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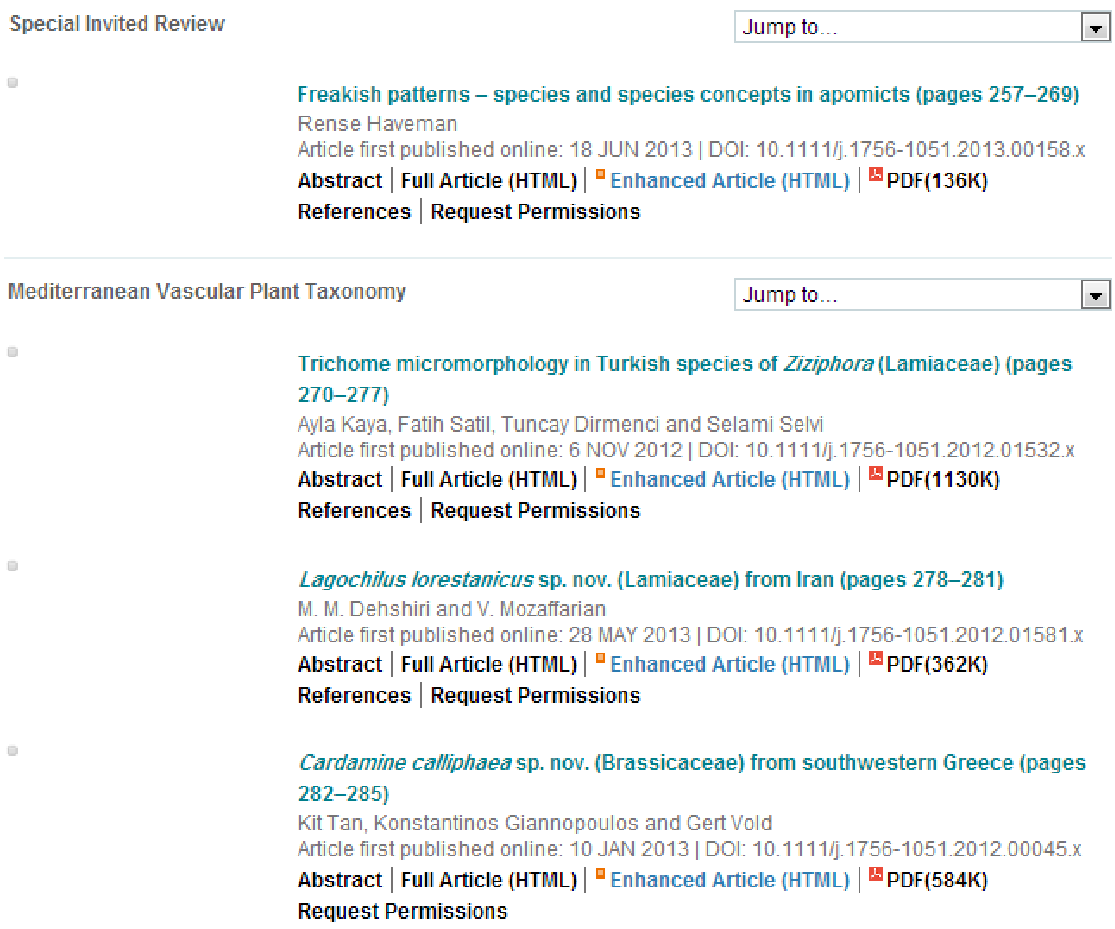

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Article first published online: 25 JAN 2013 | DOI: 10.1111/j.1756-1051.2012.01619.x

