



Article Poriella subacida Gen. & Comb Nov. for Perenniporia subacida (Peck) Donk

Rui Chen ^{1,2}, Samantha C. Karunarathna ³ and Chang-Lin Zhao ^{1,2,*}

- Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China, Ministry of Education, Southwest Forestry University, Kunming 650224, China; zongtongkai@im.ac.cn
- ² College of Biodiversity Conservation, Southwest Forestry University, Kunming 650224, China
- ³ CAS Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China; samantha@mail.kib.ac.cn
- * Correspondence: fungi@swfu.edu.cn; Tel.: +86-178-6946-2758

Abstract: *Poriella subacida* gen. & comb. nov., previously known as *Perenniporia subacida*, which causes white rot, has been documented in temperate and tropical forests. Specimens from Asia, North America, and Europe were examined, including the type specimen of *Polylorus subacidus*. Sequences of the ITS1-5.8S-ITS2 region, the 28S rDNA, the mitochondrial rDNA small subunit (mtSSU), and the gene encoding the translation elongation factor 1- α (EF1) were generated. In multigene phylogenies (maximum parsimony, maximum likelihood, Bayesian inferences), "*Perenniporia subacida*" formed a well-supported lineage, distinct from the core "*Perenniporia*" clade (type species: "*P. medulla-panis*"), and sister to the "*Yuchengia narymica*" lineage. We therefore conclude that "*P. subacida*" should be placed in the new genus "*Poriella*" gen. nov. Morphologically, "*Poriella*" is characterized by a di- to trimitic hyphal system, non-truncate basidiospores, and strongly dextrinoid, cyanophilic skeletal hyphae.

Keywords: polypore; systematics; taxonomy; white rot fungus; wood-inhabiting fungi

1. Introduction

Polyporales is one of the most intensively studied clades of fungi, being of interest to both fungal ecologists and applied scientists [1,2]. The family Polyporaceae accommodates 92 genera [3], and recently many new genera of polypores have been described, such as *Amylosporia* (B.K. Cui, C.L. Zhao & Y.C. Dai), *Crystallicutis* (El-Gharabawy and Griffith), *Hirticrusta* Matozaki (T. Hatt. and Sotome), and *Murinicarpus* (B.K. Cui and Y.C. Dai) [4–7]. The family is typified by *Polyporus* P. Micheli ex Adans. (1763) and many taxa have been separated from *Polyporus* as new genera over time [1,4,6].

Perenniporia subacida (Peck) Donk (basionym *Polyporus subacidus* Peck, 1885) is a widespread species of wood-decaying polypores with perennial, resupinate to effused-reflex basidiomes and thick-walled, non-truncate basidiospores. The species has been reported to occur in many forest ecosystems, in boreal, temperate, subtropical, and tropical regions [8–15]. This species was described by Peck (1885) as *Polyporus subacidus*, but its taxonomic position has long been debated. It has been treated in several genera, but none of these placements have been fully satisfactory [16–20]. Currently, the species is widely accepted in *Perenniporia* Murrill, which is typed by *P. medulla-panis* (Jacq.) Donk [8–13]. However, Decock and Stalpers argued for a different placement [13].

Molecular studies involving Polyporaceae, mainly based on ITS and/or nLSU sequences, have been carried out [21–27]. Further studies employing a six-gene dataset have helped to clarify the generic relationships of polyporoid fungi for 373 taxa. The latter study showed that *Perenniporia subacida* clustered in the core polyporoid clade in which it was related to *P. medulla-panis* (Jacq.) Donk [23]. Further studies of *Perenniporia* inferred



Citation: Chen, R.; Karunarathna, S.C.; Zhao, C.-L. *Poriella subacida* Gen. & Comb Nov. for *Perenniporia subacida* (Peck) Donk. *Agronomy* **2021**, *11*, 1308. https://doi.org/10.3390/ agronomy11071308

Academic Editor: Claudia Riccioni

Received: 11 May 2021 Accepted: 22 June 2021 Published: 27 June 2021

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). from nuclear ribosomal 28S and ITS sequence data revealed that *P. subacida* formed a monophyletic lineage distant from the *Perenniporia* s.s. [15,16,28].

To resolve the placement of this species, phylogenetic research was carried out employing the ITS, 28S, TEF1 and mtSSU and a comparative morphological study of the type specimen was conducted. We conclude that *Perenniporia subacida* should be treated as a distinct, new genus as described below.

2. Materials and Methods

2.1. Morphological Studies

Specimens studied are deposited at the Farlow Herbarium of Harvard University (FH), MA, USA, Beijing Forestry University (BJFC), Beijing, China and United States National Fungus Collections (BPI), New York, NY, USA. Macromorphological descriptions were on the basis of field notes and study of specimens. Color terms followed previous studies [29]. Microscopic measurements were made from slide preparations of dried specimens stained with Cotton Blue and Melzer's reagent by light microscopy [30,31]. Sections were studied using an Olympus BX40 compound microscope (Tokyo, Japan). In presenting spore size variation, 5% of measurements were excluded from each end of the range. The following abbreviations are used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB + = cyanophilous; IKI = Melzer's reagent, IKI = both non-amyloid and non-dextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = mean each spore length/width ratio, n (a/b) = number of spores (a) measured from given number of specimens (b).

2.2. Molecular Techniques and Phylogenetic Analyses

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to extract DNA from dried specimens from China and other regions, and 2xTaq PCR Mix (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to perform PCR products [30]. The primer pair ITS5 and ITS4 were amplified for the ITS region [32]. The primer pair LR0R and LR7 were for the nuclear r28S region [33]. The primer pair MS1 and MS2 were for the mitochondrial SSU region [32]. The primer pair EF1-983F and EF1-2218R were for Tef1 [34]. The PCR cycling program for ITS, mtSSU, 28S and TEF1 followed previous studies [27]. The Beijing Genomics Institute (Beijing, China) was in charge of purifying and direct sequencing of the PCR products. All sequences used in the phylogeny were downloaded from GenBank (Table 1) with references. The sequence alignment was deposited in TreeBase (submission ID 23826).

