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# *Trechisporales* emended with a segregation of *Sistotremastrales* ord. nov. (*Basidiomycota*)

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## Abstract

Trechisporales, typified by Trechispora and equivalent to Hydnodontales, is a recently introduced order within Agaricomycetes. This order only comprises one family Hydnodontaceae and 16 independent genera, but the relationships among these genera are not fully clarified. Here, via a wider sampling especially from Asia Pacific, careful morphological examinations and comprehensive multilocus-based phylogenetic analyses, the classification of Trechisporales is emended. Sertulicium and Sistotremastrum are segregated from Trechisporales, and placed in the new family Sistotremastraceae within the new order Sistotremastrales. A new genus Allotrechispora segregated from Trechispora is introduced within *Hydnodontaceae*, Trechisporales, and Boidinella, Litschauerella and Sphaerobasidium are excluded from Trechisporales. Brief summaries to genera accepted in Sistotremastrales and Trechisporales, and a key to all 12 genera accepted in Trechisporales are provided. In addition, Tomentella and Murrilloporus, potential synonyms of Trechispora, are excluded from Trechisporales and of uncertain position, respectively. At the species level, 19 new species are described with one from Allotrechispora, one from Fibrodontia, one from Subulicystidium and 16 from Trechispora, and seven new combinations are proposed with two for Allotrechispora and five for Trechispora. In addition, Trechispora yunnanensis is excluded from Trechispora. A key to all 87 species accepted in Trechispora is provided. In conclusion, an emended classification of Trechisporales within Agaricomycetes is constructed, which will help to further clarify species diversity and explore trait evolution within Trechisporales.

 $\label{eq:keywords-29} \begin{array}{l} \textbf{Keywords}-29 \ \texttt{new taxa}-\texttt{Hydnodontaceae}-\texttt{Hydnodontales}-\texttt{macrofungi}-\texttt{Sistotremastraceae}-\texttt{Taxonomy} \end{array}$ 

## Introduction

*Trechisporales* typified by *Trechispora* was newly introduced by Hibbett et al. (2007). An earlier order name *Hydnodontales* is equivalent to *Trechisporales* (Jülich 1981), but Hibbett et al. (2007) stated that *Trechispora*, a synonym with priority over *Hydnodon* (Ryvarden 2002), is the most species-rich genus in this order and thus proposed the new order name. Although not

recommended (Rec. 16A.1 of the Shenzhen Code), the proposal of *Trechisporales* is permissible according to Art. 11.10 of the Shenzhen Code (Turland et al. 2018). Since then, almost all authors has abandoned the order name *Hydnodontales*.

Trechisporales is a taxon-poor order compared with most other orders within Agaricomycetes, Basidiomycota (Wijayawardene et al. 2022b). For now, one family Hydnodontaceae and 14 independent genera, viz. Brevicellicium, Brevicellopsis, Dextrinocystis, Fibrodontia, Litschauerella, Luellia, Porpomyces, Pteridomyces, Sertulicium, Sistotremastrum, Subulicystidium, Suillosporium, Trechispora and Tubulicium are accepted in Trechisporales in studies specific to the order (Larsson 2007, Hjortstam & Ryvarden 2008, de Meiras-Ottoni et al. 2021, Spirin et al. 2021). It is worth mentioning that although two monotypic genera Dextrinodontia and Fibriciellum were also listed as members of Trechisporales (Larsson 2007, Hibbett et al. 2014, Wijayawardene et al. 2022a), their type species were previously combined to Trechispora (Larsson 1992). Therefore, Dextrinodontia and Fibriciellum are actually later synonyms of Trechispora. In addition, some recent synopses place further genera in Hvdnodontaceae, Trechisporales, including Boidinella (Kirk 2019) and Sphaerobasidium (He et al. 2019, Kirk 2019, Wijayawardene et al. 2022a), which bring the genus number to 16. However, the taxonomic position of Boidinella, Brevicellopsis, Litschauerella and Sphaerobasidium within Trechisporales has never been confirmed from a phylogenetic perspective. Morphologically, Trechisporales is highly diverse: with stipitate, clavarioid or resupinate basidiomes; smooth, grandinioid, odontioid, hydnoid or poroid hymenophores; two, four, six or eight sterigmata on basidia; smooth or variously ornamented basidiospores; but all species of Trechisporales bear a mono- or dimitic hyphal system with clamp connections. Most known species of Trechisporales may be saprotrophs on wood, while some species are considered to be ectomycorrhizal fungi or at least have a plant biotrophic lifestyle (Vanegas-León et al. 2019). For example, of the 672 nucleotide sequences of Trechispora in GenBank (https://www.ncbi.nlm.nih.gov/genbank/; access on 2 June 2022), 258 (more than one third) are named as 'uncultured Trechispora' that were generated mainly from rhizosphere and soil.

Within *Trechisporales, Sistotremastrum* and its recently segregated genus *Sertulicium* are long known to be a separate lineage from *Hydnodontaceae* that accommodates all other genera in the order (Larsson 2007). However, the *Sistotremastrum* lineage was designated as the "*Sistotremastrum* family" and a new formal family name was not introduced (Larsson 2007). This taxonomic treatment is mainly due either to restricted taxa sampled in phylogenetic analysis (Larsson 2007) or to lack of reliable phylogenetic support (Spirin et al. 2021). Indeed, all available phylogenetic studies on members of *Trechisporales* are based on only ITS and/or nrLSU regions (e.g. Larsson et al. 2004, Liu et al. 2019, Spirin et al. 2021). These two regions are generally not suitable for resolving fungal relationships at family and higher-taxonomic ranks when sampling taxa comprehensively.

At the species level, numerous new species of *Trechisporales* have been recently described worldwide in most of the accepted genera, such as *Brevicellicium* (Telleria et al. 2013a), *Dextrinocystis* (Liu et al. 2019), *Fibrodontia* (Yurchenko & Wu 2014, Liu et al. 2021), *Porpomyces* (Wu et al. 2015, Spirin et al. 2021), *Sertulicium* (Spirin et al. 2021), *Sistotremastrum* (Gruhn & Alvarado 2021, Spirin et al. 2021), *Subulicystidium* (Volobuev 2016, Ordynets et al. 2018, Liu et al. 2019), *Trechispora* (Ordynets et al. 2015, Chikowski et al. 2020, de Meiras-Ottoni et al. 2021, Liu et al. 2022) and *Tubulicium* (Liu et al. 2019, Ushijima et al. 2019). However, without the help of a well-defined phylogeny across *Trechisporales*, the taxonomic placement of certain new species may be inappropriate even based on molecular phylogenetic analyses (Telleria et al. 2013b, 2014, Xu et al. 2019, Furtado et al. 2021, Zong et al. 2021). Therefore, an emended classification of *Trechisporales* is urgently needed to provide a backbone for clarifying the species diversity and their appropriate placement within this order.

Via sampling a wider range of taxa especially from Asia Pacific, the current study aims to construct a multilocus-based phylogenetic frame of *Trechisporales* within *Agaricomycetes*.

Accordingly, one new order, one new family, one new genus and 19 new species are described, and the taxonomic position of certain previously known genera and species are adjusted.

#### **Materials & Methods**

#### **Material deposition**

Specimens studied are preserved at the Fungarium, Institute of Microbiology, Chinese Academy of Sciences (HMAS), Beijing, China, the herbarium of Institute of Microbiology, Beijing Forestry University (BJFC), Beijing, China, the herbarium of the Institute of Applied Ecology, Chinese Academy of Sciences (IFP), Shenyang, China, and the National Herbarium of Victoria (MEL), Melbourne, Australia.

#### Morphological examination

Macromorphological characters of basidiomes were examined with the aid of a Leica M 125 stereomicroscope (Wetzlar, Germany) at magnifications up to 100 times. Special color terms followed Anonymous (1969). The microscopic procedure followed Wang et al. (2021). Specimen sections were separately mounted in Cotton Blue, Melzer's reagent and 5% potassium hydroxide. Micromorphological characters were examined with an Olympus BX43 light microscope (Tokyo, Japan) at magnifications up to 1000 times. All measurements were taken from the sections mounted in Cotton Blue. When presenting the variation in the size of the basidiospores, 5% of measurements were excluded from each end of the range and are given in parentheses. Unless specified, all measurements exclude the ornamentations of basidiospores. In the morphological descriptions, L stands for the length of arithmetic average of all measured basidiospores, W for the width of arithmetic average of all measured basidiospores, Q for variation in the ratio of L to W among the studied specimens, and n (a/b) for number of basidiospores (a) measured from given number of specimens (b). Drawings were made with the aid of a drawing tube. The ornamentations of basidiospores were examined with a Hitachi SU8010 scanning election microscope (Tokyo, Japan). The sections from hymenophores of basidiomes were sprayed with gold and platinum using Leica EM ACE600 (Wetzlar, Germany).

## **Molecular sequencing**

Total DNA was extracted from basidiomes of dry specimens as templates for subsequent PCR amplifications using the CTAB rapid plant genome extraction kit (Aidlab Biotechnologies Co., Ltd, Beijing, China) according to the manufacturer's instructions. The ITS, nrLSU, tefl- $\alpha$ , rpb2 and mtSSU regions were amplified with primer pairs ITS5/ITS4 (White et al. 1990), LR0R/LR7 (Vilgalys & Hester 1990), 983F/1567R (Rehner & Buckley 2005), RPB2-f5F/RPB2b7.1R (Liu et al. 1999, Matheny 2005) and MS1/MS2 (White et al. 1990), respectively, using 2×EasyTaq<sup>®</sup> PCR SuperMix (TransGen Biotech Co., Ltd, Beijing, China). The PCR procedure was as follows: for ITS and *tef1-a*, initial denaturation at 95°C for 3 min, followed by 35 cycles at 94°C for 40 s, 54°C for 45 s and 72°C for 1 min, and a final extension of 72°C for 10 min; for nrLSU, initial denaturation at 94°C for 1 min, followed by 34 cycles at 94°C for 30 s, 50°C for 1 min, 72 °C for 1.5 min, and a final extension of 72°C for 10 min; for rpb2, initial denaturation at 94 °C for 2 min, followed by 10 cycles at 94°C for 45 s, 60°C for 45 s (minus 1°C per cycle) and 72 °C for 1.5 min, then followed by 36 cycles at 94 °C for 45 s, 53 °C for 1 min and 72°C for 1.5 min, and a final extension of 72°C for 10 min; for mtSSU, initial denaturation at 95°C for 3 min, followed by 35 cycles at 94°C for 40 s, 53°C for 45 s and 72°C for 1 min, and a final extension of 72°C for 10 min. The PCR products were sequenced with the same primers used in PCR amplification at the Beijing Genomics Institute, China. All newly generated sequences were submitted to GenBank (Table 1).

## **Phylogenetic analysis**

Besides the newly generated sequences for this study, additional related sequences were downloaded from GenBank (Table 1) and incorporated together for phylogenetic analyses. Five datasets were employed to explore the relationships among members of *Trechisporales*. The combined dataset of ITS, nrLSU, *tef1-a* and *rpb2* regions (1) was used to clarify the phylogenetic consistency of members of *Trechisporales* within *Agaricomycetes*. Besides representatives from the genera of *Trechisporales*, species from additional 20 orders within *Agaricomycetes* were also included as the ingroup taxa, while two species from *Tremellomycetes* were selected as the outgroup taxa (Table 1). The combined dataset of ITS, nrLSU, *tef1-a*, *rpb2* and mtSSU regions (2) was used to further clarify the phylogenetic relationship among genera within *Trechisporales*. The representatives from the genera of *Trechisporales* were included as the ingroup taxa, while two species from *Polyporales* were selected as the outgroup taxa (Table 1). The combined dataset of ITS, nrLSU, *tef1-a*, *rpb2* and mtSSU regions (2) was used to further clarify the phylogenetic relationship among genera within *Trechisporales*. The representatives from the genera of *Trechisporales* were included as the ingroup taxa, while two species from *Polyporales* were selected as the outgroup taxa (Table 1) according to the topology inferred from the dataset (1). Three combined datasets of ITS and nrLSU regions were used to explore the relationships among species within the genera *Fibrodontia* (3), *Subulicystidium* (4) and *Trechispora* (5), respectively. Besides the species from each target genus listed in Table 1, two species from *Dextrinocystis* and *Tubulicium* were also included as the ingroup taxa, and a species from *Porpomyces* was selected as the outgroup taxon according to the topology inferred from the dataset (2). Regarding the dataset (5) for *Trechispora*, sequences from named and unnamed species of *Scytinopogon* listed in Table 1 were also include

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-α	rpb2	mtSSU
Agaricomycetes								
Agaricales	Lepiota cristata	ZRL20151133#	China	LT716026	KY418841	KY419048	KY418992	-
	Marasmius oreades	ZRL2015086#	China	LT716048	KY418864	KY419066	KY419010	-
	Psathyrella candolleana	ZRL20151400#	China	LT716063	KY418879	KY419075	KY419024	-
Amylocorticiales	Amylocorticium cebennense	HHB-2808 <sup>#</sup>	USA	GU187505	GU187561	GU187675	GU187770	-
	Plicaturopsis crispa	MR00464 #	-	LR694209	LR694187	LR694225	LR694281	-
Atheliales	Athelia arachnoidea	CBS 418.72 #	Netherlands	GU187504	GU187557	GU187672	GU187769	-
	Byssocorticium atrovirens	BS1710033#	Sweden	LR694198	LR694175	LR694214	LR694271	-
	Piloderma fallax	S-12 #	Finland	GU187535	GU187591	GU187738	GU187797	-
Auriculariales	Auricularia heimuer	Xiaoheimao #	China	LT716074	KY418890	KY419083	KY419035	-
	Exidia crenata	PBM2527 #	-	DQ241774	AY700191	DQ408144	-	-
Boletales	Coniophora arida	FP104367 #	USA	GU187510	GU187573	GU187684	GU187775	-
	Gomphidius roseus	MB 95-038 <sup>#</sup>	Germany	DQ534570	DQ534669	GU187702	GU187818	-
	Gyrodontium sacchari	MUCL40589#	French Guiana	GU187522	GU187579	GU187703	GU187764	-
Cantharellales	<i>Clavulina</i> sp.	AFTOL-667 #	-	DQ202266	AY745694	DQ028589	DQ366286	-
	Hydnum albomagnum	AFTOL-471#	USA	DQ218305	AY700199	DQ234568	DQ234553	-
	Sistotrema confluens	AFTOL-613#	-	DQ267125	AY647214	-	DQ381837	-
Corticiales	Punctularia strigosozonata	AFTOL-1248 #	-	DQ398958	AF518642	DQ408147	DQ381843	-

 Table 1 Species and sequences used in the phylogenetic analyses.

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-a	rpb2	mtSSU
	Vuillemenia comedens	AFTOL-1247 #	-	DQ398959	AF518666	-	DQ381844	-
Geastrales	Geastrum recolligens	OSC41996#	-	-	DQ218486	DQ219230	DQ219052	-
	Pyrenogaster pityophilus	OSC59743 #	-	-	DQ218519	DQ219232	DQ219057	-
Gloeophyllales	Gloeophyllum trabeum	1320#	USA	HM536094	HM536067	HM536113	HM536112	-
	Heliocybe sulcata	IBUG-9930#	Mexico	HM536095	HM536069	HM536115	HM536114	-
Gomphales	Clavariadelphus	OSC67280#	-	-	AY574649	DQ219240	DQ219064	-
1	truncatus							
	Kavinia alboviridis	O102140 <sup>#</sup>	-	-	AY574692	DQ219250	DQ219073	-
Hymenochaetales	Fomitiporia aethiopica	MUCL 44777 #	Ethiopia	NR137575	NG059421	GU461893	JQ087956	-
2	Rigidoporus corticola	ZRL20151459#	China	LT716075	KY418899	KY419087	KY419038	-
	Peniophorella	AFTOL-ID 518 <sup>#</sup>	-	AY854081	AY700185	-	AY787221	-
	praetermissa							
Hysterangiales	Aroramyces	H4010 <sup>#</sup>	China: Hunan	-	DQ218524	DQ219118	DQ218941	-
. 0	gelatinosporus							
	Chondrogaster	OSC49298#	-	-	DQ218538	DQ219136	DQ218958	-
	pachysporus							
Iaapiales	Jaapia argillacea	CBS 252.74 #	Netherlands	GU187524	GU187581	GU187711	GU187788	-
Lepidostromatales	Lepidostroma vilgalysii	RV-MX16 <sup>#</sup>	Brazil	JN698907	JN698908	-	-	-
1	Sulzbacheromyces	Sulzbacher 1479 <sup>#</sup>	Mexico	KC170320	KC170318	-	-	-
	caatingae							
Phallales	Dictyophora duplicata	OSC38819#	-	-	DQ218481	DQ219265	DQ219087	-
	Phallus hadriani	AFTOL-683#	-	DQ404385	AY885165	DQ435792	DQ408114	-
Polyporales	Neofavolus alveolaris	Dai 11290 * #	China: Hainan	KU189768	KU189799	KU189913	KU189982	KU189949
~ 1	Polyporus squamosus	Cui 10595 * #	China: Sichuan	KU189778	KU189809	KU189925	KU189988	KU189960
	Climacodon	ZW <sup>#</sup>	-	AY854082	AY684165	AY885151	AY780941	-
	septentrionalis							
	Phlebia radiate	AFTOL-484 #	-	AY854087	AF287885	AY885156	AY218502	-
Russulales	Bondarzewia montana	AFTOL-ID 452#	Canada	DQ200923	DQ234539	DQ059044	AY218474	-
	Heterobasidion annosum	AFTOL-ID 470#	-	DQ206988	AF287866	DQ028584	AH013701	-
	Lactifluus deceptivus	AFTOL-ID 682 #	USA	AY854089	AY631899	AY885158	AY803749	-
Sebacinales	Tremellodendron	AFTOL- 699#	-	DQ411526	AY745701	DQ029196	DQ408132	-
	pallidum						<b>~</b> · · · ·	
	Piriformospora indica	AFTOL-612#	-	DQ411527	AY293202	AJ249911	DQ408131	-
Sistotremastrales	Sertulicium	Spirin 13457 *	Slovenia	MW049161	_	_	-	-
	lateclavigerum	L						
	Sertulicium guttuliferum	He 3338 * <sup>#</sup>	China: Yunnan	MK204540	MK204552	-	-	-
	Sertulicium jacksonii	Svantesson 699 *	Norway	MN937562	MN937562	_	-	_

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-a	rpb2	mtSSU
	Sertulicium	Larsson 13727 * #	France	MN937563	MN937563	-	-	-
	niveocremeum							
	Sertulicium vernale	Söderholm 3886 *	Finland	MT002311	MT664174	-	-	-
	Sistotremastrum	Miettinen 10380.1 *	China: Yunnan	MN991176	MW045423	-	-	-
	aculeatum							
	Sistotremastrum	Larsson 16097 *	Brazil	MN937564	MN937564	-	-	-
	aculeicrepitans							
	Sistotremastrum	Larsson 16004 *	Brazil	MN937567	MN937567	-	-	_
	confusum							
	Sistotremastrum	Motato-Vásquez 894 *	Brazil	MN954694	MW045424	_	_	-
	denticulatum		Dividit	1.11 () 0 10) 1	1111010121			
	Sistotremastrum	GG GUY12-180 *	-	MG913222	MG913208	_	_	_
	fibrillosum	00 00 112 100		110/13222	110/15200			
	Sistotremastrum	Miettinen 14333 *	_	MN991177	MN991177	_	_	_
	geminum	Mictulien 1 1999						
	Sistotremastrum	Spirin 8598 *	USA	MT002324	MT664173	_	_	_
	induratum	Sprin 0090	CON	111002321	111001175			
	Sistotremastrum mendax	Larsson 12022 *	Norway	MN937570	MN937570	_	_	_
	Sistotremastrum rigidum	Motato-Vásquez 833 *	Brazil	MN954693	MW045435	_	_	_
	Sistotremastrum	KHL-11849 * #	Sweden	MN937571	MN937571	_	_	_
	suecicum		Sweden	WII()57571	1011()57571			
	Sistotremastrum vigilans	Fonneland 2011-78 *	Norway	MN937572	MN937572	_	_	_
	Sistotremastrum sp.	LWZ 20171015-32 *	Vietnam	OM523376	OM339204			
	Sistotremastrum sp.	LWZ 20191107-25 * <sup>#</sup>	China: Yunnan	MW477771	MW474864	- MW478703	- MW478712	OM422784
	Sistotremastrum sp.	LWZ 20191107-25	Malaysia	OM523377	OM339205	OM416796	OM416816	OM42278
Stereopsidales	Stereopsis radicans	OLR45395 #	Belize	KC203496	KC203496	KC203516	KC203502	-
siereopsidules		KHL 12592 <sup>#</sup>	Costa Rica	KC203490	KC203490 KC203495	KC203510 KC203515	KC203502 KC203501	-
Thelephorales	Stereopsis globose Boletopsis leucomelaena	PBM2678 <sup>#</sup>	USA	DQ484064	DQ154112	GU187763	GU187820	-
inelephorales	Thelephora ganbajun	ZRL20151295 #	China	LT716082	KY418908	KY419093	KY419043	-
Tuachian anglas		CLZhao 17860 *	China: Yunnan	MW302337	MW293866	K1419095	K1419043	-
Trechisporales	Allotrechispora	CLZnao 1/800 **	China: Yunnan	MW 302337	MW 293800	-	-	-
	daweishanensis	LWZ 20100515 10 *#	A	014502250	011220204		03441/015	
	Allotrechispora gatesiae	LWZ 20180515-18 *#	Australia	OM523378	OM339206	-	OM416817	-
	Allotrechispora gatesiae	LWZ 20180515-20 *	Australia	OM523379	OM339207	OM416797	-	-
	Allotrechispora xantha	CLZhao 2632 *	China: Yunnan	MW302339	MW293868	-	-	-
	Brevicellicium	LISU 178566 *	Portugal	HE963773	HE963774	-	-	-
	atlanticum	<b>WE 20100000 101</b> **			01 1000000	01447800	0144/040	01/10000
	Brevicellicium sp.	LWZ 20190809-10b * #	China: Shandong	-	OM339208	OM416798	OM416818	OM422800
	Brevicellicium sp.	LWZ 20190918-13 *	China: Sichuan	OM523380	-	OM416799	-	OM422792

Table 1	Continued.
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Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-a	rpb2	mtSSU
	Dextrinocystis	He 5693 *	China: Fujian	MK204533	MK204546	OM416800	-	-
	calamicola							
	Dextrinocystis	He 5701 * <sup>#</sup>	China: Fujian	MK204534	MK204547	OM416801	OM416819	-
	calamicola							
	Fibrodontia alba	EYu 110703-25	China: Taiwan	KC928274	KC928275	-	-	-
	Fibrodontia alba	He 3392	China: Yunnan	OM523381	OM339209	-	-	-
	Fibrodontia alba	He 3432	China: Yunnan	OM523382	OM339210	-	-	-
	Fibrodontia alba	He 3475	China: Yunnan	OM523383	-	-	-	-
	Fibrodontia alba	He 3501	China: Yunnan	OM523384	OM339211	-	-	-
	Fibrodontia alba	He 4243	China: Jiangxi	OM523385	OM339212	-	-	-
	Fibrodontia alba	He 4255	China: Jiangxi	OM523386	OM339213	-	-	-
	Fibrodontia alba	He 4380	China: Jiangxi	OM523387	OM339214	-	-	-
	Fibrodontia alba	He 4761	China: Guangxi	MK204529	MK204541	-	-	-
	Fibrodontia alba	He 5953	China: Jiangxi	OM523388	OM339215	-	-	-
	Fibrodontia alba	He 5954a	China: Jiangxi	OM523389	OM339216	-	-	-
	Fibrodontia alba	LWZ 20170820-34 *#	China: Hubei	MT802102	MT802108	MW478698	MW478706	OM422802
	Fibrodontia alba	LWZ 20170820-39	China: Hubei	OM523390	OM339217	-	-	-
	Fibrodontia alba	LWZ 20170820-40	China: Hubei	OM523391	OM339218	-	-	-
	Fibrodontia alba	LWZ 20180415-18	Malaysia	OM523392	OM339219	-	-	-
	Fibrodontia alba	LWZ 20180923-2	China: Yunnan	OM523393	-	-	-	-
	Fibrodontia alba	LWZ 20180923-20	China: Yunnan	OM523394	OM339220	-	-	-
	Fibrodontia alba	LWZ 20180923-4	China: Yunnan	MT802107	MT802101	-	-	-
	Fibrodontia alba	LWZ 20191207-1 *	Malaysia	OM523395	OM339221	OM416802	OM416820	OM422803
	Fibrodontia alba	TNM F24944	China: Taiwan	NR153983	NG060401	-	-	-
	Fibrodontia alba	Yuan 1491	China: Yunnan	OM523396	-	-	-	-
	Fibrodontia	He 6283 *	China: Yunnan	MT802110	MT802104	MW478699	MW478710	-
	austrosinensis							
	Fibrodontia	LWZ 20190820-11b *	China: Sichuan	MT802111	MT802105	MW478700	MW478709	-
	austrosinensis							
	Fibrodontia	He 3453	China: Yunnan	MT802109	MT802103	-	-	-
	austrosinensis							
	Fibrodontia brevidens	He 3559 *	China: Hainan	MK204528	-	MW478701	MW478707	OM422791
	Fibrodontia brevidens	Wu 9807-16	-	KC928276	KC928277	-	-	-
	Fibrodontia gossypina	AFTOL-ID 599	-	DQ249274	AY646100	-	-	-
	Fibrodontia subalba	Dai 15931	China: Xinjiang	MT802106	MT802100	-	-	-
	Fibrodontia	He 6033	China: Hainan	OM523397	OM339222	-	-	-
	subaustrosinensis							

Fibrodontia         He 6279         China: Yunnan         OM523398         OM339223         -         -         -           Lenllia cystidiara         JHP 09.455 **         Portugal         MV371211         MW371211         -         -         -           Lenllia cystidiara         Di 12692 *         Ontvay         UD503822 -         -         -         -         -           Porpomyces submicitus         Dai 12692 *         Cacch Republic         KT157833         KT157838         -         -         -         -           Porpomyces submicitus         Dai 13708 **         China: Hainan         KT157143         KT157145         -	Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-a	rpb2	mtSSU
Luellia cysitiona         HP-09-455 **         Portugal         MV371211         MV371211         -         -         -         -           Luellia recondita         Dai 12692 *         Czech Republic         KT157833         KT157838         -         -         -         -           Porpomyces subuncidus         Dai 13708 **         Cina: Hianan         KT152143         KT152146         MW478702         -         -         -           Portomyces subuncidus         Dai 13708 **         China: Hianan         KT152144         KT152146         MW478702         -         -         -           Peridomyces galzini         GR0 15020 **         Fstonia         LR69420         LR694282         LR694282         -         -           Scytinopogon         TB13611         USA         -         JQ684661         -         -         -         -           Scytinopogon sp.         ME12382675         Australia         KP013088         -         -         -         -         -         -           Scytinopogon sp.         ME12382673         Australia         KP012844         KP012845         -         -         -         -           Scytinopogon sp.         ME12382673         Australia         KP012846		Fibrodontia	He 6279	China: Yunnan	OM523398	OM339223	-	-	-
Luellia recondita         O-2-35622 *         Norway         UDB38222 -         -		subaustrosinensis							
Porpomyces submucidus Porpomyces submucidus Dai 12692 *Creck Republic China: Hainan KT152143KT157333KT157383		Luellia cystidiata	JHP-09.455 * <sup>#</sup>	Portugal	MW371211	MW371211	-	-	-
Porpoonvecs submucidus         China: Hainan         KT152143         KT152144         KT152145         KT		Luellia recondita	O-F-253622 *	Norway	UDB038222	-	-	-	-
Porpomyces submucidusDai 13708 ** Deridomyces galziniChina: Hainam Beridomyces galziniKT152144 Beridomyces galziniKT152145 Beridomyces galziniMW478702 Beridomyces galziniPueridomyces galziniGB0150230 ** GB0150230 **Estonia LR694210LR694218 LR694210LR694226LR694226LR694226LR694226ScytinopogonTENN-F-066226USA-MK278574angulfsporusTENN-F-066226USA-MK278574ScytinopogonTEB13611USA-JQ684661Scytinopogon sp.BAB5120IndiaKT804576Scytinopogon sp.MEL:2382675AustraliaKP012842KP012842 <t< td=""><td></td><td>Porpomyces mucidus</td><td>Dai 12692 *</td><td>Czech Republic</td><td>KT157833</td><td>KT157838</td><td>-</td><td>-</td><td>-</td></t<>		Porpomyces mucidus	Dai 12692 *	Czech Republic	KT157833	KT157838	-	-	-
Prindomyces galzinii Preridomyces galzinii GB01502 81* Scytinopogon suppressBernicchia 812.** EstoniaItaly LR694210MN937559 LR694210ILR694188 LR694188LR694280 LR694280ILR694280 ILR694280ILR694280 <td></td> <td>Porpomyces submucidus</td> <td>Cui 5183</td> <td>China: Hainan</td> <td>KT152143</td> <td>KT152145</td> <td>-</td> <td>-</td> <td>-</td>		Porpomyces submucidus	Cui 5183	China: Hainan	KT152143	KT152145	-	-	-
Pteridomyces galzinii         GB0150230 **         Extonia         LR694120         LR694188         LR694260         LR694282         -           Scytinopogon         TENN-F-066226         USA         -         MK278574         -         -         -           Scytinopogon         TENN-F-066226         USA         -         MK278574         -         -         -           Scytinopogon         TFB13611         USA         -         JQ684661         -         -         -           argulisporus         Scytinopogon sp.         BAB5120         India         KT804576         -		Porpomyces submucidus	Dai 13708 * #	China: Hainan	KT152144	KT152146	MW478702	-	-
Scytinopogon anguilsportsTENN-F-066226USA-MK278574anguilsportsTFB13611USA-JQ684661Scytinopogon Scytinopogon sp.BAB5120IndiaKT804576Scytinopogon sp.MEL:2382675AustraliaKP013038KP012842FN012842Scytinopogon sp.MEL:2382675AustraliaKP012847FScytinopogon sp.MEL:2382623AustraliaKP012847KP012847Scytinopogon sp.MEI:2382623AustraliaKP012927KP012927 </td <td></td> <td>Pteridomyces galzinii</td> <td>Bernicchia 8122 *</td> <td>Italy</td> <td>MN937559</td> <td>MN937559</td> <td>-</td> <td>-</td> <td>-</td>		Pteridomyces galzinii	Bernicchia 8122 *	Italy	MN937559	MN937559	-	-	-
angulisporus       Scytinopogon       TFB13611       USA       -       JQ684661       -       -       -       -         Scytinopogon sp.       BAB5120       India       KT804576       -       -       -       -       -         Scytinopogon sp.       MEL:2382075       Australia       KP013088       KP013038       -       -       -       -         Scytinopogon sp.       MEL:2382092       Australia       KP012847       KP012847       -       -       -       -         Scytinopogon sp.       MEL:2382092       Australia       KP012847       KP012846       -		Pteridomyces galzinii	GB0150230 * #	Estonia	LR694210	LR694188	LR694226	LR694282	-
angulisporus         Seytinopogon         TFB13611         USA         JQ684661         -		Scytinopogon	TENN-F-066226	USA	-	MK278574	-	-	-
angulisporus Scytinopogon sp. BAB5120 India KT804576									
argulisporus Scytinopogon sp. MEL:2382675 Australia KT804576			TFB13611	USA	-	JQ684661	-	-	-
Scytinopogon sp.         BAB5120         India         KT804576         -									
Scytinopogon sp.       MEL:2382675       Australia       KP013038       KP013038       -       -       -         Scytinopogon sp.       MEL:238297       Australia       KP012847       KP012847       -       -       -         Scytinopogon sp.       MEL:2382992       Australia       KP012847       FP012847       -       -       -         Scytinopogon sp.       MEL2382623       Australia       KP01297       KP012847       -       -       -         Scytinopogon sp.       MEL2382744       Australia       KP01297       KP01297       -       -       -         Subulicystidium       He       2807       Cota       KE       MH041537       MH041570       -       -       -         Subulicystidium boidinii       KHL       12830       Costa Rica       MH041537       MH041570       -       -       -       -         Subulicystidium daii       KHL 1000       Brazil       MH000599       MH000599       -       -       -       -       -         Subulicystidium daii       LWZ 20170820-35 *       China: Hubei       OM523490       -       -       -       -       -       -       -       -       -       -       -       - </td <td></td> <td>ē 1</td> <td>BAB5120</td> <td>India</td> <td>KT804576</td> <td>-</td> <td>-</td> <td>-</td> <td>-</td>		ē 1	BAB5120	India	KT804576	-	-	-	-
Scytinopoor sp.         MEL:2382987         Australia         KP012842         KP012842         -         -         -           Scytinopogon sp.         MEL:2382992         Australia         KP012847         KP012846         -         -         -           Scytinopogon sp.         MEL:2382092         Australia         KP012986         KP012986         -         -         -           Scytinopogon sp.         MEL:2382043         Australia         KP012927         KP012927         -         -         -           Scytinopogon sp.         MEL:2382744         Australia         KP012927         KP012927         -         -         -           Subulicystidium         Ho         804         China: Guizhou         MK204539         MK204543         -         -         -           Subulicystidium boidinii         KHL 12830         Costa Rica         MH041537         MH041570         -         -         -           Subulicystidium daii         LWZ 20170820-35 *         China: Hubei         OM523399         OM339224         -         -         -           Subulicystidium daii         Xiong 221         China: Guagaxi         OM52300         -         -         -         -           Subulicystidium daii			MEL:2382675	Australia	KP013038	KP013038	-	-	-
Scytinopogon sp.       MEL:2382992       Australia       KP012847       KP012847       -       -       -         Scytinopogon sp.       MEL:2382623       Australia       KP012926       KP012927       -       -       -         Scytinopogon sp.       MEL:2382744       Australia       KP012927       KP012927       -       -       -         Subulicystidium       He 3804       China: Guizhou       MK204539       MK204543       -       -       -         Subulicystidium boidinii       KHL 12830       Costa Rica       MH041537       MH041570       -       -       -         Subulicystidium       He 2207       USA       MK204532       MK204549       -       -       -         Subulicystidium       He 2207       USA       MH000599       -       -       -       -         Subulicystidium daii       LWZ 20170820-35 *       China: Hubei       OM523399       OM339224       -       -       -       -         Subulicystidium daii       Xiong 221       China: Guangxi       OM523400       -       -       -       -         Subulicystidium daii       KHI 10360       Puerto Rico       MH041535       MH041567       -       -       -				Australia	KP012842	KP012842	-	-	-
Scytinopogon sp.MEL2382623AustraliaKP012986KP012986Scytinopogon sp.MEL2382744AustraliaKP012927KP012927SubulicystidiumHe 3804Chia: GuizhouMK204539MK204533Subulicystidium boidiniiKHL 12830Costa RicaMH041537MH041570SubulicystidiumHe 2207USAMK204543MK204549SubulicystidiumKHL 16100BrazilMH000599MH000599Subulicystidium daiiLWZ 20170820-35 *China: HubeiOM523399OM339224OM422786Subulicystidium daiiXioga 221China: GuangxiOM523400SubulicystidiumKHL 10360Puerto RicoMH041535MH041567SubulicystidiumL 1726aReunionMH041532MH041588SubulicystidiumKHL 10444Puerto RicoMH04158MH041569SubulicystidiumKHL 10444Puerto RicoMH041588MH041569SubulicystidiumKHL 10444Puerto RicoMH041588MH041569SubulicystidiumKHL 10444Puerto RicoMH041578MH041569			MEL:2382992	Australia	KP012847	KP012847	-	-	-
Seytinopogon sp.MEL2382744AustraliaKP012927KP012927KP012927SubulicystidiumHe 3804China: GuizhouMK204539MK204533Subulicystidium boidiniiKHL 12830Costa RicaMH041537MH041570SubulicystidiumHe 2207USAMK204532MK204549SubulicystidiumKHL 16100BrazilMH000599MH000599Subulicystidium daiiLWZ 20170820-35 *China: HubeiOM523309OM339224OM422786Subulicystidium daiiXiong 221China: GuangxiOM523400SubulicystidiumKHL 10360Puerto RicoMH041535MH041567Subulicystidium506781Costa RicaMH041547MH041592SubulicystidiumL 1726aReunionMH041532MH041588SubulicystidiumKHL 10444Puerto RicoMH041588MH041569SubulicystidiumKHL 10444Puerto RicoMH041588MH041569SubulicystidiumKHL 14229SwedenMH00601MH000601			MEL2382623	Australia	KP012986	KP012986	-	-	-
Subulicystidium acerosumHe 3804China: GuizhouMK204539MK204543Subulicystidium boidinii Subulicystidium brachysporumKHL 12830Costa RicaMH041537MH041570Subulicystidium brachysporumHe 2207USAMK204532MK204549Subulicystidium brachysporumKHL 16100BrazilMH000599MH000599				Australia	KP012927		-	-	-
acerosimSubulicystidium boidiniiKHL 12830Costa RicaMH041537MH041570SubulicystidiumHe 2207USAMK204532MK204549brachysporumSubulicystidiumKHL 16100BrazilMH000599MH000599Subulicystidium daiiLWZ 20170820-35 *China: HubeiOM523399OM339224OM422786Subulicystidium daiiXiong 221China: GuangxiOM523400Subulicystidium daiiXiong 221China: GuangxiOM523400Subulicystidium506781Costa RicaMH041535MH041567 <td></td> <td></td> <td></td> <td>China: Guizhou</td> <td></td> <td></td> <td>-</td> <td>-</td> <td>-</td>				China: Guizhou			-	-	-
Subulicystidium boidinii Subulicystidium brachysporumKHL 12830Costa Rica USAMH041537MH041570Subulicystidium brachysporumHe 2207USAMK204532MK204549Subulicystidium brachysporumKHL 16100BrazilMH000599MH000599Subulicystidium daiiLWZ 20170820-35 * LWZ 20170820-35 *China: Hubei China: GuangxiOM523309 OM523400OM339224 OM422786Subulicystidium daiiXiong 221China: Guangxi China: GuangxiOM523400 OM523400Subulicystidium fusiporumKHL 10360Puerto RicoMH041535MH041567Subulicystidium grandisporum506781Costa RicaMH041547MH041592Subulicystidium harpagumL 1726aReunionMH041532MH041588 <td< td=""><td></td><td>•</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>		•							
Subulicystidium brachysporumHe 2207USAMK204532MK204549Subulicystidium brachysporumKHL 16100BrazilMH000599MH000599Subulicystidium daiiLWZ 20170820-35 *China: HubeiOM523399OM339224OM422786Subulicystidium daiiXiong 221China: GuangxiOM523400Subulicystidium daiiXiong 221China: GuangxiOM523400<			KHL 12830	Costa Rica	MH041537	MH041570	-	-	-
brachysporum Subulicystidium KHL 16100 Brazil MH000599			He 2207	USA	MK204532	MK204549	-	-	-
Subulicystidium brachysporumKHL 16100BrazilMH000599MH000599Subulicystidium daiiLWZ 20170820-35 *China: Hubei China: GuangxiOM523399OM339224OM422786Subulicystidium daiiXiong 221China: Guangxi Puerto RicoOM523400Subulicystidium 									
brachysporum Subulicystidium daii LWZ 20170820-35 * China: Hubei China: Guangxi OM523399 OM339224 OM422786 Subulicystidium daii Xiong 221 China: Guangxi OM523400			KHL 16100	Brazil	MH000599	MH000599	-	-	-
Subulicystidium daiiLWZ 20170820-35 * Xiong 221China: Hubei China: Guangxi Puerto RicoOM523399 OM523400OM339224 OM422786Subulicystidium fusisporumKHL 10360Puerto RicoMH041535MH041567Subulicystidium 									
Subulicystidium daiiXiong 221China: GuangxiOM523400 </td <td></td> <td></td> <td>LWZ 20170820-35 *</td> <td>China: Hubei</td> <td>OM523399</td> <td>OM339224</td> <td>-</td> <td>-</td> <td>OM422786</td>			LWZ 20170820-35 *	China: Hubei	OM523399	OM339224	-	-	OM422786
SubulicystidiumKHL 10360Puerto RicoMH041535MH041567fusisporum506781Costa RicaMH041547MH041592grandisporumgrandisporumL1726aReunionMH041532MH041588SubulicystidiumL1726aReunionMH041532MH041588SubulicystidiumKHL 10444Puerto RicoMH041558MH041569SubulicystidiumKHL 10444SwedenMH00601MH000601						-	-	-	-
fusisporumSubulicystidium506781Costa RicaMH041547MH041592grandisporumSubulicystidiumL 1726aReunionMH041532MH041588harpagumSubulicystidiumKHL 10444Puerto RicoMH041558MH041569SubulicystidiumKHL 10444Puerto RicoMH041558MH041569SubulicystidiumKHL 14229SwedenMH00601MH000601				e		MH041567	-	-	-
Subulicystidium grandisporum506781Costa RicaMH041547MH041592grandisporum SubulicystidiumL 1726aReunionMH041532MH041588harpagum subulicystidium inornatum SubulicystidiumKHL 10444Puerto RicoMH041558MH041569Subulicystidium inornatum SubulicystidiumKHL 14229SwedenMH00601MH000601									
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SubulicystidiumL 1726aReunionMH041532MH041588harpagumSubulicystidiumKHL 10444Puerto RicoMH041558MH041569inornatumSubulicystidiumKHL 14229SwedenMH00601MH000601									
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inornatum Subulicystidium KHL 14229 Sweden MH000601 MH000601			KHL 10444	Puerto Rico	MH041558	MH041569	_	-	_
Subulicystidium KHL 14229 Sweden MH000601			• • • •						
			KHL 14229	Sweden	MH000601	MH000601	-	-	-
		longisporum							

