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Morphological and molecular identification of a new species, *Trullella yunnanensis* (Steccherinaceae, Polyporales) from southern China

Xiao He¹, Jun-Hong Dong¹ & Chang-Lin Zhao^{1,2,3}

Summary. A new wood-inhabiting fungal species, *Trullella yunnanensis* sp. nov., is described based on morphological and molecular characters. *Trullella yunnanensis* is characterised by annual, laterally stipitate basidiomata with light brownish hymenial surface and a dimitic hyphal system with clamped generative hyphae and cylindrical, colourless, thin-walled, smooth basidiospores $(3.5 - 4.5 \times 1.5 - 1.9 \mu m)$. Sequences of ITS and LSU nrRNA gene regions of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony and bayesian inference methods. The phylogenetic analyses based on ITS and ITS+nLSU sequences in Steccherinaceae showed that *Trullella yunnanensis* nested into *Trullella* and then appeared to be the sister clade to all other species of *Trullella*. Further phylogeny inferred from ITS sequences among *Trullella* revealed that *Trullella yunnanensis* formed a monophyletic entity with a high support (100% BS, 100% BP and 1.00 BPP).

Key Words. molecular phylogeny, taxonomy, wood-inhabiting fungi, Yunnan province.

Introduction

Trullella Zmitr. (Steccherinaceae, Polyporales) is typified by *T. dentipora* (Ryvarden & Iturr.) Zmitr. (Miettinen & Ryvarden 2016; Zmitrovich 2018), which is characterised by a combination of pileate or laterally stipitate basidiomata, commonly spathulate, usually light brownish, smooth upper surface with coloured zones, a dimitic hyphal system (the context monomitic and the trama dimitic) with clamped, cyanophilous generative hyphae and cylindrical, thin-walled, smooth basidiospores (Miettinen & Ryvarden 2016). So far 6 species have been accepted in the genus worldwide (Miettinen & Ryvarden 2016).

Recently, molecular studies involving *Trullella* have been carried out (Miettinen *et al.* 2012; Miettinen & Ryvarden 2016; Westphalen *et al.* 2019). Miettinen *et al.* (2012) employed a revised family-level classification of Polyporales (Basidiomycota) based on a 5-gene dataset, in which *Trullella* belonged to the family Steccherinaceae. Phylogenetic studies of the polypore genera *Antella* Miettinen, *Austeria* Miettinen, *Butyrea* Miettinen, *Citripora* Miettinen and *Trullella* Zmitr. have shown the group to be polyphyletic, based on phylogenetic and morphological evidence, in which two new species and twenty-one new combinations were introduced (Miettinen & Ryvarden 2016). On the basis of the molecular analysis of muti-gene sequences, an overview of several polypore genera in Polyporales from the Neotropics revealed that *Trullella* nested into the family Steccherinaceae and then was sister to *Nigroporus* (Miettinen *et al.* 2012; Westphalen *et al.* 2019).

During investigations on wood-inhabiting fungi in southern China, an additional taxon was found which could not be assigned to any described species. In this study, the authors examined the taxonomy and phylogeny of this new species within *Trullella* based on the internal transcribed spacer (ITS) region and the large subunit nuclear ribosomal RNA gene (nLSU) sequences.

Materials and Methods

Morphological studies

The specimens studied are deposited at the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. Macromorphological descriptions are based on field notes. Colour terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens, observed under a light microscope (Dai 2012). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, CB+ = cyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic

