Volume 107 No 1-2

Nova Hedwigia

Zeitschrift für Kryptogamenkunde

Founded by
J. Gerloff and F. Mattick

Now online

http://www.schweizerbart.de/j/nova-hedwigia

BLINDOW, I., R. MARQUARDT, D. SCHORIES & H. SCHUBERT, Charophyceae of Chile – taxonomy and distribution. Part 1. Subfamily Chareae..... 1

BLINDOW, I., D. SCHORIES & H. SCHUBERT, Charophytes of Chile – taxonomy and distribution. Part 2. Subfamily Nitelleae..... 49

SONG, Y., J.B. ZHANG, J.W. LI & L.H. QIU, *Lactifluus sinensis* sp. nov. and *L. sinensis* var. *reticulatus* var. nov. (Russulaceae) from southern China..... 91

LETCHER, P.M. & M.J. POWELL, Three new genera of soil-inhabiting chytrids in Spizellomycetaceae (Chytridiomycota)..... 105

YUAN, Y., G.J. REN & Y.C. DAI, *Dentipellis rhizomorpha* sp. nov. supported by morphological and phylogenetic analyses..... 131

GÓMEZ, F., A review on the synonymy of the dinoflagellate genera *Oxytoxum* and *Corythodinium* (Oxytoxaceae, Dinophyceae)..... 141

WU, Z.Q., Z.H. WANG, K.Y. LUO, Z.W. SHI, F. WU & C.L. ZHAO, *Skeletocutis mopanshanensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis..... 167

For continuation see page 2

J. Cramer
in der Gebrüder Borntraeger Verlagsbuchhandlung
Stuttgart 2018

Charophyceae of Chile – taxonomy and distribution. Part 1. Subfamily Chareae
Blindow, Irmgard; Marquardt, Ronny; Schories, Dirk; Schubert, Hendrik
p. 1–47, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701000 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0452

Charophytes of Chile – taxonomy and distribution. Part 2. Subfamily Nitelleae
Blindow, Irmgard; Schories, Dirk; Schubert, Hendrik
p. 49–90, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701001 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0454

Lactifluus sinensis sp. nov. and L. sinensis var. reticulatus var. nov. (Russulaceae) from southern China
Song, Yu; Zhang, Jian-Bin; Li, Jing-Wei; Qiu, Li-Hong
p. 91–103, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701002 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0451

Three new genera of soil-inhabiting chytrids in Spizellomycetaceae (Chytridiomycota)
Letcher, Peter M.; Powell, Martha J.
p. 105–129, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701003 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0458

Dentipellis rhizomorpha sp. nov. supported by morphological and phylogenetic analyses
Yuan, Yuan; Ren, Guang-Juan; Dai, Yu-Cheng
p. 131–140, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701004 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2018/0459

A review on the synonymy of the dinoflagellate genera Oxytoxum and Corythodinium (Oxytoxaceae, Dinophyceae)
Gómez, Fernando
p. 141–165, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701005 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0460

Skeletocutis mopanshanensis sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis
Wu, Zi-Qiang; Wang, Zheng-Hui; Luo, Kai-Yue; Shi, Zhong-Wen; Wu, Fang; Zhao, Chang-Lin
p. 167–177, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701006 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0461

Cryptomarasmius corbariensis (Physalacriaceae, Agaricales) in Turkey with first molecular data on the species from Eurasia
Bozok, Fuat; Taşkin, Hatıra; Büyükalaca, Saadet; Hüseyin Doğan, Hasan; Assyov, Boris
p. 179–187, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701007 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0462

A new anamorphic fungus of Nakataea from China
Ma, Li-Guo; Li, Hao-Hua; Xia, Ji-Wen; Castañeda-Ruíz, Rafael F.; Zhang, Xiu-Guo
p. 189–193, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701008 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0463

A new species of Clitocybula (Marasmiaceae) from West Bengal, India
Dutta, Arun Kumar; Antonín, Vladimír; Barui, Reddhita; Acharya, Krishnendu
p. 195–203, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701009 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2017/0464

Phylogeny and taxonomic revision of the soil chytrid, Gaertneriomyces, and description of the new genus Barromyces (Spizellomycetaceae, Chytridiomycota)
Powell, Martha J.; Letcher, Peter M.; Chen, Shu-Fen
p. 205–228, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701010 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2018/0465

Planktonic cyanobacteria from a tropical reservoir of southeastern Brazil: a picocyanobacteria rich community and new approaches for its characterization
Laux, Marcele; Werner, Vera Regina; Vialle, Ricardo A.; Ortega, José Miguel; Giani, Alessandra
p. 229–256, published: Aug 1, 2018, published online: Jul 13, 2018
ArtNo. ESP050010701011 Price: 29.00 € DOI: 10.1127/nova_hedwigia/2018/0467