Table 1. Information of the se	quences used in this study
--------------------------------	----------------------------

Succion Norma	Comple No.	GenBank Accessions				Defense
Species Name	Sample No. –	ITS	LSU	mtSSU	TEF1	Kererences
Abortiporus biennis	TFRI 274	EU232187	EU232235			[21]
A. biennis	EL65-03	JN649325	JN649325			[21]
Abundisporus roseoalbus	Dai 12269	KC415908	KC415910	KF051037	KF181131	[5]
A. pubertatis	Cui 5776	KC787565	KC787572	KF051029	KF181129	[5]
A. sclerosetosus	MUCL 41438	FJ411101	FJ393868			[28]
A. violaceus	Ryvarden 10775	KF018126	KF018134	KF051058	KF181152	[5]
Amylocystis lapponica	KHL 11755	EU118603	EU118603			[21]
Antrodia albida	CBS 308.82	DQ491414				[35]
A. albida	FP 105979	EU232272	EU232272			[36]
A. heteromorpha	CBS 200.91	DQ491415	AY515350			[35]
A. macra	MUAF 887	EU340898				[23]
Bjerkandera adusta	NBRC 4983	AB733156	AB733333			[23]
Cinereomyces lindbladii	FBCC 177	HQ659223	HQ659223			[23]
Climacocystis borealis	KH 13318	JQ031126	JQ031126			[23]
Coriolopsis caperata	LE(BIN)-0677	AB158316	AB158316			[37]
Donkioporia expansa	MUCL 35116	FJ411104	FJ393872			[28]
Earliella scabrosa	PR1209	JN165009	JN164793			[38]

	6 I.V.	GenBank Accessions				D (
Species Name	Sample No.	ITS	LSU	mtSSU	TEF1	References
Fragiliporia fragilis	Dai 13080	KJ734260	KJ734264	KJ734268	KJ790245	[5]
F. fragilis	Dai 13559	KJ734261	KJ734265	KJ734269	KJ790246	[5]
F. fragilis	Dai 13561	KI734262	KI734266	KI734270	KI790247	[5]
Ganoderma sichuanense	Wu 1006-38	IO781858	,	IX029989	IX029976	[5]
G. sichuanense	Dai 12479	IO781864		IX029988	IX029975	[5]
G. australe	Cui 9511	IN048773	IN048792	j, ,	,,,,,,	[39]
G. sinense	Wei 5327	KF494998	KF495008		KF494976	[5]
G annlanatum	Dai 12483	KF494999	KF495009		KF494977	[5]
Gelatoporia subvermispora	BRNU 592909	FI496694	FI496706		14 17 17 17	[37]
Grammethelionsis subtronica	Cui 9041	IO845096	IO845099	KF051039	KF181133	[39]
Heterobasidion annosum	PEC 5252	KC492906	KC492906	14 00 1007	iu iorroo	[23]
Hornodermonorus latissima	Cui 6625	HO876604	IF706340	KF051040	KF181134	[20]
H martius	Cui 7992	HO876603	HO654114	KF051041	KF181135	[5]
H martine	MUCI 41677	FI411092	FI303850	KI 001041	K 101100	[28]
H martine	MUCL 41678	FI/11092	FI393860			[20]
Hudnonolumorus fimbriatus	LR 40855	IN649347	IN649347			[20]
Hunochnicium lundoniae	NI 0/1031	IX12/70/	IX124704			[23]
I entinue tiorinue	DCU02 191	JX124704	A E518607	1127050		[29]
Micronorollus	D31193-101	A1210419	AF516027	027030		[30]
violaceocinerascens	MUCL 45229	FJ411106	FJ393874			[28]
M. violaceocinerascens	Cui 8459	HQ876606	HQ654113	KF051042	KF181136	[5]
Obba rivulosa	KCTC 6892	FJ496693	FJ496710			[4]
Perenniporia hainaniana	Cui 6364	JQ861743	JQ861759	KF051044	KF181138	[5]
P. hainaniana	Cui 6365	JQ861744	JQ861760	KF051045	KF181139	[5]
P. hainaniana	Cui 6366	JQ861745	JQ861761	KF494996	KF494981	[5]
P. medulla-panis	MUCL 49581	FJ411088	FJ393876			[28]
P. medulla-panis	MUCL 43250	FJ411087	FJ393875			[28]
P. medulla-panis	Cui 3274	JN112792	JN112793	KF051043	KF181137	[5]
P. substraminea	Cui 10177	JQ001852	JQ001844	KF051046	KF181140	[5]
P. substraminea	Cui 10191	JQ001853	JQ001845	KF051047	KF181141	[5]
P. substraminea	Dai 10781	KF495007	KF495018	KF494995	KF494983	[5]
Perenniporiella chaquenia	MUCL 47647	FJ411083	FJ393855		HM467609	[28]
P. chaquenia	MUCL 47648	FJ411084	FJ393856		HM467610	[28]
P. micropora	MUCL43581	FJ411086	FJ393858		HM467608	[28]
P. neofulva	MUCL 45091	FJ411080	FJ393852		HM467599	[28]
P. pendula	MUCL 46034	FJ411082	FJ393853		HM467601	[28]
Phanerochaete chrysosporium	BKM-F-1767	HQ188436	GQ470643			[37]
Phlebia unica	KHL 11786	EU118657	EU118657			[37]
Physisporinus sanguinolentus	BRNM 699576	FJ496671	FJ496725			[37]
Piloporia sajanensis	Mannine 2733a	HQ659239	HQ659239			[37]
Podoscypha venustula	CBS 65684	JN649367	JN649367			[23]
Polyporus tuberaster	CulTENN 8976	AF516598	AJ488116			[40]
Poriella subacida	Dai 8224	HQ876605	JF713024	KF218322	KF286328	[15]
P. subacida	Cui 3643	FI613655	AY336753	KF218320	KF286326	[15]
P. subacida	Cui 10053	KF495006	KF495017	KF218321	KF286327	[15]
P. subacida	MUCL 31402	FI411103	FJ393880			[28]
P. subacida	CBS 463.50	FJ805245	, , , , , , , , , , , , , , , , , , ,			Direct
P subacida	DII 2000 125	10673136				[/11]
I. Subuciuu D. subacida	DLL 2009-123	IO672014				[±⊥] [/1]
D subasida	DLL 2009-150	IO672015				[±⊥] [/1]
P. SUDUCIUU D. cultarida	DLL 2009-104	JQ0/3013				[4] [1]
P. subacida P. subacida	Dai 8859 HHb-14877-T	FJ013636 AY089739	AY089739			Direct
P. subacida	B 37	AF218403	111007707			submission [42]

Table 1. Cont.