Subalicystidium         Hjm 16400         Brazil         MH041538         MH041604         -         -         -           Subalicystidium         L1296         Reunion         MH041513         MH041565         -         -         -           Subalicystidium         Picpeabrink & Lotz- obtusisporum         Germany         MH041521         MH041566         -         -         -           Subalicystidium         L.0140         Reunion         MH041529         MH041590         -         -         -           Subalicystidium         L.0140         Reunion         MH041529         MH041590         -         -         -           Subalicystidium         TU 124388         Italy         UDB028355         UDB028355         -         -         -           Subalicystidium         918488         Colombia         MH041512         MH041608         -         -         -           Subalicystidium         918488         Colombia         MH041514         MH041608         -         -         -           Subalicystidium         TU 10894         Victnam         UDB01461         -         -         -         -           Subalicystidium tropicum         He 3968 **         China: Hainan         K2045	Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-α	rpb2	mtSSU
Subulicystidium SubulicystidiumL 1296 Prepenbrink & Lotz GermanyMH041513 		Subulicystidium	Hjm 16400	Brazil	MH041538	MH041604	-	-	-
Subulicystidium obtustsporum obtustsporum SubulicystidiumPiepenbrink & Lotz- Winter W213-31 O Winter W213-31 OGermanyMH041521MH041560Subulicystidium perlongisporum perlongisporum Turance System perlongisporumKHL 16062BrazilMH000600MH000600Subulicystidium perlongisporum perlongisporum Turance System perlongisporumTU 124388ItalyUDB028355JUB028355 <td< td=""><td></td><td>meridense</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>		meridense							
obusisporum Subulicystidium parvisporumU140ReunionMH041529MH041590							-	-	-
SubalicystidiumL 0140ReunionMH041529MH041590SubalicystidiumKHL 16062BrazilMH000600MH000600SubalicystidiumTU 124388ItalyUDB028355UDB028355Subalicystidium918488ColombiaMH041512MH041564Subalicystidium918488ColombiaMH041514MH041608SubalicystidiumKHL 10813JamaicaMH041514MH041608				Germany	MH041521	MH041566	-	-	-
parisisporum SubulicystidiumKHL 16062BrazilMH000600·····SubulicystidiumTU 124388ItalyUDB028355UDB028355······periongisporum grongisporumSubulicystidium918488ColombiaMH041512MH041564··· <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>									
Subulicystidium         KHL 16062         Brazil         MH000600         MH000600         -         -         -           Subulicystidium         TU 124388         Italy         UDB028355         UDB028355         -         -         -           Subulicystidium         918488         Colombia         MH041512         MH041564         -         -         -           Subulicystidium         918488         Colombia         MH041512         MH041668         -         -         -           Subulicystidium         KHL 10813         Jamaica         MH041514         MH041608         -         -         -           Subulicystidium ropicum         He 3583         China: Hainan         -         -         -         -         -         -         OM422787           Subulicystidium ropicum         He 3968 **         China: Hainan         -         OM523401         OM339226         -         MW478711         OM422788           Subulicystidium sp.         LWZ 20180411-4*         Malaysia         OM523401         OM339226         OM416804         -         -         -           Subulicystidium sp.         LWZ 20180816-24a         China: Bainan         OM523404         -         -         -         -			L 0140	Reunion	MH041529	MH041590	-	-	-
perlongisporum         TU 124388         Italy         UDB028355         UDB028355         -         -         -           Subulicystidium         918488         Colombia         MH041512         MH041564         -         -         -           Subulicystidium         918488         Colombia         MH041514         MH041608         -         -         -           Subulicystidium         KHL 10813         Jamaica         MH041514         MH041608         -         -         -           Subulicystidium         TU 110894         Vietnam         UDB014161         -         -         -         -           Subulicystidium tropicum         He 3583         China: Hainan         -         <									
Subulicystidium perlongisporumTU 124388ItalyUDB028355UDB028355Subulicystidium rarocrystidium918488ColombiaMH041512MH041564Subulicystidium robustiusKHL 10813JamaicaMH041514MH041608Subulicystidium robustiusTU 110894VietnamUDB014161<			KHL 16062	Brazil	MH000600	MH000600	-	-	-
perlongisporum Subulicystidium918488ColombiaMH041512MH041564SubulicystidiumKHL 10813JamaicaMH041514MH041608SubulicystidiumKHL 10813JamaicaMH041514MH041608SubulicystidiumTU 110894VietnamUDB014161Subulicystidium tropicumHe 3583China: HainanOM422787Subulicystidium tropicumHe 3968 **China: HainanMK204531MK204544-MW478711OM422788Subulicystidium sp.LWZ 20180411-4*MalaysiaOM523402-OM416803Subulicystidium sp.LWZ 2018041-5*China: BeijingOM523403OM339226OM416804Subulicystidium sp.LWZ 20190816-24aChina: SichuanOM523403OM339226OM416804 <td></td> <td>1 01</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>		1 01							
Subulicystidium rarocrystallinum918488ColombiaMH041512MH041564Subulicystidium robustiusKHL 10813JamaicaMH041514MH041608Subulicystidium tedersooiTU 110894VietnamUDB014161Subulicystidium tropicum tedersoiHe 3883China: Hainan China: Hainan <td></td> <td></td> <td>TU 124388</td> <td>Italy</td> <td>UDB028355</td> <td>UDB028355</td> <td>-</td> <td>-</td> <td>-</td>			TU 124388	Italy	UDB028355	UDB028355	-	-	-
rarocrystallinum SubulicystidiumKHL 10813JamaicaMH041514MH041608Subulicystidium tedersooiTU 110894VietnamUDB014161Subulicystidium tropicum tedersooiHe 3583China: HainanSubulicystidium tropicum Subulicystidium tropicum Bublicystidium sp.He 3968 **China: HainanMK204531MK204544-MW478711OM422787Subulicystidium sp.LWZ 20180411-4*MalaysiaOM523401OM339225 <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>									
Subulicystidium robustiusKHL 10813JamaicaMH041514MH041608Subulicystidium tedersooiTU 110894VietnamUDB014161Subulicystidium tropicum bublicystidium tropicumHe 3583China: Hainan ML 3968 **<			918488	Colombia	MH041512	MH041564	-	-	-
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1			O-F-253764	Sweden	UDB038261	_	_	_	_
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caulocystidiata			1 LON JUJ17	DIULII	1111110772				

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-α	rpb2	mtSSU
	Trechispora	He 5072	China: Hubei	OM523408	OM339230	-	-	-
	chaibuxiensis							
	Trechispora	LWZ 20170814-34	China: Hubei	OM523409	OM339231	-	-	-
	chaibuxiensis							
	Trechispora	LWZ 20170814-35	China: Hubei	OM523410	OM339232	-	-	-
	chaibuxiensis							
	Trechispora	LWZ 20170814-36	China: Hubei	OM523411	OM339233	-	-	-
	chaibuxiensis							
	Trechispora	LWZ 20170814-42	China: Hubei	OM523412	OM339234	-	-	-
	chaibuxiensis							
	Trechispora chartacea	FLOR 56185	Brazil	MK458775	-	-	-	-
	Trechispora cohaerens	TUF115568	Estonia	UDB016421	-	-	-	-
	Trechispora cf.	UC2022832	USA	KP814538	-	-	-	-
	cohaerens							
	Trechispora confinis	KHL 11064	Sweden	AF347081	AF347081	-	-	-
	Trechispora confinis	LWZ 20200809-30b	China: Sichuan	OM523413	-	-	-	-
	Trechispora confinis	LWZ 20210920-23b	China: Hubei	OM523414	OM339235	-	-	-
	Trechispora confinis	SFC20180710-18	South Korea	MK992834	-	-	-	-
	Trechispora confinis	SFC20180710-23	South Korea	MK992839	-	-	-	-
	Trechispora constricta	Dai 10488	China: Jiangxi	OM523415	-	-	-	-
	Trechispora constricta	Dai 10534	China: Jiangxi	OM523416	-	-	-	-
	Trechispora constricta	He 5899	China:	OM523417	OM339236	-	-	-
	-		Guangdong					
	Trechispora constricta	LWZ 20210924-30a	China: Henan	OM523418	OM339237	-	-	-
	Trechispora copiosa	AMO423	Brazil	MN701014	MN687972	-	-	-
	Trechispora copiosa	AMO453	Brazil	MN701018	MN687975	-	-	-
	Trechispora crystallina	LWZ 20170729-2	China: Inner	OM523419	OM339238	-	-	-
			Mongolia					
	Trechispora crystallina	LWZ 20171013-7	Vietnam	OM523420	OM339239	-	-	-
	Trechispora cyatheae	FR 0219442	France: La	UDB024014	UDB024015	-	-	-
	i i composa ogamene		Réunion	022021011	022021010			
	Trechispora cyatheae	FR 0219443	France: La	UDB024016	UDB024017	-	-	-
	2. comporta ogunicae		Réunion	022021010	022021017			
	Trechispora cyatheae	FR 0219446	France: La	UDB024020	UDB024021	-	-	-
			Réunion	52202.020	22202.021			
	Trechispora	He 6415	Malaysia	OM523421	OM339240	-	-	-
	damansaraensis		···· <b>)</b> ····					

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-a	rpb2	mtSSU
	Trechispora	LWZ 20180417-26	Malaysia	-	OM339241	-	-	-
	damansaraensis							
	Trechispora dealbata	FLOR 56182	Brazil	MK458776	-	-	-	-
	Trechispora dealbata	FLOR 56183	Brazil	MK458777	-	-	-	-
	Trechispora dentata	Dai 15277	China: Hainan	OM523505	-	-	-	-
	Trechispora dentata	Dai 22565	China	OK298491	OM049408			
	Trechispora dimitiella	Dai 17772	Singapore	OM523450	-	-	-	-
	Trechispora dimitiella	Dai 17891	Singapore	OM523451	-	-	-	-
	Trechispora dimitiella	Dai 21181	China	OK298493	OK298949			
	Trechispora dimitiella	Dai 21931	China	OK298492	OK298948			
	Trechispora	FR 0219445	France: La	UDB024018	UDB024019	-	-	-
	echinocristallina		Réunion					
	Trechispora	TUF 110414	Papua New	UDB013050	UDB013050	-	-	-
	echinocristallina		Guinea					
	Trechispora echinospora	E09/60-06	Equatorial Guinea	JX392847	JX392848	-	-	-
	Trechispora echinospora	E11/37-03	Equatorial Guinea	JX392845	JX392846	-	-	-
	Trechispora echinospora	E11/37-05	Equatorial Guinea	-	JX392849	-	-	-
	Trechispora echinospora	E11/37-10	Equatorial Guinea	JX392850	JX392851	-	-	-
	Trechispora echinospora	E11/37-11	Equatorial Guinea	JX392852	-	-	-	-
	Trechispora echinospora	E11/37-12	Equatorial Guinea	JX392853	JX392854	-	-	-
	Trechispora farinacea	KHL 8451	-	AF347082	AF347082	-	-	-
	Trechispora farinacea	KHL 8454	-	AF347083	AF347083	-	-	-
	Trechispora farinacea	KHL 8793	Sweden	AF347089	AF347089	-	-	-
	Trechispora farinacea	MA-Fungi 79474	-	JX392855	-	-	-	-
	Trechispora farinacea	TUB 011825	Germany	EU909231	EU909231	_	_	_
	Trechispora fimbriata	CLZhao 4154	China: Yunnan	MW544023	MW520173	-	-	_
	Trechispora fimbriata	Cui 7962	China: Yunnan	OM523422	-	-	-	-
	Trechispora fimbriata	Dai 17612	China: Yunnan	OM523423	OM339242	-	-	-
	Trechispora fimbriata	He 4873	China: Guangxi	OM523424	OM339243	-	-	-
	Trechispora fimbriata	He 6134	China: Yunnan	OM523425	OM339244	-	-	-
	Trechispora fimbriata	Xiong 21	China: Hunan	OM523426	-	-	-	-
	Trechispora fissurata	CLZhao 4571	China: Yunnan	MW544027	MW520177	-	-	-
	Trechispora fissurata	He 6190	China: Yunnan	OM523427	OM339245	-	-	-
	Trechispora fissurata	He 6322	China: Yunnan	OM523428	OM339246	-	-	-
	Trechispora fissurata	LWZ 20171015-11	Vietnam	OM523429	OM339247	-	-	-
	Trechispora fissurata	LWZ 20171015-16	Vietnam	OM523430	OM339248	-	-	-
	Trechispora fissurata	LWZ 20171015-35 *	Vietnam	OM523431	OM339249	-	OM416821	OM422793
	Trechispora fissurata	LWZ 20171015-4	Vietnam	OM523432	OM339250	-	-	-

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-α	rpb2	mtSSU
	Trechispora fissurata	LWZ 20180922-51	China: Yunnan	OM523433	OM339251	-	-	-
	Trechispora fissurata	LWZ 20191110-9	China: Yunnan	OM523434	OM339252	-	-	-
	Trechispora foetida	FLOR 56315	Brazil	MK458769	-	-	-	-
	Trechispora fragilis	Dai 20535	China	OK298494	OK298950			
	Trechispora gelatinosa	AMO1139	Brazil	MN701021	MN687978	-	-	-
	Trechispora gelatinosa	AMO824	Brazil	MN701020	MN687977	-	-	-
	Trechispora gracilis	LWZ 20170814-17	China: Hubei	OM523435	OM339253	-	-	-
	Trechispora gracilis	LWZ 20210626-5b	China: Jiangxi	OM523436	OM339254	-	-	-
	Trechispora gracilis	LWZ 20210919-9a	China: Hubei	OM523437	OM339255	-	-	-
	Trechispora gracilis	LWZ 20210922-7b	China: Hubei	OM523438	OM339256	-	-	-
	Trechispora havencampii	SFSU DED8300 *	Africa	NR154418	NG059993	-	-	-
	Trechispora hondurensis	HONDURAS19-F016a	Honduras	MT571523	MT636540	-	-	-
	Trechispora hondurensis	HONDURAS19-F016b	Honduras	-	MT636541	-	-	-
	Trechispora	Dai 2247	Finland	OM523439	-	-	-	-
	hymenocystis							
	Trechispora	KHL 16444	Norway	MT816397	MT816397	-	-	-
	hymenocystis		•					
	Trechispora	KHL 8795	Sweden	AF347090	AF347090	-	-	-
	hymenocystis							
	Trechispora incisa	EH 24/98	-	AF347085	AF347085	-	-	-
	Trechispora incisa	GB-0090521	Sweden	KU747093	-	-	-	-
	Trechispora incisa	GB-0090648	Sweden	KU747095	KU747087	-	-	-
	Trechispora incisa	GB-0105521	Sweden	-	KU747086	-	-	-
	Trechispora incisa	GB-0105526	Sweden	KU747094	-	-	-	_
	Trechispora incisa	He 5008 * <sup>#</sup>	China: Hebei	OM523440	OM339257	OM416805	OM416822	_
	Trechispora invisitata	UC2022935	USA	KP814182	-	-	-	-
	Trechispora invisitata	UC2023088	USA	KP814425	-	-	-	-
	Trechispora kavinioides	KGN 981002	Norway	AF347086	AF347086	-	-	-
	Trechispora laevis	TUF115551	Estonia	UDB016406	-	-	-	-
	Trechispora laevispora	Dai 21655	China	OK298495	OM108710			
	Trechispora larssonii	He 5450	China: Guizhou	OM523441	OM339258	-	-	-
	Trechispora larssonii	LWZ 20190817-11a *	China: Sichuan	OM523442	OM339259	-	OM416823	OM42279
	Trechispora larssonii	LWZ 20200818-10b	China: Sichuan	-	OM339260	-	-	-
	Trechispora latehypha	He 3924	China: Hainan	OM523443	OM339261	-	-	-
	Trechispora latehypha	He 4472	China: Fujian	OM523444	-	-	-	-
	Trechispora latehypha	He 5438 *	China: Guizhou	OM523445	_	OM416806	-	OM42279
	Trechispora latehypha	He 5848	Sri Lanka	OM523446	OM339262	-	_	-
	Trechispora latehypha	LWZ 20170611-16	China: Hainan	OM523447	OM339263	_	_	_

Table 1	Continued.
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Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-α	rpb2	mtSSU
	Trechispora longiramosa	HG 140168	China: Guizhou	OM523448	OM339264	-	-	-
	Trechispora longiramosa	CH 19233	China: Guizhou	OM523449	-	-	-	-
	Trechispora malayana	Dai 17876	Singapore	OM523452	OM339265	-	-	-
	Trechispora malayana	He 4156	Thailand	OM523453	OM339266	-	-	-
	Trechispora mellina	URM85756	Brazil	-	MH280000	-	-	-
	Trechispora microspora	O-F-253725	Sweden	UDB038247	-	-	-	-
	Trechispora minispora	AM170	Mexico	MK328885	MK328894	-	-	-
	Trechispora minispora	AM176	Mexico	MK328886	MK328895	-	-	-
	Trechispora mollis	URM 85884	Brazil	MK514945	MH280003	-	-	-
	Trechispora mollis	URM 85885	Brazil	-	MT423667	-	-	-
	Trechispora mollusca	CBS 439.48	Canada	MH856428	-	-	-	-
	Trechispora mollusca	Cui 2455	China: Qinghai	-	OM339267	-	-	-
	Trechispora mollusca	Dai 1931	Estonia	OM523454	-	-	-	-
	Trechispora mollusca	Dai 6174	China: Anhui	-	OM339268	-	-	-
	Trechispora mollusca	Dai 6191	China: Anhui	OM523455	OM339269	-	-	-
	Trechispora mollusca	Dai 7097	China: Jilin	OM523456	-	-	-	-
	Trechispora mollusca	Dai 11085	China: Inner	OM523457	OM339270	-	-	-
	_		Mongolia					
	Trechispora mollusca	Dai 11157	China: Inner	OM523458	OM339271	-	-	-
	-		Mongolia					
	Trechispora mollusca	Dai 13289	China: Gansu	OM523459	OM339272	-	-	-
	Trechispora mollusca	DLL2010-077	USA	JQ673209	-	-	-	-
	Trechispora mollusca	DLL2011-186	USA	KJ140681	-	-	-	-
	Trechispora mollusca	Li 1449	China: Hubei	OM523460	-	-	-	-
	Trechispora nivea	GB-0087593	Sweden	-	KU747088	-	-	-
	Trechispora nivea	GB-0102694	Sweden	-	KU747089	-	-	-
	Trechispora nivea	LWZ 20180804-3	China: Beijing	OM523461	OM339273	-	-	-
	Trechispora nivea	MA-Fungi 74044	-	JX392832	JX392833	-	-	-
	Trechispora nivea	MA-Fungi 76253	-	JX392837	-	-	-	-
	Trechispora nivea	MA-Fungi 76254	-	-	JX392834	-	-	-
	Trechispora nivea	MA-Fungi 76257	-	JX392826	JX392827	-	-	-
	Trechispora nivea	MA-Fungi 82479	-	-	JX392828	-	-	-
	Trechispora nivea	MA-Fungi 82481	-	-	JX392831	-	-	-
	Trechispora nivea	MA-Fungi 82483	-	JX392838	-	-	-	-
	Trechispora nivea	O 90120	Tanzania	KU747103	KU747092	-	-	-
	Trechispora cf. nivea	F-506673	Venezuela	-	KU747091	-	-	-
	Trechispora pallescens	FLOR 56184	Brazil	MK458767	-	-	-	-

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-a	rpb2	mtSSU
	Trechispora pallescens	FLOR 56188	Brazil	MK458774	-	-	-	-
	Trechispora pallescens	He 5192	Vietnam	-	MK204553	-	-	-
	Trechispora pallescens	SC1 *	-	MZ518207	MZ518091	-	-	-
	Trechispora aff.	AM21	Mexico	MK328883	MK328893	-	-	-
	pallescens							
	Trechispora aff.	RL115	Mexico	MK328887	MK328896	-	-	-
	pallescens							
	Trechispora aff.	RL132	Mexico	MK328889	MK328898	-	-	-
	pallescens							
	<i>Trechispora</i> aff.	RL133	Mexico	MK328890	MK328899	-	-	-
	pallescens							
	Trechispora papillosa	AMO713	Brazil	MN701022	MN687979	-	-	-
	Trechispora papillosa	AMO795	Brazil	MN701023	MN687981	-	-	-
	Trechispora regularis	KHL 10881	Jamaica	AF347087	AF347087	-	-	-
	Trechispora rigida	URM 85754	Brazil	MT406381	MH279999	-	-	-
	Trechispora robusta	FLOR 56179	Brazil	MK458770	-	-	-	-
	Trechispora robusta	FLOR 56190	Brazil	MK458768	-	-	-	-
	Trechispora scaber	FLOR 56189	Brazil	MK458773	-	-	-	-
	Trechispora sinensis	Dai 7227	China: Fujian	OM523462	-	-	-	-
	Trechispora sinensis	Dai 11239	China: Jiangsu	OM523463	-	-	-	-
	Trechispora sinensis	He 3714	China: Jilin	OM523464	OM339274	-	-	-
	Trechispora sinensis	He 4314	China: Jiangxi	OM523465	OM339275	-	-	-
	Trechispora sinensis	He 4668	China: Liaoning	OM523466	-	-	-	-
	Trechispora sinensis	He 4698	China: Guangxi	OM523467	OM339276	-	-	-
	Trechispora sinensis	He 5446	China: Guizhou	OM523468	OM339277	-	-	-
	Trechispora sinensis	He 5491	China: Chongqing	OM523469	OM339278	-	-	-
	Trechispora sinensis	He 5649	China: Hunan	OM523470	OM339279	-	-	-
	Trechispora sinensis	He 5652	China: Hunan	OM523471	OM339280	-	-	-
	Trechispora sinensis	He 5898	China:	OM523472	OM339281	-	-	-
			Guangdong					
	Trechispora sinensis	LWZ 20170805-14	China: Liaoning	OM523473	-	-	-	-
	Trechispora sinensis	LWZ 20170814-11	China: Hubei	OM523474	OM339282	-	-	-
	Trechispora sinensis	LWZ 20170814-27	China: Hubei	OM523475	OM339283	-	-	-
	Trechispora sinensis	LWZ 20170814-28	China: Hubei	OM523476	OM339284	-	-	-
	Trechispora sinensis	LWZ 20170815-38 *	China: Hubei	OM523477	OM339285	OM416807	-	-
	Trechispora sinensis	LWZ 20170816-16	China: Hubei	OM523478	OM339286	-	-	-
	Trechispora sinensis	LWZ 20170816-35 *	China: Hubei	OM523479	OM339287	OM416808	-	OM42279
	Trechispora sinensis	LWZ 20170817-5	China: Hunan	OM523480	OM339288	-	_	-

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-α	rpb2	mtSSU
	Trechispora sinensis	LWZ 20170909-11	China: Beijing	OM523481	OM339289	-	-	-
	Trechispora sinensis	LWZ 20180804-19	China: Beijing	OM523482	OM339290	-	-	-
	Trechispora sinensis	LWZ 20180804-20 *	China: Beijing	OM523483	OM339291	OM416809	-	-
	Trechispora sinensis	LWZ 20210923-15b	China: Henan	OM523484	OM339292	-	-	-
	Trechispora sinensis	LWZ 20210925-13b	China: Henan	OM523485	OM339293	-	-	-
	Trechispora sinensis	LWZ 20210925-3a	China: Henan	OM523486	OM339294	-	-	-
	Trechispora sinensis	LWZ 20210928-7	China: Guizhou	OM523487	OM339295	-	-	-
	Trechispora sinensis	LWZ 20210928-9	China: Guizhou	OM523488	OM339296	-	-	-
	Trechispora sinensis	Wei 7909	China: Beijing	OM523489	OM339297	-	-	-
	Trechispora stevensonii	KHL 14654	Norway	-	MH290762	-	-	-
	Trechispora stevensonii	MA-Fungi 70645	-	JX392843	JX392844	-	-	-
	Trechispora stevensonii	MA-Fungi 70669	-	JX392841	JX392842	-	-	-
	Trechispora stevensonii	TU 115499	Estonia	UDB016467	-	-	-	-
	Trechispora subfissurata	He 3907	China: Hainan	OM523490	OM339298	-	-	-
	Trechispora subfissurata	LWZ 20190613-48	China: Guangdong	OM523491	-	-	-	-
	Trechispora	LWZ 20190818-29b *	China: Sichuan	OM523492	OM339299	-	OM416824	OM42279
	subhymenocystis							
	Trechispora subhymenocystis	LWZ 20190818-32b	China: Sichuan	-	OM339300	-	-	-
	Trechispora subsinensis	He 4122	Thailand	OM523493	OM339301	_	_	-
	Trechispora subsinensis	He 4125	Thailand	OM523494	OM339302	-	-	-
	Trechispora subsinensis	He 5894	China:	OM523495	OM339303	_	_	-
	<i>F</i>		Guangdong	011020.00	011200000			
	Trechispora subsinensis	LWZ 20190611-19	China: Guangdong	OM523496	-	-	-	-
	Trechispora subsinensis	LWZ 20190611-9	China: Guangdong	OM523497	OM339304	-	-	-
	Trechispora subsphaerospora	KHL 8511	Sweden	AF347080	AF347080	-	-	-
	Trechispora taiwanensis	He 4571 *	China: Taiwan	OM523498	OM339305	_	OM416825	OM42279
	Trechispora taiwanensis	He 4574	China: Taiwan	N	OM339306	_	-	-
	Trechispora termitophila	AMO390	Brazil	MN701024	MN687982	-	-	-
	Trechispora termitophila	AMO396	Brazil	MN701025	MN687983	_	_	_
	Trechispora termitophila	AMO893	Brazil	MN701026	MN687984	_	_	-
	Trechispora thailandica	He 4101 *	Thailand	OM523499	OM339307	OM416810	-	-
	Trechispora thailandica	He 4112	Thailand	OM523500	OM339308	-	-	-
	Trechispora thailandica	He 4114	Thailand	OM523501	OM339309	-	_	_