Nova Hedwigia Vol. 107 (2018) Issue 1–2, 167–177 **Article**
published online December 19, 2017; published in print August 2018

Skeletocutis mopanshanensis sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis

Zi-Qiang Wu[1], Zheng-Hui Wang[2], Kai-Yue Luo[2], Zhong-Wen Shi[2], Fang Wu[3]* and Chang-Lin Zhao[1, 2, 4]*

[1] Key Laboratory of Forest Disaster Warning and Control of Yunnan Province, Southwest Forestry University, Kunming 650224, P.R. China

[2] College of Biodiversity Conservation and Utilization, Southwest Forestry University, Kunming 650224, P.R. China

[3] Institute of Microbiology, P.O. Box 61, Beijing Forestry University, Beijing 100083, P.R. China

[4] Yunnan Academy of Biodiversity, Southwest Forestry University, Kunming 650224, P.R. China

With 3 figures and 1 table

Abstract: A new poroid wood-inhabiting fungal species, *Skeletocutis mopanshanensis* sp. nov., is proposed based on morphological and molecular characters. The species is characterized by resupinate, white to cream basidiocarps, a dimitic hyphal system with unbranched generative hyphae and big, ellipsoid basidiospores measuring 4.7–6.6 × 3.2–4.5 µm. The internal transcribed spacer (ITS) and the large subunit (LSU) regions of nuclear ribosomal RNA gene sequences of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony and bayesian inference methods. The phylogenetic analysis based on molecular data of ITS+nLSU sequences showed that *Skeletocutis mopanshanensis* belonged to the tyromyces clade, formed a monophyletic lineage with a strong support (100% BS, 100% BP, 1.00 BPP) and was closely related to *S. yunnanensis*, and then grouped with *S. portcrosensis* and *S.* sp with a lower support. Both morphological and molecular characters confirmed the placement of the new species in *Skeletocutis*.

Key words: Phylogenetic analysis, Polypores, taxonomy, Tyromyces clade, wood-rotting fungi.

Introduction

Skeletocutis Kotl. & Pouzar (Polyporaceae, Polyporales) was erected by Kotl. & Pouzar (1958) and typed by *S. amorpha* (Fr.) Kotl. & Pouzar. It is a large, cosmopolitan genus

*Corresponding authors: fungichanglinz@163.com, fangwubjfu2014@yahoo.com

 DOI: 10.1127/nova_hedwigia/2017/0461
www.borntraeger-cramer.de
0029-5035/2017/0461 $ 2.75

characterized by a combination of annual to perennial, resupinate or pileate basidiocarps with white, cream pink to lilac, often slightly discoloured and resinous when dry; a di- to trimitic hyphal structure in which generative hyphae with clamp connections and skeletal hyphae hyaline; both types of hyphae encrusted in the dissepiments; cystidia absent, cystidioles present in most species; and hyaline, thin-walled, allantoid, cylindrical to ellipsoid basidiospores, which are negative in Melzer's reagent. In addition, the genus causes a white rot (Niemelä 1998, Núñez & Ryvarden 2001, Dai 2012, Ryvarden & Melo 2014).

Recently, Binder et al. (2013) employed molecular study based on multi-gene datasets and demonstrated that the type species of *Skeletocutis* (*S. amorpha*) belongs to the tyromyces clade and appeared to be grouped with *Tyromyces chioneus* (Fr.) P. Karst., and *Piloporia sajanensis* (Parmasto) Niemelä by using ribosomal DNA sequences. Bian et al. (2016) described a new poroid species in *Skeletocutis* based on its morphological characters and rDNA sequences, and this species also belonged to the tyromyces clade, and was related to *S. amorpha* and *S. portcrosensis* A.David.

Although *Skeletocutis* is a cosmopolitan genus, most species in the genus were found in boreal and temperate forests from the northern hemisphere (Gilbertson & Ryvarden 1986, Núñez & Ryvarden 2001, Ryvarden & Melo 2014). A comprehensive study on the *Skeletocutis* was made by Niemelä mostly based on morphological characteristics and ecological habits, and several new species were described from Europe (Niemelä 1998). Previously 23 species including five species described from China were recorded in the country (Dai 1998, 2012, Cui 2013, Bian et al. 2016). During investigations on the diversity of polypores in southwestern China, an additional undescribed species corresponding to *Skeletocutis* was found. To confirm the affinity of the undescribed species of *Skeletocutis*, phylogenetic analysis was carried out based on the ITS and nLSU sequences.

Materials and methods

The studied specimens are deposited at the herbarium of Southwest Forestry University (SWFC). Macro-morphological descriptions are based on field notes. Special colour terms follow Petersen (1996). Micro-morphological data were obtained from the dried specimens, and observed under a light microscope following Dai (2010). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic 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 given number (b) of specimens.