Abstract | **Full Article (HTML)** | Enhanced Article (HTML) | **PDF(410K)**
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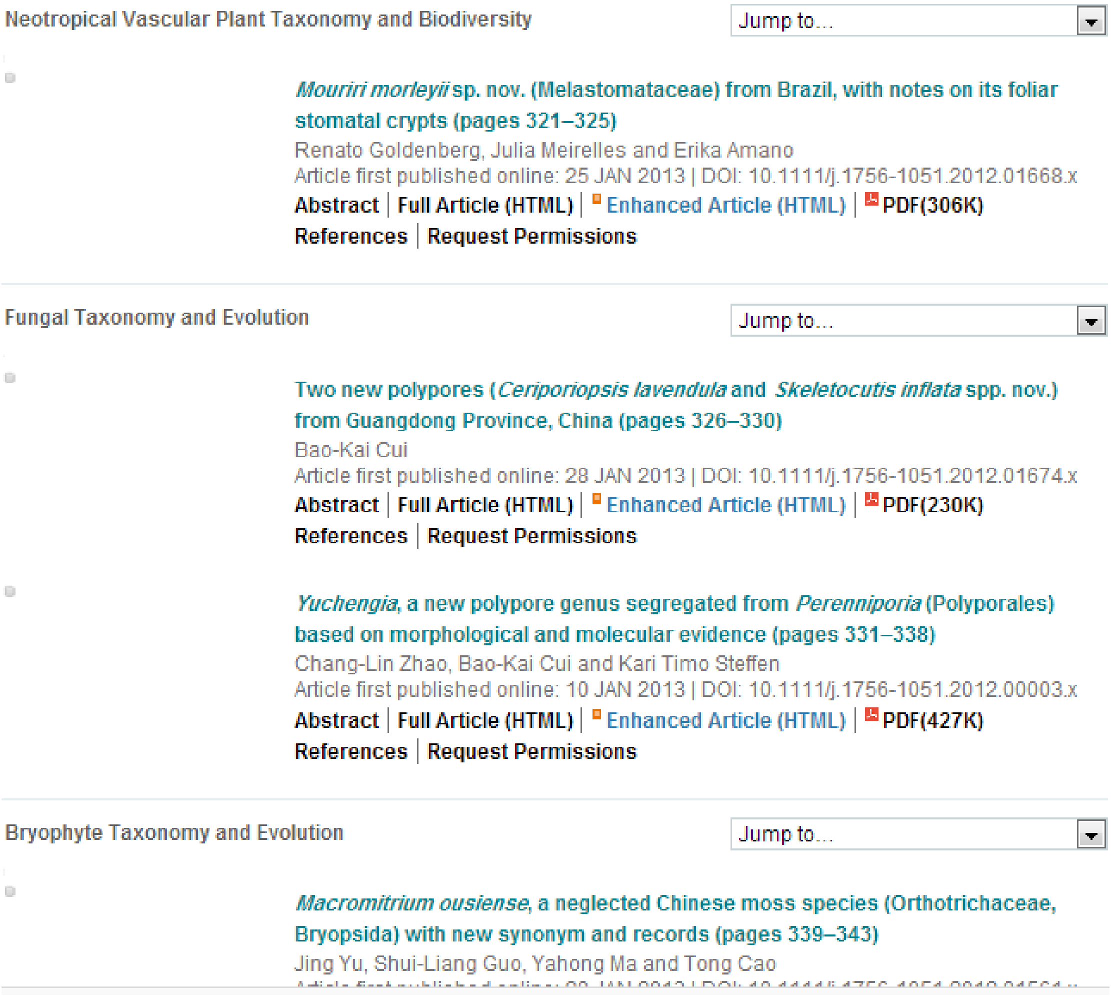

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Article first published online: 10 JAN 2013 | DOI: 10.1111/j.1756-1051.2012.00003.x
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Rense Haveman

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Mating system variation in *Veronica* (Plantaginaceae): inferences from pollen/ovule ratios and other reproductive traits (pages 372–384)

Nordic Journal of Botany 31: 331–338, 2013
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Yuchengia, a new polypore genus segregated from *Perenniporia* (Polyporales) based on morphological and molecular evidence

Chang-Lin Zhao, Bao-Kai Cui and Kari Timo Steffen

C.-L. Zhao and B.-K. Cui (baokaicui@yahoo.com.cn), Inst. of Microbiology, PO Box 61, Beijing Forestry Univ., CN-100083 Beijing, China. – K. T. Steffen, Dept of Food and Environmental Sciences, Univ. of Helsinki, FI-00014 Helsinki, Finland.

Yuchengia gen. nov. is proposed to accommodate *Perenniporia narymica*. It represents a monophyletic lineage within the core polyporoid clade based on sequences of the rDNA ITS and nLSU regions, and it is distinct from *Perenniporia* s.s. *Yuchengia* shares some characters with *Perenniporia*, both having thick-walled and cyanophilous basidiospores, but differs by having acyanophilous and amyloid skeletal hyphae dissolving in KOH, and non-dextrinoid basidiospores.