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Species name	Sample no.	GenBank accession no.		
		ITS	nLSU	NERGEBUCS
Antella americana	HHB 4100	KP135316	KP135316	Floudas & Hibbett (2015)
Antella americana	FD 199	KP135315	KP135315	Floudas & Hibbett (2015)
Antella chinensis	Dai 9019	NR120162	NG057020	Yuan (2014)
Antella chinensis	GC 150113	KY688901	KY688201	Chen <i>et al.</i> (2018)
Antrodiella semisutina	KHI 11977	IX109849	IX109849	Binder et al. (2013)
Antroduella stibitata	Vuga 07	FI613651	FI613651	Unpublished
Antroductia supratia	ED 196	VD195914	VD195914	Eleveler % Uibbett (2015)
Antroateua supuata		Kr 155514	KF150514	Floudas & Hibbett (2015)
Atraporieua neotropica	Ley Ryvaraen 44447	HQ659221	HQ659221	Miettinen & Rajchenberg (2012)
Atraporella yunnanensis	CLZhao 603	MF962481	MF962484	Wu et al. (2017)
Atraporiella yunnanensis	CLZhao 605	NR158354	NG058606	Wu et al. (2017)
Butyrea japonica	OTU 795	MT596354	MT596354	Unpublished
Butyrea japonica	10202	JN710556	JN710556	Miettinen et al. (2012)
Butyrea luteoalba	FP 105786	KP135320	KP135320	Floudas & Hibbett (2015)
Butyrea luteoalba	5403	JN710558	JN710558	Miettinen et al. (2012)
Cabalodontia gracilis	H 6013927	KY415962	KY415962	Kotiranta et al. (2017)
Cabalodontia subcretacea	OTU 1518	MT594952	MT594952	Unpublished
Cabalodontia subcretacea	UC 2023116	KP814447	KP814447	Unpublished
Cerrena unicolor	FD 299	KP135304	KP135209	Floudas & Hibbett (2015)
Citribora afrocitrina	X 595	IN710507	IN710507	Miettinen et al. (2012)
Citritore afrecitiva	X 506	J1710507	JN710507	Miettinen et el (2012)
Curipora afrocurina	X 596	JN710508	JN710508	
Cutripora bannaensis	X 243	JN710526	JN710526	Miettinen <i>et al.</i> (2012)
Flaviporus brownii	X 1216	JN710537	JN710537	Miettinen <i>et al.</i> (2012)
Flaviporus brownii	MCW 36212	KY175008	KY175008	Westphalen et al. (2018)
Flaviporus tenuis	MCW 38612	KY175003	KY175003	Westphalen et al. (2018)
Flaviporus tenuis	MCW 44213	KY175001	KY175001	Westphalen et al. (2018)
Frantisekia mentschulensis	Cui 7195	KU509497	KU509497	Unpublished
Frantisekia ussurii	Dai 8249	KC485526	KC485526	Yuan (2014)
Frantisekia ussurii	Wei 3081	KC485527	KC485527	Yuan (2014)
Junghuhnia crustacea	X 262	JN710553	JN710553	Miettinen et al. (2012)
Junghuhnia crustacea	X 1127	JN710554	JN710554	Miettinen et al. (2012)
Junghuhnia pseudocrustacea	Yuan 6160	MF139551	MF139551	Yuan et al. (2019)
Junghuhnia pseudocrustacea	Zhou 283	MF139552	MF139552	Yuan et al. (2019)
Loweomyces fractipes	MT 132012	KX378866	KX378866	Westphalen <i>et al.</i> (2016)
Loweomyces fractipes	SFC 2015090280	KX792927	KX792927	$\operatorname{Kim} et al. (2016)$
Loweomyces spissus	MCW 48814	KX378869	KX378869	Westphalen <i>et al.</i> (2016)
Loweomyces spissus	MCW 47115	KA378808	KA378808	Westphalen et al. (2016)
Mycormaphium adustum	0024 Dai 10173	JIN710575 EC485554	JN710373 EC495527	Mietunen <i>et al.</i> (2012)
Nigroporus stibitatus	EaiP 116	MT110931	MT110931	Piepenbring at al. (2020)
Nigroporus stipitatus	X 546	IN710574	IN710574	Miettinen et al. (2012)
Nigroporus zinosus	BHS 2008100	IX109857	JX109857	Binder <i>et al.</i> (2013)
Nigroporus vinosus	KA 170261	MN294801	MN294801	Unpublished
Panus fragilis	HHB 11042	KP135233	KP135328	Floudas & Hibbett (2015)
Steccherinum bourdotii	LEBIN 4136	MK795068	MK795068	Unpublished
Steccherinum bourdotii	LEBIN 3985	MK795065	MK795065	Unpublished
Steccherinum ochraceum	KHL 11902	JQ031130	JQ031130	Sjökvist et al. (2012)
Steccherinum ochraceum	Ryberg s.n.	EU118669	EU118669	Larsson (2007)
Trulla dentipora	AS 2288	KY970064	KY952634	Unpublished
Trulla dentipora	WX 95	KY969748	KY969732	Unpublished
Trulla duracina	MCW 41012	MH475309	MH475309	Westphalen et al. (2019)
Trulla duracina	RP 96	MH475310	MH475310	Westphalen et al. (2019)
Trulla meridae	AS 2150	KY980668	KY980676	Unpublished
Trulla polyporoides	JV 100868	KY446068	KY446068	Kout <i>et al.</i> (2017)
Trulla yunnanensis	CLZhao 3218	MK268831 MK268830	OM864343	Present study
Trulla yunnanensis	CLZhao 3234	MK268832 OM864348	OM864344 OM864345	Present study
Trutta yunnanensis	CLZhao 3505	OM864349	OM864346 OM864347	Present study
1 ruita yunnanensis	CLZhao 4115	FJ439513	FJ439513	Present study
Truua yunnanensis Xaadhahama (1	OED 7007	JN710607	J19710607	Present study
Xaninoporus peckianus Xanita kana muina	QFB 7987			Audet (2010)
Aaninoporus syringae	1488	D.0000	DIFLOCOC	Mieitinen et al. (2012)
Xanthoporus syringae	X 339	JN710606	JN710606	Miettinen et al. (2012)