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-a	rpb2	mtSSU
	Trechispora thelephora	URM 85757	Brazil	-	MH280001	-	-	-
	Trechispora thelephora	URM85758	Brazil	-	MH280002	-	-	-
	Trechispora thelephora	UTC 252606	Belize	-	HM104485	-	-	-
	Trechispora torrendii	KHL 15465	Brazil	-	MH290759	-	-	-
	Trechispora torrendii	URM85886	Brazil	MK515148	MH280004	-	-	-
	Trechispora tropica	LWZ 20170613-14	China: Hainan	OM523502	OM339310	-	-	-
	Trechispora tropica	LWZ 20170613-16	China: Hainan	OM523503	OM339311	-	-	-
	Trechispora tropica	LWZ 20171015-22	Vietnam	OM523504	OM339312	-	-	-
	<i>Trechispora</i> sp.	AMO799	Brazil	MN701008	MN687969	-	-	-
	Trechispora sp.	Dai 16179	China: Hainan	OM523506	OM339313	-	-	-
	Trechispora sp.	Dai 17433	Brazil	OM523507	OM339314	-	-	-
	Trechispora sp.	Dai 18781	Australia	OM523508	OM339315	-	-	-
	Trechispora sp.	Dai 22173	China	OK298496	OK298951			
	Trechispora sp.	Dai 22174	China	OK298497	OK298952			
	Trechispora sp.	F909645	Sweden	JX392817	JX392818	-	-	-
	Trechispora sp.	He 3431	China: Yunnan	OM523509	OM339316	-	-	-
	Trechispora sp.	He 3984	China: Hainan	OM523510	OM339317	-	-	-
	Trechispora sp.	He 3996	China: Hainan	OM523511	-	-	-	-
	Trechispora sp.	He 4503	China: Fujian	OM523512	OM339318	-	-	-
	Trechispora sp.	He 4641	China: Taiwan	OM523513	OM339319	-	-	-
	Trechispora sp.	He 5812	Sri Lanka	OM523514	OM339320	-	-	-
	Trechispora sp.	He 6400	Malaysia	OM523515	OM339321	-	-	-
	Trechispora sp.	HG 19350	China: Yunnan	OM523516	-	-	-	-
	Trechispora sp.	KHL 10715	-	AF347088	AF347088	-	-	-
	Trechispora sp.	KHL 16968	Brazil	MH290763	MH290763	-	-	-
	Trechispora sp.	LWZ 20170805-15	China: Liaoning	OM523517	-	-	-	-
	Trechispora sp.	LWZ 20170815-20 *	China: Hubei	OM523518	OM339322	OM416811	-	OM42280
	Trechispora sp.	LWZ 20171015-17	Vietnam	OM523519	OM339323	-	-	-
	Trechispora sp.	LWZ 20180512-12 *	Australia	OM523520	OM339324	OM416812	-	-
	Trechispora sp.	LWZ 20180513-8	Australia	OM523521	OM339325	-	-	-
	Trechispora sp.	LWZ 20180517-43 *	Australia	OM523522	OM339326	OM416813	OM416826	-
	Trechispora sp.	LWZ 20180517-44 *	Australia	OM523523	OM339327	-	OM416827	OM42279
	Trechispora sp.	LWZ 20180517-45	Australia	OM523524	OM339328	-	-	-
	Trechispora sp.	LWZ 20190816-39a *	China: Sichuan	OM523525	OM339329	OM416814	-	-
	Trechispora sp.	LWZ 20191206-27	Malaysia	OM523526	OM339330	-	-	-
	Trechispora sp.	LWZ 20191208-10	Malaysia	OM523527	-	-	-	-
	Trechispora sp.	LWZ 20200921-33a	China: Sichuan	OM523528	OM339331	-	-	-
	Trechispora sp.	LWZ 20210918-10a	China: Hubei	OM523529	OM339332	_	-	_

Class/Order	Species	Vouchers	Country	ITS	nrLSU	tef1-α	rpb2	mtSSU
	Trechispora sp.	LWZ 20210921-7a	China: Hubei	OM523530	OM339333	-	-	-
	Trechispora sp.	NCC16	Brazil	MN701007	MN687968	-	-	-
	Trechispora sp.	SP48	Brazil	MN701005	MN687965	-	-	-
	Trechispora sp.	Yuan 6129	China: Guangxi	OM523531	-	-	-	-
	Trechispora sp.	ZP-1029	China	OM523532	-	-	-	-
	Trechispora sp.	ZP-3658	China	OM523533	-	-	-	-
	Tubulicium bambusicola	He 4776 *	China: Guizhou	MK204536	MK204551	-	-	OM422789
	Tubulicium raphidisporum	He 3191 *	China: Yunnan	OM523534	OM339334	-	-	OM422801
	Tubulicium sp.	LWZ 20180414-5 * #	Malaysia	OM523535	OM339335	OM416815	OM416828	OM422790
Tremellomycetes	L.		·					
Tremellales	Bullera alba	CBS 501 #	-	AF444368	AF075500	KF037016	KF036745	-
	Dioszegia antarctica	CBS 10920#	-	DQ402529	FJ640575	KF037129	KF036858	-

<sup>#</sup> The vouchers are used in the phylogenetic analysis of Agaricomycetes in Figs 1, 2

\* The vouchers are used in the phylogenetic analysis of genera within Sistotremastrumales and Trechisporales in Fig. 3

Newly generated sequences are in bold.

Of the five datasets, each gene region was separately aligned using MAFFT 7.110 (Katoh & Standley 2013) with the G-INS-i strategy (Katoh et al. 2005) and then accordingly concatenated to five alignments (Supplementary files 1–5). The best-fit evolutionary models for the five alignments were separately estimated using jModelTest 2.1.10 (Darriba et al. 2012, Guindon & Gascuel 2003). Following these models, maximum likelihood (ML) and Bayesian inference (BI) algorithms were used to performed phylogenetic analyses. ML algorithm was conducted using raxmlGUI 2.0 (Edler et al. 2021, Stamatakis 2014) and bootstrap (BS) replicates were determined under the auto FC option (Pattengale et al. 2010). BI algorithm was conducted using MrBayes 3.2.7a (Ronquist et al. 2012). Two independent runs were employed, each with four chains and starting from random trees. Trees were sampled every 1000th generation. The first 25% of sampled trees were discarded as burn-in, while the other 75% of trees were used to construct a 50% majority consensus tree and for calculating Bayesian posterior probabilities (BPPs). Chain convergence was judged using Tracer 1.7 (Rambaut et al. 2018).

The alignment resulted from the dataset (1) was also subjected to a molecular clock analysis using BEAST 2.6.3 (Bouckaert et al. 2019). Following Wang et al. (2021), the divergence time and the corresponding credibility intervals were estimated under the lognormal relaxed molecular clock and the Yule speciation prior set. The following time points were set for calibration: 90 million years ago (Mya) as the minimum age of *Agaricales* by *Archaeomarasmius leggetti*, a fossil agaricoid species preserved in a Dominican amber (Hibbett et al. 1997); 113 Mya as the minimum age of *Hymenochaetales* by *Quatsinoporites cranhamii*, a fossil poroid species collected from Apple Bay on Vancouver Island (Smith et al. 2004); and 290 Mya as the mean age of *Agaricomycetes* by the analyses of genome data (Floudas et al. 2012). Accordingly, the offset ages for *Agaricales* and *Hymenochaetales* were, respectively, set as 90 Mya and 113 Mya with a gamma distribution prior (alpha = 20, beta = 1), while the mean age for *Agaricomycetes* was set as 290 Mya with a normal distribution prior (sigma = 1). After 200 million generations, the first 10% of the trees sampled

every 1000th generation were removed as burn-in. Chain convergence of the resulting log file was judged using Tracer 1.7 (Rambaut et al. 2018). A maximum-clade-credibility tree was summarized using TreeAnnotator 2.6.3 incorporated into BEAST 2.6.3 (Bouckaert et al. 2019).

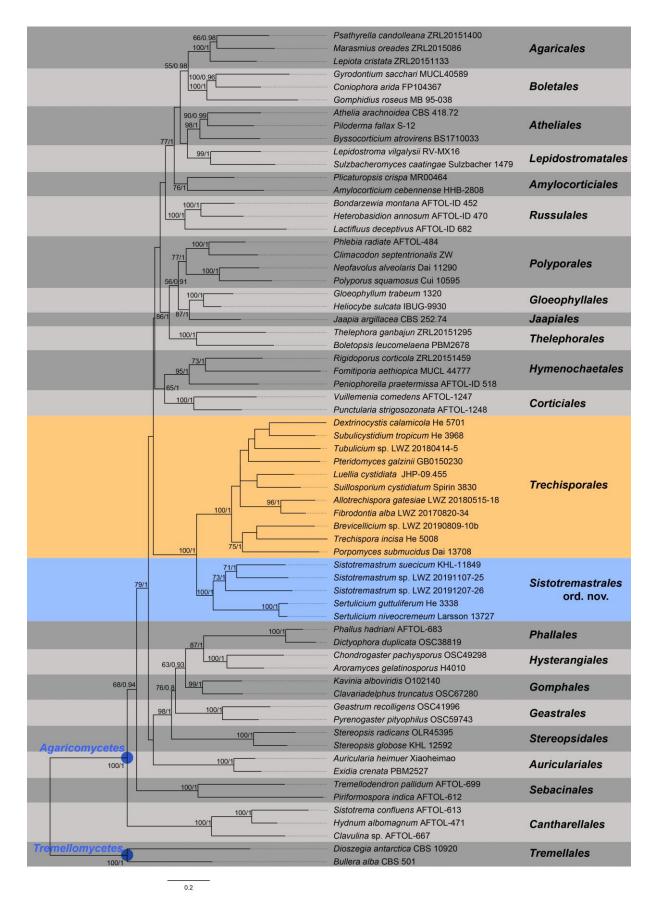
#### Results

#### Molecular phylogeny

In this study, 160 ITS, 132 nrLSU, 20 *tef1-a*, 13 *rpb2* and 21 mtSSU sequences were newly generated from 174 specimens (Table 1).

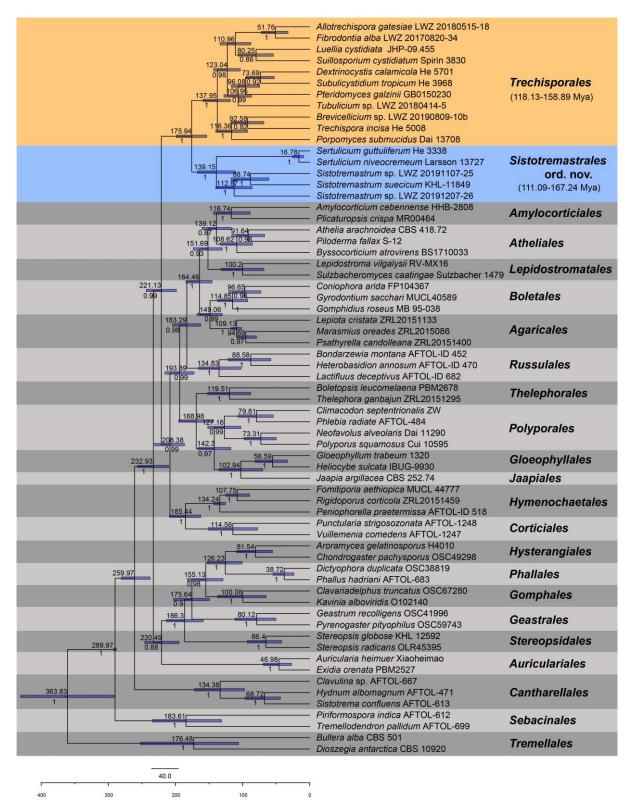
The combined dataset of ITS, nrLSU, *tef1-\alpha* and *rpb2* regions (1) comprised 65 samples and resulted in an alignment of 3842 characters with GTR + I + G as the best-fit evolutionary model. In ML algorithm, the BS search stopped after 200 replicates. In BI algorithm, after ten million generations with an average standard deviation of split frequencies of 0.004707, all chains converged, which was indicated by the effective sample sizes (ESSs) of all parameters above 3800 and the potential scale reduction factors (PSRFs) close to 1.000. Because BI and ML algorithms generated nearly congruent topologies, the topology from ML algorithm is presented along with BS values and BPPs greater than 50% and 0.8, respectively, at the nodes (Fig. 1). Regarding the molecular clock analysis, chain convergence was indicated by the ESSs above 1200. The maximum-clade-credibility chronogram is presented along with estimated divergence times of 95% highest posterior density for all clades as node bars and the crown ages and BPPs above 0.8, respectively, above and below the branches at the nodes (Fig. 2). While the monophyly of all sampled orders was well supported, this multilocus-based phylogeny strongly supported the independence of *Sertulicium* and *Sistotremastrum* (BS = 100%, BPP = 1) from other genera within Trechisporales (BS = 100%, BPP = 1), although these two genera did have a closer relationship with other genera within Trechisporales than with other orders (Fig. 1). Moreover, the 95% highest posterior density ages for the clade of Sertulicium plus Sistotremastrum compared to the clade of other genera within Trechisporales were, respectively, 111.09-167.24 Mya and 118.13-158.89 Mya with mean crown ages of 139.15 Mya and 137.95 Mya, respectively (Fig. 2). These divergence times fell in the range of mean crown ages of other orders within Agaricomycetes from 38.72 Mya (Phallales) to 134.83 Mya (Russulales) except for Sebacinales having mean crown ages of 183.61 Mya (Fig. 2). The option of combining Sertulicium, Sistotremastrum and other genera within Trechisporales as one order produced a clade with a mean crown age of 175.94 Mya considerably earlier than the option of two separate clades and most additional sampled orders (Fig. 2). In association with distinct morphological characters, one new family within one new order are described to accommodate Sertulicium and Sistotremastrum below.

The combined dataset of ITS, nrLSU,  $tef1-\alpha$ , rpb2 and mtSSU regions (2) comprised 67 samples and resulted in an alignment of 4102 characters with GTR + I + G as the best-fit evolutionary model. In ML algorithm, the BS search stopped after 150 replicates. In BI algorithm, after ten million generations with an average standard deviation of split frequencies of 0.003781, all chains converged, which was indicated by the ESSs above 3200 and the PSRFs close to 1.000. Because BI and ML algorithms generated nearly congruent topologies, the topology from ML algorithm is presented along with BS values and BPPs greater than 50% and 0.8, respectively, at the nodes (Fig. 3). This phylogeny also supported, at least did not reject, the segregation of *Sertulicium* and *Sistotremastrum* from *Trechisporales* as an independent lineage at the order level. Each sampled genus within *Trechisporales* was well differentiated from others. Moreover, within *Trechisporales* one new lineage at the genus level was revealed being composed of two recently described species in *Trechispora* and a new lineage at the species level represented by two samples. In association with morphological characters, one new genus within *Hydnodontaceae*, *Trechisporales* and one new species and two new combinations accommodated in the new genus are described below.



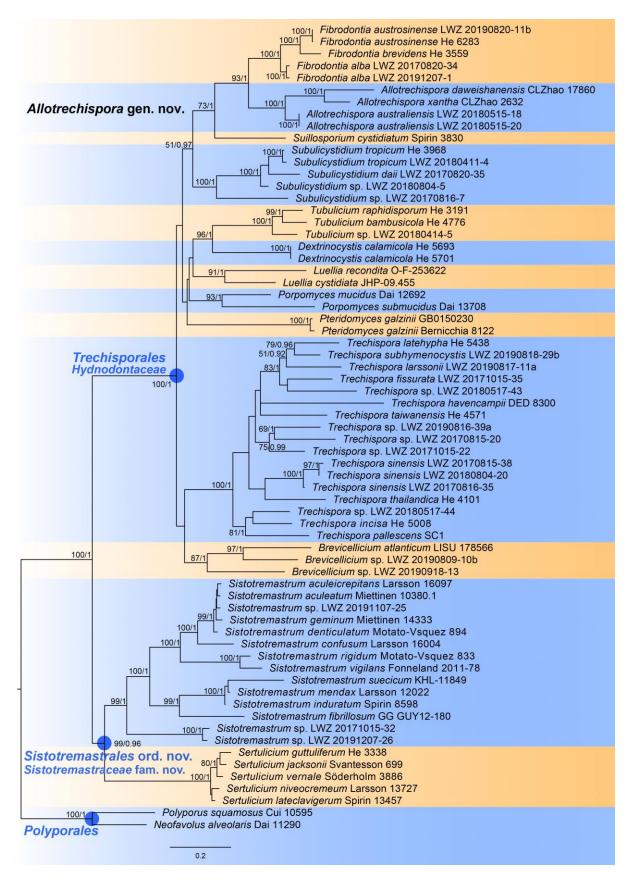
**Figure 1** – Phylogenetic position of *Sistotremastrales* and *Trechisporales* within the *Agaricomycetes* inferred from the combined dataset of ITS, nrLSU, *tef1-a* and *rpb2* regions. The topology is generated by the maximum likelihood algorithm. Bootstrap values and Bayesian

posterior probabilities, when simultaneously above 50% and 0.8, respectively, are labelled at the nodes.



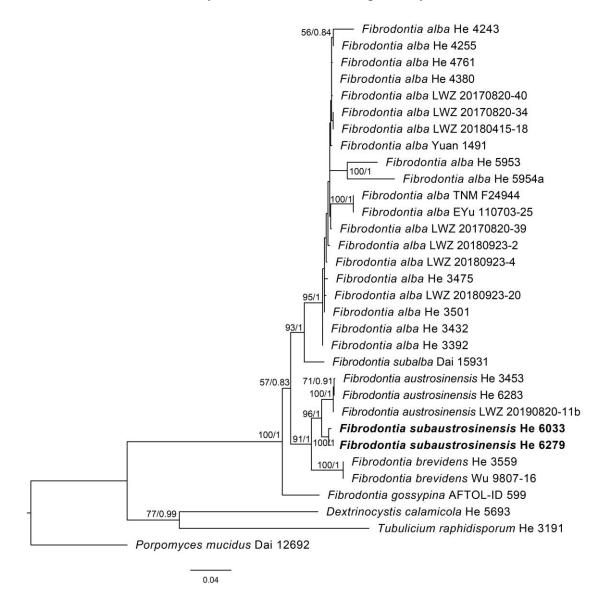
**Figure 2** – Maximum-clade-credibility chronogram and estimated divergence times of orders within the *Agaricomycetes* inferred from the combined dataset of ITS, nrLSU, *tef1-a* and *rpb2* regions. The estimated divergence times of 95% highest posterior density for all clades were indicated as node bars, and for *Sistotremastrales* and *Trechisporales* were also provided below the order names as exact numbers. The mean divergence times of clades (crown ages) and Bayesian

posterior probabilities above 0.8 were labeled above and below the branches, respectively, at the nodes.



**Figure 3** – Phylogenetic relationship among genera within *Sistotremastrales* and *Trechisporales* inferred from the combined dataset of ITS, nrLSU, *tef1-a*, *rpb2* and mtSSU regions. The topology

is generated by the maximum likelihood algorithm. Bootstrap values and Bayesian posterior probabilities, when simultaneously above 50% and 0.8, respectively, are labelled at the nodes.

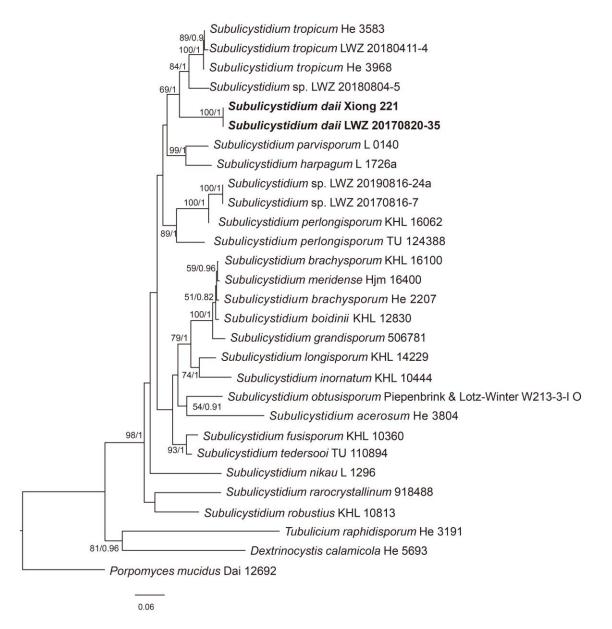


**Figure 4** – Phylogenetic relationship among species of *Fibrodontia* inferred from the combined dataset of ITS and nrLSU regions. The topology is generated by the maximum likelihood algorithm. Bootstrap values and Bayesian posterior probabilities, when simultaneously above 50% and 0.8, respectively, are labelled at the nodes. The newly described species are in boldface.

The combined dataset of ITS and nrLSU regions (3) comprised 32 samples and resulted in an alignment of 1511 characters with GTR + I + G as the best-fit evolutionary model. In ML algorithm, the BS search stopped after 350 replicates. In BI algorithm, after two million generations with an average standard deviation of split frequencies of 0. 006526, all chains converged, which was indicated by the ESSs above 1100 and the PSRFs close to 1.000. Because BI and ML algorithms generated nearly congruent topologies, the topology from ML algorithm is presented along with BS values and BPPs greater than 50% and 0.8, respectively, at the nodes (Fig. 4). The monophyly of *Fibrodontia* was strongly supported and one new lineage represented by two samples emerged within *Fibrodontia*. In association of morphological characters, this new lineage is described as one new species of *Fibrodontia* below.

The combined dataset of ITS and nrLSU regions (4) comprised 29 samples and resulted in an alignment of 1521 characters with GTR + I + G as the best-fit evolutionary model. In ML

algorithm, the BS search stopped after 350 replicates. In BI algorithm, after one million generations with an average standard deviation of split frequencies of 0. 006978, all chains converged, which was indicated by the ESSs above 700 and the PSRFs close to 1.000. Because BI and ML algorithms generated nearly congruent topologies, the topology from ML algorithm is presented along with BS values and BPPs greater than 50% and 0.8, respectively, at the nodes (Fig. 5). The monophyly of *Subulicystidium* was strongly supported, and two new lineages, each represented by two samples, emerged within *Subulicystidium*. In association of morphological characters and conditions of specimens, one of these two new lineages is described as one new species of *Subulicystidium* below.



**Figure 5** – Phylogenetic relationship among species of *Subulicystidium* inferred from the combined dataset of ITS and nrLSU regions. The topology is generated by the maximum likelihood algorithm. Bootstrap values and Bayesian posterior probabilities, when simultaneously above 50% and 0.8, respectively, are labelled at the nodes. The newly described species are in boldface.

The combined dataset of ITS and nrLSU regions (5) comprised 249 samples and resulted in an alignment of 1796 characters with GTR + I + G as the best-fit evolutionary model. In ML algorithm, the BS search stopped after 250 replicates. In BI algorithm, after ten million generations with an average standard deviation of split frequencies of 0.007705, all chains converged, which

was indicated by the ESSs above 2800 and the PSRFs close to 1.000. Because BI and ML algorithms generated nearly congruent topologies, the topology from ML algorithm is presented along with BS values and BPPs greater than 50% and 0.8, respectively, at the nodes (Fig. 6). The monophyly of *Trechispora* was strongly supported and 16 new lineages, each represented by two or more samples, emerged within *Trechispora*. In association of morphological characters, these 16 new lineages are described as 16 new species of *Trechispora* below. In addition, five species of *Scytinopogon* with clear taxonomic background, viz. *S. caulocystidiatus*, *S. dealbatus*, *S. foetidus*, *S. robustus* and *S. scaber* nested within *Trechispora* (Fig. 6) and thus are transferred to *Trechispora* below.

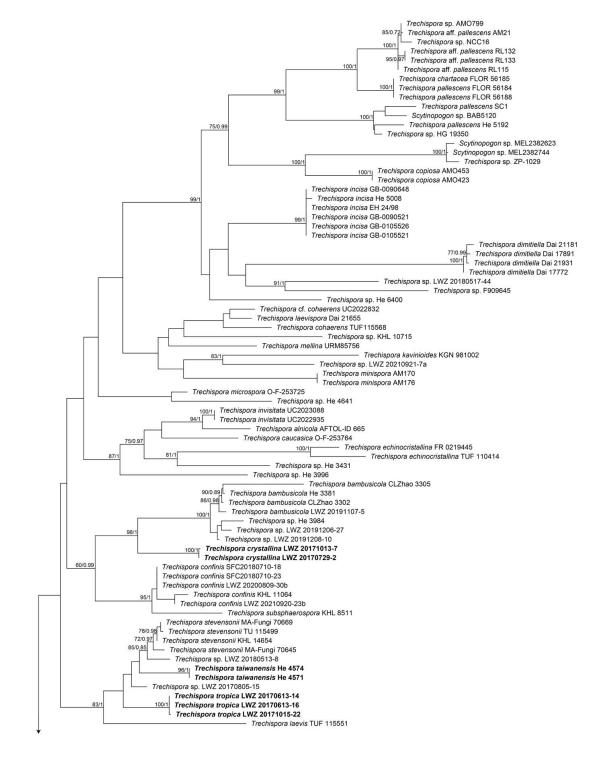


Figure 6 – Phylogenetic relationship among species of *Trechispora* inferred from the combined dataset of ITS and nrLSU regions. The topology is generated by the maximum likelihood

algorithm. Bootstrap values and Bayesian posterior probabilities, when simultaneously above 50% and 0.8, respectively, are labelled at the nodes. The newly described species are in boldface.

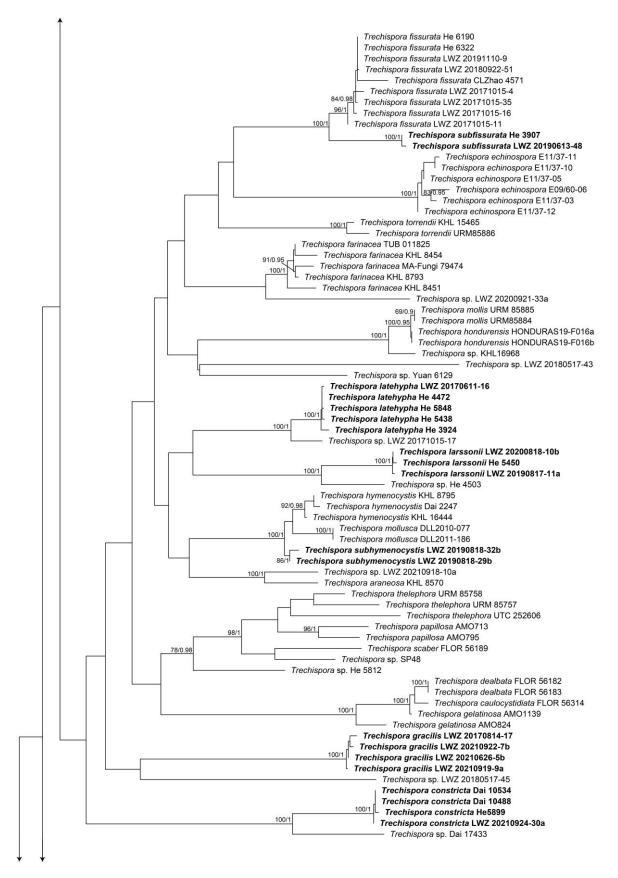


Figure 6 – Continued.



## Figure 6 – Continued.

Besides these phylogenetic analyses, molecular sequences were also employed to explore the taxonomic position of *Litschauerella*, *Sphaerobasidium* and *Trechispora yunnanense* via BLAST search. Their taxonomic positions at the higher rank are changed below. In addition, a brief summary of each genus accepted in *Trechisporales* is provided.

#### Taxonomy

Sistotremastrales L.W. Zhou & S.L. Liu, ord. nov.

Index Fungorum number: IF559875; Facesoffungi number: FoF12855 Etymology – *Sistotremastrales* (Latin), refers to the type family *Sistotremastraceae*. Type family – *Sistotremastraceae* L.W. Zhou & S.L. Liu (described below). Type genus – *Sistotremastrum* J. Erikss., Symb. bot. upsal. 16(no. 1): 62 (1958). Type species – *Sistotremastrum suecicum* Litsch. ex J. Erikss., Symb. bot. upsal. 16(no. 1): 62 (1958).

Type specimen – SWEDEN, Upland, Uppsala, Bondkyrka parish, Malma skog, Northwest of Hälltorpet, on the underside of coniferous fencing material lying in a wet spot, 4 Jan. 1933, Seth Lundell, F204406 (S, holotype).

Description – *Basidiomes* resupinate, effused, thin. *Hymenophore* smooth, grandinioid or odontioid. *Hyphal system* monomitic, all septa with clamp connections. *Cystidia* mostly absent. *Basidia* cylindrical to tubular with four to eight sterigmata. *Basidiospores* smooth, ellipsoid to cylindrical, inamyloid, acyanophilous. On wood.

Notes – Sertulicium and Sistotremastrum formerly belonging to Trechisporales are segregated as the new order. Sistotremastrales is characterized by corticioid basidiomes on wood, basidia with four to eight sterigmata and smooth basidiospores. Comparing with the circumscription of Trechisporales sensu He et al. (2019) and Spirin et al. (2021), some species in the reduced concept of Trechisporales after the exclusion of Boidinella (below), Litschauerella (below), Sertulicium, Sistotremastrum and Sphaerobasidium (below) also have smooth basidiospores, and thus are similar to species bearing basidia with four sterigmata in Sistotremastrales; however, species of Trechisporales differ in soft basidiomes, subicular hyphae with ampullate septa and presence of cystidia with various shapes (Spirin et al. 2021).

#### Sistotremastraceae L.W. Zhou & S.L. Liu, fam. nov.

Index Fungorum number: IF559876; Facesoffungi number: FoF12856

Etymology – Sistotremastraceae (Latin), refers to the type genus Sistotremastrum.

Type genus - Sistotremastrum J. Erikss., Symb. bot. upsal. 16(no. 1): 62 (1958).

Description – *Basidiomes* resupinate, effused, thin, usually up to 100 µm thick. *Hymenophore* smooth, grandinioid or odontioid, white to pale ochraceous. *Hyphal system* monomitic, all septa with clamp connections. *Cystidia* mostly absent, hyphidia rarely present. *Basidia* cylindrical to tubular, often with a slight median constriction, with four to eight sterigmata. *Basidiospores* smooth, ellipsoid to cylindrical, inamyloid, acyanophilous. On wood.

Notes – Sistotremastraceae is the single family within Sistotremastrales and comprises Sertulicium and Sistotremastrum, segregated from Trechisporales. Therefore, the unique morphological characters of Sistotremastraceae are the same as those indicated to Sistotremastrales above. From the morphological perspective, Larsson (2007) suggested the distinction of Sistotremastrum from other genera in Trechisporales and used the designation 'Sistotremastrum family'. Spirin et al. (2021) segregated Sertulicium from Sistotremastrum and indicated these two genera are unique in Trechisporales. However, Spirin et al. (2021) did not propose any formal taxonomic change at the family or higher rank mainly due to lack of reliable phylogenetic support. Here, according to multilocus-based phylogenetic analyses, we formally propose Sertulicium and Sistotremastrum in one new family and one new order independent from Hydnodontaceae and Trechisporales, respectively.

*Sertulicium* Spirin, Volobuev & K.H. Larss., in Spirin, Volobuev, Viner, Miettinen, Vlasák, Schoutteten, Motato-Vásquez, Kotiranta & Larsson, Mycol. Progr. 20(4): 460 (2021).

Type species – *Sertulicium niveocremeum* (Höhn. & Litsch.) Spirin & K.H. Larss., in Spirin, Volobuev, Viner, Miettinen, Vlasák, Schoutteten, Motato-Vásquez, Kotiranta & Larsson, Mycol. Progr. 20(4): 466 (2021)

Description – *Basidiomes* annual, resupinate, effused, very thin (usually up to 0.1 mm thick). *Hymenophore* smooth, white, cream to pale ochraceous. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline. *Cystidia* mostly absent. Hyphidia rarely present. *Basidia* clavate, hyaline, thin-walled, with four to six or six to eight sterigmata and a basal clamp connection. *Basidiospores* narrowly ellipsoid to cylindrical, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Sertulicium* was recently segregated from *Sistotremastrum* as a new genus with *S. niveocremeum* as the generic type (Spirin et al. 2021). Six combined species from other genera and a newly described species from Finland bring the species number of *Sertulicium* to seven (Spirin et al. 2021, Liu et al. 2022). While their morphological characters are not distinct, phylogenetically *Sertulicium* and *Sistotremastrum* are close but clearly separated from each other (Spirin et al. 2021, Figs 1–3).

## Sistotremastrum J. Erikss., Symb. bot. upsal. 16(no. 1): 62 (1958).

Type species – *Sistotremastrum suecicum* Litsch. ex J. Erikss., Symb. bot. upsal. 16(no. 1): 62 (1958).

Type specimen – SWEDEN, Upland, Uppsala, Bondkyrka parish, Malma skog, Northwest of Hälltorpet, on the underside of coniferous fencing material lying in a wet spot, 4 Jan. 1933, Seth Lundell, F204406 (S, holotype).