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions with some modifications that a small piece of dried fungal specimen (about 30 mg) was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 ml centrifuge tube, suspended in 0.4 ml of lysis buffer, and incubated in a 65°C water bath for 60 min. After that, 0.4 ml phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13 000 rpm for 5 min, 0.3 ml supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13000 rpm for 0.5 min. Then, 0.5 ml inhibitor removal fluid was added in AC for a centrifugation at 12000 rpm for 0.5 min. After washing twice with 0.5 ml washing buffer, the AC was transferred to a clean centrifuge tube, and 100 ml elution buffer was added to the middle of adsorbed film to elute

the genome DNA. ITS region was amplified with primer pairs ITS5 and ITS4 (White et al. 1990). Nuclear LSU region was amplified with primer pairs LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). The PCR procedure for ITS was as follows: initial denaturation at 95°C for 3 min, followed by 35 cycles at 94°C for 40 s, 58°C for 45 s and 72°C for 1 min, and a final extension of 72°C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94°C for 1 min, followed by 35 cycles at 94°C for 30 s, 48°C 1 min and 72°C for 1.5 min, and a final extension of 72°C for 10 min (Chen et al. 2015). The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) was used to edit the DNA sequence. Sequences were aligned in MAFFT 6 (Katoh & Toh 2008; http://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 21462). Sequences of *Heterobasidion annosum* (Fr.) Bref. and *Stereum hirsutum* (Willd.) Pers. obtained from GenBank were used as outgroups to root trees following Binder et al. (2013) in the ITS+nLSU analysis.

Maximum parsimony analysis was applied to the ITS+nLSU dataset sequences. Approaches to phylogenetic analysis followed Zhou et al. (2016), 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 (BT) analysis with 1,000 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 analyzed using Maximum Likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller et al. 2009). Branch support for ML analysis was determined by 1000 bootstrap replicate.

MrModeltest 2.3 (Posada & Crandall 1998, Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes3.1.2 with a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 5 million generations (ITS+nLSU), 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 that received bootstrap support for maximum likelihood (BS), maximum parsimony (BP) and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BP) and 0.95 (BPP) were considered as significantly supported, respectively.

Results

The ITS+nLSU dataset included sequences from 66 fungal specimens representing 59 species. The dataset had an aligned length of 2415 characters, of which 1400 characters are constant, 288 are variable and parsimony-uninformative, and 727 are parsimony-informative. Maximum parsimony analysis yielded two equally parsimonious trees (TL = 5654, CI = 0.306, HI = 0.692, RI = 0.557, RC = 0.170). Best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis: GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.001417 (BI).

The phylogeny (Fig. 1) inferred from ITS+nLSU sequences demonstrated seven major clades for 59 species of the Polyporales. The new species clustered into the tyromyces

Table 1. A list of species, specimens, and GenBank accession number of sequences used in this study.