4 of 13

See a sine Marro	Commite No	GenBank Accessions				Deferrences
Species Name	Sample No	ITS	LSU	mtSSU	TEF1	Kererences
Postia alni	X 1400	KC595932	KC595932			[23]
P. caesia	CIEFAP 174	JX090109	JX090129			[23]
P. guttulata	KHL 11739	EU11865	EU11865			[43]
P. venata	CIEFAP 346	JX090113	JX090133			[43]
P. lactea	X 1391	KC595939	KC595939			[23]
Pyrofomes demidoffii	MUCL 41034	FJ411105	FJ393873			[28]
Sebipora aquosa	Miettinen 8680	HQ659240	HQ659240			[22]
Skeletocutis amorpha	Miettinen 11038	FN907913	FN907913			[37]
Stereum hirsutum	NBRC 6520	AB733150	AB733325			[23]
Trametes elegans	FP105679	JN048766	JN048785			[15]
T. hirsuta	Cui 7784	JN048768	JN048787			[15]
T. hirsuta	RLG5133T	JN164854	JN164801	AF042154	JN164891	[38]
T. pubescens	PRM 900586	AY684173	AY855906			[37]
Truncospora ochroleuca	Dai 11486	HQ654105	JF706349	KF051048	KF181142	[5]
T. ochroleuca	MUCL 39726	FJ411098	FJ393865			[28]
T. ochroleuca	Cui 5671	JX941584	JX941602	KF218309	KF286315	[5]
T. ochroleuca	Cui 5673	JX941585	JX941603	KF218308	KF286314	[5]
T. ornata	Cui 5714	HQ654103	HQ654116	KF051056	KF181150	[5]
T. ohiensis	MUCL 41036	FJ411096	FJ393863			[28]
Tyromyces chioneus	Cui 10225	KF698745	KF698756			[5]
T. kmetii	Penttila 13474	KF705040	KF705041			[5]
Vanderbylia delavayi	Dai 6891	JQ861738	KF495019	KF218287	KF286293	[5]
V. fraxinea	DP 83	AM269789	AM269853			[28]
V. fraxinea	Cui 7154	HQ654095	HQ654110	KF218288	KF286294	[5]
V. fraxinea	Cui 8885	HQ876611	JF706344	KF218289	KF286295	[5]
V. fraxinea	Cui 8871	JF706329	JF706345	KF051050	KF181144	[5]
V. robiniophila	Cui 5644	HQ876609	JF706342	KF051051	KF181145	[5]
V. vicina	MUCL 44779	FJ411095	AF518666			[28]
Yuchengia narymica	Dai 7050	JN048776	JN048795	KF051053	KF181147	[39]
Y. narymica	Dai 10510	HQ654101	JF706346	KF051054	KF181148	[39]
Y. narymica	Dai 6998	JN048775	JN048794	KF051055	KF181149	[5]
Y. narymica	0709/42	JN641258	JN641265			[39]
Y. narymica	0709/157	JN641259	JN641266			[39]
Y. narymica	0809/3	JN641261	JN641268	KF051049	KF181143	[39]

Table 1. Cont.

A previous study [30] was followed for maximum parsimony analysis. The combined multiple genes dataset was analyzed under heuristic search and 1000 homogeneity replicates, giving a P value of 1.000, which is much greater than the 0.01 used in PAUP* version 4.0b10, which means there is no discrepancy among the four loci in reconstructing phylogenetic trees. Trees were constructed in PAUP* version 4.0b10 [44]. All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 bootstraps. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates [45]. DNA sequence data was also analyzed using Maximum Likelihood (ML) with RAxML-HPC2 on Abe through the Cipres Science Gateway [46], with default settings except that branch support was obtained with 1000 rapid bootstrap replicates.

Mr Modeltest 2.3 was used to estimate the best-fit evolution model for each data set for Bayesian inference (BI). The best fit models were general time reversible (GTR)+G for ITS, and general time reversible (GTR)+I+G for nr28S, mtSSU, the exons of Tef1, and the combined dataset. The partitioned mixed model, which allows for model parameters to be estimated separately for each genetic marker, was used in the Bayesian analysis. BI was performed using MrBayes 3.1.2 [47–49]. Two runs of four Markov chains were run from random starting trees for two datasets: (ITS+28S) dataset for 5 million generations and (ITS+28S+mtSSU+Tef1) dataset for 10 million generations. Trees were sampled every 100 generations. The first quarter of the generations was by default discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (ML-BS), maximum parsimony (MP-BT), and Bayesian posterior probabilities (BPP) greater than or equal to 75% (ML-BS and MP-BS) and 0.95 (BPP) were considered significantly supported.

3. Results

3.1. Molecular Phylogeny

The ITS+28S dataset included sequences from 63 fungal specimens representing 56 taxa. The dataset had an aligned length of 2112 characters, of which 1216 characters are constant, 256 are variable and parsimony-uninformative, and 640 are parsimony-informative. Maximum parsimony analysis yielded 12 equally parsimonious trees (TL = 4377, CI = 0.337, HI = 0.664, RI = 0.525, RC = 0.177). The best model for the ITS+28S dataset estimated and applied in the Bayesian analysis is general time reversible (GTR)+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to the MP analysis, with an average standard deviation of split frequencies = 0.005569 (BI).

The phylogeny (Figure 1) inferred from ITS+28S sequences resolves seven major clades for 56 species of the Polyporales. Collections of *Perenniporia subacida* formed a lineage distinct from the *Perenniporia* s.s. lineage, within the core polyporoid clade. The *P. subacida* lineage is closely related to the *Yuchengia* lineage based on *Y. narymica* (Pilát) (B.K. Cui, C.L. Zhao, and Steffen) with good support (100% BS, 100% BP, 1.00 BPP).

The four gene (ITS+28S+mtSSU+*Tef1*) sequence dataset did not show any conflicts in tree topology for the reciprocal bootstrap trees, which allowed us to combine them. The combined dataset included sequences from 61 specimens representing 29 species. The dataset had an aligned length of 3515 characters, of which 2489 characters are constant, 219 are variable and parsimony-uninformative, and 807 are parsimony-informative. Maximum parsimony analysis yielded 10 equally parsimonious trees (TL = 3075, CI = 0.498, HI = 0.502, RI = 0.747, RC = 0.372). Best model for the combined ITS+28S+mtSSU+*Tef1* estimated and applied in the Bayesian analysis: general time reversible (GTR)+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analyses resulted in a topology similar to the MP analysis, with an average standard deviation of split frequencies = 0.003420.

A further phylogeny (Figure 2) inferred from the combined ITS+28S+mtSSU+*Tef1* sequences was obtained for ten genera in *Perenniporia* s.l. and demonstrated that this taxon formed a clade together with *Y. narymica*, with strong support (100% BS, 100% BP, 1.00 BPP). The clade is distinct from *P. medulla-panis* (Jacq.) We, along with Donk, conclude that it belongs to a distinct, new genus, hereafter called *Poriella*.

3.2. Taxonomy

Poriella C.L. Zhao, gen. nov.

MycoBank: 840061.

It is characterized by producing resupinate to effused-reflex basidiomata with dingyyellowish to pale tan to ochraceous surface and a di-trimitic hyphal system with unbranched and strongly dextrinoid skeletal hyphae, and thick-walled, non-dextrinoid, cyanophilous basidiospores.

Type species: Poriella subacida (Peck) C.L. Zhao.