Table 1. List of species, specimens and GenBank accession numbers of sequences used in t	this study.
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average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from a given number (b) of specimens.

Molecular procedures and phylogenetic analyses

The EZNA HP Fungal DNA Kit (Omega Biotechnologies Co., Ltd, Kunming) was used to obtain PCR products from dried specimens, according to the manufacturer's instructions with some modifications. The ITS region was amplified with the primer pair ITS5 and ITS4 (White *et al.* 1990). The nuclear LSU region was amplified with the primer pair LR0R and LR7 (http://www.biology.duke.edu/ fungi/mycolab/primers.htm). The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, P.R. China. All newly generated sequences were deposited in GenBank (Table 1).

Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) was used to edit the DNA sequence. Sequences were aligned in MAFFT 7 (http://mafft.cbrc.jp/align ment/server/) using the "G-INS-i" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 27002). Sequences of *Cerrena unicolor* (Bull.) Murrill and *Panus fragilis* O.K.Mill. obtained from GenBank were used as an outgroup to root trees following Justo *et al.* (2017) in the ITS and ITS+nLSU analyses (Figs 1, 2) and *Mycorrhaphium adustum* (Schwein.) Maas Geest. was used as an outgroup to root the tree in the ITS analysis (Fig. 3).

Maximum parsimony analyses were applied to the ITS and ITS+nLSU dataset sequences. Approaches to phylogenetic analyses followed Zhao & Wu (2017), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BP) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics: tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree (MPT) generated. Sequences were also analysed using Maximum Likelihood (ML) with RAxML-HPC2 on Abe through the Cipres Science Gateway (www.phylo.org; Miller et al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). BI was calculated with MrBayes 3.1.2 with a general time reversible (GTR+I+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronguist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 1500 thousand generations (Fig. 1), for 2 million generations (Fig. 2), and for 40 thousand generations (Fig. 3) and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received maximum likelihood bootstrap value (BS) >75%, maximum parsimony bootstrap value (MP) >75%, or Bayesian posterior probabilities (BPP) >0.95.