Species name	Sample no.	GenBank accession no.		References
		ITS	nLSU	
Abortiporus biennis	TFRI 274	EU232187	EU232235	Binder et al. 2005
Antrodia albida	CBS 308.82	DQ491414	AY515348	Kim et al. 2007
A. heteromorpha	CBS 200.91	DQ491415	AY515350	Kim et al. 2007
Antrodiella americana	Gothenburg 3161	JN710509	JN710509	Binder et al. 2013
A. semisupina	FCUG 960	EU232182	EU232266	Binder et al. 2005b
Bjerkandera adusta	NBRC 4983	AB733156	AF287848	Binder et al. 2005
Ceriporiopsis alboaurantia	Cui 4136	KF845948	KF845955	Zhao et al. 2015b
C. balaenae	H7002389	FJ496669	FJ496717	Tomšovský et al. 2010
C. consobrina	Rivoire 977	FJ496667	FJ496716	Tomšovský et al. 2010
C. fimbriata	Dai 11672	KJ698633	KJ698637	Zhao et al. 2015b
C. gilvescens	BRNM 710166	FJ496684	FJ496720	Tomšovský et al. 2010
C. gilvescens	BRNM 667882	FJ496685	FJ496719	Tomšovský et al. 2010
C. guidella	HUBO 7659	FJ496687	FJ496722	Tomšovský et al. 2010
C. rosea	Dai 13584	KJ698636	KJ698640	Zhao et al. 2015b
C. semisupina	Cui 10222	KF845949	KF845956	Zhao et al. 2015b
C. semisupina	Cui 10189	KF84595	KF845958	Zhao et al. 2015b
Cinereomyces lindbladii	KHL 12078	FN907906	FN907906	Binder et al. 2013
Climacocystis borealis	KH 13318	JQ031126	JQ031126	Binder et al. 2013
Coriolopsis caperata	LE(BIN)-0677	AB158316	AB158316	Tomšovský et al. 2010
Dacryobolus karstenii	KHL 11162	EU118624	EU118624	Binder et al. 2005
Daedalea quercina	DSM 4953	DQ491425	DQ491425	Kim et al. 2007
Earliella scabrosa	PR 1209	JN165009	JN164793	Binder et al. 2005
Fomitopsis pinicola	CBS 221.39	DQ491405	DQ491405	Kim et al. 2007
F. rosea	ATCC 76767	DQ491410	DQ491410	Kim et al. 2007
Fragiliporia fragilis	Dai 13080	KJ734260	KJ734264	Zhao et al. 2015a
F. fragilis	Dai 13559	KJ734261	KJ734265	Zhao et al. 2015a
F. fragilis	Dai 13561	KJ734262	KJ734266	Zhao et al. 2015a
Ganoderma lingzhi	Wu 1006-38	JQ781858	–	Zhao et al. 2015a
Gelatoporia subvermispora	BRNU 592909	FJ496694	FJ496706	Tomšovský et al. 2010
Grammothelopsis subtropica	Cui 9035	JQ845094	JQ845097	Zhao et al. 2015a
Heterobasidion annosum	PFC 5252	KC492906	KC492906	Binder et al. 2013
Hornodermoporus martius	MUCL 41677	FJ411092	FJ393859	Robledo et al. 2009
Hypochnicium lyndoniae	NL 041031	JX124704	JX124704	Binder et al. 2005
Junghuhnia nitida	KHL 11903	EU118638	EU118638	Binder et al. 2005
Mycoacia fuscoatra	KHL 13275	JN649352	JN649352	Tomšovský et al. 2010
M. nothofagi	KHL 13750	GU480000	GU480000	Tomšovský et al. 2010
Obba rivulosa	KCTC 6892	FJ496693	FJ496710	Miettinen & Rajchenberg 2012
O. valdiviana	FF 503	HQ659235	HQ659235	Miettinen & Rajchenberg 2012
Perenniporia medulla-panis	MUCL 49581	FJ411087	FJ393875	Robledo et al. 2009
Perenniporiella neofulva	MUCL 45091	FJ411080	FJ393852	Robledo et al. 2009
Phlebia livida	FCUG 2189	AF141624	AF141624	Tomšovský et al. 2010

P. radiata	UBCF 19726	HQ604797	HQ604797	Binder et al. 2013
P. subserialis	FCUG 1434	AF141631	AF141631	Tomšovský et al. 2010
Piloporia sajanensis	Mannine 2733a	HQ659239	HQ659239	Tomšovský et al. 2010
Podoscypha venustula	CBS 65684	JN649367	JN649367	Binder et al. 2013
Polyporus tuberaster	CulTENN 10197	AF516596	AJ488116	Binder et al. 2013
Postia guttulata	KHL 11739	EU11865	EU11865	Kim et al. 2007
Sebipora aquosa	Miettinen 8680	HQ659240	HQ659240	Miettinen and Rajchenberg 2012
Skeletocutis amorpha	Miettinen 11038	FN907913	FN907913	Tomšovský et al. 2010
S. jelicii	H 6002113	FJ496690	FJ496727	Tomšovský et al. 2010
S. mopanshanensis	CLZhao 1152	MF924720	MF924722	Present study
S. mopanshanensis	CLZhao 1184	MF924721	MF924723	Present study
S. nivea	ES 2008	JX109858	JX109858	Tomšovský et al. 2010
S. ochroalba	JK 1208/8	KF840389	–	Tomšovský et al. 2010
S. portcrosensis	LY 3493	FJ496689	FJ496689	Tomšovský et al. 2010
S. sp.	NMM-2009	FJ791129	–	Tomšovský et al. 2010
S. yunnanensis	Dai 15709	KU950434	KU950436	Bian et al. 2016
S. yunnanensis	Dai 15712	KU950435	KU950437	Bian et al. 2016
Steccherinum fimbriatum	KHL 11905	EU118668	EU118668	Tomšovský et al. 2010
S. ochraceum	KHL 11902	JQ031130	JQ031130	Tomšovský et al. 2010
Stereum hirsutum	NBRC 6520	AB733150	AB733325	Tomšovský et al. 2010
Truncospora ochroleuca	MUCL 39726	FJ411098	FJ393865	Robledo et al. 2009
Tyromyces chioneus	Cui 10225	KF698745	KF698756	Zhao et al. 2015b
Xanthoporus syringae	Gothenburg 1488	JN710607	JN710607	Tomšovský et al. 2010

clade and was formed a monophyletic lineage with a high support (100% BS, 95% BP, 0.99 BPP), and was closely related to *Skeletocutis yunnanensis* L.S.Bian, C.L.Zhao & F.Wu with a high support (96% BS, 87% BP, 0.98 BPP), and then grouped with *S. portcrosensis* and *S.* sp with a lower support.