Etymology: *Poriella* (Lat.): referring to its similar appearance to the genus *Perenniporia*. Basidiomata perennial, resupinate to effused-reflex. Pore surface is dingy-yellowish to pale tan to ochraceous. Pores round to angular. Subiculum cream to buff, thin. Tubes concolorous with pore surface, corky. Hyphal system di-trimitic, generative hyphae hyaline, thin-walled, with clamp connections; skeletal hyphae predominant, unbranched, strongly dextrinoid, cyanophilous, rarely dissolving in KOH. Basidiospores ellipsoid, non-truncate, hyaline, thick-walled, smooth, non-dextrinoid, CB+.

Poriella subacida (Peck) C.L. Zhao, comb. nov. Figures 3 and 4. MycoBank: 840062.

- Basionym: Polyporus subacidus Peck, Ann. Rep. N.Y. St. Mus. nat. Hist. 38: 92, 1885.
- =Poria subacida (Peck) Sacc., Syll. fung. (Abellini) 6: 325 (1888).

=Chaetoporus subacidus (Peck) Bondartsev & Singer, Annls mycol. 39(1): 51 (1941).

- =Oxyporus subacidus (Peck) Komarova, Mycoth. Eston. 3: 13 (1961).
- *=Perenniporia subacida* (Peck) Donk, Persoonia 5(1): 76 (1967).

=Poria colorea Overh. & Englerth, Bull. Yale Univ. School For. 50: 21 (1942).

=Poria fuscomarginata Berk. ex Cooke, Grevillea 15(no. 73): 24 (1886).

=Poria subaurantia Berk. ex Cooke, Grevillea 15(no. 73): 27 (1886).



Figure 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Poriella subacida* and related species in Polyporales based on ITS+28S sequences. Branches are labeled with maximum likelihood bootstrap higher than 70%, parsimony bootstrap proportions higher than 50% and Bayesian posterior probabilities more than 0.95, respectively. Clade names [23].



Figure 2. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Poriella subacida*, and related species in *Perenniporia* s.l. based on the combined ITS+28S+mtSSU+TEF1 sequence datasets. Branches are labeled with maximum likelihood bootstrap higher than 70%, parsimony bootstrap proportions higher than 50% and Bayesian posterior probabilities more than 0.95, respectively. Clade names follow [15].

Fruiting body: Perennial, resupinate to effused-reflex, becomes corky when dried, about 22 cm or more at the longest dimension, 15 cm or more at the widest dimension, and up to 17 mm thick at the center. Pore surface pale yellowish to dingy-yellowish when fresh, dingy-yellowish to pale tan to ochraceous when dry; pores round to angular, 4–6 per mm; dissepiments thin, entire. Subiculum thin, cream to buff, up to 1 mm thick. Tubes concolorous with pore surface, up to 16 mm thick.



Figure 3. Basidiomata of *Poriella subacida* (Holotype, BPI 844697). Scale bar = 1 cm.



Figure 4. Microscopic structures of *Poriella subacida* (Holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Cystidioles. (d) Hyphae from trama. (e) Hyphae from context. Bars: $A = 5 \mu m$; $B-E = 10 \mu m$.

Hyphal structure: Hyphal system di-trimitic; generative hyphae with clamp connections; skeletal hyphae strongly dextrinoid, CB+; dissolving in KOH.

Context: Generative hyphae infrequent, hyaline, thin-walled, 2.5–4 μ m in diameter; skeletal hyphae dominant, thick-walled with a wide lumen, unbranched, subparallel, 3–5.5 μ m in diameter; skeletal-binding hyphae hyaline, thick-walled, frequently branched, flexuous, interwoven, 1–2 μ m in diameter.

Tubes: Generative hyphae infrequent, hyaline, thin-walled, 2.5–3.5 μ m in diameter; skeletal hyphae dominant, thick-walled with a wide lumen, unbranched, subparallel, 3–4.5 μ m in diameter; skeletal-binding hyphae hyaline, thick-walled, frequently branched, flexuous, interwoven, 0.7–1.7 μ m in diameter. Cystidia absent, but fusoid cystidioles present, hyaline, thin-walled, 13–16 \times 3–4.5 μ m. Basidia barrel-shaped, with four sterigmata and a basal clamp connection, 20–22.5 \times 7–8 μ m; basidioles similar in shape to basidia, but slightly smaller.

Basidiospores: Ellipsoid, not truncate, hyaline, thick-walled, smooth, non-dextrinoid, CB+, (4.2–)4.5–6.2(–6.4) × (3.2–)3.6–4.6(–4.9) μ m, L = 5.25 μ m, W = 3.92 μ m, Q = 1.13–1.42 (*n* = 450/15).

Associated wood-rot: White.

Substrates and distribution: Mainly on conifers, but also on hardwood, causes white rot in *Abies* Mill and *Tsuga* Carr. and common on dead fallen trees in many areas. A boreal eastern species in Europe, widely distributed in forest regions of Asia and North America [8,10,11].