Results

Molecular phylogeny

The ITS dataset (Fig. 1) included sequences from 57 fungal specimens representing 31 species in Steccherinaceae. The dataset had an aligned length of 1077 characters, of which 495 characters are constant, 97 are variable and parsimony-uninformative, and 485 are parsimony-informative. Maximum parsimony analysis yielded 9 equally parsimonious trees (TL = 2636, CI = 0.4108, HI = 0.5892, RI = 0.6918, RC = 0.2842). Best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis: GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.009995 (BI).

The phylogenetic tree (Fig. 1) inferred from the ITS sequences in Steccherinaceae, showed that *Trullella yunnanensis* nested into the genus *Trullella* and then was sister to all sampled species of *Trullella* with low support.

The ITS+nLSU dataset (Fig. 2) included sequences from 59 fungal specimens representing 32 species in Steccherinaceae. The dataset had an aligned length of 1730 characters, of which 1046 characters are constant, 99 are variable and parsimony-uninformative, and 585 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 3034, CI = 0.4021, HI = 0.5979, RI = 0.6843, RC = 0.2752). Best model for the ITS+nLSU dataset esticqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.016430 (BI)



Fig. 1. Maximum parsimony strict consensus tree of Steccherinaceae illustrating the phylogeny of Trullella yunnanensis and related species based on ITS sequences. Branches are labelled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95, respectively.

and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS) = 234.

Further phylogeny (Fig. 2) inferred from the combined ITS+nLSU sequences in Steccherinaceae, showed that Trullella yunnanensis clustered into Trullella and then was sister to a clade containing T. dentipora and T. duracina with low support.

The ITS dataset (Fig. 3) included sequences from 13 fungal specimens representing 6 taxa in Trullella. The dataset had an aligned length of 965 characters in the dataset, of which 655 characters are constant, 85 are variable and parsimony-uninformative, and 225 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 435, CI= 0.8713, HI = 0.1287, RI = 0.9100, RC = 0.7928). Best model for ITS estimated and applied in the Bayesian analysis: GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis resulted in the same topology with an average standard deviation of split frequencies = 0.008519 (BI).

The molecular analysis (Fig. 3) inferred from ITS sequences in genus Trullella, demonstrated that Trullella yunnanensis formed a monophyletic entity with a high 100% BS, 100% BP and 1.00 BPP in Trullella.

Taxonomic Treatment

Trullella yunnanensis C.L. Zhao sp. nov. Type: China, Yunnan Province, Puer, Laiyanghe National Forest Park, on fallen branch of angiosperm, 30 Sept. 2017, C. L. Zhao CLZhao 3234 (holotype SWFC).

MycoBank no.: MB 843170

GenBank no.: C. L. Zhao 3218 (ITS MK268831; nLSU OM864343); C. L. Zhao 3234 (ITS MK268830; nLSU OM864344); C. L. Zhao 3505 (ITS MK268832; nLSU OM864345); C. L. Zhao 4115 (ITS OM864348; nLSU OM864346); C. L. Zhao 8244 (ITS OM864349; nLSU OM864347).

Basidiomata annual, laterally stipitate, solitary. Pileus reniform to semicircular, applanate, 1 - 2.5 cm from the base to margin, 2 - 4 cm wide, up to 0.5 mm thick; upper surface smooth, radially striate, cream to yellow when juvenile, light brownish when old, zonate; the margin acute, entire. Pores round, 7 – 10 per mm,



Fig. 2. Maximum parsimony strict consensus tree of Steccherinaceae illustrating the phylogeny of *Trullella yunnanensis* and related species based on ITS+nLSU sequences. Branches are labelled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95, respectively.