Description – *Basidiomes* annual, resupinate, effused, thin to rather substantial (up to 0.2 mm thick). *Hymenophore* smooth, grandinioid, odontioid, white, cream to buff-yellow. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline. *Cystidia* mostly absent. Hyphidia present. *Basidia* clavate, hyaline, thin-walled, with two to four, four to six or six to eight sterigmata and a basal clamp connection. *Basidiospores* narrowly ellipsoid to cylindrical, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes - Sistotremastrum was erected for S. niveocremeum and S. suecicum with the latter species as the generic type (Eriksson 1958). Later, six species, viz. S. aculeocrepitans, S. chilense, S. fibrillosum, S. guttuliferum, S. lateclavigerum and S. roseum were successively added to this genus (Boidin & Gilles 1994, Telleria et al. 2013b, 2014, Dhingra et al. 2014, Gruhn et al. 2018). However, of these eight species, S. chilense, S. lateclavigerum and S. niveocremeum were recently transferred to Sertulicium, and S. guttuliferum was considered to be a synonym of Sertulicium granuliferum by Spirin et al. (2021). Besides, Spirin et al. (2021) also newly described eight species in Sistotremastrum. In addition, Sistotremastrum limonadense was newly described from French Guiana (Gruhn & Alvarado 2021), but this species was later transferred to Sertulicium (Liu et al. 2022). In summary, a total of 12 species is accepted in Sistotremastrum. Although being placed in Trechisporales, Sistotremastrum has long been considered to be separated from additional genera in the single family *Hydnodontaceae* within this order (Larsson 2007). Unlike the previous phylogeny lack of reliable support at the family rank (Spirin et al. 2021), the current multilocus-based phylogenetic analyses support the proposal of Sistotremastrum in one new family Sistotremastraceae within one new order Sistotremastrales independent from Trechisporales (Figs 1-3).

Trechisporales K.H. Larss., in Hibbett et al., Mycol. Res. 111(5): 541 (2007).

Type genus – *Trechispora* P. Karst., Hedwigia 29: 147 (1890) = *Hydnodon* Banker, Mycologia 5(6): 297 (1913).

Type species – *Trechispora onusta* P. Karst., Hedwigia 29: 147 (1890) = *T. hymenocystis* (Berk. & Broome) K.H. Larss., Mycol. Res. 98(10): 1167 (1994).

Description – *Basidiomes* resupinate, effused, stipitate or clavarioid. *Hymenophore* smooth, grandinioid, hydnoid or poroid to partly irpicoid. *Hyphal system* monomitic to dimitic, all septa with clamp connections. *Cystidia* present or absent. *Basidia* cylindrical with two to four sterigmata. *Basidiospores* smooth or ornamented, subglobose, ellipsoid, subangular or fusiform, inamyloid, acyanophilous. On wood or ground.

Notes – Comparing with the circumscription of *Trechisporales* sensu He et al. (2019) and Spirin et al. (2021), the current concept of *Trechisporales* is reduced according to the exclusion of *Boidinella* (below), *Litschauerella* (below), *Sertulicium, Sistotremastrum* and *Sphaerobasidium* (below). For now, *Trechisporales* is composed of one family *Hydnodontaceae* comprising 12 genera.

Hydnodontaceae Jülich, Biblthca Mycol. 85: 372 (1982) [1981].

Type genus – Hydnodon Banker, Mycologia 5(6): 297 (1913) = Trechispora P. Karst., Hedwigia 29: 147 (1890).

Type species – *Hydnodon thelephorus* (Lév.) Banker [as '*thelephorum*'], Mycologia 5(6): 297 (1913) = *Trechispora thelephora* (Lév.) Ryvarden, Syn. Fung. (Oslo) 15: 32 (2002).

*= Subulicystidiaceae* Jülich, Biblthca Mycol. 85: 391 (1982) [1981].

Description – *Basidiomes* resupinate, effused, stipitate or clavarioid. *Hymenophore* smooth, grandinioid, odontioid, hydnoid or poroid to partly irpicoid, mycelial cords present or absent. *Hyphal system* monomitic to dimitic, all septa with clamp connections, subicular hyphae with or without ampullate septa. *Cystidia* present in some species, mostly absent. *Basidia* cylindrical with two to four sterigmata, often with a slight median constriction. *Basidiospores* smooth or ornamented, subglobose, ellipsoid, subangular or fusiform, inamyloid, acyanophilous. *Conidiospores* sometimes present. On wood or ground.

Notes – After the exclusion of *Boidinella* (below), *Litschauerella* (below), *Sertulicium*, *Sistotremastrum* and *Sphaerobasidium* (below), all genera formerly accepted in *Trechisporales* and a new genus *Allotrechispora* (described below) are accommodated in *Hydnodontaceae*.

The family names *Hydnodontaceae* and *Subulicystidiaceae* (as well as *Litschauerellaceae*, see *Litschauerella* under excluded genera from *Trechisporales*) were published simultaneously by Jülich (1981). Under this circumstance, the choice of name is governed by Art. 11.5 of the Shenzhen Code (Turland et al. 2018) and the first effectively published choice establishes priority. Hibbett et al. (2014) listed *Subulicystidiaceae* as a synonym of *Hydnodontaceae*, thereby establishing the priority of the latter name.

#### Allotrechispora L.W. Zhou & S.L. Liu, gen. nov.

Index Fungorum number: IF559877; Facesoffungi number: FoF12857

Etymology – Allotrechispora (Latin), refers to the segregation from Trechispora.

Diagnosis – Differs from *Trechispora* in the absence of stipitate or clavarioid basidiomes, and the absence of ampullate septa on subicular hyphae (Eriksson et al. 1981, de Meiras-Ottoni et al. 2021).

Type species – Allotrechispora gatesiae L.W. Zhou, S.L. Liu & T.W. May (described below).

Type specimen – AUSTRALIA, Tasmania, Tahune Adventures, The Look-in Look-out, on fallen *Atherosperma moschatum*, 15 May 2018, *L.W. Zhou*, LWZ 20180515-18 (holotype in MEL, isotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, loosely attached to the substrates. *Hymenophore* smooth to tuberculate, white to cinnamon-buff, cracked with age. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline, thin-walled. *Cystidia* absent. *Basidia* subcylindrical to subclavate, hyaline, thin-walled, with four sterigmata and a basal clamp connection. *Basidiospores* oblong ellipsoid to ellipsoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – Compared to other genera in *Trechisporales*, *Allotrechispora* is characterized by cream to cinnamon-buff, corticioid basidiomes, a monomitic hyphal system, absence of isodiametric subhymenial hyphae, absence of cystidia, and smooth, oblong ellipsoid to ellipsoid basidiospores. *Allotrechispora* is phylogenetically closest to *Fibrodontia* (the clade containing both genera has BS = 74%, BPP = 0.99; Fig. 3), and these two genera are more or less similar by the absence of cystidia and smooth, ellipsoid basidiospores. However, *Fibrodontia* differs in the odontioid hymenophore and a dimitic hyphal system.

Allotrechispora daweishanensis (C.L. Zhao) L.W. Zhou & S.L. Liu, comb. nov.

Index Fungorum number: IF559878; Facesoffungi number: FoF12858

Basionym. Trechispora daweishanensis C.L. Zhao, in Zong, Liu, Wu & Zhao, Phytotaxa 479(2): 153 (2021).

 $\equiv$  Brevicellicium daweishanense (C.L. Zhao) Z.B. Liu & Yuan Yuan, Frontiers in Microbiology 13(no. 818358): 15 (2022).

Notes – *Trechispora daweishanensis* was recently described from southwestern China (Zong et al. 2021). Although the authors stated that their phylogeny indicates this species nested within *Trechispora*, this genus was not recovered as a well-supported clade (Fig. 1 in Zong et al. 2021). A later phylogenetic analysis revealed the separation of *T. daweishanensis* from *Trechispora*, but unfortunately this phylogeny sampling taxa incomprehensively was incorrectly recognized and *T. daweishanensis* was accordingly transferred to *Brevicellicium* (Liu et al. 2022). According to the current phylogeny (Fig. 3), *T. daweishanensis* does not belong to *Trechispora* and *Brevicellicium*, but falls within a distinct clade described as a new genus *Allotrechispora* in *Trechisporales*. Therefore, *T. daweishanensis* is transferred to *Allotrechispora*.

Allotrechispora gatesiae L.W. Zhou, S.L. Liu & T.W. May, sp. nov.

Figs 7, 8

Index Fungorum number: IF559879; Facesoffungi number: FoF12859

Etymology – *gatesiae* (Latin), refers to the Australian mycologist, Dr. Genevieve Gates, who kindly arranged the author Li-Wei Zhou's field trip in Tasmania, Australia.

Diagnosis – Characterized by the largest basidiospores in the genus.

Typus – AUSTRALIA, Tasmania, Tahune Adventures, The Look-in Look-out, on fallen trunk of *Atherosperma moschatum*, 15 May 2018, *L.W. Zhou*, LWZ 20180515-18 (holotype in MEL, isotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, loosely attached to the substrates. *Hymenophore* tuberculate, straw-yellow when fresh, straw-yellow to cinnamon-buff, cracked with age. *Margin* thinning out, fimbriate, slightly paler than hymenophore surface, becoming indistinct with age.

*Hyphal system* monomitic; generative hyphae with clamp connections, hyaline, thin-walled, frequently branched and septate, loosely interwoven, 2–3  $\mu$ m in diam. *Cystidia* absent. *Basidia* cylindrical, hyaline, thin-walled, with four sterigmata and a basal clamp connection, 20–27 × 6–8  $\mu$ m; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* oblong ellipsoid to ellipsoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous, (5–)5.2–6.8(–7) × (3.7–)3.8–4.3(–5)  $\mu$ m, L = 6.0  $\mu$ m, W = 4.1  $\mu$ m, Q = 1.4–1.5 (*n* = 60/2).

Other specimen (paratype) examined – AUSTRALIA, Tasmania, Tahune Adventures, The Look-in Look-out, on fallen trunk of *Atherosperma moschatum*, 15 May 2018, *L.W. Zhou*, LWZ 20180515-20 (HMAS).

Notes – As far as macromorphology, *Allotrechispora gatesiae* is distinct from other species in this genus by its colored basidiomes. The basidiospores in *A. gatesiae* are larger than those in *A. daweishanensis* ( $3.8-5 \times 2.7-3.5 \mu m$ ; Zong et al. 2021: as *Trechispora*). In comparison to *Allotrechispora gatesiae*, basidiospores are overlapping in size in *A. xantha* ( $4.3-5.7 \times 3.2-4 \mu m$ ; transferred from *Trechispora xantha* below), but this species has a lower length to width ratio of basidiospores (1.32-1.41; Zong et al. 2021: as *Trechispora*).

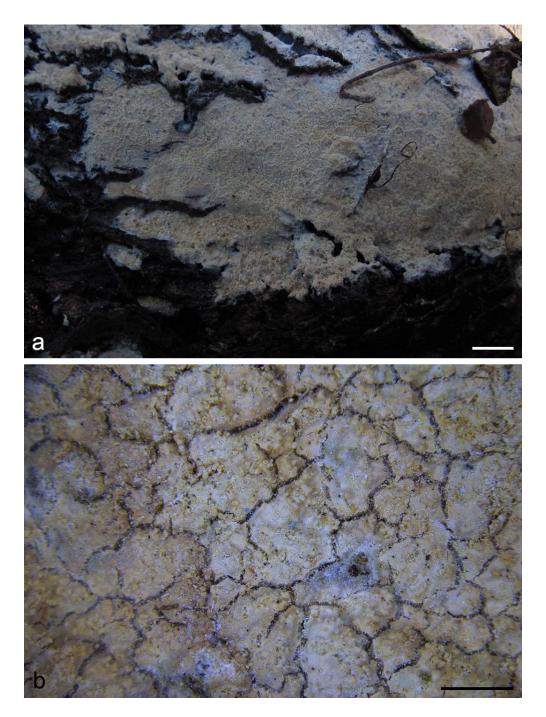
Allotrechispora xantha (C.L. Zhao) L.W. Zhou & S.L. Liu, comb. nov.

Index Fungorum number: IF559880; Facesoffungi number: FoF12860

Basionym. Trechispora xantha C.L. Zhao, in Zong, Liu, Wu & Zhao, Phytotaxa 479(2): 155 (2021).

 $\equiv$  Brevicellicium xanthum (C.L. Zhao) Z.B. Liu & Yuan Yuan, Frontiers in Microbiology 13(no. 818358): 15 (2022).

Notes – *Trechispora xantha* was described from southwestern China together with *T. daweishanensis*, and these two species have a close phylogenetic relationship (Zong et al. 2021). Together with *T. daweishanensis*, *T. xantha* was inappropriately transferred to *Brevicellicium* (Liu et al. 2022). The current phylogeny supports that *T. xantha* and *T. daweishanensis* fall within the clade of the new genus *Allotrechispora* (Fig. 3). Therefore, *T. xantha* is transferred to *Allotrechispora*.



**Figure 7** – Basidiomes of *Allotrechispora gatesiae* (LWZ 20180515-18, holotype). Scale bars: a = 1 cm, b = 2 mm.

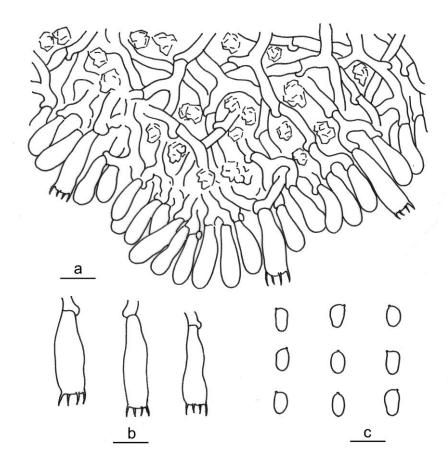
Brevicellicium K.H. Larss. & Hjortstam, in Hjortstam & Larsson, Mycotaxon 7(1): 117 (1978).

Type species – *Brevicellicium exile* (H.S. Jacks.) K.H. Larss. & Hjortstam, Mycotaxon 7(1): 118 (1978).

Description – *Basidiomes* annual, resupinate, effused, thin, membranaceous. *Hymenophore* smooth, grandinioid, white, cream to yellowish. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline, thin-walled, distinctly isodiametric. *Cystidia* absent. *Basidia* shortly cylindrical, hyaline, thin-walled, with four sterigmata and a basal clamp connection. *Basidiospores* usually subangular with a distinct apiculus, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Brevicellicium* was erected by Hjortstam & Larsson (1978) with *B. exile* as the generic type. *Brevicellicium* is a cosmopolitan genus and is characterized by isodiametric subhymenial hyphae, short basidia, and smooth, often subangular basidiospores with a distinct

apiculus. Jülich (1981) put *Brevicellicium* in *Hydnodontaceae*, and Larsson (2007) accepted this placement at the family level and further put it in *Trechisporales*. Later, Telleria et al. (2013a) confirmed the classification of *Brevicellicium* within *Hydnodontaceae*, *Trechisporales* from the phylogenetic perspective. For now, ten species are accepted in *Brevicellicium*, while the taxonomic position of certain species needs to be further tested by molecular evidence (Telleria et al. 2013a). Moreover, two unnamed single-specimen lineages, viz. LWZ 20190809-10b and LWZ 20190918-13, both from Sichuan, China are revealed from the current multilocus-based phylogenetic analyses (Figs 1–3).



**Figure 8** – Microscopic structures of *Allotrechispora gatesiae* (drawn from the holotype). a Vertical section of basidiomes. b Basidia. c Basidiospores. Scale bars =  $10 \mu m$ .

Brevicellopsis Hjortstam & Ryvarden, Syn. Fung. (Oslo) 25: 15 (2008).

Type species – *Brevicellopsis allantospora* (Hjortstam & Ryvarden) Hjortstam & Ryvarden, Syn. Fung. (Oslo) 25: 15 (2008).

Description – *Basidiomes* annual, resupinate, effused, thin, membranaceous, soft, fragile. *Hymenophore* odontioid, greyish white to pale ochraceous. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline, slightly isodiametric. *Cystidia* absent. *Basidia* shortly cylindrical, hyaline, thin-walled, with four sterigmata and a basal clamp connection. *Basidiospores* allantoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Brevicellopsis* was erected to accommodate *B. allantospora* (Hjortstam & Ryvarden 2008) that is a species originally described from Africa as a member of *Brevicellicium* (Hjortstam & Ryvarden 1980). This monotypic genus differs from *Brevicellicium* mainly by odontioid hymenophore and allantoid basidiospores (Hjortstam and Ryvarden 2008). Presumably due to the segregation from *Brevicellicium*, *Brevicellopsis* was also considered to potentially belong to *Trechisporales* (Hibbett et al. 2014). Phylogenetic analyses need to be employed to exactly delimit the taxonomic position of *Brevicellopsis*.

Dextrinocystis Gilb. & M. Blackw., Mycotaxon 33: 376 (1988).

Type species – *Dextrinocystis capitata* (D.P. Rogers & Boquiren) Gilb. & M. Blackw., Mycotaxon 33: 378 (1988).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, easily separated from the substrate. *Hymenophore* smooth, cream to buff, not cracked. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline. *Cystidia-like* branches present on subicular hyphae, embedded, hyaline, thick-walled, encrusted at apex. Cystidia subulate, projecting beyond hymenium, bi- or multi-rooted, hyaline, distinctly thick-walled with a narrow lumen, slightly encrusted at apex, distinctly dextrinoid. *Basidia* subcylindrical to subclavate, hyaline, thin-walled, with four sterigmata and a basal clamp connection. *Basidiospores* oblong-ellipsoid to short cylindrical, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Dextrinocystis* was segregated from *Epithele* to accommodate *E. capitata* that is strikingly distinguished by strongly dextrinoid cystidia (Gilbertson & Blackwell 1988). This monotypic genus was doubtfully put in *Trechisporales* (Larsson 2007). Later, another two species also with dextrinoid cystidia, viz. *D. calamicola* and *D. macrospora* were added to this genus (Nakasone 2013, Liu et al. 2019). Of the three species accepted in *Dextrinocystis*, *D. calamicola* was included in a phylogenetic analysis that unambiguously confirmed that within *Trechisporales* this genus has a closer relationship with *Tubulicium*, as indicated by morphological characters (Liu et al. 2019). This topology is also recovered by the current phylogeny (Fig. 3).

Fibrodontia Parmasto, Consp. System. Corticiac. (Tartu): 174 (1968).

Type species – Fibrodontia gossypina Parmasto, Consp. System. Corticiac. (Tartu): 207 (1968).

Description – *Basidiomes* annual, resupinate, effused, thin, soft-membranaceous, easily detached. *Hymenophore* grandinioid, odontioid, white to pale cinnamon-buff. *Hyphal system* dimitic, generative hyphae with clamp connections, hyaline; skeletal hyphae hyaline to yellowish, thick-walled with a wide lumen. *Cystidia* absent. *Basidia* subcylindrical to subclavate, hyaline, thin-walled, with four sterigmata and a basal clamp connection. *Basidiospores* broadly ellipsoid to ovoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous or slightly cyanophilous. On wood.

Notes – *Fibrodontia gossypina* was newly described as the generic type of a new genus *Fibrodontia* (Parmasto 1968). Although *Fibrodontia* is morphologically close to *Hyphodontia* (Eriksson et al. 1981) and was formerly treated as a synonym of *Hyphodontia* (Langer 1994), the molecular evidence indicated that this genus belongs to *Hydnodontaceae* (Binder et al. 2005) and thus the genus was placed in *Trechisporales* (Larsson 2007). Six species were accepted in *Fibrodontia* (Liu et al. 2021), while one additional species is described below, bringing the total species number in this genus to seven. It is noteworthy that Baltazar et al. (2016) proposed *Cystidiodendron fimbriatum* (the generic type of *Cystidiodendron*) as conspecific with *F. gossypina*. To solve the taxonomic delimitation of these two genera, the species affinity of *C. fimbriatum* and *F. gossypina* has to be tested via molecular evidence (Liu et al. 2021). Ideally, the lectotype of *C. fimbriatum* collected in 1933 or potentially a later collection designated as an epitype can be sequenced.

#### Fibrodontia subaustrosinensis S.L. Liu, S.H. He & L.W. Zhou, sp. nov. Figs 9, 10

Index Fungorum number: IF559881; Facesoffungi number: FoF12861

Etymology – *subaustrosinensis* (Latin), refers to the new species resembling *Fibrodontia austrosinensis* in morphology.

Diagnosis – Differs from *Fibrodontia austrosinensis* by longer basidia and slightly larger basidiospores (Liu et al. 2021).

Typus – CHINA, Yunnan, Xichou County, Xiaoqiaogou Forest Park, on fallen angiosperm trunk, 16 Nov. 2019, *S.H. He*, He 6279 (holotype in BJFC 033223, isotype in HMAS).

Description – *Basidiomes* annual, resupinate, easily detached, without odor or taste, soft corky and brittle when dry, up to 13 cm long, 3 cm wide and 0.2 mm thick. *Hymenophore* grandinioid, white to cream when fresh, usually with curry-yellow to olive tinge, olivaceous buff to honey-yellow when dry. *Margin* white, cottony, up to 0.5 mm wide.

*Hyphal system* dimitic; generative hyphae with clamp connections. Subiculum composed of a loose layer of distinct hyphae; generative hyphae, hyaline, thin- to slightly thick-walled, occasionally branched, smooth, 2–3.5 µm in diam; skeletal hyphae rare, hyaline to yellowish, thick-walled with a wide to narrow lumen, unbranched, smooth, slightly flexuous, 2–3 µm in diam. Aculei composed of a central core of compact hyphae and subhymenial and hymenial layers, at apex terminal hyphae slightly tapered; generative hyphae distinct, hyaline, thin- to slightly thick-walled, occasionally branched, smooth, subparallel, 2–3 µm in diam; skeletal hyphae rare, hyaline to yellowish, thick-walled with a wide to narrow lumen, unbranched, smooth, slightly flexuous, more or less parallel along the aculei, 2–3 µm in diam. *Basidia* suburniform to clavate, thin-walled, with four sterigmata and a basal clamp connection,  $20-27 \times 3.8-5$  µm; basidioles similar in shape to basidia, but smaller. *Basidiospores* ellipsoid to ovoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous, (4.5–)4.8–6 × (3.9–)4–5(–5.5) µm, L = 5.2 µm, W = 4.4 µm, Q = 1.2 (*n* = 60/2).

Other specimen (paratype) examined – CHINA, Hainan, Changjiang County, Bawangling National Forest Park, on dead branch of living tree of *Arenga pinnata*, 16 Nov. 2019, *S.H. He*, He 6033 (BJFC).

Notes – *Fibrodontia subaustrosinensis* closely resembles *F. austrosinensis*, but the latter species has shorter basidia (13–16  $\mu$ m in length) and slightly smaller basidiospores (4.2–5.2 × 3.5–4.5  $\mu$ m; Liu et al. 2021). *Fibrodontia brevidens* is also similar to *F. subaustrosinensis* by the yellowish hymenophore with an olive tinge, but differs in the presence of moderately encrusted skeletal hyphae and smaller basidiospores (4–4.5 × 3.5–4.5  $\mu$ m; Yurchenko & Wu 2014).

Luellia K.H. Larss. & Hjortstam, Svensk bot. Tidskr. 68(1): 59 (1974).

Type species – *Luellia recondita* (H.S. Jacks.) K.H. Larss. & Hjortstam, Svensk bot. Tidskr. 68(1): 60 (1974).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, closely attached to the substrates. *Hymenophore* smooth, brown. *Hyphal system* monomitic, generative hyphae clamped or not, yellowish brown. *Cystidia* absent. *Basidia* clavate to pyriform, hyaline, thin-walled, with two to four sterigmata. *Basidiospores* fusiform to navicular, with distinct apiculus, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Luellia* was erected by Larsson & Hjortstam (1974), who at that time accommodated two species in the genus, viz. *L. furcata* and *L. recondita*. Later, *Luellia cystidiata* was added to this genus (Hauerslev 1979). Morphologically, *Luellia* is characterized by brown hymenophore with mostly encrusted hyphae and thin-walled, inamyloid basidiospores, and was placed in *Atheliaceae*, *Atheliales* (Jülich 1981). However, even though morphological characters did not suggest affinity to other genera in *Trechisporales*, Larsson (2007) considered that *Luellia* is a member of *Hydnodontaceae*, *Trechisporales* on the basis of unpublished molecular evidence, which is also confirmed by Spirin et al. (2021) and the current phylogeny (Fig. 3).

#### Porpomyces Jülich, Persoonia 11(4): 425 (1982).

Type species – Porpomyces mucidus (Pers.) Jülich, Persoonia 11(4): 425 (1982).

Description – *Basidiomes* annual, resupinate, soft. *Hymenophore* poroid, white to pale ochraceous, pores round to angular. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline, with ampullate septa in hyphal cords. *Cystidia* absent. *Basidia* barrel-shaped, hyaline, thin-walled, with four sterigmata and a basal clamp connection. *Basidiospores* subglobose to ellipsoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Porpomyces* was erected as a monotypic genus typified by *P. mucidus* (Jülich 1982). This species was formerly considered to be close to *Ceriporiopsis* and thus placed in *Polyporales* 

(Gilbertson & Ryvarden 1985), but later molecular evidence indicated that it is close to *Trechispora* instead of *Ceriporiopsis* (Larsson 2001). Therefore, *Porpomyces* was listed as one of the exemplar genera of *Trechisporales* when this order was newly proposed (Hibbett et al. 2007). Three species are accepted in *Porpomyces* and its poroid hymenophore and ampullate hyphal septa make it morphologically similar to *Trechispora* (Spirin et al. 2021). However, *Porpomyces* bears smooth basidiospores, while all known poroid species in *Trechispora* have ornamented basidiospores.



**Figure 9** – Basidiomes of *Fibrodontia subaustrosinensis* (He 6279, holotype). Scale bars: a = 1 cm, b = 1 mm.

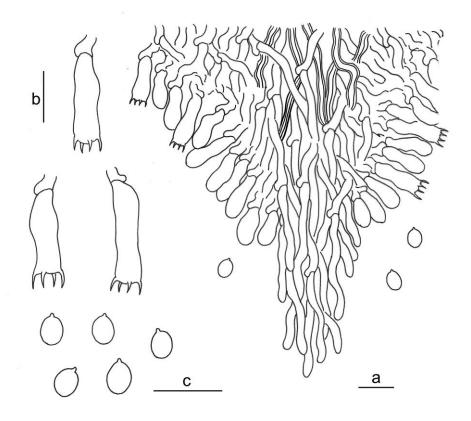
Pteridomyces Jülich, Persoonia 10(3): 331 (1979).

Type species – Pteridomyces galzinii (Bres.) Jülich, Persoonia 10(3): 331 (1979).

Description – Basidiomes annual, resupinate, effused, thin. Hymenophore grandinioid, odontioid. Hyphal system monomitic to dimitic, generative hyphae with clamp connections, hyaline. Hyphal pegs consisting of parallelly arranged, thin-walled, hyaline hyphae. Cystidia

present or absent, fusoid. *Basidia* narrowly clavate, hyaline, thin-walled, with two to four sterigmata and a basal clamp connection. *Basidiospores* cylindrical, allantoid or navicular, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Pteridomyces* was erected as a monotypic genus to accommodate *Epithele galzinii* (Jülich 1979). Later, Boidin and his colleagues broadened the morphological delimitation of *Pteridomyces* from a monomitic to dimitic hyphal system by adding seven species to this genus (Boidin & Lanquetin 1983, Boidin & Gilles 1986a, 1988, Boidin et al. 1989). Hjortstam (1991) redelimited the taxonomic status of the eight species of *Pteridomyces*, and treated *Pteridomyces* as a synonym of *Athelopsis*, a disposition which is not widely recognized. However, due to the morphological affinity to *Athelopsis*, *Pteridomyces* was placed in *Atheliaceae*, *Atheliales*, when Larsson (2007) dealt with the taxonomic position of corticioid fungi. Subsequently, a new species of *Pteridomyces* was described from Chilean Patagonia based solely on morphological characters (Gorjón & Hallenberg 2013). Recently, Spirin et al. (2021) and Sulistyo et al. (2021) with the aid of phylogenetic analyses suggested that *Pteridomyces* is an independent genus in *Hydnodontaceae*, *Trechisporales*. The current phylogenies also recovered this topology (Figs 1–3).



**Figure 10** – Microscopic structures of *Fibrodontia subaustrosinensis* (drawn from the holotype). a Vertical section of basidiomes. b Basidia. c Basidiospores. Scale bars =  $10 \mu m$ .

Subulicystidium Parmasto, Consp. System. Corticiac. (Tartu): 120 (1968).

Type species – *Subulicystidium longisporum* (Pat.) Parmasto, Consp. System. Corticiac. (Tartu): 121 (1968).

= Aegeritina Jülich, Int. J. Mycol. Lichenol. 1(3): 282 (1984). Type species – Aegeritina tortuosa (Bourdot & Galzin) Jülich, Int. J. Mycol. Lichenol. 1(3): 282 (1984).

Description – *Basidiomes* annual, resupinate, effused, thin, soft. *Hymenophore* smooth, more or less arachnoid, white, cream to olivaceous buff. *Margin* not differentiated. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline, thin-walled. *Cystidia* subulate, projecting beyond hymenium, hyaline, thick-walled and regularly covered with rectangular crystals except at the apex. *Basidia* suburniform, hyaline, thin-walled, with four sterigmata and a basal

clamp connection. *Basidiospores* cylindrical, fusiform to sigmoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.

Notes – *Subulicystidium* was erected as a monotypic genus with *S. longisporum* as the generic type (Parmasto 1968). Molecular evidence unambiguously supported this genus as a member of *Hydnodontaceae*, *Trechisporales*, although there was a lack of clear morphological affinity (Larsson 2007). Recently, 13 species were newly described in *Subulicystidium* on the basis of morphological and phylogenetic evidence (Ordynets et al. 2018, Liu et al. 2019). One more species of *Subulicystidium* is described below, which bring the species number of this genus to 24. *Subulicystidium* is morphologically distinct from other genera in *Trechisporales* in the presence of a crystalline sheath on the cystidia.

The monotypic genus *Aegeritina* comprises *A. tortuosa*, accepted as the asexual stage of *Subulicystidium longisporum* (Eriksson et al. 1984). With the transition to one fungus-one name, Stalpers et al. (2021) recommended retention of the earlier generic name *Subulicystidium* over *Aegeritina*.

#### Subulicystidium daii S.L. Liu & L.W. Zhou, sp. nov.

Figs 11, 12

Index Fungorum number: IF559882; Facesoffungi number: FoF12862

Etymology – *daii* (Latin), refers to the Chinese mycologist, Prof. Dr. Yu-Cheng Dai, who opened the door of fungal taxonomy for the author Li-Wei Zhou.

Diagnosis – Differs from *Subulicystidium acerosum* by the absence of needle-like crystals and wider basidiospores (1.8–2.2  $\mu$ m in width in *S. acerosum*; Liu et al. 2019).

Typus – CHINA, Hubei, Wudangshan Town, Wudangshan National Forest Park, on fallen angiosperm branch, 20 Aug. 2017, *L.W. Zhou*, LWZ 20170820-35 (holotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, very thin, loosely attached to the substrates, up to 9 cm long, 4 cm wide. *Hymenophore* smooth, cream to straw-yellow when fresh, cream to ash-grey with age, not cracked. *Margin* undifferentiated.

*Hyphal system* monomitic; generative hyphae with clamp connections, hyaline, slightly thickwalled, frequently branched and septate, loosely subparallel, 2–3.5 µm in diam. *Cystidia* abundant, subulate, projecting beyond hymenium, hyaline, thick-walled, regularly covered with rectangular crystals except at the apex,  $50-80 \times 3-5$  µm. *Basidia* subclavate to suburniform, hyaline, thinwalled, with four sterigmata and a basal clamp connection,  $16-22 \times 5-7$  µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* fusiform to slightly vermicular, hyaline, thinwalled, smooth, inamyloid, indextrinoid, acyanophilous,  $(15-)15.5-17.5(-18.5) \times 2.3-3$  µm, L = 16.5 µm, W = 2.6 µm, Q = 6.5-6.9 (n = 60/2).

Other specimen (paratype) examined – CHINA, Guangxi, Longzhou County, Nonggang National Nature Reserve, on fallen angiosperm branch, 3 July 2007, *H.X. Xiong*, Xiong 221 (IFP 009160).

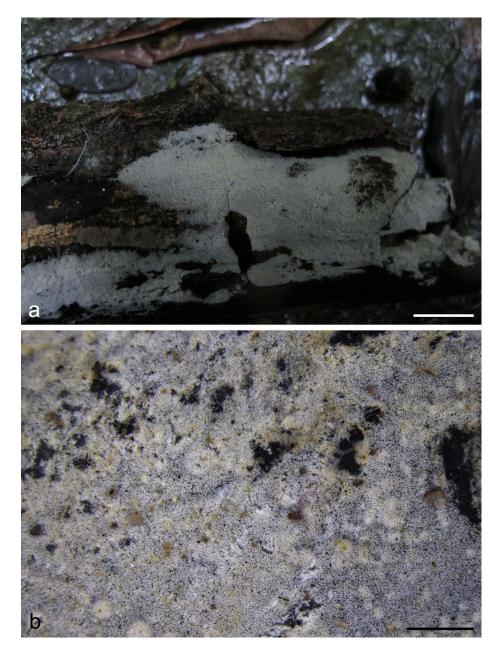
Notes – Besides *Subulicystidium acerosum*, *S. daii* also resembles *S. cochleum* and *S. perlongisporum* by the long (above 15  $\mu$ m in length) and straight or slightly curved basidiospores; however, *S. cochleum* differs in the presence of a bundle of needle-like crystals at the cystidial crystalline sheath ends, while *S. perlongisporum* differs in narrower basidiospores (1.5–2.5  $\mu$ m in width; Ordynets et al. 2018).

#### Suillosporium Pouzar, Česká Mykol. 12(1): 31 (1958).

Type species – Suillosporium cystidiatum (D.P. Rogers) Pouzar, Česká Mykol. 12(1): 31 (1958).

Description – *Basidiomes* annual, resupinate, effused, thin. *Hymenophore* smooth, grandinioid, odontioid, white to cream. *Margin* not differentiated. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline. *Cystidia* (septocystidia) thin-walled, more or less encrusted. *Basidia* shortly clavate, hyaline, thin-walled, with two to four sterigmata. *Basidiospores* fusiform to navicular, thin- to slightly thick-walled, smooth, inamyloid, indextrinoid, weakly cyanophilous. On wood.