Additional specimen examined: CANADA, Ontario, Gull lake, on Thuja occidentalis L., July 25 1919, J.H. Faull (5088) (FH 00605379); Lake Timagami, Timagami Is., on fallen trunk of Abies balsamea (L.) Mill., September 10 1918, J.H. Faull (3365) (FH 00605372); Lake Rosseau, on Tsuga Carr., September 1902, Harper (587) (FH 00605380); Lake Rosseau, on Pinus Linn log, October 1903, S.A. Haper (832) (FH); Lake Rosseau, on fallen log of Abies balsamea (L.) Mill., 18 August 1921, J.H. Faull (6013) (FH 00605381); Humber Valley, on roots of Thuja occidentalis L., September 1914, J.H. Faull (169) (FH 00605373); Humber Valley, on dead hardwood, September 1914, J.H. Faull (156) (FH 00605375); Sudbury District, Cleland Tp., on dead coniferous wood, 15 September 1918, J.H. Faull (3502) (FH 00605377). CHINA, Fujian Province, Wuyishan Nature Reserve, on fallen angiosperm trunk, 21 October 2005, Dai 7316 (IFP); Guizhou Province, Jiangkou County, Fanjingshan Nature Reserve, on fallen angiosperm trunk, 21 August 2010, Yuan 5511 (IFP); Heilongjiang Province, Yichun, Fenglin Nature Reserve, on fallen trunk of Picea Dietr., 2 August 2011, Cui 9849, 9853 (BJFC); Yunnan Province, Baoshan, Gaoligong Mountain, on angiosperm trunk, 23 September 2007, Yuan 3850, 3854 (IFP); Zhejiang Province, Linan, Tianmushan Nature Reserve, on fallen trunk of Picea Dietr., 11 October 2005, Cui 2705 2712 (BJFC). FINLAND, Pera-Pohjanma, Pisavaara National Park, on fallen trunk of Picea Dietr., 14 September 1997, Dai 2648 (BJFC); Pisavaara National Park, on Picea Dietr., 4 November 2011, Dai 12619 (BJFC). USA, Arizona, Coronado National Forest, on conifer, 28 August 1958, Lowe (9407) (FH 00605393); Connecticut, New Haven, Sleeping Giant State Park, on fallen trunk of Betula L., 22 July 2012, Dai 12773 (BJFC); as above, on fallen trunk of Tsuga Carr., 22 July 2012, Dai 12785 (BJFC); as above, 24 July 2012, Dai 10287 (BJFC); as above, on fallen trunk of Pinus Linn, 24 July 2012, Dai 10285 (BJFC); Idaho, Bovill County, on dead fallen trunk of Pinus Linn, 2 October 1920, A.S. Rhoads (15891)(FH 00605391); Priest River, on Picea engelmanni, September 1915, J.R. Weir (9551) (FH 00605392); Priest River, on Abies grandis (Dougl ex D Don) Lindl, September 1915, J.R. Weir (8152) (FH 00605394); Kansas, Rooks County, Rockport, on underside of old log, 9 December 1893, (1315) (FH 00605389); Maine, Norcross, on fallen Populus L. log, 20 August 1940, D.H. Linder s.n. (FH 00605344), Kittery Point, on log of Quercus L., 28 July 1922, J.R. Weir (897)(FH 00605347); Linekin, on Picea Dietr., September 1899, Burt (2125B) (FH); as above, 16 August 1899, Burt 2127 (FH); Massachusetts, Norfolk County, Sharon, 28 June 1946, A.P.D.Piguet (54) (FH 00605353); Michigan, Neebish, September 1911, E.T.Harper & S.A.Harper s.n. (FH 00605383); Isle Royal, Rock Harbor, August 1904, E.T.Harper & S.A.Harper s.n. (FH 00605384); Pleasant Ridge, on fallen Tsuga Carr., 25 September 1915, P.Spaulding & J.F.Collins s.n. (FH 00605345); New York, Osceola, on Tsuga Carr., August 1885, C.H. Peck, BPI 844697 (Holotype, BPI); as above, on Picea Dietr. log, FH 0053717 (FH); Dryden, Ringwood Preserve, on old wood, 9 June 1952, W.B.Cooke & V.G.Cooke (29105) (FH 00605356); Ithaca, on Betula lutea F.Michx., nom. illeg. 21 March 1935, W.L. White (1568) (FH 00605360); Floodwood, on conifer, August 1900, Burt 2122B (FH); Floodwood, on Picea Dietr. log, 20 August 1900, 2123B (FH); Pennsylvania: Bedford County, New Paris, on fallen Quercus L., 1 September 1916, J.H. Faull (1490) (FH 00605366); Lackawanna County, Carbondale, on Tsuga Carr. log, 13 December 1898, Burt 2124C (FH); Tennessee, Knox County, Ball Camp Pike, on Pinus Linn log, 18 December 1938, L.R. Hesler (11907) (FH 00605387); Vermont: Addison County, Ripton, on hardwood log, 31 October 1896, (FH 00605346); Addison County, Ripton, on Picea Dietr., 4 November 1896, Burt 2126A (FH); Addison County, Ripton, on Picea Dietr., 31 October 1896, Burt 2126B (FH); Abby, on Tsuga Carr. log, 31 October 1896, Burt 2123A (FH); Underhill, on hardwood, 18 May 1880, Pringle (1025) (FH 00605350); as above, on dead conifer, August 1897, Burt 2121A, B, C (FH); as above, on fallen trunk of *Tsuga* Carr., September 1902, Harper 625 (FH); Dunamase, on Tsuga Carr. log, 14 September 1896, Burt 2121E (FH); Dunamase, on Tsuga Carr., October 1896, Burt 2122A (FH); Snake Mountain, January 1896, 2124A (FH); as above, September 1902, Harper 746 (FH); Washington: Marymere Falls, Olympic National Park, on Pseudotsuga taxifolia (Lamb.) Britton, WB (27590) (FH 00605395); Clallam County, Sol Duc Hot Springs, on fallen Tsuga heterophylla (Raf.) Sarg., 4 July 1920, J.R. Weir (650) (FH 00605396); as above, on fallen trunk of Picea sitchensis (Bong.) Carr., 14 July 1920, J.R. Weir (609) (FH 00605397); Wisconsin, June 21 1946, Neuman (162) (FH 00605386).

4. Discussion

The taxonomic position of this taxon has been long debated [16–20]. It was transferred to *Perenniporia* by Donk [20], and this placement has been generally accepted [8–12]. Due to a combination of characteristics (completely unbranched skeletal hyphae and ellipsoid and non-truncate basidiospores), Decock and Staplers [13] mentioned that the species did not belong to *Perenniporia*. Based on phylogenetic and morphological grounds, Robledo et al. confirmed that this taxon should be separated from *Perenniporia*, and could be recognized as a distinct genus morphologically as well [28]. Previous studies also confirmed that this species formed a clade distinct from the *P. medulla-panis* clade [5,6,28]. The present study confirms these results from previous studies and formally describes the new genus, *Poriella* with *P. subacida* as type species.

Other species of *Perenniporia* and *Poriella subacida* share the morphological features of unbranched skeletal hyphae and non-truncate basidiospores, such as *Perenniporia africana* (Ipulet and Ryvarden) in Uganda [50,51], *P. contraria* (Berk. and M.A. Curtis) Ryvarden in Cuba, and *P. ellipsospora* (Ryvarden and Gilb.) in North America [10]. A comparison of *Poriella* and related genera is presented in Table 2.

 Table 2. A comparison of Poriella subacida and related genera and species.

Conora	Hyphal	Basidiospore	Chemical Re	Deference	
System		Morphology	Skeletal Hyphae	Basidiospores	Kelefence
Perenniporia s.s.	dimitic	ellipsoid, truncate or not	dextrinoid or not, CB+	variable dextrinoid, CB+	[13]
Perenniporiopsis	trimitic	oblong-ellipsoid, truncate	dextrinoid, CB– in the context, CB+ in the trama	dextrinoid, CB+	[6]
Perenniporiella	dimitic	globose to subglobose, non-truncate	non-dextrinoid to strongly dextrinoid, slightly to distinctly cyanophilous	slightly dextrinoid, CB+	[51]
Poriella subacida Yuchengia narymica	di-trimitic dimitic	ellipsoid, non-truncate ellipsoid, non-truncate	strongly dextrinoid, CB+ amyloid, CB-	non-dextrinoid, CB+ IKI–, CB+	This study [38]

CB+ = cyanophilous, CB- = acyanophilous.