dissepiments thin, entire, white to cream when juvenile, light brownish when old. Stipe cylindrical, up to 5.5 mm long, up to 3 mm in diam. Context leathery in fresh condition, corky to leathery in dried condition, cream, very thin, up to 0.2 mm thick. Tubes concolorous with poroid surface, corky, up to 0.3 mm long. *Hyphal structure*. Hyphal system dimitic; generative hyphae with clamp connections, IKI–, CB+; tissues unchanged in KOH. *Context.* Generative hyphae dominant, colourless, thin- to slightly thick-walled, branched, $3.5 - 5 \mu m$ in diam.; skeletal hyphae, colourless, thick-walled with a narrow to wide lumen, unbranched, interwoven, $4 - 5.5 \mu m$ in diam. *Tubes.* Generative hyphae colourless,

thin-walled, rarely branched, $2.5 - 4 \mu m$ in diam.; skeletal hyphae dominant, colourless, thick-walled with a narrow to wide lumen, unbranched, interwoven, $3.5 - 5 \mu m$. Hyphal pegs common, $25 - 45 \times 8 - 20 \mu m$. Cystidia and cystidioles absent; basidia clavate to barrel-shaped, with four sterigmata and a basal clamp connection, $9 - 14 \times 3 - 3.5 \mu m$; basidioles dominant, mostly pear-shaped, but slightly smaller than basidia. *Spores*. Basidiospores cylindrical and curved, colourless, thin-walled, smooth, IKI–, CB–, $(3 -) 3.5 - 4.5 (-5) \times 1.5 - 1.9 \mu m$, L = 4 µm, W = 1.6 µm, Q = 2.41 - 2.57 (n = 150/5). Figs 4, 5, 6.



Fig. 3. Maximum parsimony strict consensus tree illustrating the phylogeny of *Trullella yunnanensis* and related species in *Trullella* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95, respectively.

RECOGNITION. *Trullella yunnanensis* differs from all its congeners by the following combination of traits: annual, laterally stipitate, solitary basidiomata; round and small pores (7 - 10 per mm); a dimitic hyphal system with clamped generative hyphae, CB+; cylindrical and curved basidiospores, $3.5 - 4.5 \times 1.5 - 1.9 \text{ µm}$.

DISTRIBUTION. Known only from the type locality. SPECIMENS EXAMINED. CHINA. Yunnan Province, Puer, Laiyanghe National Forest Park, on the angiosperm trunk, 30 Sept. 2017, C. L. Zhao CLZhao 3218; Zhenyuan County, Wuliangshan National Nature Reserve, on

the angiosperm trunk, 2 Oct. 2017, C. L. Zhao CLZhao



Fig. 4. Basidiomata of Trullella yunnanensis (holotype). Scale bars: A 2 cm; B – E 1 cm; F 0.5 mm. PHOTOS: XIAO HE.



Fig. 5. Microscopic structures of *Trullella yunnanensis* (drawn from the holotype). **A** basidiospores; **B** basidia and basidioles; **C** hyphae from trama; **D** hyphae from context. Scale bars: **A**, **B** 5 µm; **C**, **D** 10 µm. DRAWN BY XIAO HE.

3505; Jingdong County, Wuliangshan National Nature Reserve, on fallen branch of angiosperm, 5 Oct. 2017, *C. L. Zhao* CLZhao 4115; on the trunk of *Pinus*, 22 Aug. 2018, *C. L. Zhao* CLZhao 8244 (SWFC).



Fig. 6. Microscopic structures of *Trullella yunnanensis* (draw from the holotype). A a section of hymenium and hyphal pegs in it. Scale bar: 10 μ m. DRAWN BY XIAO HE.

HABITAT. Lignicolous.

CONSERVATION STATUS. Not evaluated.

ETYMOLOGY. Refers to the locality (Yunnan Province) of the type specimens.

NOTES. In the present study, a new species, *Trullella yunnanensis* is described based on phylogenetic analyses and morphological characters.

Phylogenetically, the consensus BI phylogram of ITS and 28S sequences data set showed that eleven families were included in the order Polyporales and three families Steccherinaceae Parmasto, Podoscyphaceae D.A.Reid and Meripilaceae Jülich grouped together, in which Trullella was nested into Steccherinaceae and was sister to Nigroporus (Westphalen et al. 2019). In the present study, Trullella yunnanensis clusters into Trullella and then groups with T. dentipora and T. duracina (Figs 1, 2) and T. meridae (Miettinen & Ryvarden) Zmitr. (Fig. 3). However, morphologically, T. dentipora differs from T. yunnanensis by its ochraceous basidiomata upper surface and larger pores (2 – 5/mm; Ryvarden & Iturriaga 2003). Trullella duracina differs in its larger basidiospores $(4.3 - 5.3 \times 1.6)$ - 1.9 μm; Miettinen & Ryvarden 2016). Trullella meridae differs in its hard and cracking basidiomata and smaller pores (10 - 12/mm; Miettinen & Ryvarden 2016).