Notes – Suillosporium was erected as a monotypic genus to accommodate Pellicularia cystidiata (Pouzar 1958). Suillosporium was put in Botryobasidiaceae (Jülich 1981) and morphologically related to Botryobasidium (Eriksson et al. 1984). Later, three additional species were added to Suillosporium (Boidin & Gilles 1986b, Langer & Langer 2004, Kotiranta & Saarenoksa 2006). Although Larsson (2007) doubted the placement of Suillosporium at higher ranks and considered its taxonomic position as uncertain, He et al. (2019) still treated this genus in Botryobasidiaceae. This issue was for the first time clarified on the basis of phylogenetic evidence by Spirin et al. (2021), whose analyses indicated it as a member of Hydnodontaceae, Trechisporales. The current phylogenies also recovered this topology (Figs 1–3).



**Figure 11** – Basidiomes of *Subulicystidium daii* (LWZ 20170820-35, holotype). Scale bars: a = 1 cm, b = 1 mm.

### Trechispora P. Karst., Hedwigia 29: 147 (1890).

Type species – *Trechispora onusta* P. Karst., Hedwigia 29: 147 (1890) = *T. hymenocystis* (Berk. & Broome) K.H. Larss., Mycol. Res. 98(10): 1167 (1994).

*= Pseudohydnum* Rick, Annls mycol. 2(5): 409 (1904) Nom. illegit. non *Pseudohydnum* P. Karst., Not. Sällsk. Fauna et Fl. Fenn. Förh. 9: 374 (1868).

= *Hydnodon* Banker, Mycologia 5(6): 297 (1913).

= *Fibuloporia* Bondartsev & Singer, in Singer, Mycologia 36(1): 67 (1944).

= *Scytinopogon* Singer, Lloydia 8(3): 139 (1945).

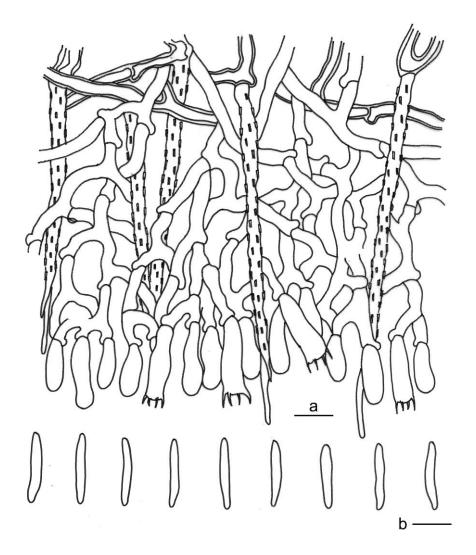
= *Echinotrema* Park.-Rhodes, Trans. Br. mycol. Soc. 38(4): 367 (1955).

= *Fibriciellum* J. Erikss. & Ryvarden, Cortic. N. Eur., 3 Coronicium-Hyphoderma (Oslo): 373 (1975).

= Osteomorpha G. Arnaud ex Watling & W.B. Kendr., Naturalist (Hull), ser. 3 104(no. 948): 1 (1979).

= Cristelloporia I. Johans. & Ryvarden, Trans. Br. mycol. Soc. 72(2): 189 (1979).

= Dextrinodontia Hjortstam & Ryvarden, Mycotaxon 12(1): 172 (1980).



**Figure 12** – Microscopic structures of *Subulicystidium daii* (drawn from the holotype). a Vertical section of basidiomes. b Basidiospores. Scale bars =  $10 \mu m$ .

Description – *Basidiomes* annual, resupinate, effused, stipitate, or clavarioid, soft, loosely attached to the substrates. *Hymenophore* smooth, grandinioid, odontioid, hydnoid or poroid, white, cream to cinnamon-buff, mycelial cords often present. *Hyphal system* monomitic to dimitic, generative hyphae with clamp connections, hyaline, with typical ampullate septa, crystals common on subicular hyphae. *Cystidia* present or absent. *Basidia* cylindrical, often with a slight median constriction, hyaline, thin-walled, with two to four sterigmata and a basal clamp connection. *Basidiospores* usually subglobose to ellipsoid, rarely allantoid or subangular, hyaline, thin-walled, smooth, verrucose or aculeate, inamyloid, indextrinoid, acyanophilous. Conidiospores sometimes present. On soil or wood.

Notes – *Trechispora* was erected as a monotypic genus for the corticioid species *T. onusta* (Karsten 1890). Later, its species diversity was extremely enriched (e.g. Liberta 1966, 1973, Larsson 1994, 1996). The concept was further enlarged, especially by absorbing *Hydnodon* with stipitate basidiomes (Ryvarden 2002) and *Scytinopogon* with clavarioid basidiomes (de Meiras-Ottoni et al. 2021). When the family *Hydnodontaceae* and the order *Hydnodontales* were erected, *Trechispora* was included as one of exemplar genera (Jülich 1981). Furthermore, *Trechispora* is the automatic type genus of *Trechisporales* (equivalent to *Hydnodontales*; Hibbett et al. 2007). The shared morphological characters of species in *Trechispora* are remarkable ampullate hyphal septa, and in addition most species in this genus have ellipsoid, ornamented basidiospores, but there is considerable diversity in basidiome form.

It is noteworthy that of the currently accepted members of *Trechispora*, *T. clancularis*, *T. molliuscula*, *T. mollusca* and *T. silvae-ryae* were, respectively, placed at one time in four monotypic genera *Echinotrema*, *Dextrinodontia*, *Fibuloporia* and *Fibriciellum* based on morphological characters (Larsson 1992, 1994).

Echinotrema was introduced for E. clanculare, a resupinate species from the United Kingdom, described as having a hymenium of "parallel sinuous plates" and echinulate basidiospores, with these characters compared by the original author to those of Lindtneria and Sistotrema (Parker-Rhodes 1955). Larsson (1994) examined the type collection, which he described as having a poroid to irpicoid hymenium, and found frequently ampullate septa and aculeate basidiospores. Although Larsson (1994) found some unusual features in E. clanculare, especially the basidia with an oblique medial widening, such structures were present in some other species of Trechispora, and consequently he did not consider that there were sufficient grounds to recognize Echinotrema as distinct from Trechispora. Dextrinodontia was erected to accommodate an African new species D. molliuscula (Hjortstam & Ryvarden 1980). This genus was listed as a member of Hydnodontaceae, Trechisporales with doubt by Larsson (2007) and as a potential member of Trechisporales by Hibbett et al. (2014). Fibriciellum was described to accommodate a new species F. silvae-ryae from Sweden (Eriksson & Ryvarden 1975), and later was placed in Hydnodontaceae, Trechisporales (Larsson 2007). Recently, an ITS sequence (MZ159622) of F. silvae-ryae was submitted to GenBank. Although this ITS sequence was generated from a voucher collected from England instead of type locality, as the single molecular sequence of this species, its BLAST search revealed an affinity to members of Trechispora. For now, we accept Echinotrema, Dextrinodontia and Fibriciellum as synonyms of Trechispora but the placement of species used to typify the three genera should be further clarified ideally with the aid of multilocus-based phylogenetic analyses from more samples.

*Fibuloporia* was introduced for *F. mollusca* (based on *Boletus molluscus* Pers.) by Singer (1944) with minimal discussion and no indication that the fungus has ornamented basidiospores, from which it can be gathered that the erroneous interpretation of *B. molluscus* as a smooth-spored species was being followed. For discussion of the complex situation around the typification of *B. molluscus* see Larsson (1994, 2001). With acceptance of material collected by Persoon and designated by Donk as the neotype of *B. molluscus*, the name must be interpreted as based on a species with rough basidiospores, thus the placement in *Trechispora* by Liberta (1973), which is followed by subsequent authors including Larsson (1994). Given that sequenced material is available for *Trechispora mollusca*, there is no doubt about the synonymy of *Fibuloporia* and *Trechispora*.

Scytinopogon is another noteworthy synonym of Trechispora. This genus, typified by Scytinopogon pallescens, was erected for clavarioid species (Singer 1945). Although macromorphology initially indicated placement of Scytinopogon in the family Clavariaceae, Scytinopogon microscopically deviates by rather short basidia and ellipsoid basidiospores with ornamentations and thus was put in its own new family Scytinopogonaceae as the type genus (Jülich 1981). Jülich (1981) also suggested the morphological affinity of Scytinopogon to Hydnodon (a synonym of Trechispora; Ryvarden 2002) and Trechispora, and placed Scytinopogonaceae in Hydnodontales (equivalent to Trechisporales; Hibbett et al. 2007).

Molecular evidence not only supported the close relationship between *Scytinopogon* and *Trechispora* (Larsson et al. 2011), but also grouped these two genera in a clade with strong support (Birkebak et al. 2013, de Meiras-Ottoni et al. 2021) or weak support (Desjardin & Perry 2015). de Meiras-Ottoni et al. (2021) stated that the weak support in the phylogeny of Desjardin & Perry (2015) resulted from one problematic sequence in their dataset. Moreover, de Meiras-Ottoni et al. (2021) carefully compared the morphological characters of types of *Scytinopogon* and *Trechispora*, and indicated that both share the remarkable ampullate hyphal septa and ellipsoid, ornamented basidiospores. Therefore, *Scytinopogon* was formally proposed as a later synonym of *Trechispora* (de Meiras-Ottoni et al. 2021). The current phylogeny sampling more taxa of *Trechispora* clearly supports the monophyly of this genus with inclusion of species formerly belonging to *Scytinopogon* (Fig. 6). After transferring five species from *Scytinopogon* to *Trechispora* (combined below), only two species, viz. *S. echinosporus* and *S. parvus* are still left in *Scytinopogon* due to unavailable of their molecular sequences.

The illegitimate genus name *Pseudohydnum* J. Rick is included under *Trechispora* following Donk (1956), who treated the type species *P. guepinioides* as a synonym of *Hydnum thelephorum* (*Trechispora thelephora*).

Osteomorpha was introduced for an asexual species O. fragilis that was associated with a species of Trechispora. Stalpers et al. (2021) discussed the connection between Osteomorpha and Trechispora and concluded that the two genera are synonymous.

Cristelloporia was described by Johansen & Ryvarden (1979) for Cristelloporia dimitica I. Johans. & Ryvarden, a resupinate, poroid fungus with asperulate, ellipsoid to irregularly lobed basidiospores and needle-like crystals among dimitic hyphae, found in Ghana, Africa. The authors noted that "When first examined under the microscope, C. dimitica was considered to be a new species of Trechispora Karst. and there are several characters pointing towards this genus, including the aculeate spores, the needle-like crystals and the many pleurobasidia". However, they concluded that "it would be better placed in the Polyporaceae [i.e. as a new genus] because of the very distinct dimitic hyphal system giving the fruitbodies a cottony and coriaceous consistency so typical for many resupinate polypores". Cristelloporia is listed as a synonym of Trechispora by Index Fungorum, following the entry in the 10th edition of Dictionary of the Fungi (Kirk et al. 2008) where the source of the synonym is noted as "Larsson in litt." which would refer to Larsson (1992) and this placement is followed by Gorjón (2020) and He et al. (2019). Larsson (1992) considered that the type, Cristelloporia dimitica, was synonymous with C. brasiliensis Corner and Heterobasidion pahangense Corner. Because Trechispora dimitica Hallenb. blocked transfer of C. dimitica to Trechispora, Larsson (1992) took up the next available epithet, brasiliensis, but without making a valid transfer to Trechispora. Later, C. brasiliensis was validly transferred to Trechispora by Chikowski et al. (2020) on the basis of morphological characters. Even though sequences are not available for T. brasiliensis, we accept the placement in Trechispora taken up by Larsson (1992) and Chikowski et al. (2020), which renders Cristelloporia a synonym of Trechispora. Note that Hattori (2003) treated Heterobasidion pahangense as an independent species (combined in Cristelloporia). Of the three other species placed in Cristelloporia: C. trimitica was found by Hattori (2003) to represent a trimitic species of Trametes, for which the type collection was contaminated by another fungus with echinulate spores; the position of C. asperispora has not been re-examined since it was originally described from Kenya; and for C. rutilantiformis see under Murilloporus under Genus of uncertain position (below).

Trechispora caulocystidiata (A.N.M. Furtado & M.A. Neves) L.W. Zhou & S.L. Liu, comb. nov.

Index Fungorum number: IF559883; Facesoffungi number: FoF12863

*Basionym. Scytinopogon caulocystidiatus* A.N.M. Furtado & M.A. Neves, in Furtado, Daniëls, Reck & Neves, Mycotaxon 136(1): 113 (2021).

Notes – *Trechispora caulocystidiata* was recently described as a new species in *Scytinopogon* on the basis of morphological and molecular data (Furtado et al. 2021). Although Furtado et al. (2021) noticed that *Trechispora* has been formally treated as having priority over *Scytinopogon* (de

Meiras-Ottoni et al. 2021), they did not put this new species in *Trechispora* due to lack of a comprehensive phylogeny. The current phylogeny (Fig. 6) undoubtedly supports that *S. caulocystidiatus* nests within *Trechispora*, and thus we make this combination. The detailed description of *T. caulocystidiata* can be found in Furtado et al. (2021).

Trechispora chaibuxiensis S.L. Liu, L.W. Zhou & S.H. He, sp. nov. Figs 13–15

Index Fungorum number: IF559885; Facesoffungi number: FoF12864

Etymology - chaibuxiensis (Latin), refers to Chaibuxi Grand Canyon Scenic Spot.

Diagnosis – Differs from *Trechispora subsinensis* (described below) in the presence of hyphoid cystidia.

Typus – CHINA, Hubei, Wufeng County, Chaibuxi Grand Canyon Scenic Spot, on fallen angiosperm branch, 14 Aug. 2017, *L.W. Zhou*, LWZ 20170814-34 (holotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, thin, soft and fragile, easily separated from substrates, up to 5 cm long, 2 cm wide. *Hymenophore* odontioid with numerous small aculei, sometimes fertile at the apex of the aculei, cream to straw-yellow when fresh, straw-yellow when dry, up to 0.3 mm long. *Margin* white, fimbriate, up to 0.5 mm wide.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, slightly thick-walled, moderately branched and septate, interwoven, 2.5–4.5 µm diam, ampullate septa up to 6 µm wide. Aculei composed of a central core of compact hyphae and subhymenial and hymenial layers; generative hyphae distinct, hyaline, thin to slightly thick-walled, occasionally branched, smooth, subparallel, 2–3.5 µm in diam, apical ends in aculei with basidia and rare hyphoid cystidia. Crystals usually present, bipyramidic, aggregated. *Hyphoid cystidia* rare, smooth, thin-walled, fusoid,  $20-35 \times 3-5$  µm. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection,  $12-20 \times 3.5-4.5$  µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* broadly ellipsoid, hyaline, thin-walled, aculeate, inamyloid, indextrinoid, acyanophilous,  $(2.6-)2.8-3.3 \times (2-)2.2-2.8(-2.9)$  µm, L = 3 µm, W = 2.6 µm, Q = 1.1-1.2 (n = 90/3).

Other specimens (paratypes) examined – CHINA, Hubei, Wufeng County, Chaibuxi Grand Canyon Scenic Spot, on fallen angiosperm branch, 14 Aug. 2017, *L.W. Zhou*, LWZ 20170814-35 (HMAS), *L.W. Zhou*, LWZ 20170814-36 (HMAS), *L.W. Zhou*, LWZ 20170814-42 (HMAS); on fallen angiosperm branch, 15 Aug. 2017, *S.H. He*, He 5072 (BJFC 024590).

Notes – *Trechispora chaibuxiensis* is characterized by the odontioid hymenophore with numerous small aculei, a monomitic hyphal system, the presence of hyphoid cystidia and basidia in apical ends of aculei, and broadly ellipsoid, aculeate basidiospores. Besides *Trechispora subsinensis*, *T. chaibuxiensis* could also be confused with *T. nivea*, but the latter species has a hymenophore with longer aculei (up to 1 mm in length) and lacks cystidia (Larsson 1995). Similar to *Trechispora chaibuxiensis*, other species such as *T. caulocystidiata*, *T. gelatinosa* and *T. minispora* also have cystidial structures, but they differ in the clavarioid basidiomes (de Meiras-Ottoni et al. 2021).

Trechispora constricta S.L. Liu, S.H. He & L.W. Zhou, sp. nov.

Figs 16–18

Index Fungorum number: IF559886; Facesoffungi number: FoF12865

Etymology – constricta (Latin), refers to constriction on the spines of basidiospores.

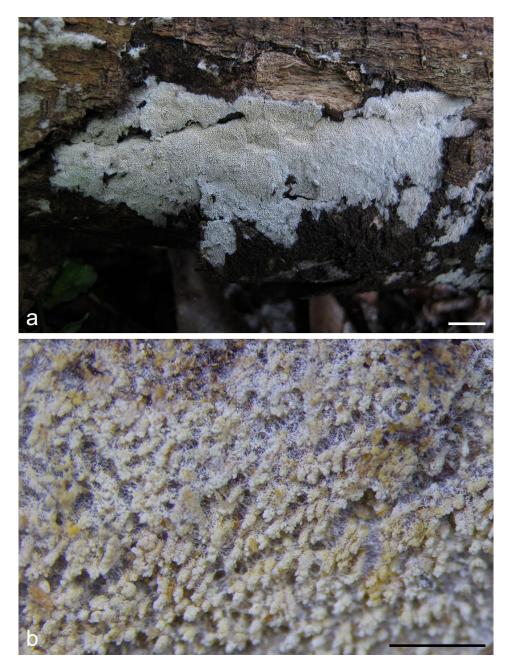
Diagnosis – Characterized by the presence of a slight constriction on the spines of basidiospores.

Typus – CHINA, Jiangxi, Fenyi County, Dagangshan Nature Reserve, on rotten angiosperm wood, 19 Sept. 2008, *Y.C. Dai*, Dai 10534 (holotype in BJFC 004783).

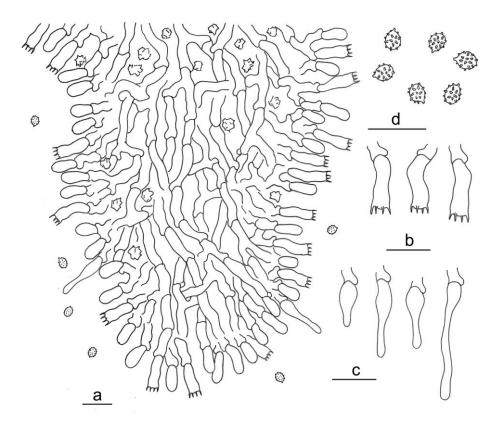
Description – *Basidiomes* annual, resupinate, effused, thin, soft, easily separated from substrates, up to 3 cm long, 2 cm wide. *Hymenophore* odontioid, white to cream when fresh, cream to buff-yellow with age, not cracked. Aculei 5–8 per mm, up to 0.5 mm long. *Margin* thinning out as byssoid, white.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin-walled, moderately branched, septate, interwoven,  $3-5 \mu m$  in diam, ampullate septa up to 7  $\mu m$  wide. Tramal generative hyphae distinct, hyaline, thin-walled, moderately branched, smooth, subparallel,  $3-6 \mu m$  in diam. Crystals usually present, rhomboidal. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection,  $11-15 \times 4-5.5 \mu m$ ; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline to yellowish, thin-walled, aculeate, with a slight constriction in the middle-upper part of spines, inamyloid, indextrinoid, acyanophilous,  $3-4 \times 2.3-2.9(-3) \mu m$ , L =  $3.4 \mu m$ , W =  $2.6 \mu m$ , Q = 1.3 (n = 60/2).

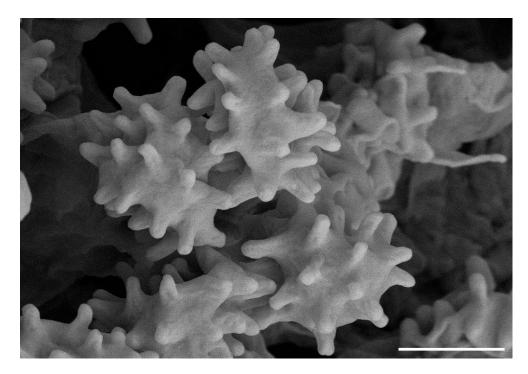
Other specimens (paratypes) examined – CHINA, Jiangxi, Fenyi County, Dagangshan Nature Reserve, on rotten angiosperm wood, 18 Sept. 2008, *Y.C. Dai*, Dai 10488 (BJFC 004737); Guangdong, Shixing County, Chebaling National Nature Reserve, on angiosperm stump, 14 June 2019, *S.H. He*, He 5899 (BJFC 030774).



**Figure 13** – Basidiomes of *Trechispora chaibuxiensis* (LWZ 20170814-34, holotype). Scale bars: a = 1 cm, b = 1 mm.



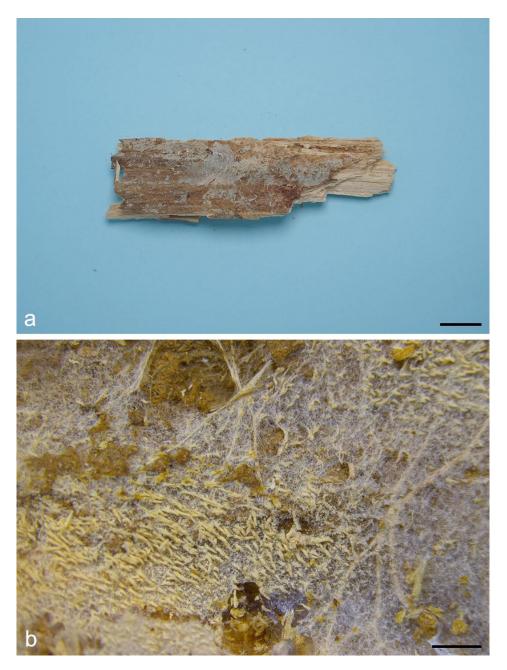
**Figure 14** – Microscopic structures of *Trechispora chaibuxiensis* (drawn from the holotype). a Vertical section of basidiomes. b Basidia. c Cystidia. d Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 15** – Scanning electron micrograph of basidiospores of *Trechispora chaibuxiensis* (scanned from the holotype). Scale bar =  $3 \mu m$ .

Notes – *Trechispora constricta* is characterized by wide generative hyphae (3–6  $\mu$ m in diam) and aculeate basidiospores with a slight constriction in the middle-upper part of spines (Fig. 18). *Trechispora constricta* resembles *T. tropica* (described below), but the latter species differs also in

smaller basidiospores (2.5–3  $\times$  2.2–2.5  $\mu m)$  besides lack of a constriction on the spines of basidiospores.



**Figure 16** – Basidiomes of *Trechispora constricta* (Dai 10534, holotype). Scale bars: a = 1 cm, b = 1 mm.

Trechispora crystallina S.L. Liu & L.W. Zhou, sp. nov.

Figs 19–21

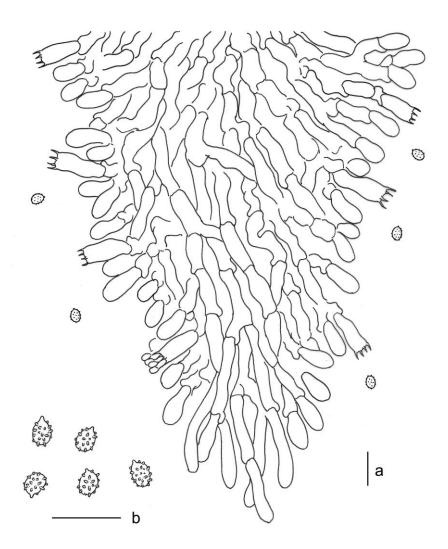
Index Fungorum number: IF559887; Facesoffungi number: FoF12866

Etymology – crystallina (Latin), refers to crystals.

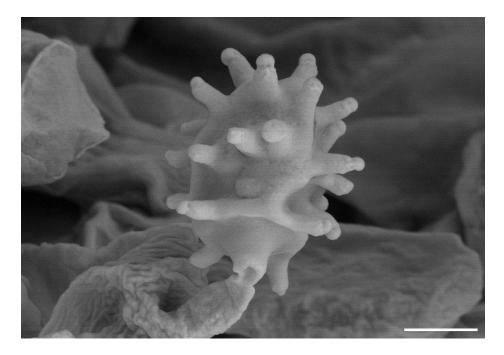
Diagnosis – Characterized by crystals abundant in subiculum and trama, and verrucose basidiospores.

Typus – VIETNAM, Ho Chi Minh City, Le Thi Rieng Park, on living angiosperm tree, 13 Oct. 2017, *L.W. Zhou*, LWZ 20171013-7 (holotype in HMAS).

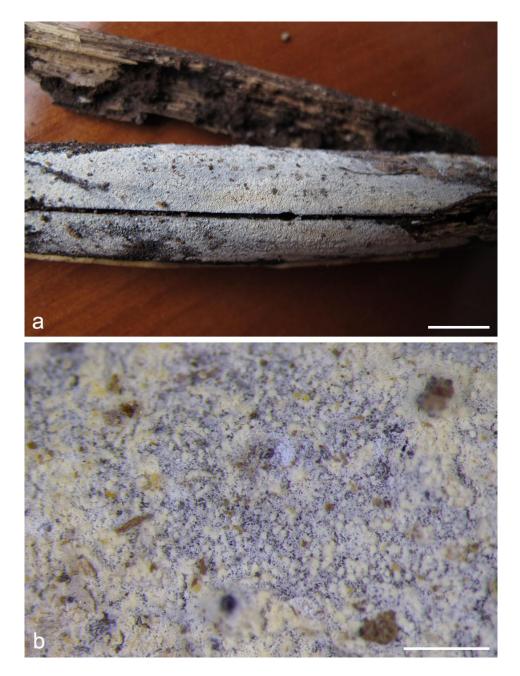
Description – *Basidiomes* annual, resupinate, effused, thin, soft and fragile, easily separated from substrates, up to 10 cm long, 2.5 cm wide. *Hymenophore* grandinioid with numerous small aculei, white to cream when fresh, cream to straw-yellow when dry. *Margin* white, slightly fimbriate, up to 0.2 mm wide.



**Figure 17** – Microscopic structures of *Trechispora constricta* (drawn from the holotype). a Vertical section of basidiomes. b Basidiospores. Scale bars =  $10 \mu m$ .



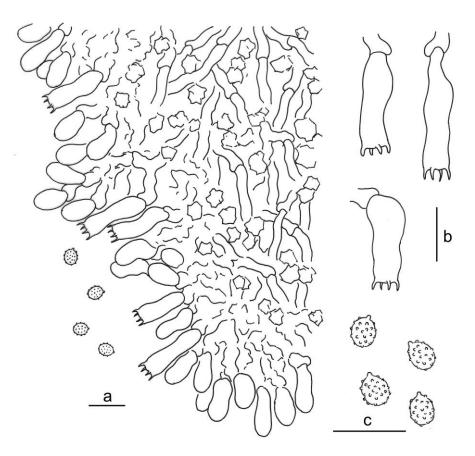
**Figure 18** – Scanning electron micrograph of basidiospores of *Trechispora constricta* (scanned from the holotype). Scale bar =  $2 \mu m$ .



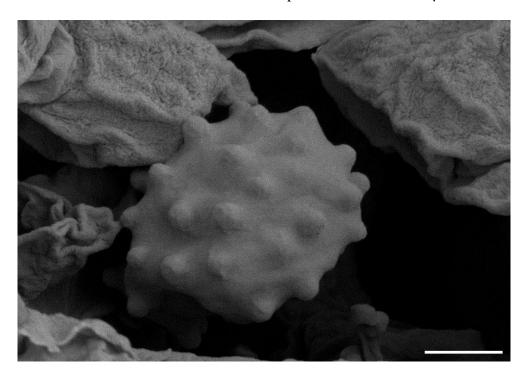
**Figure 19** – Basidiomes of *Trechispora crystallina* (LWZ 20171013-7, holotype). Scale bars: a = 1 cm, b = 0.5 mm.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subiculum composed of indistinct generative hyphae; subicular hyphae hyaline, thin-walled, frequently branched and septate, interwoven, 2–3.5 µm in diam, ampullate septa up to 6 µm wide. Tramal generative hyphae distinct, hyaline, thin-walled, frequently branched, smooth, interwoven, 3–5 µm in diam. Crystals occurring in both subiculum and trama, as small, aggregated rhomboidal flakes. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection,  $17-22 \times 4-6$  µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin to slightly thick-walled, vertucose, inamyloid, indextrinoid, acyanophilous,  $(3.2-)3.5-4.2(-5) \times (2.8-)3-3.6(-3.8)$  µm, L = 4 µm, W = 3.2 µm, Q = 1.2-1.3 (*n* = 60/2).

Other specimen (paratype) examined – CHINA, Inner Mongolia, Tongliao, Daqinggou National Nature Reserve, on fallen angiosperm twig, 29 July 2017, *L.W. Zhou*, LWZ 20170729-2 (HMAS).



**Figure 20** – Microscopic structures of *Trechispora crystallina* (drawn from the holotype). a Vertical section of basidiomes b Basidia. c Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 21** – Scanning electron micrograph of basidiospores of *Trechispora crystallina* (scanned from the holotype). Scale bar =  $2 \mu m$ .

Notes – Trechispora crystallina resembles T. cyatheae and T. torrendii by whitish to yellowish, grandinioid hymenophore, thin subiculum and a monomitic hyphal system with thin-

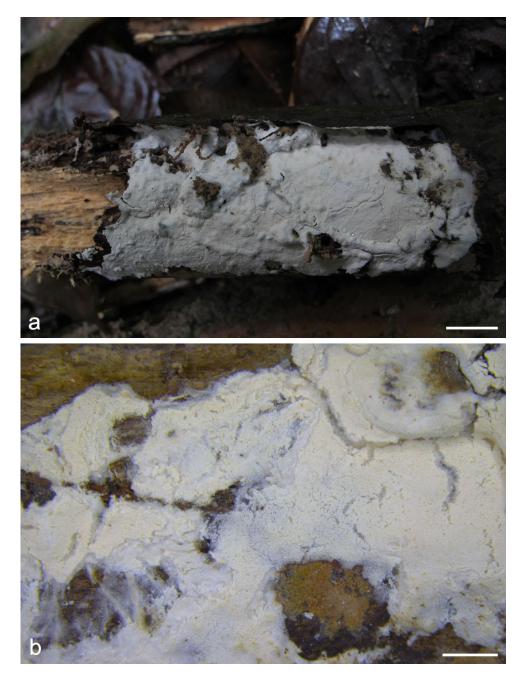
walled hyphae (Ordynets et al. 2015, Chikowski et al. 2020). However, *T. cyatheae* differs in aculeate, smaller basidiospores  $(3-3.5 \times 2-3 \ \mu\text{m}$  including spines) and growth exclusively on *Cyathea glauca*, an endemic species of tree fern to La Réunion, France (Ordynets et al. 2015); and *T. torrendii* differs in the absence of crystals and aculeate, smaller basidiospores  $(3.2-3.5 \times 2.8-3.2 \ \mu\text{m}$  including spines; Chikowski et al. 2020).

*Trechispora damansaraensis* S.L. Liu, L.W. Zhou & S.H. He, sp. nov. Figs 22–23

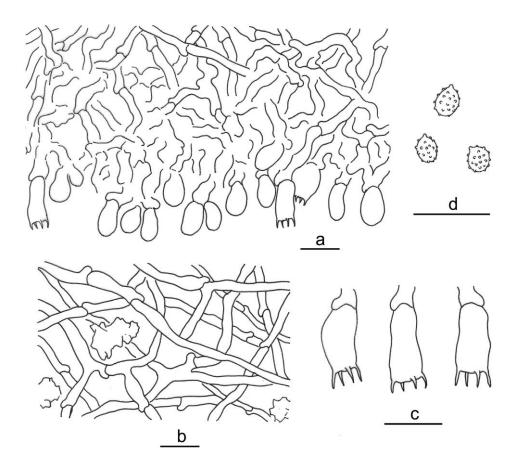
Index Fungorum number: IF559888; Facesoffungi number: FoF12867 Etymology – *damansaraensis* (Latin), refers to Kota Damansara Community Forest Reserve.

Diagnosis – Characterized by the combination of cream, smooth hymenophore and the occasional presence of crystals.

Typus – MALAYSIA, Selangor, Kota Damansara Community Forest Reserve, on fallen angiosperm branch, 17 Apr. 2018, *L.W. Zhou*, LWZ 20180417-26 (holotype in HMAS).



**Figure 22** – Basidiomes of *Trechispora damansaraensis* (LWZ 20180417-26, holotype). Scale bars: a = 1 cm, b = 1 mm.



**Figure 23** – Microscopic structures of *Trechispora damansaraensis* (drawn from the holotype). a Vertical section of basidiomes. b Hyphae in subiculum. c Basidia. d Basidiospores. Scale bars =  $10 \mu m$ .

Description – *Basidiomes* annual, resupinate, effused, thin, soft and fragile, loosely attached to the substrates. *Hymenophore* smooth, farinaceous, white to cream when fresh, cream, occasionally cracked with age. *Margin* thinning out, fimbriate, slightly paler than hymenophore, becoming indistinct with age. Mycelial cords present, white, 0.5 mm wide. *Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin to slightly thick-walled, frequently branched and septate, interwoven, 1–4 µm in diam, ampullate septa up to 5 µm wide, thin, flexuous. Subhymenium composed of indistinct generative hyphae, 2–4 µm in diam, much branched, flexuous. Crystals occasionally present, as aggregated rhomboidal flakes. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, thin-walled, with four sterigmata and a basal clamp connection, 9–12 × 5–6.5 µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin to slightly thick-walled, aculeate, inamyloid, indextrinoid, acyanophilous, (2.8–)3–3.8 × (2.1–)2.3–3(–3.2) µm, L = 3.2 µm, W = 2.7 µm, Q = 1.2 (*n* = 60/2).

Other specimen (paratype) examined – MALAYSIA, Selangor, Kota Damansara Community Forest Reserve, on fallen angiosperm branch, 7 Dec. 2019, *S.H. He*, He 6415 (BJFC 033359).