Taxonomy

Skeletocutis mopanshanensis C.L.Zhao, **sp. nov.** Figs 2, 3

MycoBank no.: MB 823081

Diagnosis: The species is distinct by its resupinate basidiocarps with white to cream hymenophores, round pores measuring 4–5 per mm, a dimitic hyphal system with unbranched generative hyphae, tramal hyphae subparallel along the tubes and covered by fine crystals, and ellipsoid basidiospores measuring 4.7–6.6 × 3.2–4.5 µm.

Holotypus: CHINA. Yunnan Prov., Yuxi, Xinping County, Mopanshan National Forest Park, on fallen branch of *Pinus yunnanensis*, 18 January 2017, CLZhao 1184 (SWFC).

Etymology: *Mopanshanensis* (Lat.): referring to the locality (Mopanshan) of the type specimen.

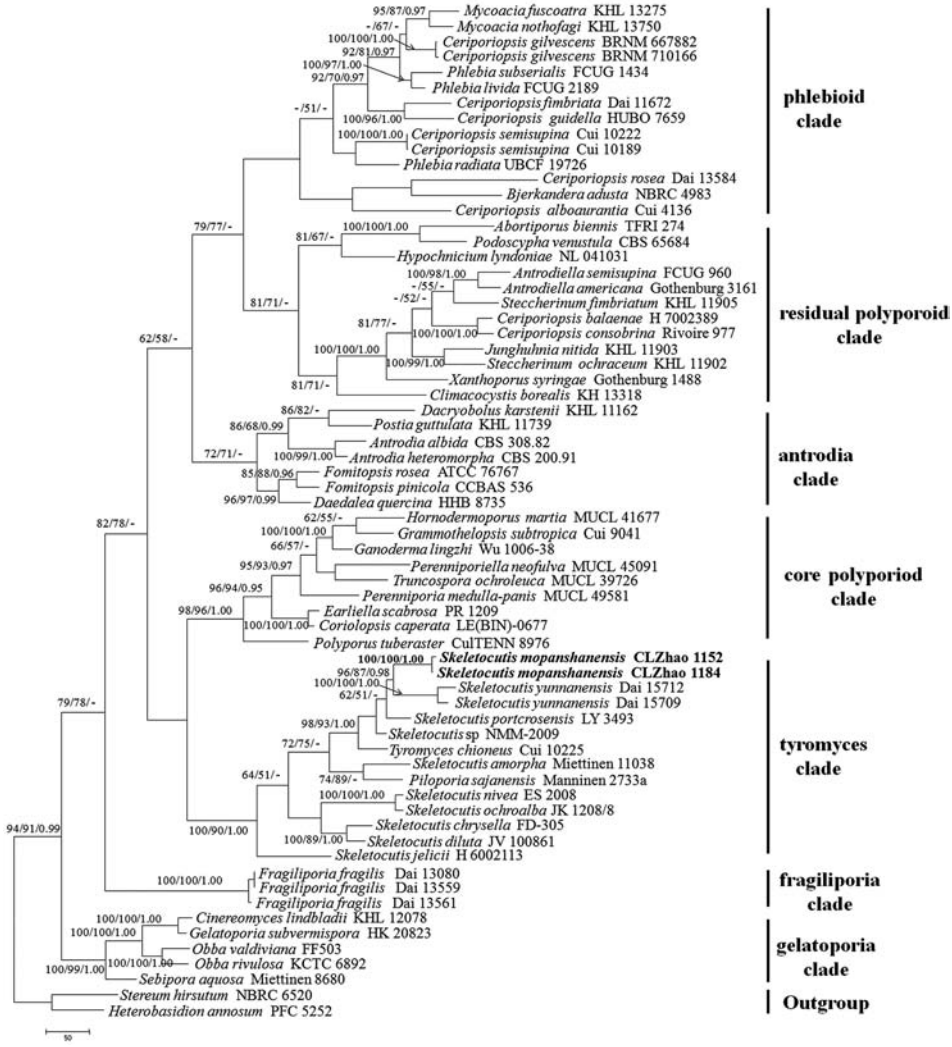

Fig. 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Skeletocutis mopanshanensis* and related species in Polyporales based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap higher than 70%, parsimony bootstrap proportions higher than 50% and Bayesian posterior probabilities more than 0.95 respectively. Clade names follow Binder et al. (2013).