In geographical distribution, *Trullella* species are a rarely studied group of Basidiomycota (Dai 2012; Miettinen & Ryvarden 2016), and one species, *Trullella duracina*, was recorded in China (Dai 2012). However, the diversity of wood-rotting fungi is still not well known, especially in East Asian areas, many recently described taxa of wood-rotting fungi were from these areas (Dai 2012; Li & Cui 2013; Chen *et al.* 2014; Bian & Dai 2015; Han & Cui 2015; Song *et al.* 2016; Cui *et al.* 2019; Shen *et al.* 2019; Zhu *et al.* 2019). In the present study, *T. yunnanensis*, is from East Asia, too. It is possible that new taxa will be found after further investigations and molecular analyses.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

References

Audet, S. (2010). Essai de découpage systématique du genre Scutiger (Basidiomycota): Albatrellopsis, Albatrellus, Polyporoletus, Scutiger et description de six nouveaux genres. *Mycotaxon* 111 (1): 431 – 464. https://doi.org/10.5248/111.431

- Bian, L. S. & Dai, Y. C. (2015). Coltriciella globosa and C. pseudodependens spp. nov. (Hymenochaetales) from southern China based on morphological and molecular characters. Mycoscience 56: 190 – 197. https:// doi.org/10.1016/j.myc.2014.06.001
- Binder, M., Justo, A., Riley, R., Salamov, A., Lopez-Giraldez, F., Sjökvist, E., Copeland, A., Foster, B., Sun, H., Larsson, E., Larsson, K-H., Townsend, J., Grigoriev, I. V. & Hibbett, D. S. (2013). Phylogenetic and phylogenomic overview of the Polyporales. *Mycologia* 105 (6): 1350 – 1373. https://doi.org/10.3852/13-003
- Chen, C. C., Wu, S. H. & Chen, C. Y. (2018). Twelve species of Polypores (Basidiomycetes) new to Taiwan. *Fungal Sci.* 33 (1): 7 – 19.
- Chen, J. J., Korhonen, K., Li, W. & Dai, Y. C. (2014). Two new species of the *Heterobasidion insulare* complex based on morphology and molecular data. *Mycoscience* 55: 289 – 298. https://doi.org/10. 1016/j.myc.2013.11.002
- Cui, B. K., Li, H. J., Ji, X., Zhou, J. L., Song, J., Si, J., Yang, Z. L. & Dai, Y. C. (2019). Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. *Fung. Diversity* 97: 137 – 392. https://doi.org/10.1007/s13225-019-00427-4
- Dai, Y. C. (2012). Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53: 49 – 80. https://doi.org/10.1007/s10267-011-0134-3
- Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* 39: 783 791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x
- Floudas, D. & Hibbett, D. S. (2015). Revisiting the taxonomy of *Phanerochaete* (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. *Fungal Biol.* 119 (8): 679 – 719. https://doi.org/10.1016/j.funbio.2015.04.003
- Hall, T. A. (1999). BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95 – 98.
- Han, M. L. & Cui, B. K. (2015). Morphological characters and molecular data reveal a new species of *Fonitopsis* (Polyporales) from southern China. *Mycoscience* 56: 168–176. https://doi.org/10.1016/j.myc.2014.05.004
- Justo, A., Miettinen, O., Floudas, D., Ortiz-Santana, B., Sjökvist, E., Lindner, D., Nakasone, K., Niemelä, T., Larsson, K. H., Ryvarden, L. & Hibbett, D. S. (2017). A revised family-level classification of the Polyporales (Basidiomycota). *Fungal Biol.* 121: 798 – 824. https://doi.org/10.1016/j.funbio.2017.05.010
- Kim, N. K., Park, J. Y., Park, M. S., Lee, H., Cho, H. J., Eimes, J., Kim, C. & Lim, Y. W. (2016). Five New Wood Decay Fungi (Polyporales and Hymenochaetales) in Korea. *Mycobiology* 44 (3): 146 – 154. https://doi.org/10.5941/MYCO.2016.44.3.146