Notes – *Trechispora minima* mostly resembles *T. damansaraensis* by smooth hymenophore, a monomitic hyphal system and occasional presence of crystals in subiculum, but differs in parallel generative hyphae in subiculum, narrower basidia (4.5–5  $\mu$ m in width) and subglobose to broadly ellipsoid basidiospores (Larsson 1996).

Trechispora dealbata (Berk.) L.W. Zhou & S.L. Liu, comb. nov.

Index Fungorum number: IF559889; Facesoffungi number: FoF12868

Basionym. Clavaria dealbata Berk., Hooker's J. Bot. Kew Gard. Misc. 8: 275 (1856).

≡ Scytinopogon dealbatus (Berk.) Corner, Beih. Nova Hedwigia 33: 89 (1970).

Notes – de Meiras-Ottoni et al. (2021) showed that *Scytinopogon dealbatus* nested within *Trechispora* on the basis of molecular data, but they did not propose any taxonomic change because of lack of morphological information on relevant specimens. Later but almost simultaneously, Furtado et al. (2021) provided a detailed morphological description of *S. dealbatus*, noting that 'additional DNA regions and species are needed before concluding that *Scytinopogon* and *Trechispora* are fully synonymous'. The current phylogenies sampling more gene regions (Fig. 3) and sequence-available species of *Scytinopogon* and *Trechispora* (Fig. 6) undoubtedly support *Scytinopogon* and *Trechispora* as congeneric. Therefore, we transfer *S. dealbatus* to *Trechispora* as *T. dealbata*.

Trechispora foetida (A.N.M. Furtado & M.A. Neves) L.W. Zhou & S.L. Liu, comb. nov.

Index Fungorum number: IF559890; Facesoffungi number: FoF12869

*Basionym. Scytinopogon foetidus* A.N.M. Furtado & M.A. Neves, in Furtado, Daniëls, Reck & Neves, Mycotaxon 136(1): 119 (2021).

Notes – *Scytinopogon foetidus* was newly described together with *S. caulocystidiatus* (Furtado et al. 2021). Similar to the treatment of *S. caulocystidiatus*, we transfer *S. foetidus* to *Trechispora* as *T. foetida*. The detailed description of *T. foetida* can be found in Furtado et al. (2021).

#### Trechispora gracilis S.L. Liu & L.W. Zhou, sp. nov.

Index Fungorum number: IF559891; Facesoffungi number: FoF12870

Etymology – gracilis (Latin), refers to thin basidiomes.

Diagnosis – Characterized by the combination of thin, corticioid basidiomes with ash-grey, smooth hymenophore and the absence of crystals.

Typus – CHINA, Jiangxi, Jiujiang, Bailudong Academy, on fallen gymnosperm branch, 26 June 2021, *L.W. Zhou*, LWZ 20210626-5b (holotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, easily separated from substrates, up to 10 cm long, 2 cm wide, 50  $\mu$ m thick. *Hymenophore* smooth, arachnoid, cream to light ash-grey when fresh, ash-grey when dry, not cracked. *Margin* white, thinning out as byssoid, 0.5 mm wide.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae long-celled, hyaline, slightly thick-walled, frequently branched and septate, interwoven, 2.5–3.5  $\mu$ m in diam, ampullate septa up to 5  $\mu$ m wide. Subhymenium composed of indistinct generative hyphae, much branched. Crystals absent. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection, 10–13 × 4–5  $\mu$ m; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, aculeate, inamyloid, indextrinoid, acyanophilous, (2.5–)2.8–3.2 × (2–)2.3–2.8(–2.9)  $\mu$ m, L = 3.0  $\mu$ m, W = 2.5  $\mu$ m, Q = 1.2 (*n* = 60/2).

Other specimens (paratypes) examined – CHINA, Hubei, Huanggang, Dabieshan National Nature Reserve, on fallen gymnosperm branch, 19 Sept. 2021, *L.W. Zhou*, LWZ 20210919-9a (HMAS); Macheng, Shizifeng Nature Reserve, on fallen twig of *Pinus*, 22 Sept. 2021, *L.W. Zhou*, LWZ 20210922-7b (HMAS); Wufeng County, Chaibuxi Grand Canyon Scenic Spot, on fallen angiosperm twig, 17 Aug. 2017, *L.W. Zhou*, LWZ 20170814-17 (HMAS).

Notes – *Trechispora gracilis* resembles *T. damansaraensis* by thin basidiomes and smooth hymenophore; however, *T. damansaraensis* differs in white to cream hymenophore, the occasional presence of crystals in subiculum and slightly longer basidiospores  $(3-3.8 \ \mu m \ in \ length)$ .

## Trechispora larssonii S.L. Liu, L.W. Zhou & S.H. He, sp. nov.

Index Fungorum number: IF559892; Facesoffungi number: FoF12872

Etymology – *larssonii* (Latin), refers to the Swedish mycologist, Prof. Dr. Karl-Henrik Larsson, who has made most significant contributions to the taxonomy of *Trechispora*.

Figs 27-29

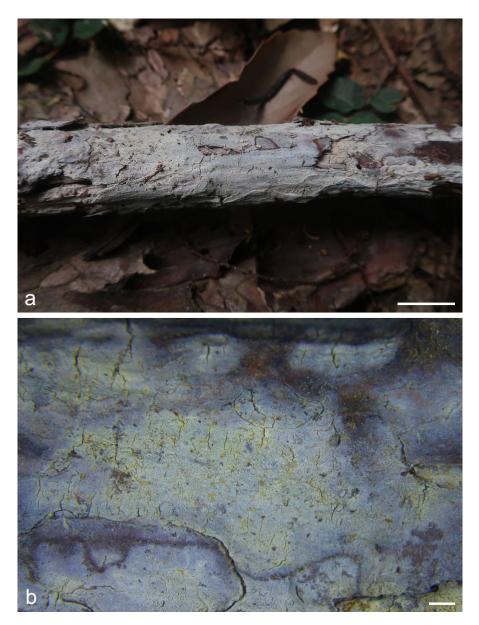
Figs 24-26

Diagnosis – Differs from *Trechispora minima* by the common presence of crystals and verrucose basidiospores (Larsson 1996).

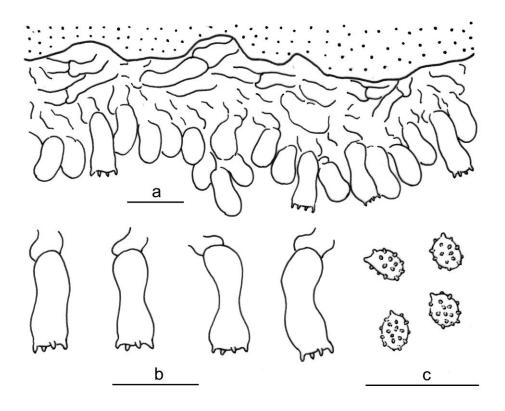
Typus – CHINA, Sichuan, Muchuan County, Qincaiping Nature Reserve, on fallen gymnosperm twig, 17 Aug. 2019, *L.W. Zhou*, LWZ 20190817-11a (holotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, fragile, easily separated from substrates, up to 15 cm long, 2 cm wide. *Hymenophore* smooth, farinaceous, white to cream when fresh, cream to buff-yellow with age, finely cracked. *Margin* thinning out as byssoid, narrow, white to cream.

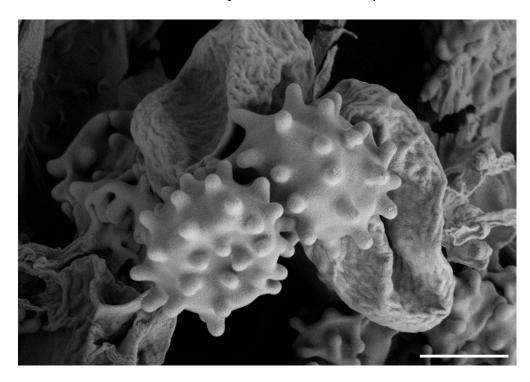
*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin-walled, moderately branched and septate, subparallel, 2.5–5 µm in diam, ampullate septa up to 7 µm wide. Subhymenial hyphae short-celled and wide, 3–5 µm in diam, much branched. Crystals common, as aggregated rhomboidal flakes. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, thin-walled, with four sterigmata and a basal clamp connection,  $7-13 \times 4-5$  µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, verrucose, inamyloid, indextrinoid, acyanophilous,  $(2.5-)2.8-3.3(-3.5) \times (2.5-)2.1-2.8(-3.3)$  µm, L = 3 µm, W = 2.5 µm, Q = 1.2 (*n* = 60/2).



**Figure 24** – Basidiomes of *Trechispora gracilis* (LWZ 20210626-5b, holotype). Scale bars: a = 1 cm, b = 1 mm.



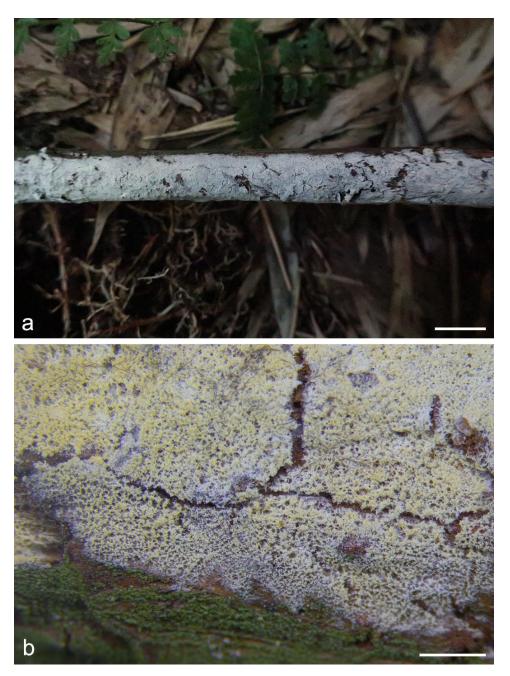
**Figure 25** – Microscopic structures of *Trechispora gracilis* (drawn from the holotype). a Vertical section of basidiomes. b Basidia. c Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 26** – Scanning electron micrograph of basidiospores of *Trechispora gracilis* (scanned from the holotype). Scale bar =  $3 \mu m$ .

Other specimens (paratypes) examined – CHINA, Sichuan, Meigu County, Dafengding National Nature Reserve, on fallen gymnosperm branch, 18 Aug. 2020, *L.W. Zhou*, LWZ 20200818-10b (HMAS); Guizhou, Chishui County, *Alsophila* National Nature Reserve, on dead branch of living *Osmunda vachellii*, 7 July 2018, *S.H. He*, He 5450 (BJFC 026511).

Notes – Besides *Trechispora minima*, which differs by occasional occurrence of crystals and aculeate basidiospores (Larsson 1996), *T. larssonii* is also similar to *T. damansaraensis* by smooth and farinaceous hymenophore, but *T. damansaraensis* differs in slightly narrower generative hyphae in subiculum and subhymenium (up to 4  $\mu$ m), the occasional presence of crystals, and aculeate, slightly longer basidiospores (3–3.8  $\mu$ m in length).



**Figure 27** – Basidiomes of *Trechispora larssonii* (LWZ 20190817-11a, holotype). Scale bars: a = 1 cm, b = 1 mm.

Trechispora latehypha S.L. Liu, S.H. He & L.W. Zhou, sp. nov.

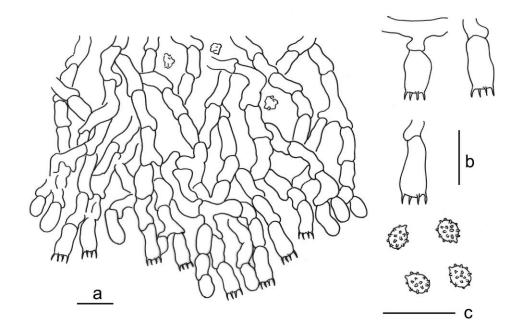
Figs 30–32

Index Fungorum number: IF559893; Facesoffungi number: FoF12873

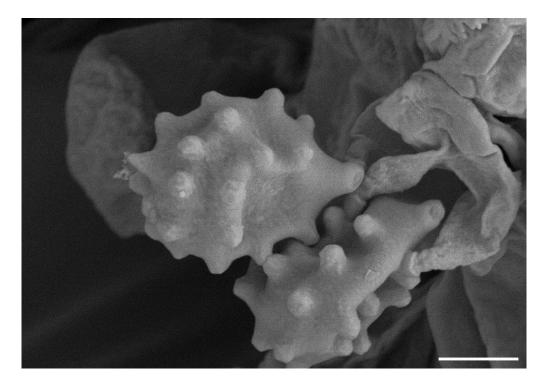
Etymology - latehypha (Latin), refers to wide subhymenial hyphae.

Diagnosis – Characterized by the rows of short-celled and wide hyphae in subhymenia, thick-walled generative hyphae in subiculum, and aculeate basidiospores.

Typus – CHINA, Guangdong, Renhua County, Danxiashan National Nature Reserve, on fallen angiosperm trunk, 4 June 2019, *S.H. He*, He 5848 (holotype in BJFC 030723).



**Figure 28** – Microscopic structures of *Trechispora larssonii* (drawn from the holotype). a Vertical section of basidiomes. b Basidia. c Basidiospores. Scale bars =  $10 \mu m$ .

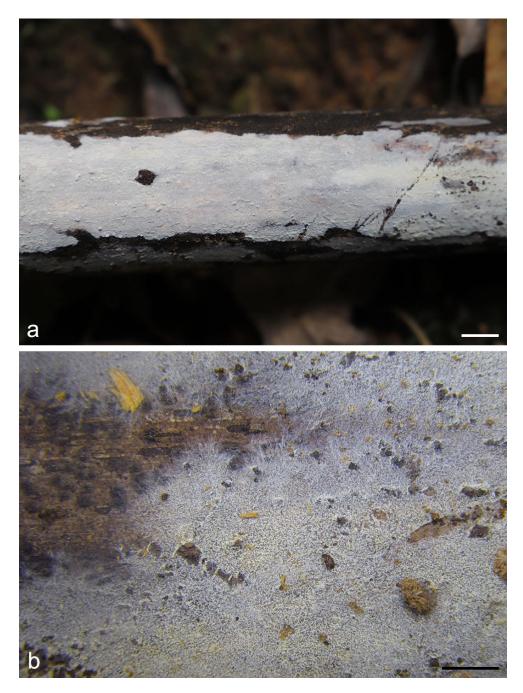


**Figure 29** – Scanning electron micrograph of basidiospores of *Trechispora larssonii* (scanned from the holotype). Scale bar =  $2 \mu m$ .

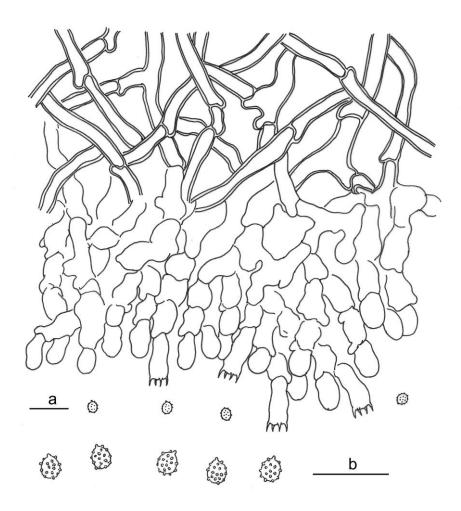
Description – *Basidiomes* annual, resupinate, effused, thin, soft, fragile, inseparable from substrate, up to 15 cm long, 4 cm wide. *Hymenophore* smooth, arachnoid, white to cream when fresh, cream to buff-yellow with age, finely cracked with age. *Margin* white, thinning out as byssoid, 1 mm wide.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae longcelled, hyaline, slightly thick-walled to thick-walled, moderately branched and septate,  $3.5-6 \mu m$  in diam. Subhymenial hyphae short-celled and wide, hyaline, thin-walled,  $4.5-7 \mu m$  in diam, much branched. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thinwalled, with four sterigmata and a basal clamp connection,  $13-16 \times 4-5.5 \mu m$ ; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, aculeate, inamyloid, indextrinoid, acyanophilous,  $(2.9-)3-3.5(-3.8) \times (2.2-)2.4-2.9(-3) \mu m$ , L = 3.2  $\mu m$ , W = 2.6  $\mu m$ , Q = 1.2 (*n* = 60/2).

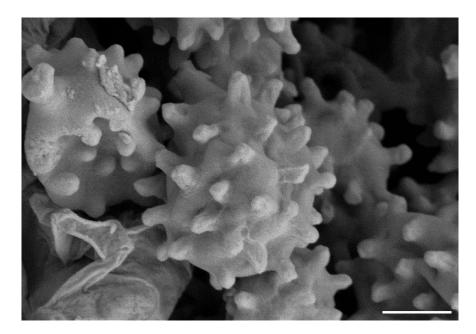
Other specimens (paratypes) examined – CHINA, Fujian, Wuyishan, Wuyishan National Nature Reserve, on fallen branch of *Tsuga*, 17 Aug. 2016, *S.H. He*, He 4472 (BJFC 023913). Guangdong, Renhua County, Danxiashan National Nature Reserve, on fallen angiosperm trunk, 4 June 2019, *S.H. He*, He 5838 (BJFC 030705). Hainan, Qiongzhong County, Limushan National Forest Park, on fallen angiosperm trunk, 16 June 2017, *L.W. Zhou*, LWZ 20170611-16 (HMAS); Wuzhishan, Wuzhishan National Forest Park, on dead branch of living angiosperm, 10 June 2016, *S.H. He*, He 3924 (BJFC 022426).



**Figure 30** – Basidiomes of *Trechispora latehypha* (He 5848, holotype). Scale bars: a = 1 cm, b = 2 mm.



**Figure 31** – Microscopic structures of *Trechispora latehypha* (drawn from the holotype). a Vertical section of basidiomes; b. Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 32** – Scanning electron micrograph of basidiospores of *Trechispora latehypha* (scanned from the holotype). Scale bar =  $2 \mu m$ .

Notes – *Trechispora latehypha* is similar to *T. larssonii* by more or less smooth hymenophoral configuration and rows of short-celled and wide subhymenial hyphae. However, *T.* 

*larssonii* has thin-walled subicular hyphae and verrucose basidiospores. *Trechispora farinacea* also resembles *T. latehypha* by short-celled and wide subhymenial hyphae, but differs in more or less grandinioid to nearly hydnoid hymenophore, and subglobose to broadly ellipsoid basidiospores (Larsson 1995). In addition, *T. farinacea* is a common species in the north temperate zone, especially in Europe (Bernicchia & Gorjón 2010), whereas *T. latehypha* is only known in southern China.

*Trechispora longiramosa* S.L. Liu, G. He, Shuang L. Chen & L.W. Zhou, sp. nov. Figs 33–35 Index Fungorum number: IF559894; Facesoffungi number: FoF12874

Etymology – *longiramosa* (Latin), refers to long terminal branches of basidiomes.

Diagnosis – Characterized by U-shaped, dense, long, thin terminal branches with acute tips and a fishy odor.

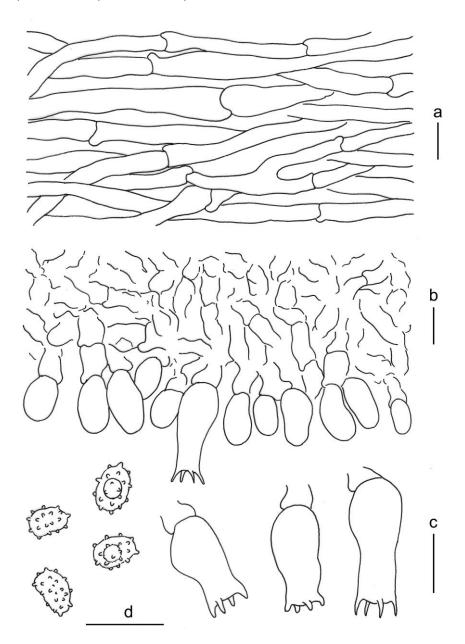
Typus – CHINA, Guizhou, Libo County, Maolan National Nature Reserve, on ground, 17 July 2019, *G. He*, CH 19233 (holotype in HMAS).



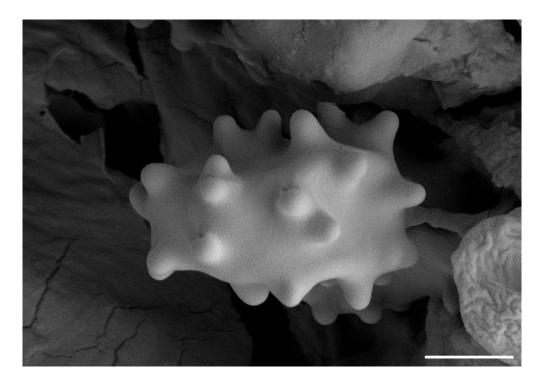
**Figure 33** – Basidiomes of *Trechispora longiramosa* (CH 19233, holotype). a Fresh specimen. b Hymenophore on branches of dried specimens. Scale bars: a = 1 cm, b = 1 mm.

Description – *Basidiomes* annual, clavarioid, solitary or in small groups, densely branched, moderately open, fleshy consistency, cream to buff turning yellowish brown towards the apex when fresh, olivaceous buff turning dark brown towards the apex when dry, with fishy odor, 7 cm high. Branches polychotomous, axils U-shaped, tips acute, white to honey-yellow. Stipe white to cream,  $5-15 \times 1-2$  mm.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin-walled, cylindrical, moderately branched and septate, subparallel, 3–8 µm in diam; ampullate septa usually present in the hyphae at the base of the stipe, up to 10 µm wide. Subhymenial hyphae short-celled and wide, 4–8 µm in diam, much branched. *Cystidia* absent. *Basidia* suburniform to subclavate, hyaline, thin-walled, with four sterigmata and a basal clamp connection, agglutinated,  $15-23 \times 8-11$  µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline to yellowish, slightly thick-walled, aculeate with spines slightly swelled in 5% potassium hydroxide, inamyloid, indextrinoid, acyanophilous,  $(4-)4.8-6 \times (3-)3.3-4(-4.5)$  µm, L = 5.2 µm, W = 3.8 µm, Q = 1.4 (*n* = 60/2).



**Figure 34** – Microscopic structures of *Trechispora longiramosa* (drawn from the holotype). a Hyphae in subiculum. b Vertical section of basidiomes. c Basidia. d Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 35** – Scanning electron micrograph of basidiospores of *Trechispora longiramosa* (scanned from the holotype). Scale bar =  $3 \mu m$ .

Other specimen (paratype) examined – CHINA, Guizhou, Libo County, Maolan National Nature Reserve, on ground, 13 July 2014, *G. He*, HG 140168 (MCCNNU 00968).

Notes – Micromorphologically, *T. longiramosa* is similar to *T. copiosa* by similar shape and size of basidiospores; however, *T. copiosa* differs in V-shaped branches and pale greyish yellow to beige basidiomes (de Meiras-Ottoni et al. 2021).

Trechispora malayana S.L. Liu, S.H. He & L.W. Zhou, sp. nov.

Figs 36–38

Index Fungorum number: IF559895; Facesoffungi number: FoF12875

Etymology - malayana (Latin), refers to the Malay Peninsula.

Diagnosis – Characterized by the combination of hydnoid hymenophore, the presence of mycelial cords, and long spines on basidiospores (0.6–1  $\mu$ m in length).

Typus – SINGAPORE, Bukit Timah Nature Reserve, on rotten angiosperm wood, 20 July 2017, *Y.C. Dai*, Dai 17876 (holotype in BJFC 025408).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, fragile, easily separated from substrates, up to 10 cm long, 5 cm wide. *Hymenophore* hydnoid, cream to buff-yellow with age. Aculei white when fresh, 5–6 per mm, up to 0.8 mm long. *Margin* thinning out as byssoid, white, up to 1.5 mm wide. Mycelial cords present, white, 0.5 mm wide.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin-walled, frequently branched and septate, interwoven, 1.5–4 µm in diam, ampullate septa up to 6 µm wide. Tramal generative hyphae distinct, hyaline, thin-walled, frequently branched, smooth, subparallel to interwoven, 2–4 µm in diam. Crystals usually present, bipyramidic, aggregated. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection,  $20-28 \times 4-5$  µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, aculeate, inamyloid, indextrinoid, acyanophilous,  $3.3-4.1(-4.5) \times (2.3-)2.5-3(-3.5)$  µm, L = 3.8 µm, W = 2.9 µm, Q = 1.3-1.4 (n = 60/2).

Other specimen (paratype) examined – THAILAND, Krabi, Khao Phanom Bencha National Park, on rotten angiosperm trunk, 28 July 2016, *S.H. He*, He 4156 (BJFC 023598).

Notes – *Trechispora malayana* may be confused with *T. nivea*, but *T. nivea* differs in slightly thick-walled tramal hyphae and shorter spines on basidiospores (up to 0.3  $\mu$ m in length; Larsson 1995).

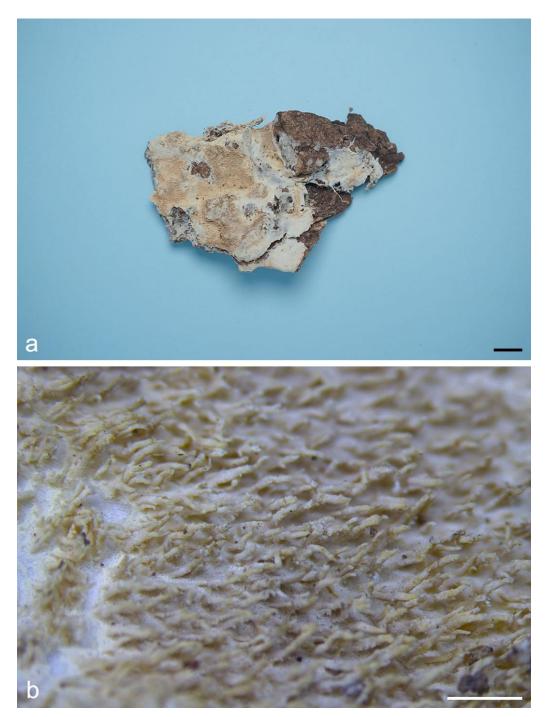
# Trechispora robusta (Rick) L.W. Zhou & S.L. Liu, comb. nov.

Index Fungorum number: IF559896; Facesoffungi number: FoF12876 *Basionym. Clavaria robusta* Rick, Egatea 16: 120 (1931).

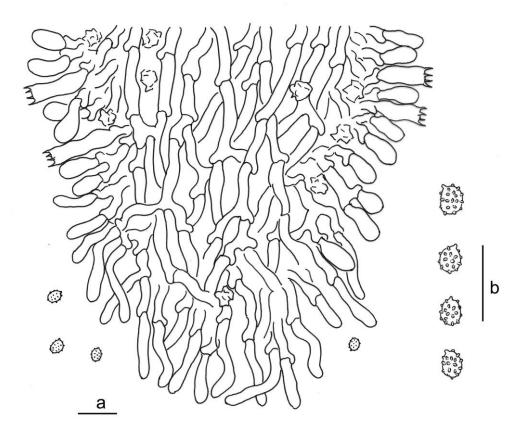
Basionym. Clavaria robusta Rick, Egalea 16: 120 (1931).

≡ Scytinopogon robustus (Rick) Corner, Beih. Nova Hedwigia 33: 91 (1970).

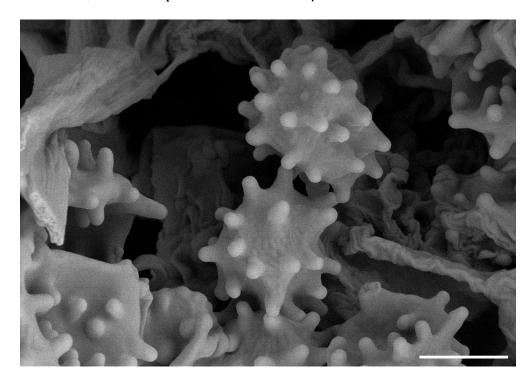
Notes – The proposal of this combination is on the basis of the same reason as that for *Trechispora dealbata* indicated above. The detailed description of *T. robusta* can be found in Furtado et al. (2021).



**Figure 36** – Basidiomes of *Trechispora malayana* (Dai 17876, holotype). Scale bars: a = 1 cm, b = 1 mm.



**Figure 37** – Microscopic structures of *Trechispora malayana* (drawn from the holotype). a Vertical section of basidiomes; b. Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 38** – Scanning electron micrograph of basidiospores of *Trechispora malayana* (scanned from the holotype). Scale bar =  $3 \mu m$ .

*Trechispora scabra* (Berk. & M.A. Curtis) L.W. Zhou & S.L. Liu, comb. nov. Index Fungorum number: IF559897; Facesoffungi number: FoF12877 Basionym. Thelephora scabra Berk. & M.A. Curtis, Amer. J. Sci. Arts, Ser. 2 11: 94 (1851). ≡ Scytinopogon scaber (Berk. & M.A. Curtis) D.A. Reid, Persoonia 2(2): 161 (1962).

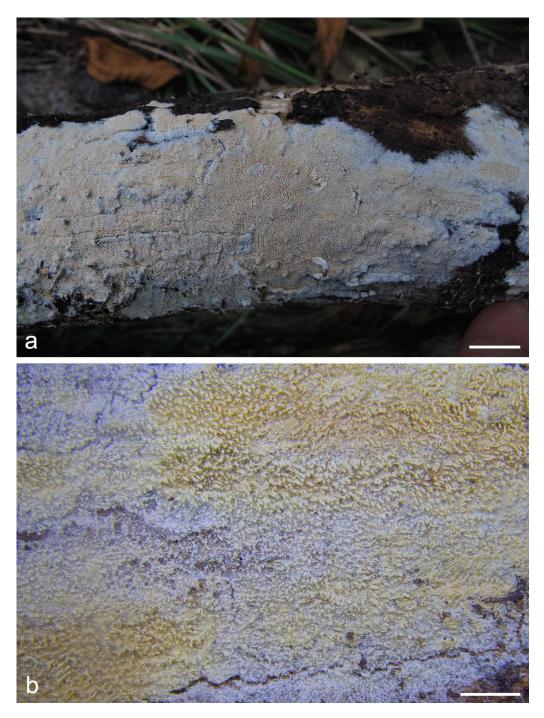
Notes – The proposal of this combination is on the basis of the same reason as that for *Trechispora dealbata* indicated above. The detailed description of *T. scabra* can be found in Furtado et al. (2021).

Trechispora sinensis S.L. Liu, L.W. Zhou & S.H. He, sp. nov. Figs 39–41

Index Fungorum number: IF559898; Facesoffungi number: FoF12878

Etymology – sinensis (Latin), refers to China.

Diagnosis – Differs from Trechispora subsinensis (described below) in vertucose basidiospores.



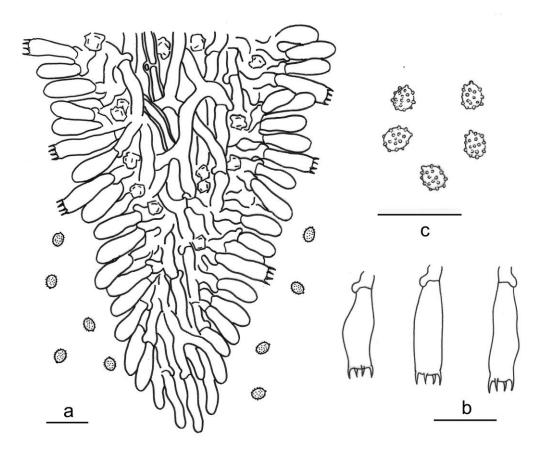
**Figure 39** – Basidiomes of *Trechispora sinensis* (LWZ 20180804-19, holotype). Scale bars: a = 1 cm; b = 2 mm.

Typus – CHINA, Beijing, Mentougou, Donglingshan Scenic Spot, on fallen angiosperm branch, 4 Aug. 2018, *L.W. Zhou*, LWZ 20180804-19 (holotype in HMAS).

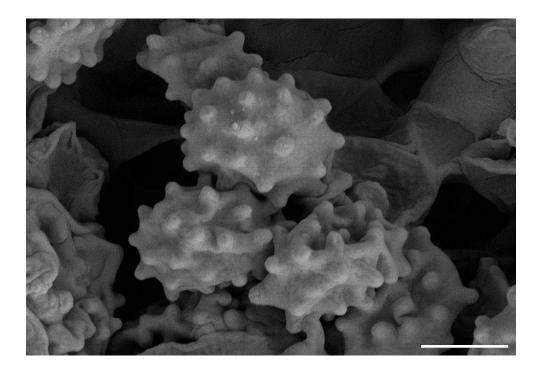
Description – *Basidiomes* annual, resupinate, effused, thin, soft, fragile, easily separated from substrates, up to 12 cm long, 5 cm wide. *Hymenophore* odontioid with numerous small aculei, cream to straw-yellow when fresh, cinnamon-buff when dry. *Margin* white, fimbriate, up to 3 mm wide.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin or thick-walled, moderately branched and septate, interwoven, 2–3.5 µm in diam, ampullate septa up to 5 µm wide. Aculei composed of a central core of compact hyphae and subhymenial and hymenial layers; generative hyphae distinct, hyaline, thin or thick-walled, moderately branched, smooth, subparallel to interwoven, 2–3.5 µm in diam. Crystals abundant, bipyramidic, aggregated. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, thin-walled, with four sterigmata and a basal clamp connection,  $11-15 \times 3.8-5$  µm; basidioles similar in shape to basidia, but smaller. *Basidiospores* broadly ellipsoid, hyaline, thin-walled, verrucose, inamyloid, indextrinoid, acyanophilous,  $2.8-3.3 \times (2.2-)2.5-2.9$  µm, L = 3 µm, W = 2.7 µm, Q = 1.1-1.2 (n = 90/3).