Perenniporia Murrill is a large, cosmopolitan genus. Species in this genus usually have dextrinoid and cyanophilous skeletal hyphae, and ellipsoid to distinctly truncate basidiospores which usually are thick-walled, cyanophilous and variably dextrinoid (Dai et al. 2002, Decock and Stalpers 2006). During a revision of the taxonomy and analyzing the phylogenetic relationships of species of *Perenniporia* from different areas, we reconsidered the placement of *Perenniporia narymica* (Pilát) Pouzar. This species is characterized by acyanophilous and amyloid skeletal hyphae that dissolve in KOH, and non-dextrinoid basidiospores. Both characters distinguish *Perenniporia narymica* from *Perenniporia*. Furthermore, phylogenetic inference based on LSU-ITS shows this species to be only distantly related to *P. medulla-panis* (Jacq.) Donk. On this basis, we propose a new genus to address this species.

Material and methods

Morphological studies

Chinese voucher specimens are deposited at BJFC and IFP. The microscopic routine used in the study follows Dai (2010). Sections were studied at magnification up to 1000× using a Nikon Eclipse E 80i microscope and phase contrast illumination. Drawings were made with the aid of a drawing tube. Microscopic features, measurements and drawings were made from slide preparations stained with Cotton Blue and Melzer's reagent. Spores were measured from sections cut from the tubes. In presenting spore size variation, 5% of measurements were excluded from each end of the range, and are given in parentheses. In the text the following abbreviations are used: IKI = Melzer's reagent, IKI– = negative in Melzer's reagent, KOH = 5% potassium hydroxide, CB = Cotton Blue, CB+ = cyanophilous, CB– = acyanophilous, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between studied specimens, n = number of measured spores from a given number of specimens. Special color terms are from Petersen (1996).

Molecular procedures and phylogenetic analyses

Phire Plant Direct PCR Kit (Finnzymes) procedure was used to extract total genomic DNA from the fruit bodies and for the polymerase chain reaction (PCR), and PCR amplification was confirmed on 1% agarose electrophoresis gels stained with ethidium bromide (Stöger et al. 2006). The internal transcribed spacer (ITS) regions were amplified with the primers ITS4 and ITS5 (White et al. 1990) and the large subunit (nLSU) with the primers LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). DNA sequencing was performed at Beijing Genomics Institute. All newly generated sequences have been submitted to GenBank and are listed in Table 1.

Sequences were aligned with BioEdit (Hall 1999) and ClustalX (Thomson et al. 1997). Alignment was manually adjusted when necessary. Sequence alignment was deposited at TreeBase (<http://purl.org/phylo/treebase>; submission ID 12005).

Maximum parsimony and Bayesian analyses were conducted for the nLSU and combined ITS + nLSU dataset. All characters were equally weighted and gaps were treated as missing data. The tree construction procedure was performed in PAUP* (Swofford 2002). Trees were inferred using the heuristic search option with TBR

Table 1. List of species, specimens and GenBank accession number of sequences. * = sequences newly generated from the current study.