- Kotiranta, H., Kulju M. & Miettinen, O. (2017). Caudicicola gracilis (Polyporales, Basidiomycota), a new polypore species and genus from Finland. Ann. Bot. Fenn. 54: 159 – 167. https://doi.org/10.5735/085.054.0325
- Kout, J., Vlasák, J. & Vlasák, J. (2017). Antrodia multiformis and A. tenerifensis spp. nov. (Fomitopsidaceae, Basidiomycota): new brown rot polypores. Mycol. Progr. 16 (7): 737 – 742. https://doi.org/10. 1007/s11557-017-1310-4
- Larsson, K. H. (2007). Re-thinking the classification of corticioid fungi. *Mycol. Res.* 111 (9): 1040 – 1063. https://doi.org/10.1016/j.mycres.2007.08.001
- Li, H. J. & Cui, B. K. (2013). Two new Daedalea species (Polyporales, Basidiomycota) from South China. Mycoscience 54: 62 – 68. https://doi.org/ 10.1016/j.myc.2012.07.005
- Miettinen, O., Larsson, E., Sjökvist, E. & Larsson, K. H. (2012). Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic Polypores (Polyporales, Basidiomycota). *Cladistics* 28 (3): 251 – 270. https://doi. org/10.1111/j.1096-0031.2011.00380.x
- & Rajchenberg, M. (2012). *Obba* and *Sebipora*, new polypore genera related to *Cinereomyces* and *Gelatoporia* (Polyporales, Basidiomycota). *Mycol. Progr.* 11 (1): 131 147. https://doi.org/10.1007/s11557-010-0736-8
- & Ryvarden, L. (2016). Polypore Genera Antella, Austeria, Butyrea, Citripora, Metuloidea and Trulla (Steccherinaceae, Polyporales). Ann. Bot. Fenn. 53: 157 – 172. https://doi.org/10.5735/085.053.0403
- Miller, M. A., Holder, M. T., Vos, R., Midford, P. E., Liebowitz, T., Chan, L., Hoover, P. & Warnow, T. (2009). The CIPRES Portals. CIPRES. URL: http://www.phylo.org/ sub_sections/portal. (Archived by WebCite(r) at http:// www.webcitation.org/5imQlJeQa). [Accessed 7 Dec. 2011].
- Nylander, J. A. A. (2004). MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Uppsala.
- Petersen, J. H. (1996). *Farvekort. The Danish Mycological Society's colour-chart.* Foreningen til Svampekundskabens Fremme, Greve.
- Piepenbring, M., Maciá-Vicente, J. G., Codjia, J. E. I., Glatthorn, C., Kirk, P., Meswaet, Y., Minter, D., Olou, B. A., Reschke, K., Schmidt, M. & Yorou, N. S. (2020). Mapping mycological ignorance — checklists and diversity patterns of fungi known for West Africa. *IMA Fungus* 11: 13. https://doi.org/10. 1186/s43008-020-00034-y
- Ronquist, F. & Huelsenbeck, J. P. (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572 – 1574. https://doi.org/ 10.1093/bioinformatics/btg180
- Ryvarden, L. & Iturriaga, T. (2003). Studies in neotropical polypores 10. New polypores from Venezuela.