Three species have been mentioned as possible synonyms of this highly variable species. *Poria colorea* Overh. & Englerth, described from Western *Tsuga* Carr. and has generally been considered to be conspecific with *Polyporus subacidus*. *Poria fuscomarginata* Berk. ex Cooke was commented on by Murrill [52] who found the type material to be badly

preserved and scanty. He concluded that "it was suggested little." *Poria subaurantia* Berk. ex Cooke was considered a synonym of *Polyporus subacidus* by Murrill [53]. Judging by their descriptions, these fungi show a range of variation that is acceptable for *P. subacidus*.

Our molecular phylogenetic analyses revealed that the genus *Poriella* is closely related to *Yuchengia narymica* and then grouped with *Vanderbylia* based on the ITS+28S gene regions and the combined ITS+28S+mtSSU+*Tef1* sequences (Figures 1 and 2). Morphologically, two species share the same hyphal system and basidiospores. However, *Y. narymica* differs markedly from the acyanophilous, amyloid skeletal hyphae [38,53–55]. *Vanderbylia* mainly differs in its pileate basidiomata, a dimitic hyphal system with distinctly arboriform vegetative hyphae in the hymenophoral trama and obovoid basidiospores [10,56].

Poriella subacida is primarily a boreal taxon and is widely distributed in forest regions of northern Asia, North America and Europe [8,10,11]. It mainly grows on conifers, especially *Picea* Dietr., but also on *Larix* and *Pinus* Linn. In Europe, it has also been found occasionally on hardwoods like *Populus* L. and *Prunus* L. [8], and other hardwoods in North America and Asia [10,11]. The species is also present in tropical areas (e.g., in Africa) [57], but these records should be treated with caution. Ipulet and Ryvarden [50] recently described *Perenniporia africana* Ipulet and Ryvarden, from Uganda, with seemingly the same combination of characteristics, i.e., unbranched skeletal hyphae and non-truncate basidiospores [57,58]. A list of characteristics of *Poriella subacida* comb. nov. from different regions is presented in Table 3.

Table 3. A list of characteristics of Poriella subacida comb. nov. from different regions.

Specimens	Locality	Basidiospores (µm)	Average	Q	Pores/mm	Substrate
BPI 844697 (Type)	USA, NY	$(4.2-)4.4-5.7(-6.2) \times (3.1-)3.5-4.3(-4.5)$	5.2×3.9	1.35	4–5	on <i>Tsuga</i> Carr.
BPI 844698	USA, NY	$(4.7-)5-6(-6.4) \times (3.6-)3.9-4.6(-4.8)$	5.4 imes 4.1	1.36	4-5	on Tsuga Carr.
BPI 844699	USA, NY	$(4.3-)4.5-5.7(-6.2) \times (3.2-)3.6-4.4(-4.6)$	5.2×3.9	1.35	4-5	on Tsuga Carr.
BPI 885858	USA, NY	$(4.9-)5.1-6.2(-6.5) \times (3.4-)3.7-4.6(-4.8)$	5.6×4.2	1.3	4-5	on Tsuga Carr.
FH0053717	USA, NY	$(4.8-)5-5.6(-5.8) \times (3.7-)3.9-4.5(-4.7)$	5.3×4.2	1.33	4-5	on the log of Picea asperata Mast.
Hesler 11907	USA, TN	$(4.4-)4.6-5.3(-5.5) \times (3.5-)3.7-4.3(-4.6)$	4.9 imes 4	1.2	4-5	on the log of Pinus Linn
00605389	USA, KS	$(4.1-)4.5-5.1(-5.3) \times (3-)3.4-4.5(-4.8)$	4.8 imes 3.8	1.3	4-6	on underside of old log
Lowe 9407	USA, AZ	$(4.6-)4.9-5.8(-6) \times (3.9-)4.3-4.9(-5.1)$	5.4 imes 4.5	1.2	4-6	on the log of Picea asperata Mast.
00605344	USA, ME	$(4.3-)4.6-5.2(-5.4) \times (3.4-)3.6-4.2(-4.6)$	4.9 imes 3.9	1.2	4-5	on fallen Populus L. log
00605372	Canada, Ontario	$(4.4-)4.6-5.8(-6) \times (3-)3.3-4.2(-4.5)$	5.3 imes 3.8	1.2	4-6	on fallen trunk of Abies Mill
Cui 9849	China, Heilongjiang	$(4.9-)5.2-5.7(-5.9) \times (3.9-)4.1-4.4(-4.6)$	5.4 imes 4.2	1.3	4-5	on fallen trunk of Picea Dietr.
Yuan 3854	China, Yunnan	$(5-)5.2-5.8(-6) \times (3.9-)4.1-4.4(-4.5)$	5.6×4.2	1.3	4-6	on angiosperm trunk
Cui 2712	China, Zhejiang	$(4.9-)5.1-5.7(-6) \times (3.9-)4-4.4(-4.6)$	5.4 imes 4.2	1.3	4-5	on fallen trunk of Picea Dietr.
Dai 2648	Finland, Pohjanmaa	$(4.3-)4.7-5.7(-6.1) \times (3-)3.3-3.9(-4.1)$	5.3×3.6	1.3	4-6	on fallen trunk of Picea Dietr.
Dai 12619	Finland, Pohjanmaa	$(4.5-)4.6-5.8(-6.4) \times (3.1-)3.5-4.1(-4.6)$	5.2 imes 3.8	1.3	4–5	on Picea Dietr.

Poriella subacida causes white rot of conifers and hardwoods and also butt and root rots of living conifers. Due to the cream to golden yellow mycelia felts that develop in the decayed wood, this rot is commonly called "feather rot" [10].

Author Contributions: Conceptualization, C.-L.Z. and R.C.; methodology, C.-L.Z. and R.C.; software, R.C.; validation, R.C., C.-L.Z. and S.C.K.; formal analysis, R.C.; resources, C.-L.Z.; data curation, R.C.; writing—original draft preparation, R.C.; writing—review and editing, C.-L.Z. and S.C.K.; visualization, R.C.; supervision, C.-L.Z. and S.C.K.; project administration, C.-L.Z.; funding acquisition, C.-L.Z. and S.C.K. All authors have read and agreed to the published version of the manuscript.

Funding: This research was supported by the Yunnan Fundamental Research Project (Grant No. 202001AS070043) and the High-level Talents Program of Yunnan Province (YNQR-QNRC-2018-111).

Data Availability Statement: Publicly available datasets were analyzed in this study. This data can be found here: https://www.ncbi.nlm.nih.gov/; https://www.mycobank.org/page/Simple%20 names%20search; http://purl.org/phylo/treebase, submission ID 23826; accessed on 25 June 2021.