FRUITING BODY: Basidiocarps annual, resupinate, very difficult to separate from substrate, soft leathery, without odour or taste when fresh, becoming soft corky to fragile upon drying, up to 7 cm long, 4 cm wide and 1 mm thick at centre. Pore surface white when fresh, white to cream upon drying; pores round, 4–5 per mm; dissepiments thin, entire. Sterile margin distinct, white, up to 2 mm wide. Subiculum white to cream, soft corky,

Fig. 2. Basidiomata of *Skeletocutis mopanshanensis*. Bars: 1.5 cm (holotype).

up to 0.3 mm thick. Tubes concolorous with pore surface, soft corky to fragile, up to 0.7 mm long.

Hyphal structure: Hyphal system dimitic; generative hyphae with clamp connections, hyaline, thin-walled; skeletal hyphae thick-walled with a wide lumen; all hyphae IKI-, CB-, unchanged in KOH.

Subiculum: Generative hyphae hyaline, unbranched, covered by fine crystals, interwoven, 2.5–4 µm in diameter; skeletal hyphae dominant, hyaline, thick-walled with a wide lumen, occasionally branched, interwoven, 3–5 µm in diameter.

Tubes: Generative hyphae hyaline, thin-walled, unbranched, covered by fine crystals, interwoven, 2–3 µm in diameter; skeletal hyphae dominant, hyaline, thick-walled with a wide lumen, occasionally, interwoven, 2.5–4.5 µm in diameter. Cystidia absent, but fusoid cystidioles occasionally present, hyaline, thin-walled, 7–10 × 2–3 µm; basidia burrel-shaped to pyriform, with four sterigmata and a basal clamp connection, 9–13 × 5.5–8 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores: Basidiospores ellipsoid, hyaline, thin-walled, smooth, IKI-, CB-, (4.5–)4.7–6.6(–6.8) × (3–)3.2–4.5(–4.8) µm, L = 5.51 µm, W = 3.69 µm, Q =1.41–1.65 (n = 60/2).

Rot type: A white rot.

Additional specimen (paratype) examined: CHINA. Yunnan Prov., Yuxi, Xinping county, Mopanshan National Forest Park, on fallen branch of *Pinus yunnanensis*, 18 January 2017, CLZhao 1152 (SWFC).

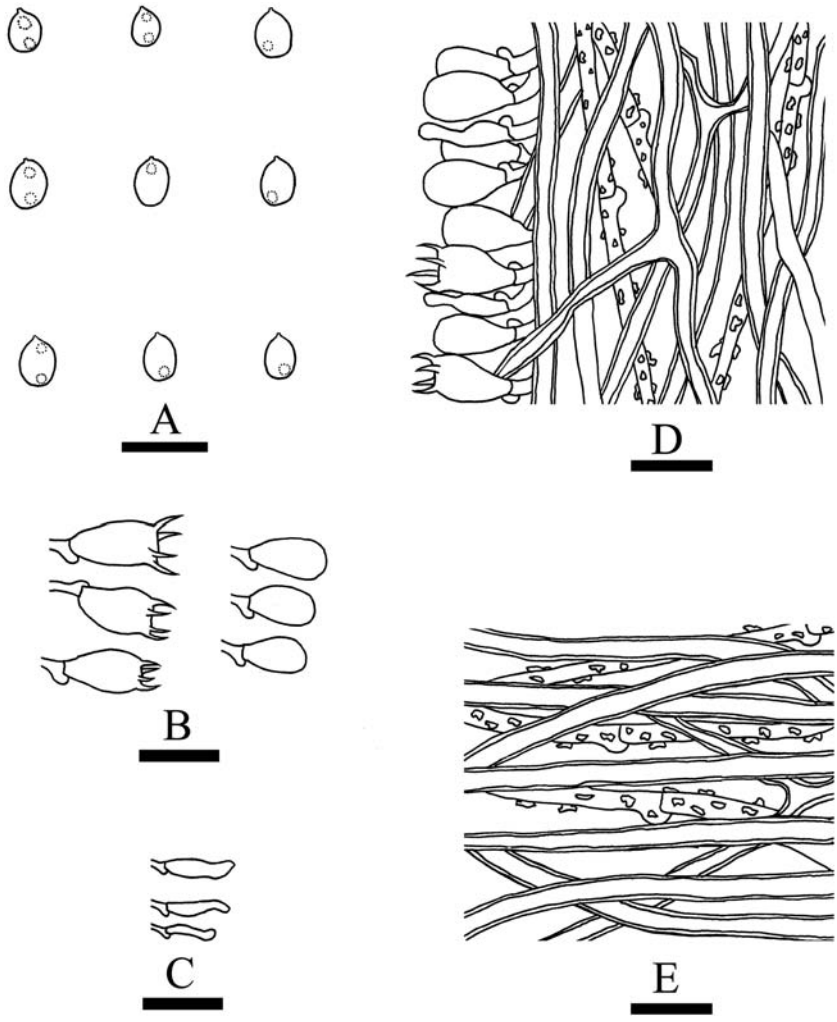

Fig. 3. Microscopic structures of *Skeletocutis mopanshanensis* (drawn from the holotype). a. Basidiospores; b. Basidia and basidioles; c. Cystidioles; d. Hyphae from trama; e. Hyphae from subiculum. Bars: A, B, C, D = 10 μm.

