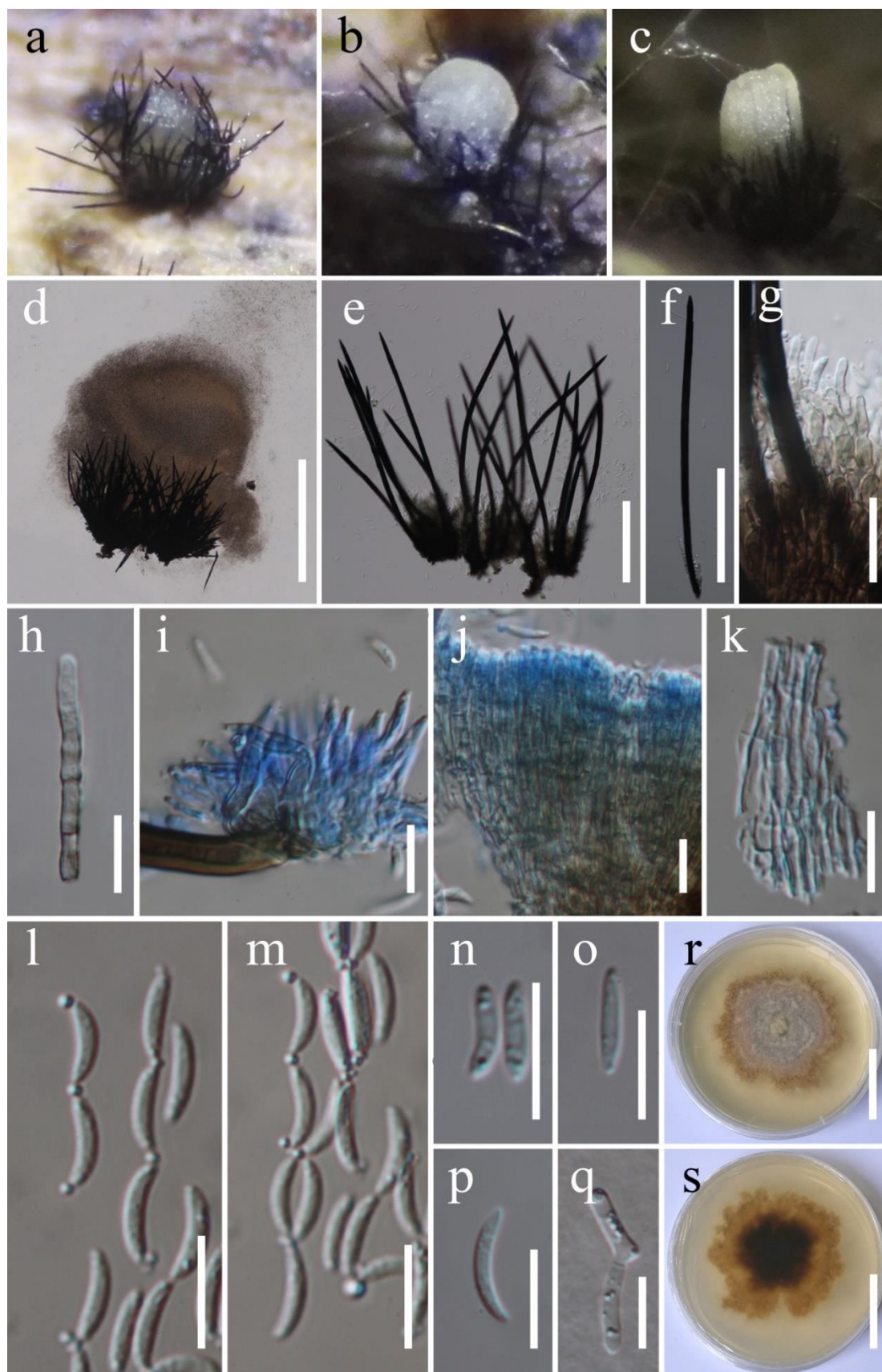


Fig. 2 – *Brunneodinemasporium jonesii* (GZAAS 16–0062, holotype). a–c Conidiomata on host surface. d Conidioma. e–f Conidioma setae. g–h Conidiophores and conidiogenous cells. i–k Basal stroma of conidioma and conidiophores stained with cotton blue. l–p Conidia (Note: conidia are connected by mucilaginous balls). q Germinating conidium. r–s Colonies on PDA from above and below. – Scale bars: d = 500 μ m, e–f = 100 μ m, g = 20 μ m, h–q = 10 μ m, r–s = 20 mm.

walled, 178–290 μm long, 5–7.5 μm wide, arising from basal stroma. *Conidiophores* lining the basal stroma into a densely-packed mass, brown, multi-septate, unbranched or branched, cylindrical, thin-walled, smooth, 53–71 \times 1.3–2 μm (\bar{x} = 63 \times 1.7 μm , n = 20). *Conidiogenous cells* integrated, determinate, phialidic with a collarete and clear periclinal thickening at apex, pale brown, smooth, subcylindrical to lageniform, 6.5–13 μm long \times 1–2.5 μm wide (\bar{x} = 9 \times 1.8 μm , n = 50). *Conidia* hyaline to subhyaline, aseptate, thin-walled, smooth, fusiform, straight or curved, obtuse to subobtusely rounded at apex, truncate to rounded at the base, aguttulate or guttulate, 6–9.5 \times 1.5–2 μm wide (\bar{x} = 8 \times 1.7 μm , n = 50), with mucilaginous balls released at the conidial ends; connecting the conidia in short false chains. Chains of conidia arising from conidiogenous cells aggregated into a conspicuous slimy, dome-shaped mass. Sexual morph: not observed.