Other specimens (paratypes) examined – CHINA, Beijing, Mentougou, Donglingshan Scenic Spot, on fallen angiosperm branch, 4 Aug. 2018, *L.W. Zhou*, LWZ 20180804-20 (HMAS); on fallen angiosperm twig, 9 Sept. 2017, *L.W. Zhou*, LWZ 20170909-11 (HMAS). Chongqing, Simianshan National Scenic Spot, on fallen angiosperm branch, 8 July 2018, *S.H. He*, He 5491 (BJFC 026552). Hubei, Wufeng County, Houhe National Nature Reserve, on fallen angiosperm branch, 16 Aug. 2017, *L.W. Zhou*, LWZ 20170816-35 (HMAS). Hunan, Sangzhi County, Badagongshan National Nature Reserve, on fallen angiosperm branch, 17 Aug. 2017, *L.W. Zhou*, LWZ 20170817-5 (HMAS).



**Figure 40** – Microscopic structures of *Trechispora sinensis* (drawn from the holotype). a Vertical section of basidiomes. b Basidiospores. **c** Basidia. Scale bars =  $10 \mu m$ .



**Figure 41** – Scanning electron micrograph of basidiospores of *Trechispora sinensis* (scanned from the holotype). Scale bar =  $3 \mu m$ .

Notes – *Trechispora sinensis* has a wide distribution throughout China, including in multiple provincial regions, like Beijing, Chongqing, Guangdong, Guangxi, Guizhou, Hubei, Hunan, Jiangsu, Jiangxi, Jilin and Liaoning. *Trechispora sinensis* may be confused with *T. chaibuxiensis* and *T. subsinensis*; however, *T. chaibuxiensis* differs in the presence of hyphoid cystidia, while *T. subsinensis* differs in predominantly thick-walled tramal hyphae and aculeate basidiospores.

Trechispora subfissurata S.L. Liu, S.H. He & L.W. Zhou, sp. nov.

Figs 42–44

Index Fungorum number: IF559899; Facesoffungi number: FoF12879 Etymology – *subfissurata* (Latin), refers to the similarity to *Trechispora fissurata*.

Diagnosis – Differs from *Trechispora fissurata* by its thinner basidiomes and not cracked hymenophore with shorter aculei (Zhao & Zhao 2021).

Typus – CHINA, Hainan, Baisha County, Yinggeling National Nature Reserve, on dead branch of living angiosperm, 9 June 2016, *S.H. He*, He 3907 (holotype in BJFC 022409).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, fragile, easily separated from substrates, up to 8 cm long, 3 cm wide, 0.5 mm thick. *Hymenophore* odontioid to hydnoid with numerous aculei up to 0.4 mm long, white to cream when fresh, cream to buff-yellow when dry. *Margin* white to cream, fimbriate, up to 2 mm wide.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular generative hyphae hyaline, thick-walled, moderately branched and septate, subparallel to interwoven, 2.5–4.5  $\mu$ m in diam, ampullate septa up to 6  $\mu$ m wide. Aculei composed of a central core of compact hyphae and subhymenial and hymenial layers; tramal generative hyphae distinct, hyaline, thick-walled, moderately branched, smooth, subparallel, 2.5–4  $\mu$ m in diam. Crystals usually present, bipyramidic, aggregated. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection, 11–15 × 4–5.5  $\mu$ m; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin- to slightly thick-walled, aculeate with spines that have a sharp apex, inamyloid, indextrinoid, acyanophilous, 2.8–3.5 × 2.5–3  $\mu$ m, L = 3.1  $\mu$ m, W = 2.8  $\mu$ m, Q = 1.1 (n = 60/2).

Other specimen (paratype) examined – CHINA, Guangdong, Ruyuan County, Nanling National Forest Park, on the base of living angiosperm, 13 June 2019, *L.W. Zhou*, LWZ 20190613-48 (HMAS).

Notes – *Trechispora subfissurata* is characterized by aculeate basidiospores with spines that have a sharp apex. This character makes *T. subfissurata* similar to *T. echinospora* and *T. fissurata* (Phookamsak et al. 2019, Zhao & Zhao 2021). However, *T. echinospora* differs in the absence of crystals in subiculum and trama, and globose basidiospores (Phookamsak et al. 2019), while *T. fissurata* differs in thicker basidiomes (up to 0.8 mm in thickness) with longer aculei (up to 0.9 mm in length; Zhao & Zhao 2021).

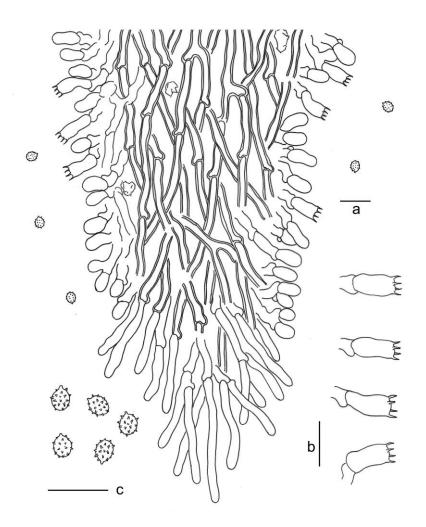


**Figure 42** – Basidiomes of *Trechispora subfissurata* (He 3907, holotype). Scale bars: a = 1 cm, b = 1 mm.

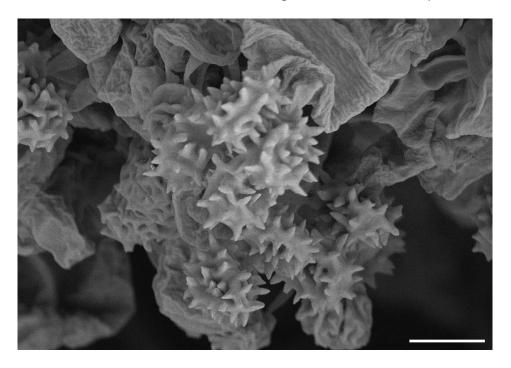
Trechispora subhymenocystisS.L. Liu, H.S. Yuan & L.W. Zhou, sp. nov.Figs 45–47Index Fungorum number: IF559900; Facesoffungi number: FoF12880Figs 45–47

Etymology – subhymenocystis (Latin), refers to the similarity to Trechispora hymenocystis.

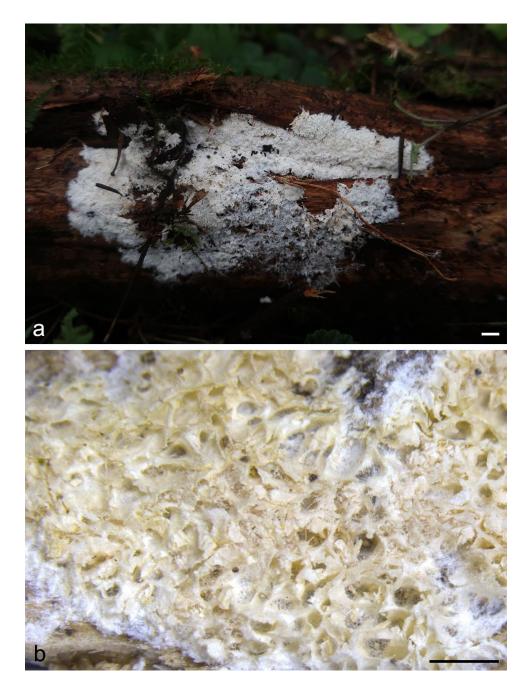
Diagnosis – Differs from *Trechispora hymenocystis* in lack of sphaerocysts in subiculum (Larsson 1994).



**Figure 43** – Microscopic structures of *Trechispora subfissurata* (drawn from the holotype). a Vertical section of basidiomes. b Basidia. c Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 44** – Scanning electron micrograph of basidiospores of *Trechispora subfissurata* (scanned from the holotype). Scale bar = 5  $\mu$ m.



**Figure 45** – Basidiomes of *Trechispora subhymenocystis* (LWZ 20190818-32b, holotype). Scale bars: a = 1 cm, b = 1 mm.

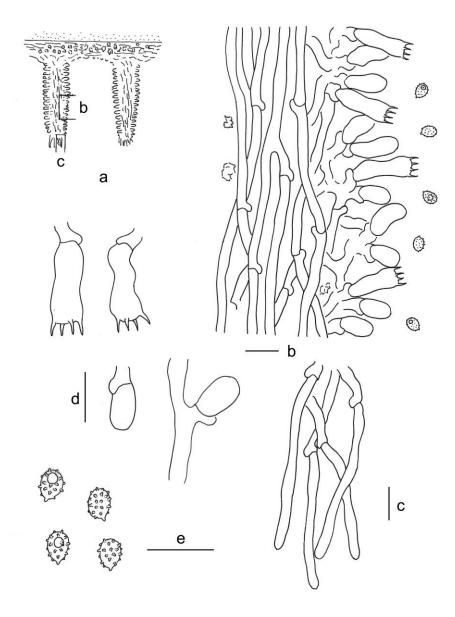
Typus – CHINA, Sichuan, Meigu County, Dafengding National Nature Reserve, on fallen trunk of *Cryptomeria fortunei*, 18 Aug. 2019, *L.W. Zhou*, LWZ 20190818-32b (holotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, soft, fragile, easily separated from substrates, soft when fresh, becoming soft corky when dry, up to 6 cm long, 4 cm wide. Pore surface white when fresh, buff, cinnamon-buff to yellowish brown when dry; pores round to angular, 3–4 per mm; dissepiments thin, entire. Subiculum white, soft corky, thin, about 0.1 mm thick. Tubes cinnamon-buff to yellowish brown, soft, up to 1.5 mm long. *Margin* white, fimbriate, rhizomorphic.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular generative hyphae hyaline, thin-walled, moderately branched and septate, subparallel to interwoven,  $2.5-5 \mu m$  in diam, ampullate septa up to 7  $\mu m$  wide; crystals abundant, irregular. Generative hyphae in tubes hyaline, thin-walled, moderately branched and septate, more or less parallel,  $2.5-4 \mu m$  in diam;

crystals rare, irregular. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection,  $13-22 \times 5-7 \mu m$ ; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline to yellowish, slightly thick-walled, aculeate with tubercles on spines, inamyloid, indextrinoid, acyanophilous,  $(3.5-)3.8-4.5(-4.8) \times (2.8-)3-3.5(-3.9) \mu m$ , L = 4.1 µm, W = 3.1 µm, Q = 1.3 (*n* = 60/2).

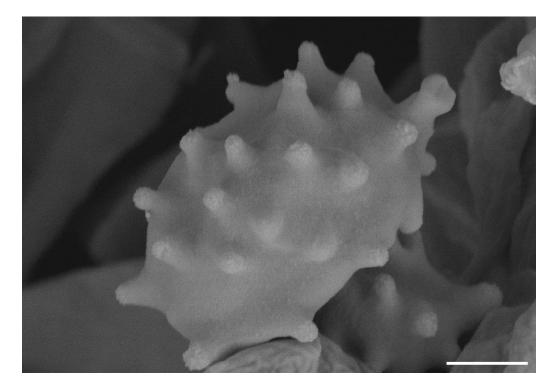
Other specimens (paratypes) examined – CHINA, Sichuan, Meigu County, Dafengding National Nature Reserve, on fallen trunk of *Cryptomeria fortunei*, 18 Aug. 2019, *L.W. Zhou*, LWZ 20190818-29b (HMAS). Yunnan, Xianggelila, Shuoduhu, on fallen trunk of *Abies*, 31 Aug. 2006, *H.S. Yuan*, Yuan 2027 (IFP 007168); Xianggelila, Qianhushan, on fallen trunk of *Abies*, 1 Sept. 2006, *H.S. Yuan*, Yuan 2089 (IFP 007171).



**Figure 46** – Microscopic structures of *Trechispora subhymenocystis* (drawn from the holotype). a Vertical section through basidiomes showing position of b and c. b Section through a dissepiment edge. c Section at the apex of a dissepiment. d Basidia and basidioles. e Basidiospores. Scale bars =  $10 \mu m$ .

Notes – The tuberculate ornamentations on spines of basidiospores, which were first reported in *T. hymenocystis* (Larsson 1994), make *Trechispora subhymenocystis* similar to *T. araneosa*, *T.* 

hondurensis, T. hymenocystis and T. minima. However, T. araneosa and T. minima differ in nonporoid hymenophores (Larsson 1995, 1996), T. hondurensis differs in smaller basidiospores (3.67–  $3.84 \times 2.76-2.89 \mu m$ ; Haelewaters et al. 2020), and T. hymenocystis differs in the presence of sphaerocysts in cords and the adjacent part of subiculum and larger basidiospores (4.5–5.5 × 3.5– 4.5 µm; Larsson 1994). Trechispora subhymenocystis also resembles T. mollusca by poroid hymenophore, a monomitic hyphal system, and ellipsoid, aculeate basidiospores; however, T. mollusca differs in white to light ochraceous hymenophore, slightly thick-walled subicular hyphae and shorter basidiospores (2.5–4 µm in length; Liberta 1973, Larsson 1994, Bernicchia & Gorjón 2010).



**Figure 47** – Scanning electron micrograph of basidiospores of *Trechispora subhymenocystis* (scanned from the holotype). Scale bar =  $2 \mu m$ .

Trechispora subsinensis S.L. Liu, S.H. He & L.W. Zhou, sp. nov.

Figs 48-50

Etymology – subsinensis (Latin), refers to the similarity to Trechispora sinensis.

Diagnosis – Differs from Trechispora sinensis in aculeate basidiospores.

Index Fungorum number: IF559901; Facesoffungi number: FoF12881

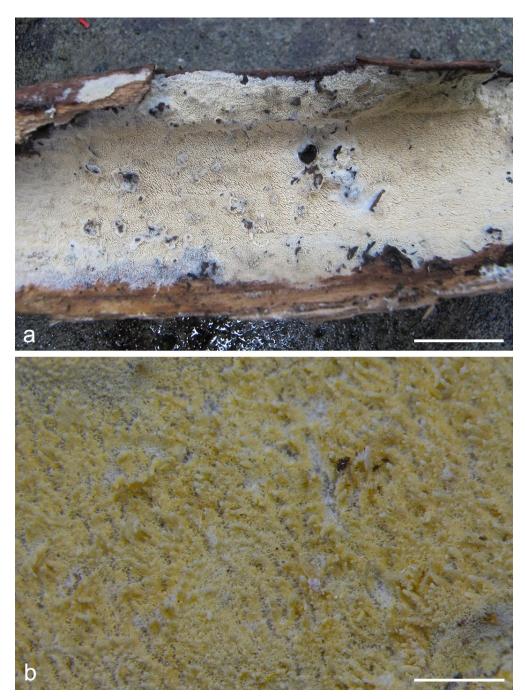
Typus – CHINA, Guangdong, Guangzhou, Baiyunshan National Scenic Spot, on fallen angiosperm branch, 11 June 2019, *L.W. Zhou*, LWZ 20190611-9 (holotype in HMAS).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, fragile, easily separated from substrates, up to 9 cm long, 3 cm wide. *Hymenophore* odontioid with numerous small aculei, cream when fresh, straw-yellow to bluish grey when dry. *Margin* white, fimbriate, up to 0.5 mm wide.

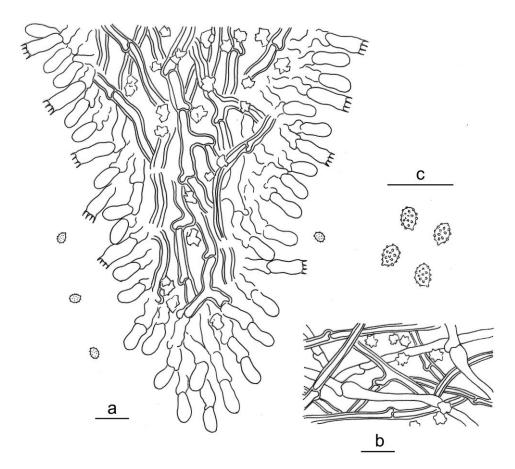
*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin to thick-walled, moderately branched and septate, interwoven, 2–3.5 µm in diam, ampullate septa up to 5 µm wide. Aculei composed of a central core of compact hyphae and subhymenial and hymenial layers; tramal generative hyphae distinct, hyaline, thick-walled, moderately branched, smooth, subparallel to interwoven, 2–3.5 µm in diam. Crystals usually present, bipyramidic, aggregated. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, thin-walled, with four sterigmata and a basal clamp connection,  $11-15 \times 3.8-5$  µm; basidioles similar in shape to basidia, but smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, aculeate, inamyloid, indextrinoid, acyanophilous,  $(2.5-)2.7-3.5(-4) \times (2-)2.3-2.8(-3)$  µm, L = 3 µm, W = 2.5 µm, Q = 1.2 (n = 90/3).

Other specimens (paratypes) examined – CHINA, Guangdong, Guangzhou, Baiyunshan National Scenic Spot, on dead branch of living angiosperm, 11 June 2019, *L.W. Zhou*, LWZ 20190611-19 (HMAS); Zhaoqing, Dinghushan National Nature Reserve, on fallen angiosperm trunk, 10 June 2019, *S.H. He*, He 5894 (BJFC 030763). THAILAND, Chiang Mai, Mork Fa Waterfall, on dead branch of living angiosperm, 25 July 2016, *S.H. He*, He 4122 (BJFC 023564), on rotten bamboo, 25 July 2016, *S.H. He*, He 4125 (BJFC 023567).

Notes – *Trechispora subsinensis* morphologically resembles *T. chaibuxiensis*, *T. fimbriata*, *T. nivea* and *T. sinensis* (Larsson 1995, Zhao & Zhao 2021), and phylogenetically these five species also nested within a strongly supported clade (BS = 97%, BPP = 1; Fig. 6). *Trechispora chaibuxiensis* differs in the presence of hyphoid cystidia, *T. fimbriata* in cracked hymenial surface and longer aculei (0.5–0.9 mm; Zhao & Zhao 2021), *T. nivea* in slightly thick-walled tramal hyphae and longer aculei (up to 1 mm; Larsson 1995), and *T. sinensis* in vertucose basidiospores.



**Figure 48** – Basidiomes of *Trechispora subsinensis* (LWZ 20190611-9, holotype). Scale bars: a = 1 cm; b = 1 mm.



**Figure 49** – Microscopic structures of *Trechispora subsinensis* (drawn from the holotype). a Vertical section of basidiomes. b Hyphae in subiculum. c Basidiospores. Scale bars =  $10 \mu m$ .

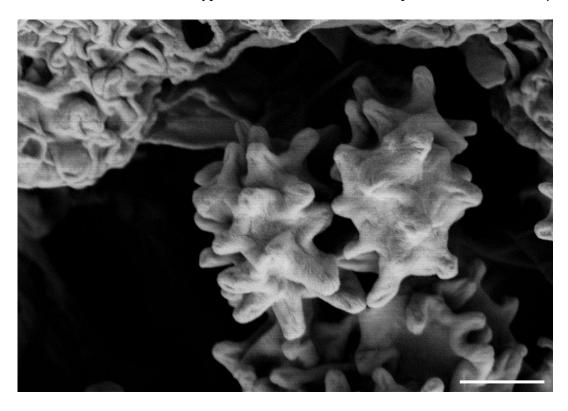


Figure 50 – Scanning electron micrograph of basidiospores of *Trechispora subsinensis* (scanned from the holotype). Scale bar =  $2 \mu m$ .

Trechispora taiwanensis S.L. Liu, S.H. He & L.W. Zhou, sp. nov.

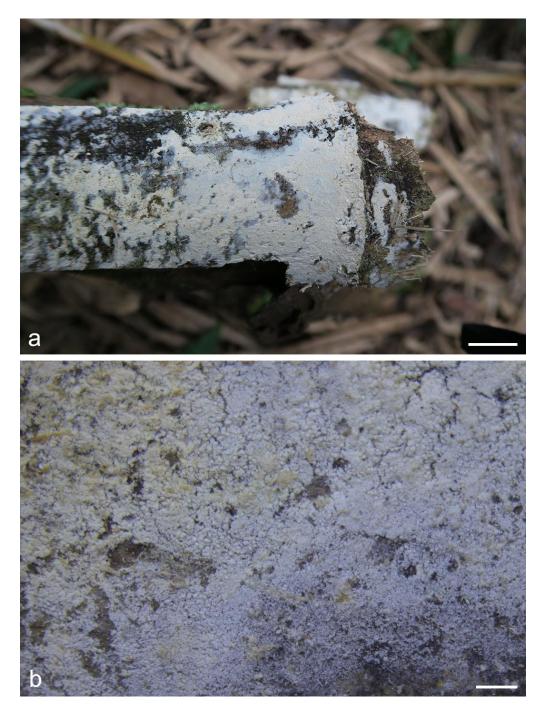
Index Fungorum number: IF559902; Facesoffungi number: FoF12882

Etymology - taiwanensis (Latin), refers to Taiwan, China.

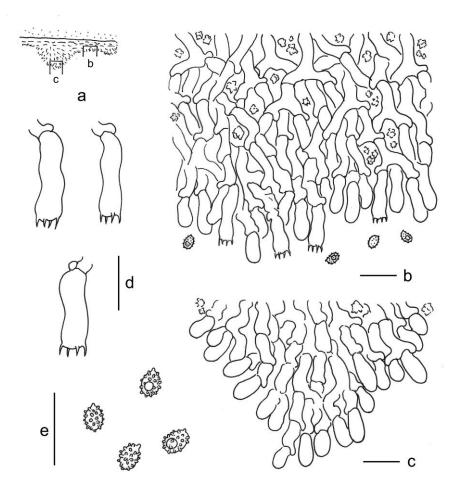
Diagnosis – Differs from *Trechispora thailandica* (described below) in narrower basidiospores.

Typus – CHINA, Taiwan, Nantou County, Lianhuachi Nature Reserve, on dead bamboo, 6 Dec. 2016, *S.H. He*, He 4571 (holotype in BJFC 024012).

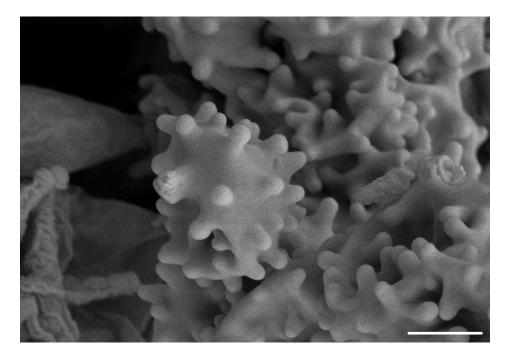
Description – *Basidiomes* annual, resupinate, effused, thin, soft, fragile, loosely attached to the substrates, up to 10 cm long, 5 cm wide. *Hymenophore* smooth to grandinioid with numerous small aculei, farinaceous, cream when fresh, cream to straw-yellow with age, finely cracked with age. *Margin* thinning out as byssoid, 2–3 mm wide.



**Figure 51** – Basidiomes of *Trechispora taiwanensis* (He 4571, holotype). Scale bars: a = 1 cm, b = 1 mm.



**Figure 52** – Microscopic structures of *Trechispora taiwanensis* (drawn from the holotype). a Vertical section through basidiomes showing position of b and c. b Section through base of a spine. c Section through apex of a spine. d Basidia. e Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 53** – Scanning electron micrograph of basidiospores of *Trechispora taiwanensis* (scanned from the holotype). Scale bar =  $2 \mu m$ .

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae long-celled, hyaline, thin-walled, frequently branched and septate, subparallel to interwoven, 2.5–4.5 µm in diam, ampullate septa up to 6 µm wide. Aculei composed of a central core of compact hyphae and subhymenial and hymenial layers; generative hyphae distinct, hyaline, thin or thick-walled, moderately branched, smooth, subparallel, 2.5–5.5 µm in diam. Crystals present, bipyramidic, aggregated. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection,  $13-16 \times 4-5.5$  µm; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thinwalled, aculeate, inamyloid, indextrinoid, acyanophilous, sometimes with one oil drop in the protoplasm,  $3-4(-4.2) \times 2-2.8(-3.2)$  µm, L = 3.3 µm, W = 2.5 µm, Q = 1.2-1.5 (*n* = 60/2).

Other specimen (paratype) examined – CHINA, Taiwan, Nantou County, Lianhuachi Nature Reserve, on dead bamboo, 6 Dec. 2016, *S.H. He*, He 4574 (BJFC 024015).

Notes – Macromorphologically, *T. taiwanensis* resembles *T. laevis*, but *T. laevis* differs in straight or concave basidiospores at the ventral side (Larsson 1996). In addition, *T. taiwanensis* is so far only known on bamboo in subtropical Asia, whereas *T. laevis* grows on coniferous wood in North Europe (Larsson 1996).

Trechispora thailandica S.L. Liu, S.H. He & L.W. Zhou, sp. nov.

Figs 54–56

Index Fungorum number: IF559903; Facesoffungi number: FoF12883

Etymology - thailandica (Latin), refers to Thailand.

Diagnosis – Differs from Trechispora taiwanensis in wider basidiospores.

Typus – THAILAND, Chiang Mai, Doi Saket, on rotten bamboo, 24 July 2016, *S.H. He*, He 4101 (holotype in BJFC 023542).

Description – *Basidiomes* annual, resupinate, effused, thin, soft, easily separated from substrates, up to 9 cm long, 3 cm wide. *Hymenophore* grandinioid with round and obtuse aculei, white to cream when fresh, cream to buff-yellow with age, finely cracked with age. *Margin* thinning out as byssoid.

*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin-walled, frequently branched and septate, subparallel, 2.5–5  $\mu$ m in diam. Tramal generative hyphae distinct, hyaline, thin-walled, moderately branched, smooth, interwoven, 3–5  $\mu$ m in diam. Crystals usually present, bipyramidic, aggregated. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection, 11–15 × 4–5.5  $\mu$ m; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline to yellowish, thin-walled, aculeate, inamyloid, indextrinoid, acyanophilous, (3.5–)3.8–4.3(–4.5) × (2.5–)2.8–3.5  $\mu$ m, L = 4  $\mu$ m, W = 3  $\mu$ m, Q = 1.3 (*n* = 60/2).

Other specimens (paratypes) examined – THAILAND, Chiang Mai, Doi Saket, on rotten bamboo, 24 July 2016, *S.H. He*, He 4112 (BJFC 023554), He 4114 (BJFC 023556).

Notes – *Trechispora thailandica* resembles *T. cyatheae* by the white to cream, grandinioid hymenophore and ellipsoid basidiospores; however, *T. cyatheae* has smaller basidiospores ( $3-3.5 \times 2-3 \mu m$  including spines) and grows exclusively on *Cyathea glauca*, an endemic species of tree fern to La Réunion, France (Ordynets et al. 2015).

*Trechispora tropica* S.L. Liu & L.W. Zhou, sp. nov.

Figs 57–59

Index Fungorum number: IF559904; Facesoffungi number: FoF12884

Etymology – *tropica* (Latin), refers to tropics.

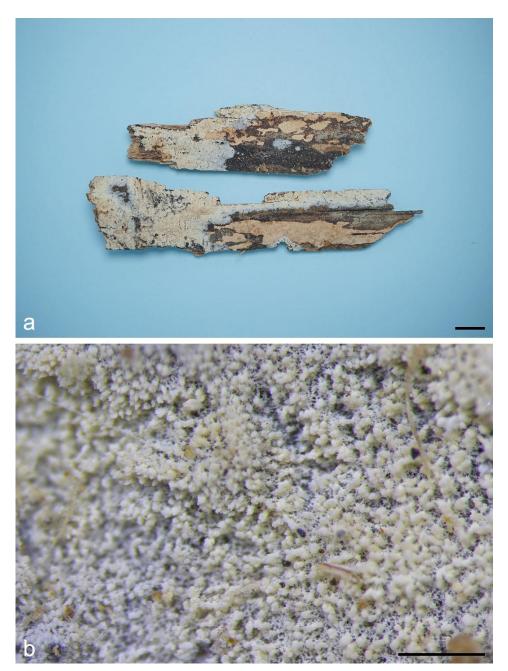
Diagnosis – Characterized by the absence of crystals in trama and subhymenium, and cystidium-like hyphal ends at the apex of aculei.

Typus – CHINA, Hainan, Ledong County, Jianfengling National Forest Park, on fallen angiosperm branch, 13 June 2017, *L.W. Zhou*, LWZ 20170613-14 (holotype in HMAS).

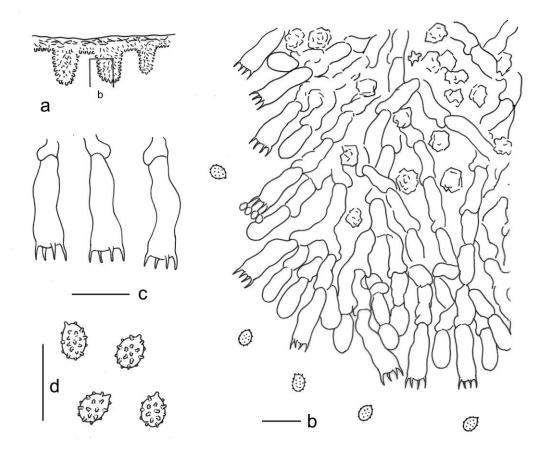
Description – *Basidiomes* annual, resupinate, effused, thin, soft and fragile, easily separated from substrates, up to 11 cm long, 5 cm wide. *Hymenophore* grandinioid to odontioid with

numerous, small aculei, white to cream when fresh, cream to straw-yellow when dry. *Margin* white, fimbriate, up to 2 mm wide.

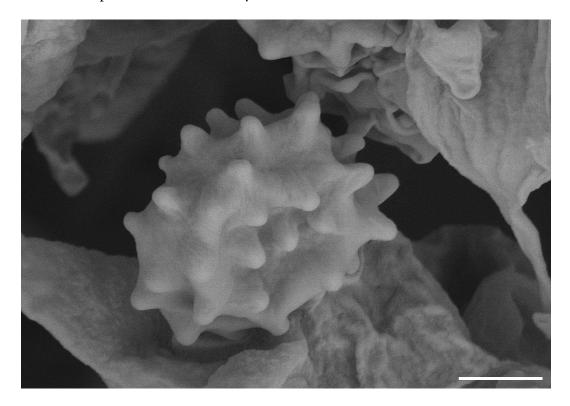
*Hyphal system* monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thin-walled, frequently branched and septate, subparallel, 2.5–6  $\mu$ m in diam, ampullate septa up to 8  $\mu$ m wide. Aculei composed of a central core of compact hyphae and subhymenial and hymenial layers; generative hyphae distinct, hyaline, thin or thick-walled, frequently branched, smooth, subparallel, 2.5–5.5  $\mu$ m in diam; hyphal ends present at apex, cystidium-like, long-celled, 2.5–4  $\mu$ m in diam. Crystals only present in subiculum, usually flat and basically rhomboidal. *Cystidia* absent. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection, 7–10 × 4–5  $\mu$ m; basidioles in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, aculeate, inamyloid, indextrinoid, acyanophilous, 2.5–3 × 2.2–2.5(–2.6)  $\mu$ m, L = 2.8  $\mu$ m, W = 2.3  $\mu$ m, Q = 1.2 (*n* = 60/2).



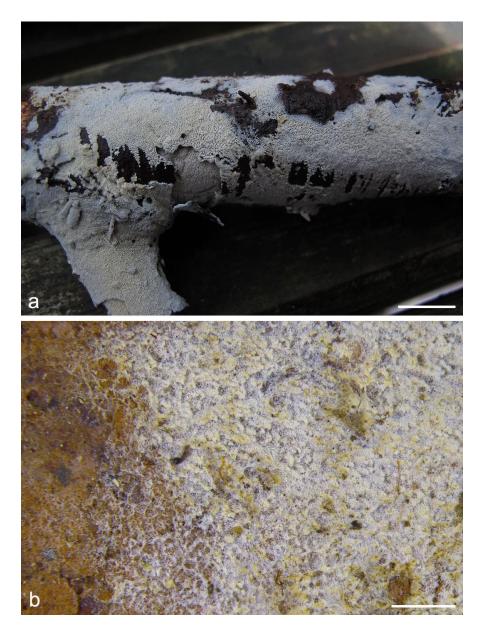
**Figure 54** – Basidiomes of *Trechispora thailandica* (He 4101, holotype). Scale bars: a = 1 cm, b = 0.5 mm.



**Figure 55** – Microscopic structures of *Trechispora thailandica* (drawn from the holotype). a Vertical section through basidiomes showing position of b. b Section through apex of a spine. c Basidia. d Basidiospores. Scale bars =  $10 \mu m$ .



**Figure 56** – Scanning electron micrograph of basidiospores of *Trechispora thailandica* (scanned from the holotype). Scale bar =  $2 \mu m$ .



**Figure 57** – Basidiomes of *Trechispora tropica* (LWZ 20170613-14, holotype). Scale bars: a = 1 cm; b = 1 mm.

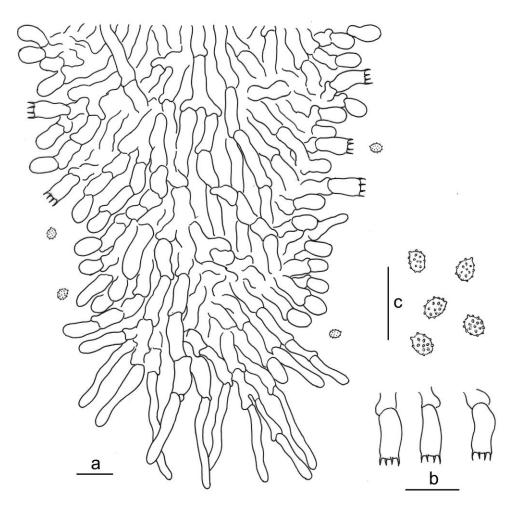
Other specimens (paratypes) examined – CHINA, Hainan, Ledong County, Jianfengling National Forest Park, on fallen angiosperm branch, 13 June 2017, *L.W. Zhou*, LWZ 20170613-16 (HMAS). VIETNAM, Da Lat, Bidoup Nui Ba National Park, on fallen angiosperm branch, 15 Oct. 2017, *L.W. Zhou*, LWZ 20171015-22 (HMAS).