Discussion

In the present study, a new species, *Skeletocutis mopanshanensis*, is described based on phylogenetic analysis and morphological characters. The species has unique morphological characters in *Skeletocutis* and forms a monophyletic lineage within the tyromyces clade.

Previously, seven clades were found in the Polyporales: antrodia clade, core polyporoid clade, fragiliporia clade, gelatoporia clade, phlebioid clade, residual polyporoid clade and tyromyces clade (Binder et al. 2013). According to our result based on the combined ITS+nLSU sequence data (Fig. 1), *Skeletocutis mopanshanensis* is nested into the tyromyces clade with strong support (100% BS, 100% BP, 1.00 BPP).

In our analysis (Fig. 1), *Skeletocutis mopanshanensis* grouped with *S. yunnanensis*, and then grouped with *S. portcrosensis* inferred from the ITS+nLSU analysis. However, morphologically *S. yunnanensis* differs from *S. mopanshanensis* by its angular pores and smaller and cylindric basidiospores (3.5–4.5 ×1–1.2 µm; Bian et al. 2016). *Skeletocutis portcrosensis* can be distinguished by arachnoid margins and a monomitic hyphal system and smaller, cylindric basidiospores (4–5 ×1.5–1.8 µm; Ryvarden & Melo 2014).

Having wider basidiospores (> 2 µm in width) reminds of two similar species in the *Skeletocutis*: *S. percandida* (Malençon & Bertault) Jean Keller and *S. sensitiva* (Lloyd) Ryvarden. The former differs from *S. mopanshanensis* by cottony basidiocarps with white rhizomorph and cylindrical basidiospores; in addition, it grows on hardwood (Ryvarden & Melo 2014). The latter is separated from *S. mopanshanensi* by its resupinate to effused-reflexed basidiocarps with orange pore surface and smaller basidiospores (4–4.5 × 3–3.5 µm; Núñez & Ryvarden 2001).

Acknowledgments

We express our gratitude to Yong-He Li (Yunnan Academy of Biodiversity, Southwest Forestry University) for his support on molecular work. The research is supported by the National Natural Science Foundation of China (Project No. 31700023) and Science and Technology Talent Support Program of Three Areas in Yunnan Province (Project No. 21700329).

References

BIAN, L.S., C.L. ZHAO & F. WU 2016: A new species of *Skeletocutis* (Polyporales, Basidiomycota) from Yunnan of China. – Phytotaxa **270**: 267–276. doi: 10.1007/S10267-010-0068-1

BINDER, M., D.S. HIBBETT, K.H. LARSSON, E. LARSSON, E. LANGER et al. 2005: The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). – Syst. Biodivers. **3**: 113–157. doi: 10.1017/S1477200005001623

BINDER, M., A. JUSTO, R. RILEY, A. SALAMOV, F. LÓPEZ-GIRÁLDEZ et al. 2013: Phylogenetic and phylogenomic overview of the Polyporales. – Mycologia **105**: 1350–1373. doi: 10.3852/13-003

CHEN, J.J., L.L. SHEN & B.K. CUI 2015: Morphological characters and molecular data reveal a new species of *Hydnocristella*. – Nova Hedwigia **101**: 139–146. doi: 10.1127/nova_hedwigia/2015/0255

CUI, B.K. 2013: Two new polypores (*Ceriporiopsis lavendula* and *Skeletocutis inflata* spp. nov.) from Guangdong Province, China. – Nord. J. Bot. **31**: 326–330. doi:10.1111/j.1756-1051.2012.01674.x

DAI, Y.C. 1998: Changbai wood-rotting fungi 9. Three new species and other species in *Rigidoporus*, *Skeletocutis* and *Wolfiporia* (Basidiomycota, Aphyllophorales). – Ann. Bot. Fenn. **35**: 143–154.

DAI, Y.C. 2010: Hymenochaetaceae (Basidiomycota) in China. – Fungal Divers. **45**: 131–343. doi:10.1007/s13225-010-0066-9

DAI, Y.C. 2012: Polypore diversity in China with an annotated checklist of Chinese polypores. – Mycoscience **53**: 49–80. doi: 10.1007/s10267-011-0134-3

FELSENSTEIN, J. 1985: Confidence intervals on phylogenetics: an approach using bootstrap. – Evolution **39**: 783–791.