		GenBank no.	
Species name	Sample no.	ITS	LSU
Abundisporus fuscopurpureus	Cui 8638	JN048771	JN048790
A. pubertatis	Dai 12140	JN048772	JN048791
Antrodia alpina	RLG 6107	EU232207	EU232282
A. carbonica	FP 105585-R	EU232211	EU232285
A. xantha	TFRI 879	EU232210	EU232284
Basidioradulum radula	NH 9453	AF347105	AF347105
Bjerkandera adusta	DAOM 215869	DQ060097	AF287848
Boletopsis leucomelaena	ID 1527	DQ484064	DQ154112
Byssomerulius corium	KHL 8593	AY463389	AY586640
Ceraceomyces violascens	KHL 11169	EU118611	EU118612
Ceriporia viridans	KHL 8765	AF347109	AF347109
Ceriporiopsis aneirina	MUAF 888	EU340895	EU368503
Dacryobolus karstenii	KHL 11162	EU118624	EU118624
Diplomitoporus lindbladii	HHB 5629	AJ006682	AY333814
D. lindbladii	Dai 6414	JN641256*	JN641263*
Ganoderma australe	Cui 9511	JN048773*	JN048792*
G. lucidum	Cui 9164	JN048774*	JN048793*
Globulicium hiemale	5444b	DQ873595	DQ873595
Gloeoporus dichrous	KHL 11173	EU118627	EU118627
G. pannocinctus	FCUG 2109	AF141612	AF141612
Hyphoderma capitatum	KHL 8464	DQ677491	DQ677491
H. orphanellum	NH 12208	DQ677500	DQ677500
Hyphodermella corrugata	KHL 3663	EU118630	EU118630
Meruliopsis taxicola	Kuljok 00/75	EU118648	EU118648
Perenniporia corticola	Cui 1465	JN048759	JN048779
P. corticola	Cui 2655	HQ654093	HQ848483
P. corticola	Cui 1248	HQ848472	HQ848482
P. corticola	Dai 7330	HQ654094	HQ654108
P. detrita	MUCL 42649	FJ411099	FJ393866
P. fraxinea	DP 83	AM269789	AM269853
P. fraxinea	Cui 7154	HQ654095	HQ654110
P. fraxinea	Cui 8871	JF706329	JF706345
P. fraxinea	Cui 8885	HQ876611	JF706344
P. latissima	Cui 6625	HQ876604	JF706340
P. maackiae	Cui 8929	HQ654102	JF706338
P. maackiae	Cui 5605	JN048760	JN048780
P. martia	Cui 7992	HQ876603	HQ654114
P. martia	MUCL 41677	FJ411092	FJ393859
P. martia	MUCL 41678	FJ411093	FJ393860
P. medulla-panis	MUCL 49581	FJ411088	FJ393876
P. medulla-panis	MUCL 43250	FJ411087	FJ393875
P. medulla-panis	Dai 10780	HQ654099	JF713023
P. medulla-panis	Cui 3274	JN112792	JN112793
P. ochroleuca	Dai 11486	HQ654105	JF706349
P. ochroleuca	MUCL 39563	FJ411097	FJ393864
P. ochroleuca	MUCL 39726	FJ411098	FJ393865
P. ohiensis	MUCL 41036	FJ411096	FJ393863
P. ohiensis	Cui 5714	HQ654103	HQ654116
P. pyricola	Cui 9149	JN048762	JN048782
P. pyricola	Dai 10265	JN048761	JN048781
P. rhizomorpha	Cui 7507	HQ654107	HQ654117
P. robiniophila	Cui 5644	HQ876609	JF706342
P. robiniophila	Cui 7144	HQ876608	JF706341
P. robiniophila	Cui 9174	HQ876610	JF706343
P. subacida	Dai 8224	HQ876605	JF713024
P. subacida	Cui 3643	FJ613655	AY336753
P. subacida	MUCL 31402	FJ411103	AY333796
P. tenuis	Cui 5523	HQ848474	HQ848480
P. tephropora	Cui 6331	HQ848473	HQ848484
P. tephropora	Cui 8040	JN048763	HQ654118
P. tephropora	Cui 9029	HQ876601	JF706339
P. truncatospora	Cui 6987	JN048778	HQ654112
P. truncatospora	Dai 5125	HQ654098	HQ848481

(Continued)

Table 1. (Continued).

Species name	Sample no.	GenBank no.	
		ITS	LSU
P. vicina	MUCL 44779	FJ411095	FJ393862
Perenniporiella chaquenia	MUCL 49758	FJ411085	FJ393857
Phanerochaete sordida	KHL 12054	EU118653	EU118653
Poriodontia subvinosa	H 10493	FN907920	FN907920
Postia guttulata	KHL 11739	EU118650	EU118650
Pyrofomes albomarginatus	Cui 8838	JN048765*	JN048784*
P. albomarginatus	Cui 8844	JN048764*	JN048783*
Rickenella mellea	Lamoure 74	U66438	U66438
Trametes elegans	BCC 23751	FJ372692	FJ372714
T. elegans	Dai 10748	JN048766	JN048785
T. hirsuta	Cui 7784	JN048768	JN048787
T. ochracea	PRM 900601	AY684177	AY855908
T. suaveolens	Dai 10729	JN048770	JN048789
Trichaptum abietinum	FCUG 2581	AF141636	AF141636
Yuchengia narymica	Dai 7050	JN048776*	JN048795*
Y. narymica	Dai 10510	HQ654101	JF706346
Y. narymica	0308/21-J	JN641257*	JN641264*
Y. narymica	0709/42	JN641258*	JN641265*
Y. narymica	0709/157	JN641259*	JN641266*
Y. narymica	0808/10	JN641260*	JN641267*
Y. narymica	0809/3	JN641261*	JN641268*
Y. narymica	1009/22	JN641262*	JN641269*
Y. narymica	Dai 6998	JN048775*	JN048794*
Y. narymica	Dai 6989	JN048777*	JN048796*
Y. narymica	Dai 7016	JF706331*	JF706347*

branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all equally parsimonious trees were saved. Clade stability was assessed using a bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each generated Maximum Parsimonious Tree (MPT).