Acknowledgments: Special thanks are conveyed to Yu-Cheng Dai (BJFU, China), Bao-Kai Cui (BJFU, China), and Donald H. Pfister (Harvard University) for allowing me to study their specimens.

Conflicts of Interest: The authors declare no conflict of interest. All the experiments undertaken in this study comply with the current laws of the People's Republic of China.

References

- 1. James, T.Y.; Stajich, J.E.; Hittinger, C.T.; Rokas, A. Toward a fully resolved fungal tree of life. *Annu. Rev. Microbiol.* **2020**, *15*, 1–46. [CrossRef] [PubMed]
- Justo, A.; Miettinen, O.; Floudas, D.; Ortiz-Santana, B.; Sjökvist, E.; Lindner, D.; Nakasone, K.; Niemelä, T.; Larsson, K.H.; Ryvarden, L.; et al. A revised family-level classification of the Polyporales (Basidiomycota). *Fungal Biol.* 2017, 121, 798–824. [CrossRef] [PubMed]
- 3. Kirk, P.M.; Cannon, P.F.; David, J.C.; Minter, D.W.; Stalpers, J.A. *Ainsworth and Bisby's Dictionary of the Fungi*, 10th ed.; CAB International Press: Wallingford, UK, 2008. [CrossRef]
- 4. Cui, B.K.; Li, H.J.; Ji, X.; Zhou, J.L.; Song, J.; Si, J.; Yang, Z.L.; Dai, Y.C. Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. *Fungal Divers.* **2019**, *97*, 137–392. [CrossRef]
- 5. El-Gharabawy, H.M.; Leal-Dutra, C.A.; Griffith, G.W. *Crystallicutis* gen. nov. (Irpicaceae, Basidiomycota), including *C. damiettensis* sp. nov., found on *Phoenix dactylifera* (date palm) trunks in the Nile Delta of Egypt. *Fungal Biol.* **2021**, *125*, 447–458. [CrossRef]
- 6. Matozaki, T.; Hattori, T.; Maekawa, N.; Nakagiri, A.; Ishikawa, N.K.; Sotome, K. *Hirticrusta* gen. nov. segregated from *Neofomitella* in Polyporaceae (Polyporales). *Mycoscience* 2020, *5*, 240–248. [CrossRef]
- Ma, X.; Zhao, C.L. Crepatura ellipsospora gen. et sp. nov. in Phanerochaetaceae (Polyporales, Basidiomycota) bearing a tuberculate hymenial surface. Mycol. Prog. 2019, 18, 785–793. [CrossRef]
- 8. Ryvarden, L.; Melo, I. Poroid fungi of Europe. Syn. Fung. 2014, 31, 1-455.
- 9. Peck, C.H. Report of the botanist. Ann. Rep. N. Y. State Mus. Nat. Hist. 1885, 38, 77–138.
- Gramss, G.R.; Gilbertson, L.; Ryvarden, L. North American Polypores. Volume 1: Abortiporus—Lindtneria. 433 S., 209 Abb. Oslo 1986. Fungiflora A/S. J. Basic Microbiol. 1987. [CrossRef]
- 11. Núñez, M.; Ryvarden, L. East Asian polypores 2. Syn. Fung. 2001, 14, 165–522.
- 12. Dai, Y.C.; Niemelä, T.; Kinnunen, J. The polypore genera *Abundisporus* and *Perenniporia* (Basidiomycota) in China, with notes on Haploporus. *Ann. Bot. Fenn.* **2002**, *39*, 169–182.
- 13. Decock, C.; Stalpers, J. Studies in *Perenniporia*: *Polyporus unitus*, *Boletus medulla-panis*, the nomenclature of *Perenniporia*, *Poria* and *Physisporus*, and a note on European *Perenniporia* with a resupinate basidiome. *Taxon* **2006**, *53*, 759–778. [CrossRef]
- 14. Dai, Y.C. Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* **2012**, *53*, 49–80. [CrossRef]
- 15. Zhao, C.L.; Cui, B.K.; Dai, Y.C. New species and phylogeny of *Perenniporia* based on morphological and molecular characters. *Fungal Divers.* **2013**, *58*, 47–60. [CrossRef]
- 16. Shen, S.; Xu, T.M.; Jason, K.; Zhao, C.L. Morphological and molecular identification of a new species of *Perenniporia* (Polyporales, Basidiomycota) in North America. *Phytotaxa* **2018**, *351*, 63–71. [CrossRef]
- 17. Saccardo, P.A. Sylloge hymenomycetum, Vol. II. Polyporeae, Hydneae, Thelephoreae, Clavarieae, Tremellineae. *Sylloge Fungorum* **1888**, *6*, 1–928.
- 18. Bondartsev, A.; Singer, R. Zur systematik der Polyporaceae. Ann. Mycol. 1941, 39, 43-65.
- 19. Parmasto, E. Eesti seente eksikaat. Mycotheca Est. 1961, 3, 51-75.
- 20. Donk, M.A. Notes on European polypores II. Persoonia 1967, 5, 47-130.
- 21. Larsson, K.H. Re-thinking the classification of corticioid fungi. Mycol. Res. 2007, 111, 1040–1063. [CrossRef]
- 22. Miettinen, O.; Larsson, K.H.; Sjökvist, E.; Larsson, K.L. Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic polypores (Polyporales, Basidiomycota). *Cladistics* **2012**, *28*, 251–270. [CrossRef]
- Binder, M.; Justo, A.; Riley, R.; Salamov, A.; López-Giráldez, F.; Sjökvist, E.; Copeland, A.; Foster, B.; Sun, H.; Larsson, E.; et al. Phylogenetic and phylogenomic overview of the Polyporales. *Mycologia* 2013, 105, 1350–1373. [CrossRef]
- 24. Dai, Y.C.; Cui, B.K.; Si, J.; He, S.H.; Hyde, K.D.; Yuan, H.S.; Lui, X.Y.; Zhou, L.W. Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. *Mycol. Prog.* **2015**, *14*, 62. [CrossRef]
- 25. Miettinen, O.; Spirin, V.; Vlasák, J.; Rivoire, B.; Stenroos, S.; Hibbett, D. Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). *MycoKeys* **2016**, *17*, 1–46. [CrossRef]
- 26. Zhou, M.; Dai, Y.C.; Vlasák, J.; Yuan, Y. Molecular phylogeny and global diversity of the genus *Haploporus* (Polyporales, Basidiomycota). *J. Fungi* **2021**, *7*, 96. [CrossRef] [PubMed]
- 27. Liu, Z.B.; Zhou, M.; Yuan, Y.; Dai, Y.C. Global diversity and taxonomy of *Sidera* (Hymenochaetales, Basidiomycota): Four new species and keys to species of the genus. *J. Fungi.* **2021**, *7*, 251. [CrossRef]
- 28. Robledo, G.L.; Amalfi, M.; Castillo, G.; Rajchenberg, M.; Decock, C. *Perenniporiella chaquenia* sp. nov. and further notes on *Perenniporiella* and its relationships with *Perenniporia* (Poriales, Basidiomycota). *Mycologia* **2009**, 101, 657–673. [CrossRef]
- 29. Petersen, J.H. Farvekort: The Danish Mycological Society's Colour Chart; Foreningen til Svampekundskabens Fremme: Greve, Denmark, 1996.
- 30. Zhao, C.L.; Wu, Z.Q. *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Mycol Prog.* **2017**, *16*, 93–100. [CrossRef]
- 31. Huang, R.X.; Zhao, C.L. Three new species of *Phlebia* (Polyporales, Basidiomycota) based on the evidence from morphology and DNA sequence data. *Mycol. Prog.* **2020**, *19*, 753–767. [CrossRef]
- 32. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In *PCR Protocols: A Guide to Methods and Applications;* Innis, M.A., Gelfand, D.H., Sninsky, J.J., White, T.J., Eds.; Academic Press: San Diego, CA, USA, 1990; pp. 315–322.