GILBERTSON, R.L. & L. Ryvarden: 1986: North American polypores. – Fungiflora, Oslo.

HALL, T.A. 1999: Bioedit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. – Nucleic Acids Symp. Ser. **41**: 95–98.

KATOH, K. & H. TOH 2008: Recent developments in the MAFFT multiple sequence alignment program. – Briefings in Bioinformatics **9**: 286–298.

KIM, K.M., J.S. LEE & H.S. JUNG 2007: *Fomitopsis incarnatus* sp. nov. based on generic evaluation of *Fomitopsis* and *Rhodofomes*. – Mycologia **99**: 833–841. doi:10.3852/mycologia.99.6.833

KOTLÁBA, F. & Z. POUZAR 1958: Polypori novi vel minus cogniti Cechoslovakiae 3. – Ceská Myk ologie **12**: 95–104.

MIETTINEN, O. & M. RAJCHENBERG 2012: *Obba* and *Sebipora*, new polypore genera related to *Cinereomyces* and *Gelatoporia* (Polyporales, Basidiomycota). – Mycol. Prog. **11**: 131–147. doi:10.1007/s11557-010-0736-8

MILLER, M.A., M.T. HOLDER, R. VOS, P.E. MIDFORD, T. LIEBOWITZ et al. 2008: The CIPRES Portals. CIPRES. URL: http://www.phylo.org/sub_sections/portal. 2009-08-04. (Archived by WebCite(r) at http://www.webcitation.org/5imQlJeQa)

NIEMELÄ, T. 1998: The *Skeletocutis subincarnata* complex (Basidiomycetes), a revision. – Acta Bot. Fennica **161**: 1–35.

NÚÑEZ, M. & L. RYVARDEN 2001: East Asian polypores 2. – Syn. Fung. **14**: 165–522.

NYLANDER, J.A.A. 2004: MrModeltest v2. Program distributed by the author. – Evolutionary Biology Centre, Uppsala University.

PETERSEN, J.H. 1996: Farvekort. The Danish Mycological Society's colour-chart. – Foreningentil Svampekundskabens Fremme, Greve.

POSADA, D. & K.A. CRANDALL 1998: Modeltest: testing the model of DNA substitution. – Bioinformatics **14**: 817–818.

ROBLEDO, G.L., M. AMALFI, G. CASTILLO, M. RAJCHENBERG & C. DECOCK 2009: *Perenniporiella chaquenia* sp. nov. and further notes on *Perenniporiella* and its relationships with *Perenniporia* (Poriales, Basidiomycota). – Mycologia **101**: 657–673. doi: 10.3852/08-040

RONQUIST, F. & J.P. HUELSENBECK 2003: MRBAYES 3: bayesian phylogenetic inference under mixed models. – Bioinformatics **19**: 1572–1574. doi: 10.1093/bioinformatics/btg180

RYVARDEN, L. & I. MELO 2014: Poroid fungi of Europe. – Syn Fung **31**: 1–455. – Fungiflora, Oslo.

SWOFFORD, D.L. 2002: PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sinauer Associates, Massachusetts.

TOMŠOVSKÝ, M., A. MENKIS & R. VASAITIS 2010: Phylogenetic relationships in European *Ceriporiopsis* species inferred from nuclear and mitochondrial ribosomal DNA sequences. – Fungal Biology **114**: 350–358.

WHITE, T.J., T. BRUNS, S. LEE & J. TAYLOR 1990: Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. – In: INNIS, M.A., D.H. GELFAND, J.J. SNINSKY & T.J. WHITE (eds.): PCR Protocols: A guide to methods and applications. – Academic Press, San Diego, pp. 315–322.

ZHAO, C.L., B.K. CUI, J. SONG & Y.C. DAI 2015a: Fragiliporiaceae, a new family of Polyporales (Basidiomycota). – Fungal Divers **70**: 115–126. doi: 10.1007/s13225-014-0299-0

ZHAO, C.L., F. WU, H.X. LIU & Y.C. DAI 2015b: A phylogenetic and taxonomic study on *Ceriporiopsis* s. str. (Polyporales) in China. – Nova Hedwigia **101**: 403–417. doi: 10.1127/nova_hedwigia/2015/0282

ZHOU, L.W., J. VLASAK, C. DECOCK, A. ASSEFA, J. STENLID, D. ABATE et al. 2016: Global diversity and taxonomy of the *Inonotu*s linteus complex (Hymenochaetales, Basidiomycota): *Sanghuangporus* gen. nov.,*Tropicoporus excentrodendri* and *T. guanacastensis* gen. et spp. nov., and 17 new combinations. – Fungal Diversity **77**: 335–347. doi: 10.1007/s13225-015-0335-8

Manuscript submitted August 31, 2017; accepted October 20, 2017.