Notes – *Trechispora tropica* is phylogenetically close to *T. laevis*, *T. stevensonii* and *T. taiwanensis* (Fig. 6). However, *T. laevis* differs in smooth hymenophore (Larsson 1996), *T. stevensonii* in the presence of arthroconidia (Larsson 1995), and *T. taiwanensis* in longer basidiospores (3–4  $\mu$ m in length) sometimes with one oil drop in the protoplasm and the growth on bamboo.

Tubulicium Oberw., Sydowia 19(1-3): 53 (1966) [published June 1965].

Type species – *Tubulicium vermiferum* (Bourdot) Oberw. ex Jülich, Persoonia 10(3): 335 (1979).

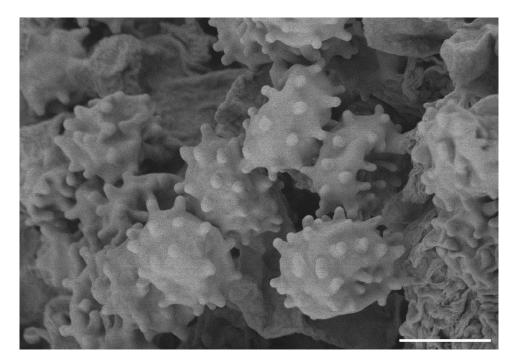
*= Tubulixenasma* Parmasto, Izv. Akad. Nauk Estonsk. SSR, Ser. Biol. 14: 231 (1965) [published July 1965]. Type species *– Tubulixenasma vermiferum* (Bourdot) Parmasto, Eesti NSV Tead. Akad. Toim., Biol. seer 14(2): 231 (1965). Description – *Basidiomes* annual, resupinate, effused, thin, closely adnate. *Hymenophore* smooth, more or less arachnoid, white, cream to buff. *Hyphal system* monomitic, generative hyphae with clamp connections, hyaline, thin- to slightly thick-walled. *Cystidia* (*lyocystidia*) conical, subulate, projecting beyond hymenium, multi-rooted, hyaline, distinctly thick-walled, slightly amyloid, covered with dendroid branching hyphae. *Basidia* suburniform, hyaline, thin-walled, with four sterigmata and a basal clamp connection. *Basidiospores* navicular to sigmoid, hyaline, thin-walled, smooth, inamyloid, indextrinoid, acyanophilous. On wood.



**Figure 58** Microscopic structures of *Trechispora tropica* (drawn from the holotype). a Vertical section of basidiomes b Basidia. c Basidiospores. Scale bars =  $10 \mu m$ .

Notes – *Tubulicium* was erected for two species, viz. *Hypochnus dussii* and *Peniophora vermifera* (Oberwinkler 1965). However, the combinations of these two species to *Tubulicium* by Oberwinkler (1965) were invalid according to the International Code of Botanical Nomenclature (Montreal Code published in 1961). Later, Jülich (1979) validated these two combinations. *Tubulicium* was formerly put in the family *Tubulicrinaceae* (Jülich 1981), but later molecular evidence indicated that it belonged in the trechisporoid clade (Larsson et al. 2004). Therefore, Larsson (2007) formally accepted it as a member of *Hydnodontaceae*, *Trechisporales*, although there was lack of clear affinity to other genera within *Trechisporales* in morphology. Recently, two new species of *Tubulicium* were almost simultaneously described on the basis of morphological and phylogenetic evidence (Liu et al. 2019, Ushijima et al. 2019). Besides bringing the species number of *Tubulicium* to 11, these two studies also confirmed the taxonomic placement of *Tubulicium* proposed by Larsson (2007), which is also recovered by the current phylogenies (Figs 1, 2, 3). Morphologically, *Tubulicium* is characterized by the presence of multirooted, subulate and thick-walled cystidia covered by dendroid-branching hyphae (Liu et al. 2019, Ushijima et al. 2019).

*Tubulixenasma* Parmasto is an obligate synonym of *Tubulicium*, because it is based on the same type species, *Peniophora vermifera*. *Tubulicium* and *Tubulixenasma* were published in the same year, but according to the title page of *Sydowia* volume 19, the paper on "Primitive Basidiomyceten" by Oberwinkler "wurde als Sonderdruck im Juni 1965 ausgegeben [was issued as an offprint in June 1965]" while Parmasto (1965) appeared in July of that year, according to Hjortstam et al. (1988).



**Figure 59** Scanning electron micrograph of basidiospores of *Trechispora tropica* (scanned from the holotype). Scale bar =  $4 \mu m$ .

### Genera excluded from *Trechisporales*

### Boidinella Nakasone, Cryptog. Mycol. 32(2): 192 (2011).

Type species – *Boidinella globulispora* (Boidin & Lanq.) Nakasone, Cryptog. Mycol. 32(2): 193 (2011).

Notes – *Boidinella* was introduced for *B. cystidiolophora* (originally described in *Sistotremella*) and the type species *B. globulispora* (originally described in *Dendrothele*) by Nakasone (2011). The genus was characterized by the combination of "effuse, soft, densely farinaceous or membranous basidioma, urniform basidia with 4-sterigmata, obclavate lcptocystidia, dendrohyphidia, and basidiospores with smooth, slightly thickened. cyanophilous walls". There are no sequences for either species currently in GenBank. Nevertheless, *Boidinella* was placed in *Hydnodontaceae*, *Trechisporales* by Kirk (2019) who does not indicate the source of this placement. Until molecular data are available, the genus is best treated as a member of the *Cantharellales* as indicated by the original author according to morphological characters (Nakasone 2011), which are distinct from members in *Trechisporales*.

### Litschauerella Oberw., Sydowia 19(1-3): 43 (1966) [1965].

Type species – *Litschauerella abietis* (Bourdot & Galzin) Oberw. ex Jülich, Persoonia 10(3): 335 (1979).

Notes – *Litschauerella* is a small and not well-known genus. Larsson (2007) place this genus in *Trechisporales* with doubt. Two authors of the current paper, viz. S.L. Liu and S.H. He, and their colleagues for the first time generated molecular sequences from a species in this genus, but they did not mention its taxonomic position (Liu et al. 2019). Here, via BLAST search of ITS

(MK204555) and nrLSU (MK204556) regions from *Litschauerella gladiola* represented by the specimen He 3171 (BJFC 021566) from Yunnan, China, we confirmed that this species has an affinity to *Hymenochaetales* rather than *Trechisporales*. Although *L. gladiola* is not the generic type, its placement based on molecular evidence does provide more doubts about the position of *Litschauerella* within *Trechisporales*. Given above, no evidence supports the taxonomic position of *Litschauerella* in *Trechisporales* and thus we tentatively exclude it from *Trechisporales*. We note that the family *Litschauerellaceae* (Jülich 1981) is based on *Litschauerella*, but even if *Litschauerella* should prove to belong in *Hydnodontaceae*, this latter family name could stand as the two families were introduced in the same publication, and *Hydnodontaceae* has already been established as the preferred choice over *Subulicystidiaceae* and, if necessary, a similar choice could be made against *Litschauerellaceae*.

#### Sphaerobasidium Oberw., Sydowia 19(1-3): 57 (1966) [1965].

Type species – *Sphaerobasidium minutum* (J. Erikss.) Oberw. ex Jülich, Persoonia 10(3): 335 (1979).

Notes – For unexplained reasons, He et al. (2019) and Kirk (2019) listed *Sphaerobasidium* in *Hydnodontaceae* despite the fact that molecular data on the type species of this genus indicate a placement in the vicinity of *Tubulicrinis* in the *Hymenochaetales* (Larsson et al. 2006, Larsson 2007). BLAST search with all three available sequences of *Sphaerobasidium minutum* (GenBank accession numbers: AJ406446, DQ873652 and DQ873653) also suggests its affinity to *Hymenochaetales* rather than *Trechisporales*.

*Tomentella* P. Karst., Bidr. Känn. Finl. Nat. Folk 48: 419 (1889) non *Tomentella* Pers. ex Pat., Hyménomyc. Eur. (Paris): 154 (1887).

Type species – Tomentella sulphurea (Pers.) P. Karst., Bidr. Känn. Finl. Nat. Folk 48: 419 (1889).

Notes – The type of the illegitimate name *Tomentella* P. Karst. was placed at one time in *Trechispora* as *Trechispora sulphurea*, but was subsequently accepted as a species of *Phlebiella* as *P. sulphurea* and considered synonymous with *Trechispora vaga*, such as by Ginns & Lefebvre (1993). While *Tomentella sulphurea* (based on *Corticium sulphureum*) and *Trechispora vaga* (based on *Phlebia vaga*) are both sanctioned, the former has the earlier basionym as is the name that should be taken up when the two names are treated as referring to the same species. Larsson (2007) placed *Phlebiella* outside of *Hydnodontaceae*, in the "*Phlebiella* family". Piątek (2005) pointed out that *Phlebiella* was not validly published and should be known as *Xenasmatella*. While the name *Xenasmatella vaga* exists for another species, no combination has been made yet in *Xenasmatella* for *T. sulphurea*. Despite the unresolved issues around the correct name for *Tomentella sulphurea*, it is clear that *Tomentella* P. Karst. does not belong in *Hydnodontaceae*, despite the placement in that family by Index Fungorum (http://www.indexfungorum.org/).

#### Genus of uncertain position

#### Murrilloporus Ryvarden, Mycotaxon 23: 192 (1985).

Type species – Murrilloporus rutilantiformis (Murrill) Ryvarden, Mycotaxon 23: 192 (1985).

Notes – Trametes rutilantiformis, type of the monotypic genus Murrilloporus, was placed by Stalpers (1996) in Heterobasidion, at that time making Murrilloporus a synonym of Heterobasidion. Later, Hattori (2003) synonymized Loweporus corticicola with Trametes rutilantiformis and placed the latter in Cristelloporia, making Murrilloporus a synonym of Cristelloporia. In this case, given that Cristelloporia is now a synonym of Trechispora, Murrilloporus would also be placed under Trechispora. However, T. rutilantiformis differs from Trechispora in the combination of coriaceous basidiomes with context up to 1 cm thick and dextrinoid skeletal hyphae. Given this morphological divergence from Trechispora, sequencing is required to confirm the appropriate placement of Trametes rutilantiformis.

# Species excluded from Trechispora

Trechispora yunnanensis C.L. Zhao, in Xu, Chen & Zhao, Phytotaxa 424(4): 256. (2019).

Notes – *Trechispora yunnanensis* was recently described from Yunnan, China (Xu et al. 2019). Chikowski et al. (2020) noted that the deposited molecular sequences of this species are questionable according to BLAST search. Although the morphological characters of *T. yunnanensis* partially fit the concept of *Trechispora*, we confirmed that the ITS and nrLSU regions of this species (put in reverse order in the columns in Table 1 of the original publication) actually represent two taxa, respectively, from the orders *Trechisporales* and *Hymenochaetales* instead of being a single taxon. Therefore, the identity of type specimens of *T. yunnanensis* needs to be further clarified. For now, we tentatively exclude this species from *Trechispora, Trechisporales*.

# Key to 12 genera in Trechisporales

1. Basidiomes clavarioid or pileate-stipitate, on ground or termite mounds	Trechispora A
1. Basidiomes resupinate, on wood	
2. Hymenophore poroid	3
2. Hymenophore non-poroid	
3. Basidiospores smooth	
3. Basidiospores ornamented	Trechispora B
4. Hymenophore brown	
4. Hymenophore usually light colored	5
5. Cystidia present, distinct	
5. Cystidia absent or indistinct	9
6. Cystidia distinctly dextrinoid	Dextrinocystis
6. Cystidia amyloid or negative in Melzer's reagent	7
7. Cystidia neither bi- nor multi-rooted, multiseptated	Suillosporium
7. Cystidia bi- or multi-rooted, not multiseptated	8
8. Cystidia regularly encrusted with rectangular crystals	Subulicystidium
8. Cystidia usually covered with dendroid hyphae	Tubulicium
9. Generative hyphae with ampullate septa	Trechispora C
9. Generative hyphae without ampullate septa	10
10. Subhymenial hyphae isodiametric	
10. Subhymenial hyphae not isodiametric	
11. Hymenophore firmly granular or almost smooth; basidiospores rhomboid or s	short ellipsoid
	Brevicellopsis
11. Hymenophore distinctly odontioid; basidiospores narrowly allantoid	Brevicellicium
12. Hyphal system dimitic	Fibrodontia
12. Hyphal system monomitic	13
13. Sterile hyphal pegs present	Pteridomyces
13. Sterile hyphal pegs absent	Allotrechispora

# Key to 87 species in *Trechispora* (separated into three parts following the key to 12 genera in *Trechisporales*)

Trechispora A (Basidiomes clavarioid or pileate-stipitate, on ground or termite mounds)1. Hymenophore pileate-stipitate.21. Hymenophore clavarioid.42. Aculei up to 0.4 mm long; basidiospores < 3.5 µm wide.</td>7. hypogeton2. Aculei up to 1 mm long; basidiospores > 3.5 µm wide.33. The stipe and abhymenial surface white to sordid cream.T. gillesii3. The stipe and abhymenial surface light yellow brown.T. thelephora

4. Hymenophore on termite mounds	T. termitophila
4. Hymenophore on ground	5
5. Hymenophore more or less minutely papillate or hydnoid	6
5. Hymenophore smooth	
6. Hymenophore white	
6. Hymenophore pale orange to reddish	T. papillosa
7. Hymenophore light brown to reddish brown when fresh	
7. Hymenophore pure white, greyish yellow to beige when fresh	
8. Inflated hyphae absent in subiculum, basidia with two sterigmata	T. havencampii
8. Inflated hyphae present in subiculum, basidia with four sterigmata	
9. Subicular hyphae 3.5–8 µm in diam	T. foetidus
9. Subicular hyphae inflated to 6–23 µm in diam	T. robusta
10. Hymenia with cystidial structures	
10. Hymenia without cystidial structures	
11. Cystidia clavate	T. minispora
11. Cystidia lanceolate, narrowly utriform or capitate	
12. Basidiospores subglobose, Q = 1.06	T. caulocystidiatus
12. Basidiospores ellipsoid, Q = 1.29	T. gelatinosa
13. Inflated hyphae present in subiculum	14
13. Inflated hyphae absent in subiculum	16
14. Branches U-shaped, cream to buff turning yellowish brown towards the ap	exT. longiramosa
14. Branches V-shaped, pale greyish yellow to beige	
15. Basidiomes pale yellow when dry	T. copiosa
15. Basidiomes reddish brown when dry	T. dealbata
16. Hymenia unilateral	T. chartacea
16. Hymenia amphigenous	T. pallescens

# Trechispora B (Basidiomes resupinate, on wood, hymenophore poroid)

1. Hyphal system dimitic	2
1. Hyphal system monomitic	3
2. Basidiospores ventrally concave	T. brasiliensis
2. Basidiospores ventrally convex	T. dimitiella
3. Basidiospores subglobose to subangular, sparsely verrucose	T. polygonospora
3. Basidiospores subglobose to broadly ellipsoidal, densely aculeate	4
4. Cystidial structures present	T. regularis
4. Cystidial structures absent	5
5. Basidiospores including spines $> 6 \mu m \log$	T. clancularis
5. Basidiospores including spines < 6 µm long	6
6. Subicular hyphae slightly thick-walled, up to 3 µm wide	7
6. Subicular hyphae thin-walled, up to 6 µm wide	8
7. Ampullate septa present on subicular hyphae	T. mollusca
7. Ampullate septa absent on subicular hyphae	
8. Crystals in subiculum as numerous rodlets	T. candidissima
8. Crystals in subiculum as rhomboidal plates or various shapes	9
9. Sphaerocysts present in cords and the adjacent part of subiculum	T. hymenocystis
9. Sphaerocysts absent	
10. Basidiospores $< 3.8 \ \mu m \log$ , $< 3 \ \mu m wide$	T. hondurensis
10. Basidiospores > 3.8 $\mu$ m long, > 3 $\mu$ m wide	T. subhymenocystis

Trechispora C (Basidiomes resupinate, on wood, hymenophore non-poroid)	
1 Basidiospores smooth	

-	•	1	,	 1	1	<i>,</i>
1. Basidiospor	res smooth			 		2
1						

2. Hyphal system dimitic	
2. Hyphal system monomitic	
3. Hymenophore hydnoid	
3. Hymenophore smooth	
4. Hymenophore hydnoid.	
4. Hymenophore smooth to farinaceous	
5. Basidiospores subglobose, angular to turbinate	
5. Basidiospores ellipsoid to lacrymoid	8
6. Hymenophore pellicular, smooth	T. mellina
6. Hymenophore more or less adnate, farinaceous	
7. Basidiospores turbinate	
7. Hymenophore subglobose	v
8. Crystals bipyramid, aggregate	-
8. Crystals differently shaped	
9. Basidiospores > 4 µm long	
9. Basidiospores $< 4 \mu m \log$	
10. Crystals as rodlets with incised ends	
10. Crystals otherwise	
11. Basidiospores thick-walled	<i>v</i>
11. Basidiospores thin-walled	
12. Hyphal system dimitic	
12. Hyphal system monomitic	
13. Thick-walled conidia present	
13. Thick-walled conidia absent	
14. Conidia rugose	
14. Conidia smooth	
15 Crystalling anhars sovered by numerous needle like grystals present	T 1 · · · 11 ·
15. Crystalline sphere covered by numerous needle-like crystals present	
15. Crystalline sphere covered by numerous needle-like crystals absent	
<ul><li>15. Crystalline sphere covered by numerous needle-like crystals absent</li><li>16. Subicular crystals acicular</li></ul>	16 <i>T. dimitica</i>
<ul><li>15. Crystalline sphere covered by numerous needle-like crystals absent</li><li>16. Subicular crystals acicular</li><li>16. Subicular crystals differently shaped</li></ul>	16 T. dimitica T. minuta
<ol> <li>Crystalline sphere covered by numerous needle-like crystals absent</li> <li>Subicular crystals acicular</li> <li>Subicular crystals differently shaped</li> <li>Basidiomes reflexed</li> </ol>	16 T. dimitica T. minuta T. fastidiosa
<ol> <li>Crystalline sphere covered by numerous needle-like crystals absent</li> <li>Subicular crystals acicular</li> <li>Subicular crystals differently shaped</li> <li>Basidiomes reflexed</li> <li>Basidiomes not reflexed</li> </ol>	
<ul> <li>15. Crystalline sphere covered by numerous needle-like crystals absent</li> <li>16. Subicular crystals acicular</li> <li>16. Subicular crystals differently shaped</li> <li>17. Basidiomes reflexed</li> <li>17. Basidiomes not reflexed</li> <li>18. Basidiomes &lt; 50 μm thick</li> </ul>	
<ul> <li>15. Crystalline sphere covered by numerous needle-like crystals absent</li></ul>	
<ul> <li>15. Crystalline sphere covered by numerous needle-like crystals absent</li></ul>	
<ol> <li>Crystalline sphere covered by numerous needle-like crystals absent</li></ol>	
<ul> <li>15. Crystalline sphere covered by numerous needle-like crystals absent</li></ul>	
<ul> <li>15. Crystalline sphere covered by numerous needle-like crystals absent</li></ul>	
15. Crystalline sphere covered by numerous needle-like crystals absent 16. Subicular crystals acicular 17. Basidiomes reflexed 17. Basidiomes not reflexed 18. Basidiomes < 50 $\mu$ m thick 18. Basidiomes > 50 $\mu$ m thick 19. Hymenophore smooth 19. Hymenophore non-smooth 20. Basidia with two sterigmata 21. Basidiospores > 4.5 $\mu$ m long, > 3.5 $\mu$ m wide	
<ul> <li>15. Crystalline sphere covered by numerous needle-like crystals absent</li></ul>	
<ul> <li>15. Crystalline sphere covered by numerous needle-like crystals absent</li></ul>	
15. Crystalline sphere covered by numerous needle-like crystals absent 16. Subicular crystals acicular 17. Basidiomes reflexed 17. Basidiomes not reflexed 18. Basidiomes < 50 $\mu$ m thick 18. Basidiomes > 50 $\mu$ m thick 19. Hymenophore smooth 19. Hymenophore non-smooth 20. Basidia with two sterigmata 20. Basidia with four sterigmata 21. Basidiospores > 4.5 $\mu$ m long, > 3.5 $\mu$ m wide 22. Basidiospores ventrally concave 22. Basidiospores ventrally straight or convex	
15. Crystalline sphere covered by numerous needle-like crystals absent.16. Subicular crystals acicular.17. Basidiomes reflexed.17. Basidiomes not reflexed.18. Basidiomes < 50 μm thick.	16 
15. Crystalline sphere covered by numerous needle-like crystals absent.16. Subicular crystals acicular.16. Subicular crystals differently shaped.17. Basidiomes reflexed.17. Basidiomes not reflexed.18. Basidiomes < 50 µm thick.	16 
15. Crystalline sphere covered by numerous needle-like crystals absent.16. Subicular crystals acicular.16. Subicular crystals differently shaped.17. Basidiomes reflexed.17. Basidiomes not reflexed.18. Basidiomes < 50 µm thick.	16 
15. Crystalline sphere covered by numerous needle-like crystals absent.16. Subicular crystals acicular.17. Basidiomes reflexed.17. Basidiomes not reflexed.18. Basidiomes < 50 μm thick.	16 
15. Crystalline sphere covered by numerous needle-like crystals absent.16. Subicular crystals acicular.17. Basidiomes reflexed.17. Basidiomes not reflexed.18. Basidiomes < 50 µm thick.	16 
15. Crystalline sphere covered by numerous needle-like crystals absent.16. Subicular crystals acicular.16. Subicular crystals differently shaped.17. Basidiomes reflexed.17. Basidiomes not reflexed.18. Basidiomes < 50 µm thick.	16 
15. Crystalline sphere covered by numerous needle-like crystals absent16. Subicular crystals acicular	16 
15. Crystalline sphere covered by numerous needle-like crystals absent16. Subicular crystals acicular	16 
15. Crystalline sphere covered by numerous needle-like crystals absent16. Subicular crystals acicular	16 

27. Basidiospores in shape regular	
28. Basidiospores sparsely ornamented	
28. Basidiospores densely ornamented	
29. Basidiospores turbinate, verrucose	T. subsphaerospora
29. Basidiospores ellipsoid, aculeate	T. stellulata
30. Subicular generative hyphae thick-walled	T. latehypha
30. Subicular generative hyphae thin-walled	
31. Basidiospores verrucose	T. larssonii
31. Basidiospores aculeate	
32. Crystals abundant in subhymenium	T. cyatheae
32. Crystals occasionally present or absent in subhymenium	
33. Crystals as single or aggregated rodlets with incised ends	
33. Crystals as aggregate rhomboidal flakes	
34. Basidia < 5 µm wide, basidiospores subglobose to broadly ellipsoid	
34. Basidia $> 5 \mu m$ wide, basidiospores ellipsoid	
35. Hymenophore colliculose or grandinioid	
35. Hymenophore odontioid to hydnoid	
36. Hymenophore yellowish to ochraceous; conidia present	
36. Hymenophore white to cream; conidia absent	
37. Basidiospores verrucose, ventrally straight or convex	
37. Basidiospores aculeate, ventrally concave	
38. On bamboo	
38. Not on bamboo	
39. Basidiospores mostly < 2.8 μm wide	
39. Basidiospores mostly > 2.8 $\mu$ m wide	
40. Basidiospores ventrally concave	
40. Basidiospores ventrally straight or convex	
41. Basidiospores globose to subglobose	
41. Basidiospores ellipsoid to broadly ellipsoid	
42. Basidiospores verrucose	
42. Basidiospores aculeate	2
43. Crystals butterfly-shaped in subiculum	
43. Crystals as prisms to rhomboidal flakes in subiculum	
44. Tramal hyphae distinctly thick-walled	
44. Tramal hyphae thin-walled or slightly thick-walled	
45. Hymenophore aculei $> 0.4$ mm long	
45. Hymenophore aculei < 0.4 mm long	
46. Margin undifferentiated	
46. Margin thinning out, fimbriate	<sup>U</sup>
47. Basidiomes irpicoid.	
47. Basidiomes typically odontioid or hydnoid	
48. Hymenophore aculei sparse, cream to buff-yellow when fresh	
48. Hymenophore aculei dense, white when fresh	
49. Basidiospores with sharp spines	
49. Basidiospores without sharp spines	
50. Basidiospores verrucose	
50. Basidiospores voltacose	
51. Basidiospores thick-walled	
51. Basidiospores thin-walled	
52. Crystals absent, basidiospores globose	
52. Crystals present, basidiospores ellipsoid to broadly ellipsoid	-
53. Arthroconidia present.	
1	

53. Arthroconidia absent	54
54. Crystals absent in trama	55
54. Crystals present in trama	
55. Basidiospores excluding spines $< 3.5 \mu$ m long, $< 3 \mu$ m wide	T. tropica
55. Basidiospores excluding spines $> 3.5 \mu$ m long, $> 3 \mu$ m wide	T. verruculosa
56. Tramal hyphae 3–6 μm wide, spines of basidiospores constricted	T. constricta
56. Tramal hyphae 2–4 µm wide, spines of basidiospores not constricted	57
57. Basidia present at the apical ends of aculei, hyphoid cystidia present	T. chaibuxiensis
57. Basidia absent at the apical ends of aculei, hyphoid cystidia absent	
58. Tramal hyphae thin-walled, spines on basidiospores $> 0.6 \mu m \log$	T. malayana
58. Tramal hyphae slightly thick-walled, spines on basidiospores $< 0.3 \ \mu m \ long$	T. nivea

### Discussion

In this study, the relationships among members of *Trechisporales* within *Agaricomycetes* are for the first time explored with the help of the most comprehensive multilocus-based phylogenetic analyses. In association with morphological characters, a new family *Sistotremastraceae* within a new order *Sistotremastrales* are introduced for *Agaricomycetes* to accommodate *Sertulicium* and *Sistotremastrum* (type genus) segregated from *Trechisporales*; a new genus *Allotrechispora* is proposed within *Hydnodontaceae*, *Trechisporales*; one new species is introduced for each of *Allotrechispora*, *Fibrodontia* and *Subulicystidium*, and 16 new species for *Trechispora* are described; seven new combinations are proposed for *Allotrechispora* and *Trechispora*; and *Boidinella*, *Litschauerella* and *Sphaerobasidium* are excluded from *Hydnodontaceae*, *Trechispora* by unnanensis from *Trechispora* with uncertain taxonomic position at these ranks. Moreover, a brief introduction to two accepted genera within *Sistotremastrales* and all 12 accepted genera within *Trechisporales*, along with keys to these 12 genera of *Trechisporales* and to all 87 species of *Trechispora* are provided. In addition, *Tomentella* P. Karst. non-Pers. ex Pat. and *Murrilloporus*, potential synonyms of *Trechispora*, are excluded from *Trechisporales* and of uncertain position, respectively.

Sistotremastrum, as the type genus of the new family Sistotremastraceae and the new order Sistotremastrales, was formerly known as the 'Sistotremastrum family' within Trechisporales, and distantly related to other genera belonging to Hydnodontaceae, the single formally named family of this order (Larsson 2007). Recently, Spirin et al. (2021) segregated an additional genus Sertulicium from Sistotremastrum, and also suggested that Sertulicium and Sistotremastrum should be independent at the family level from Hydnodontaceae. However, even if the morphological characters of Sertulicium and Sistotremastrum are distinct, the dataset of nrLSU region failed to generate a strongly supported phylogeny (Spirin et al. 2021). The current phylogenies, for the first time both sampling taxa comprehensively and employing multiloci, recover the clade of Sertulicium and Sistotremastrum as highly distinct from Hydnodontaceae at the family level and also from Trechisporales at the order level within Agaricomycetes (Figs 1-3). Although the close relationship between Sistotremastrales and Trechisporales cannot be rejected, it is assumed that all nodes in phylogenetic trees will receive strong supports when sampling enough gene regions, like the phenomena in recent phylogenomic analyses (Nagy et al. 2014, Kiss et al. 2019, Miyauchi et al. 2020, Jiang et al. 2021, Li et al. 2021). In addition, in the current phylogeny (Fig. 1), the clade being composed of five well-accepted independent orders, viz. Geastrales, Gomphales, Hysterangiales, Phallales and Stereopsidales, receives almost full statistical support (BS = 98%, BPP = 1), while *Gloeophyllales*, *Jaapiales*, *Polyporales* and *Thelephorales* also group together with strong support (BS = 86%, BPP = 1). Therefore, the phylogenetic affinity between these two orders is not the obstacle to separating them. Moreover, the divergence time of this clade also fits well within the range of all known orders in Agaricomycetes (Fig. 2). A recent whole-scale phylogenomic analysis has proved that the current fungal classification at higher ranks is basically consistent with the evolutionary divergence in Basidiomycota (Li et al. 2021). That is to say that the divergence time can be considered to be one of important supports for circumscribing fungal orders

as used here. Given above, the segregation of *Sistotremastrales* from *Trechisporales* is justified following the practice of integrated taxonomy.

Within the small family *Sistotremastraceae* and order *Sistotremastrales*, only two genera accommodating 19 species are known to date (Dhingra et al. 2014, Gruhn & Alvarado 2021, Spirin et al. 2021). Although this study does not describe new species of *Sertulicium* and *Sistotremastrum*, three unnamed single-specimen lineages are recovered in *Sistotremastrum*, viz. LWZ 20171015-32 collected from Vietnam, LWZ 20191107-25 from Yunnan, China and LWZ 20191207-26 from Malaysia (Fig. 3). This indicates that more species in *Sistotremastraceae*, *Sistotremastrales* await description. Moreover, the phylogenetic relationships among species of *Sistotremastrum* indicate that additional new genera may need to be segregated as was *Sertulicium* (Fig. 3).

Besides one new species of *Subulicystidium*, one unnamed single-specimen (LWZ 20180804-5) lineage and one unnamed double-specimen (LWZ 20170816-7 and LWZ 20190816-24a) lineage were newly revealed in this genus (Fig. 5). Following a desired taxonomic practice (Aime et al. 2021), the unnamed single-specimen new lineage is better not to be described as a new species until more related samples can be examined. Regarding the unnamed double-specimen new lineage, it was phylogenetically related to *S. perlongisporum* (Fig. 5). However, the phylogenetic identity of *S. perlongisporum* is not clear (Fig. 5; Volobuev 2016, Ordynets et al. 2018). More importantly, the condition of both specimens in this new lineage is not good enough to justly determine the morphological characters. Therefore, we leave this unnamed double-specimen new lineage open until more related samples in a good condition can be secured.

With the inclusion of 16 new species, a total of 87 species are accepted in *Trechispora*. In addition, 29 unnamed single-specimen new lineages were revealed in this genus (Fig. 6) and their taxonomic identities await to be further determined with more related samples (Aime et al. 2021). Consequently, more than one hundred species could be present in *Trechispora*. Although *Trechispora* is strongly supported as a monophyletic genus (Figs 3, 6), it is noticed that nearly one quarter of known species (21 out of 87) in *Trechispora* are not subjected to phylogenetic analyses with molecular data. Taking the segregation of *Allotrechispora* into consideration, the monophyly of *Trechispora* still needs to be tested by sampling the remaining one quarter of known species in phylogenetic analyses.

As the most species-rich genus in Trechisporales, Trechispora produces highly diverse morphological characters. The most striking character is the clavarioid basidiomes adopted by synonymizing Scytinopogon (de Meiras-Ottoni et al. 2021), which was originally put in Clavariaceae (Corner 1950, García-Sandoval et al. 2005) but later moved to Trechisporales (Jülich 1981, Birkebak et al. 2013). In addition, even for the species of Trechispora with resupinate basidiomes, their hymenophoral configurations can range from smooth, grandinioid, hydnoid to poroid. Previous study on Hymenochaetales indicated that grandinioid hymenophoral configuration represents an adaptive advantage in balancing protection and dispersal of basidiospores (Wang et al. 2021). Even though of interest, the trait evolution of basidiomes in Trechispora is not yet explored. Microscopically, as sexual reproductive cells of species in Basidiomycota (Wallen & Perlin 2018), the morphology of basidiospores is considered to be one of the most important and distinguishable taxonomic characters. In species of Trechispora, the surface of basidiospores is morphologically diverse, including contrasts between ornamented vs. not ornamented and ornamentation-verrucose vs. ornamentation-aculeate. However, the biological and ecological functions of these diverse characters in the process of sexual reproduction are unknown. Besides variation in morphology, the nutritional modes of Trechispora may be saprotrophic or biotrophic (Vanegas-León et al. 2019). The answer to how and why the nutritional modes shift from one mode to another will help to understand the evolutionary history of *Trechispora*. In the current phylogeny of Trechispora (Fig. 6), the interspecific relationships are not well resolved, and moreover the phylogenetic identity of certain species, like T. nivea and T. pallescens, is not clear. To solve the above-mentioned series of evolutionary issues in macromorphology, micromorphology and nutrition mode, a much higher resolution of phylogenetic relationships among species of Trechispora is needed. Undoubtedly, gene regions additional to ITS and nrLSU should be used to

construct an intrageneric phylogeny with reliable statistical supports. Moreover, omics analyses of certain representative species could help to elucidate the evolutionary dynamics of corresponding traits, like fungal multicellularity (Kiss et al. 2019) and symbiosis (Miyauchi et al. 2020).

In conclusion, via a wider sampling especially from Asia Pacific, careful morphological examinations and comprehensive multilocus-based phylogenetic analyses, an emended classification of *Trechisporales* within *Agaricomycetes* is constructed. This classification will help to further clarify species diversity and explore trait evolution within *Trechisporales*.

#### Supplementary material

File S1 Alignment resulted from the dataset (1). File S2 Alignment resulted from the dataset (2). File S3 Alignment resulted from the dataset (3).

File S4 Alignment resulted from the dataset (4).

File S5 Alignment resulted from the dataset (5).

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