- 33. Lutzoni Lab. Available online: http://lutzonilab.org (accessed on 4 June 2021).
- 34. Rehner, S.A.; Buckley, E.A. Beauveria phylogeny inferred from nuclear ITS and EF1-alpha sequences: Evidence for cryptic diversification and links to Cordyceps teleomorphs. *Mycologia* **2005**, *97*, 84–98. [PubMed]
- Kim, K.M.; Lee, J.S.; Jung, H.S. Fomitopsis incarnatus sp. nov. based on generic evaluation of Fomitopsis and Rhodofomes. Mycologia 2007, 99, 833–841. [CrossRef]
- 36. Vlasak, J.; Vlasa, K.J., Jr.; Cui, B.K. *Antrodia kmetii*, a new European polypore similar to *Antrodia variiformis*. *Cryptogam*. *Mycol*. **2013**, *34*, 203–209. [CrossRef]
- 37. Tomšovský, M.; Menkis, A.; Vasaitis, R. Phylogenetic relationships in European *Ceriporiopsis* species inferred from nuclear and mitochondrial ribosomal DNA sequences. *Fungal Biol.* **2010**, *114*, 350–358. [CrossRef] [PubMed]
- Justo, A.; Hibbett, D.S. Phylogenetic classification of *Trametes* (Basidiomycota, Polyporales) based on a five-marker dataset. *Taxon* 2011, 60, 1567–1583. [CrossRef]
- Zhao, C.L.; Cui, B.K.; Steffen, K.T. Yuchengia, a new polypore genus segregated from *Perenniporia* (Polyporales, Basidiomycota) based on morphological and molecular characters. *Nord. J. Bot.* 2013, *31*, 331–338. [CrossRef]
- Sotome, K.; Hattori, T.; Ota, Y.; Toanun, C.; Salleh, B.; Kakishima, M. Phylogenetic relationships of *Polyporus* and morphologically allied genera. *Mycologia* 2008, 100, 603–615. [CrossRef]
- 41. Brazee, N.J.; Lindner, D.L.; Fraver, S.; D'Amato, A.W.; Milo, A.M. Wood-inhabiting, polyporoid fungi in aspen-dominated forests managed for biomass in the U.S. Lake States. *Fungal Ecol.* **2012**, *5*, 600–609. [CrossRef]
- 42. Tabata, M.; Harrington, T.C.; Chen, W.; Abe, Y. Molecular phylogeny of species in the genera *Amylostereum* and *Echinodontium*. *Mycoscience* **2000**, *41*, 585–593. [CrossRef]
- 43. Pildain, M.B.; Rajchenberg, M. The phylogenetic position of *Postia* s.l. (Polyporales, Basidiomycota) from Patagonia, Argentina. *Mycologia* **2013**, 105, 357–367. [CrossRef]
- 44. Swofford, D.L. PAUP*: Phylogenetic Analysis Using Parsimony (*and Other Methods). Version 4.0b10; Sinauer Associates: Sunderland, MA, USA, 2002.
- 45. Felsenstein, J. Confidence intervals on phylogenetics: An approach using bootstrap. *Evolution* **1985**, *39*, 783–791. [CrossRef] [PubMed]
- Miller, M.A.; Holder, M.T.; Vos, R.; Midford, P.E.; Liebowitz, T.; Chan, L.; Hoover, P.; Warnow, T. The CIPRES Portals. (Archived by WebCite(r)). 4 August 2009. Available online: http://www.phylo.org/sub_sections/portal; http://www.webcitation.org/ 5imQlJeQa (accessed on 4 June 2021).
- 47. Posada, D.; Crandall, K.A. Modeltest: Testing the model of DNA substitution. Bioinformatics 1998, 14, 817-818. [CrossRef]
- 48. Nylander, J.A.A. *MrModeltest v2. Program Distributed by the Author. Evolutionary Biology Centre;* Uppsala University: Uppsala, Sweeden, 2004.
- 49. Ronquist, F.; Huelsenbeck, J.P. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 2003, 19, 1572–1574. [CrossRef] [PubMed]
- 50. Ipulet, P.; Ryvarden, L. New and interesting polypores from Uganda. Syn. Fung. 2005, 20, 87–99.
- 51. Decock, C.; Ryvarden, L. *Perenniporiella* gen. nov. segregated from *Perenniporia*, including key to neotropical *Perenniporia* species with pileate basidiomes. *Mycol. Res.* **2003**, *107*, 93–103. [CrossRef]
- 52. Murrill, W.A. Some described species of Poria. Mycologia 1919, 11, 231–244. [CrossRef]
- 53. Murrill, W.A. Light-colored resupinate polypores II. Mycologia 1920, 12, 299–308.
- 54. Pilát, A. Additamenta ad floram Sibiriae Asiaeque orientalis mycologicam. Pars Tertia. Bull. Soc. Mycolog. 1936, 51, 351–426.
- 55. Pouzar, Z. Notes on four European polypores. Česká Mykol. 1984, 38, 203–204.
- 56. Decock, C.; Ryvarden, L. Studies in neotropical polypores. Some coloured resupinate *Perenniporia* species. *Mycol. Res.* **1999**, *103*, 1138–1144. [CrossRef]
- 57. Ryvarden, L.; Johansen, I. A Preliminary Polypore Flora of East Africa; Fungiflora: Oslo, Norway, 1980.
- 58. Ryvarden, L. Genera of polypores: Nomenclature and taxonomy. Syn. Fung. 1991, 5, 1–363.