Culture characteristics – *Conidia* germinating on water agar (WA) within 24 h and germ tubes produced from conidium. Colonies growing on potato dextrose agar medium (PDA), form irregular, surface rough, edge undulate, reaching 30 mm in two weeks at 28°C, initially pale brown and changing to brown when aged. *Mycelium* superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.

Material examined – CHINA, Guangxi Province, Fang Cheng Gang, on decaying wood in a freshwater stream, 15 May 2016, Yong-Zhong Lu, JHC17-1 (GZAAS 16–0062, **holotype**); ex-type living culture, GZCC 16–0050.

Notes – *Brunneodinemasporium jonesii* is introduced here as a novel species based on morphological distinctions and phylogenetic analysis. Combined LSU and ITS sequence data recognize *B. jonesii* as belonging to the genus *Brunneodinemasporium* and formed a distinct clade with the type species *B. brasiliense* with high support (100% BS and 1.00 PP) (Fig. 1). Morphologically, these two species are similar in conidiophores and setae, but they differ from each other by conidia shape. *Brunneodinemasporium brasiliense* have a single, unbranched, flexuous, tubular appendage at each end, but *B. jonesii* lacks this feature. Instead, the conidia are connected by mucilaginous balls in *B. jonesii*. Therefore, we introduced *B. jonesii* as the second species of *Brunneodinemasporium*.

Tainosphaeria jonesii Y.Z. Lu, J.K. Liu & K.D. Hyde, sp. nov.

Fig. 3

Index Fungorum number – IF 552517

Facesoffungi number – FoF 02639;

Holotype – GZAAS 16–0065

Etymology – Named in honour of Professor E.B. Gareth Jones for his contributions to tropical mycology.

Saprobic on decaying wood in freshwater stream. *Mycelium* composed of partly immersed and partly superficial, hyaline to pale brown, septate, with glistening conidial masses. Asexual morph: *Conidiophores* 44–98 (113) μm long 2.5–3.5 μm wide (\bar{x} = 71 \times 3 μm , n = 20), superficial, mononematous, macronematous, crowded, erect, unbranched, dark brown below half, pale brown towards the apex, septate, unbranched, smooth-walled, tapering to a terminal, single phialide. *Conidiogenous cells* phialidic, proliferating percurrently, subcylindrical, light brown, narrowing below the collarete. *Collarettes* light brown, funnel-shaped, 3.5–5 μm at the opening, 1.5–3 μm deep. *Conidia* 14–19 \times 2–3 μm wide (\bar{x} = 17 \times 2.5 μm , n = 50), hyaline, aseptate, thin-walled, smooth, fusiform, gently curved, rarely straight, obtuse to subobtusely rounded at the apex, truncate at base, eguttulate or guttulate, with single, unbranched, 6–8.5 μm long, flexuous, tubular appendage at each end, apparently separated from the conidium by a septum. Sexual morph: Undetermined.

Culture characteristics – *Conidia* germinating on water agar (WA) within 12 h and germ tubes produced from conidium. Colonies growing on potato dextrose agar medium (PDA), irregular, surface rough, edge undulate, reaching 30 mm in two weeks at 28°C, initially brown then becoming dark brown gradually, but greenish-brown in the center all the times. *Mycelium* superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.



Fig. 3 – *Tainosphaeria jonesii* (GZAAS 16–0065, holotype). a–b Conidia on host surface. c Conidiophore on host substrate. d Conidiophores with conidium. e Phialide with a developing conidium. f Apical phialide. g Germinating conidium. h–k Conidia. l–m Colonies on PDA from above and below. – Scale bars: c–e = 20 μ m, f–k = 10 μ m, l–m = 20 mm.

Material examined – CHINA, Guangxi Province, Fang Cheng Gang, on decaying wood in freshwater stream, 15 May 2016, Yong-Zhong Lu, JHC 21-4 (GZAAS 16–0065, **holotype**); ex-type living culture, GZCC 16–0053. CHINA, Guangxi Province, He Chi, on decaying wood in a mountain, 19 May 2016, Yong-Zhong Lu, ML 06-2 (GZAAS 16–0077); living culture, GZCC 16–0065.