Mycologia 95 (6): 1066 – 1077. https://doi.org/10. 1080/15572536.2004.11833021

- Shen, L. L., Wang, M., Zhou, J. L., Xing, J. H., Cui, B. K. & Dai, Y. C. (2019). Taxonomy and phylogeny of *Postia*. Multi-gene phylogeny and taxonomy of the brownrot fungi: *Postia* (Polyporales, Basidiomycota) and its related genera. *Persoonia* 42: 101 – 126. https://doi. org/10.3767/persoonia.2019.42.05
- Sjökvist, E., Larsson, E., Eberhardt, U., Ryvarden, L. & Larsson, K. H. (2012). Stipitate steroid basidiocarps have evolved multiple times. *Mycologia* 104 (5): 1046 – 1055. https://doi.org/10.3852/11-174
- Song, J., Chen, J. J., Wang, M., Chen, Y. Y. & Cui, B. K. (2016). Phylogeny and biogeography of the remarkable genus *Bondarzewia* (Basidiomycota, Russulales). *Sci. Rep.* 6: 34568. https://doi.org/10.1038/srep34568
- Swofford, D. L. (2002). PAUP*: phylogenetic analysis using parsimony (*and other methods). version 4.0b10. Sinauer Associates, Sunderland, Massachusetts.
- Westphalen, M. C., Rajchenberg, M., Tomšovský M. & Gugliotta, A. M. (2018). A re-evaluation of Neotropical *Junghuhnia* s.lat. (Polyporales, Basidiomycota) based on morphological and multigene analyses. *Personia* 41: 130 – 141. https://doi.org/10.3767/persoonia.2018.41.07
- _____, Tomšovský M., Rajchenberg, M. & Gugliotta, A. M. (2016). Morphological and phylogenetic studies of two new neotropical species of *Loweomyces* (Polyporales, Basidiomycota). *Mycol. Progr.* 15: 967 975. https://doi.org/10.1007/s11557-016-1223-7
- ____, ___, Gugliotta, A. M. & Rajchenberg, M. (2019). An overview of *Antrodiella* and related genera of Polyporales from the Neotropics. *Mycologia* 111 (5): 813 – 831. https://doi.org/10.1080/00275514.2019. 1633895
- White, T. J., Bruns, T., Lee, S. & Taylor, J. (1990).
 Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: M. A. Innis, D. H. Gelfand, J. J. Sninsky & T. J. White (eds), *PCR protocols: a guide to methods and applications*, pp. 315

– 322. Academic Press, San Diego:. https://doi.org/ 10.1016/B978-0-12-372180-8.50042-1

- Wu, Z. Q., Shen, S., Luo, K. Y., Wang, Z. H. & Zhao, C. L. (2017). Morphological and molecular identification of a new species of *Atraporiella* (Polyporales, Basidiomycota) in China. *Phytotaxa* 332 (1): 31 40. https://doi.org/10.11646/phytotaxa.332.1.3
- Yuan, H. S. (2014). Molecular phylogenetic evaluation of *Antrodiella* and morphologically allied genera in China. *Mycol. Progr.* 13 (2): 353 – 364. https://doi. org/10.1007/s11557-013-0921-7
- ____, Lu, X. & Qin, W. M. (2019). Molecular and morphological analyses separate *Junghuhnia pseudocrustacea* sp. nov. (Basidiomycota) from *Junghuhnia crustacea* complex. *Nova Hedwigia* 108(1): 255 264. https://doi.org/10.1127/nova_hedwigia/2018/0497
- Zhao, C. L. & Wu, Z. Q. (2017). Ceriporiopsis kunningensis sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. Mycol. Progr. 16: 93 – 100. https://doi.org/10. 1007/s11557-016-1259-8
- Zhu, L., Song, J., Zhou, J. L., Si, J. & Cui, B. K. (2019). Species diversity, phylogeny, divergence time and biogeography of the genus Sanghuangporus (Basidiomycota). Frontiers Microbiol. 10: 812. https://doi.org/10.3389/fmicb.2019.00812
- Zmitrovich, I. V. (2018). Conspectus systematis Polyporacearum v. 1.0. Folia Cryptogam. Petrop. 6: 3 – 145.

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