Mr Modeltest (Nylander 2004, Posada and Crandall 1998) was used to determine the best-evolution for each data set for Bayesian inference (BY). Bayesian inference was calculated with Mr Bayes with a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist and Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 3 million generations, and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum parsimony (MP) and Bayesian posterior probabilities (BPP) greater or equal than 75% (MP) and 0.95 (BPP) were considered as significantly supported.

Yuchengia B. K. Cui & K. T. Steffen gen. nov.

MycoBank no. MB 563490

Carpophorum annuum, resupinatum. Contextum cremeum vel bubalinum; facies pororum cremea vel luteola, pori angulati. Systema hypharum dimiticum, hyphae generatoriae fibulatae, hyphae skeletales amyloideae, CB−. Basidiosporae hyalinae, ellipsoideae, IKI−, CB+.

Type: *Yuchengia narymica* (Pilát) B. K. Cui, C. L. Zhao & K. T. Steffen.

Etymology

The new genus was named *Yuchengia* in honor of the Chinese mycologist, Dr Yucheng Dai.

Description

Basidiocarps annual, resupinate. Pore surface cream to yellowish buff; pores angular, dissepiments thin, entire. Subiculum cream to buff, thin. Tubes concolorous with pore surface, hard corky. Hyphal system dimitic; generative hyphae hyaline, thin-walled, rarely branched, with clamp connections; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, usually unbranched, interwoven, weakly to distinctly amyloid in Melzer's reagent, acyanophilous, dissolving in KOH. Cystidia absent, cystidioles variably present; basidia clavate, with four sterigmata and a basal clamp connection; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, not truncate, hyaline, thick-walled, smooth, IKI−, CB+.

Yuchengia narymica (Pilát) B. K. Cui, C. L. Zhao & K. T. Steffen comb. nov. (Fig. 1)

MycoBank no. MB 563491

Basionym: *Trametes narymica* Pilát, Bull. Trimest. Soc. Mycol. Fr. 51 (1936, p. 364).
Based on the same type: *Perenniporia narymica* (Pilát) Pouzar (1984, p. 204).

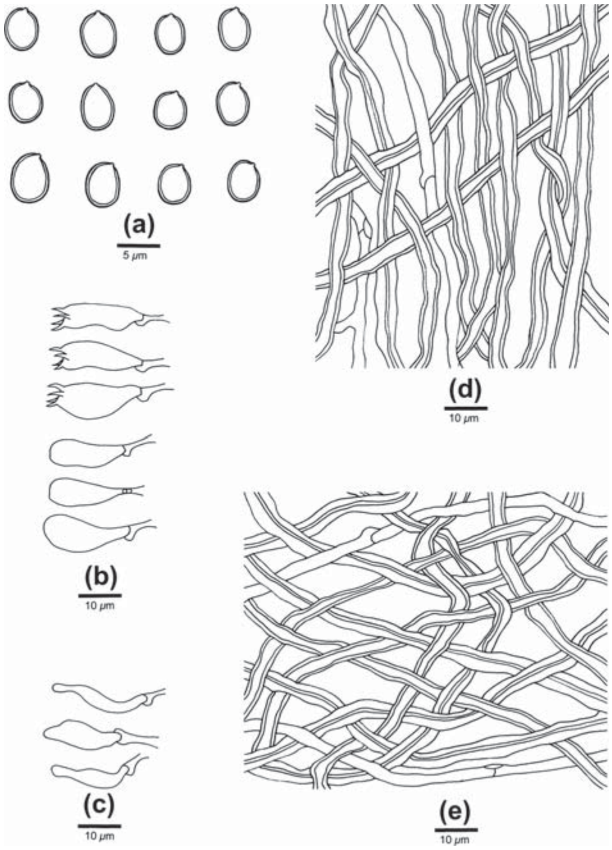

Figure 1. Microscopic structures of *Yuchengia narymica* comb. nov. (drawn from Dai 6989). (a) basidiospores, (b) basidia and basidioles, (c) cystidioles, (d) hyphae from trama, (e) hyphae from subiculum.