Notes – Two strains of *Tainosphaeria jonesii* were isolated from the specimens collected from Guangxi Province, China. This is the first record of *Tainosphaeria* for China, while the other two previously described species were from Puerto Rico and Thailand (Fernández & Huhndorf 2005, Liu et al. 2016). *Tainosphaeria jonesii* was found as an asexual morph on natural woody substrates, and is morphologically similar to *T. siamensis*. However, the phylogeny (Fig. 1) indicates that they are different species. Although the statistical support (70% BS / 0.90 PP, data not shown) is not reach to the significant standard (75% BS / 0.95 PP), this might cause by the population of the genus, as well as only two genes included. However, from the topology it clearly showed that they could be phylogenetically distinct species. Moreover, we also compared the new species with *Tainosphaeria siamensis* by using single gene, and there are 7 bp and 10 bp differences in LSU and ITS respectively which also confirmed that they are phylogenetically distinct species even though they share similar morphology. Therefore, we introduced it as a novel *Tainosphaeria* species.

Acknowledgments

This work was funded by the grants of the National Natural Science Foundation of China (NSFC Grant No. 31460011) and the agricultural science and technology foundation of Guizhou province (Nos. NY[2013]3042) from the Science and Technology Department of Guizhou province, China. J.K Liu would like to thank the Phylogeny and Biodiversity of *Botryosphaeriaceae* in Southwest China (Qian KeHe LH 2015-7061).

References

- Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B et al. 2015 – Fungal diversity notes 111–252— taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 75, 27–274.
- Chomnunti P, Hongsanan S, Hudson BA, Tian Q et al. 2014 – The sooty moulds. *Fungal Diversity* 66, 1–36.
- Crous PW, Verkley GJM, Christensen M, Castañeda-Ruiz RF, Groenewald JZ. 2012 – How important are conidial appendages?. *Persoonia* 28, 126–137.
- Fernández FA, Huhndorf SM. 2005 – New species of *Chaetosphaeria*, *Melanopsammella* and *Tainosphaeria* gen. nov. from the Americas. *Fungal Diversity* 18, 15–57.
- Glez-Peña D, Gómez-Blanco D, Reboiro-Jato M, Fdez-Riverola F, Posada D. 2010 – ALTER: program-oriented conversion of DNA and protein alignments. *Nucleic Acids Research* 38, 14–18.
- Hashimoto A, Sato G, Matsuda T, Matsumura M et al. 2015 – Taxonomic revision of *Pseudolachnea* and *Pseudolachnella* and establishment of *Neopseudolachnella* and *Pseudodinemasporium* gen. nov. *Mycologia* 107, 383–408.
- Huelsenbeck JP, Ronquist F. 2001 – MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* 17, 754–755.
- Huhndorf SM, Miller AN, Fernández FA. 2004 – Molecular systematics of the *Sordariales*: the order and the family *Lasiosphaeriaceae* redefined. *Mycologia* 96, 368–387.
- Index Fungorum. 2016 – <http://www.indexfungorum.org/names/Names.asp>.
- Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat DJ et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. *Fungal Diversity* 74, 3–18.
- Katoh K, Standley DM. 2013 – MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30, 772–780.
- Liu JK, Chomnunti P, Cai L, Phookamsak R et al. 2010 – Phylogeny and morphology of *Neodeightonia palmicola* sp. nov. from palms. *Sydowia* 62, 261–276.

- Liu JK, Hyde KD, Jones EBG, Ariyawansa HA et al. 2015 – Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity* 72, 1–197.
- Liu JK, Yang J, Maharachchikumbura SSN, McKenzie EHC et al. 2016 – Novel *chaetosphaeriaceous* hyphomycetes from aquatic habitats. *Mycological Progress* 15, 1157–1167.
- Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC et al. 2016 – Families of *Sordariomycetes*. *Fungal Diversity* 79, 1–317.
- Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC et al. 2015 – Towards a natural classification and backbone tree for *Sordariomycetes*. *Fungal Diversity* 72, 199–301.
- Miller MA, Pfeiffer W, Schwartz T. 2010 – Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In *Proceedings of the Gateway Computing Environments Workshop 2010 (GCE)*, pp 1–8.
- Nylander JAA. 2004 – MrModeltest 2.0. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.
- Rambaut A. 2012 – FigTree version 1.4.0. Available at <http://tree.bio.ed.ac.uk/software/figtree>.
- Rannala B, Yang Z. 1996 – Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. *Journal of Molecular Evolution* 43, 304–311.
- Ronquist F, Huelsenbeck JP. 2003 – MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19, 1572–1574.
- Stamatakis A. 2006 – RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 22, 2688–2690.
- Stamatakis A, Hoover P, Rougemont J. 2008 – A rapid bootstrap algorithm for the RAxML web-servers. *Systematic Biology* 75, 758–771.
- Vilgalys R, Hester M. 1990 – Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172, 4238–4246.
- White TJ, Bruns T, Lee S, Taylor JW. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applications* 18, 315–322.
- Zhaxybayeva O, Gogarten JP. 2002 – Bootstrap, Bayesian probability and maximum likelihood mapping: exploring new tools for comparative genome analyses. *BMC Genomics* 3, 1.