Description

Basidiocarps annual, resupinate, corky, without odour or taste when fresh, becoming hard corky upon drying, up to 16 cm long, 7 cm wide, 1 cm thick at center. Pore surface cream coloured when fresh, light buff to cream buff upon drying; pores angular, 4–5 per mm; dissepiments thin, entire. Sterile margin narrow, cream to cream buff, up to 1 mm wide. Subiculum cream, thin, up to 0.5 mm thick. Tubes concolorous with pore surface, hard corky, up to 9.5 mm long. Hyphal system dimitic; generative hyphae with clamp connections; skeletal hyphae weakly to distinctly amyloid in Melzer's reagent, CB−, dissolving in KOH. Generative hyphae in subiculum hyaline, thin-walled, occasionally branched, 2.3–4.0 µm in diameter; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, unbranched, interwoven, 1.9–4.8 µm in diameter. Generative hyphae in trama hyaline, thin-walled, rarely branched, 2.0–3.5 µm in diameter; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, unbranched, interwoven, 1.8–4.6 µm in diameter. Cystidia absent, fusoid cystidioles present, hyaline, thin-walled, 14.2–20.7 × 3.6–6.3 µm; basidia clavate, with four sterigmata and a basal clamp connection, 16.8–19.2 × 5.8–8.8 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, not truncate, hyaline, thick-walled, smooth, IKI−, CB+, (4.1–)4.2–5.2(–5.3) × (3.1–)3.2–4.0(–4.1) µm, L = 4.83 µm, W = 3.74 µm, Q = 1.24–1.33 (n = 120/4).

Ecology and distribution

Lignicolous, causing a white rot. Found in east Asia, North America and Europe.

Additional specimens examined

Russia. Siberia, Narym, on *Betula verrucosa*, 1933 PRM 811202 (Type in PRM). – China. Jilin Province, Antu County, Changbaishan Nature Reserve, on rotten stump of *Populus*, 27 Aug 2005 Dai 7050 (BJFC). – USA. PA, Schwenksville, swamp, creek, on *Bebula*, Vlasák 0809/3; PA, Schuyilkill canal, on hardwood, Vlasák 1009/22. – Slovakia. Uliě, Rožok NPR, on *Fagus*, Oct 1990 Vlasák 9010/32; Petrovce, country border line, on *Fagus*, Oct 1998 Vlasák 9810/12.

Molecular phylogeny

The nLSU dataset comprised 61 sequences representing 26 taxa and *Bjerkandera adusta* (Willd.) P. Karst. was chosen as the outgroup taxon for rooting purposes (Fig. 2). The dataset included 1327 characters, of which 1087 characters were constant, 79 were variable and parsimony-uninformative, and 161 were parsimony-informative. Parsimony analysis recovered 100 equally parsimonious trees (TL = 460, CI = 0.513, RI = 0.736, HI = 0.487, RC = 0.378). The Bayesian analysis resulted in average standard deviation of split frequencies = 0.008115.

The combined ITS + nLSU dataset included sequences from 73 fungal specimens representing 49 taxa and *Boletopsis leucomelaena* (Pers.) Fayod was chosen as the outgroup for rooting purposes based on data from Miettinen and Rajchenberg (2012). The dataset consists of 1626 base pairs with 676 parsimony informative positions. Parsimony analysis yielded 100 equally parsimonious trees (TL = 1,486, CI = 0.236, RI = 0.653, HI = 0.639) and a consensus tree is shown in Fig. 3. Bayesian analysis resulted in average standard deviation of split frequencies = 0.004046.

Discussion

The taxonomic position of *Yuchengia narymica* has long been debated. The species was first described as *Trametes narymica* Pilát by Pilát (1936). Later, Pouzar (1984) proposed it as *Perenniporia narymica*, and this was widely accepted (Gilbertson and Ryvarden 1987, Ryvarden and Gilbertson 1994, Núñez and Ryvarden 2001, Dai et al. 2002). Decock and Stalpers (2006) mentioned that the species does not belong to *Perenniporia*, and suggested it might belong in *Diplomitoporus* Domański because of its non-branched skeletal hyphae and thin-walled basidiospores, and maybe in *Antrodiella* Ryvarden & I. Johans. too. However, the study of the type specimen reveals that the basidiospores are distinctly thick-walled. This character would exclude both of these genera.

The specimens of *Yuchengia narymica* from different regions which were studied are listed in Table 2. *Perenniporia narymica* has an annual growth habit, resupinate basidiocarps, and a dimitic hyphal system with clamped generative hyphae. It is characterized by amyloid and acyanophilous skeletal hyphae dissolving in KOH, and thick-walled

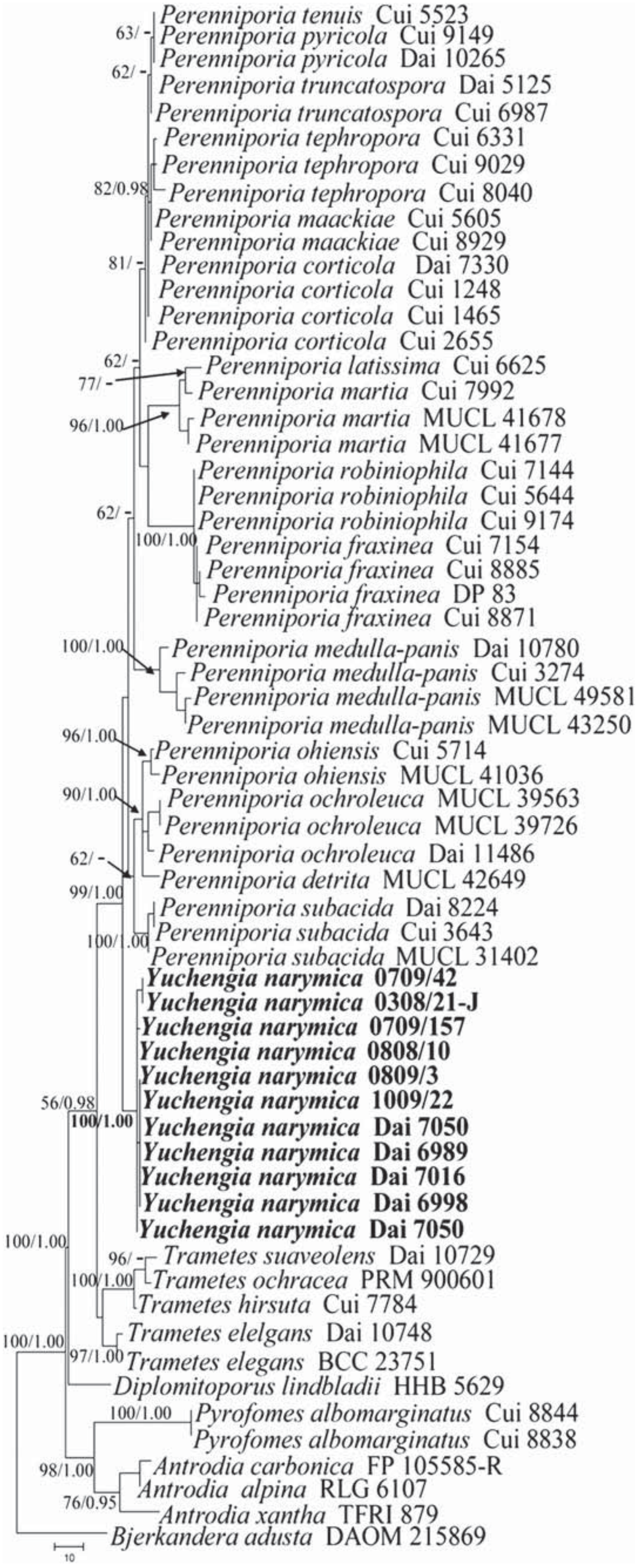

Figure 2. Phylogeny of *Yuchengia* and *Perenniporia* generated by Maximum Parsimony and Bayesian analysis based on nLSU sequences. Parsimony bootstrap proportions (before the slash sign) higher than 50% and Bayesian posterior probabilities (after the slash sign) larger than 0.95 are indicated along the branches.

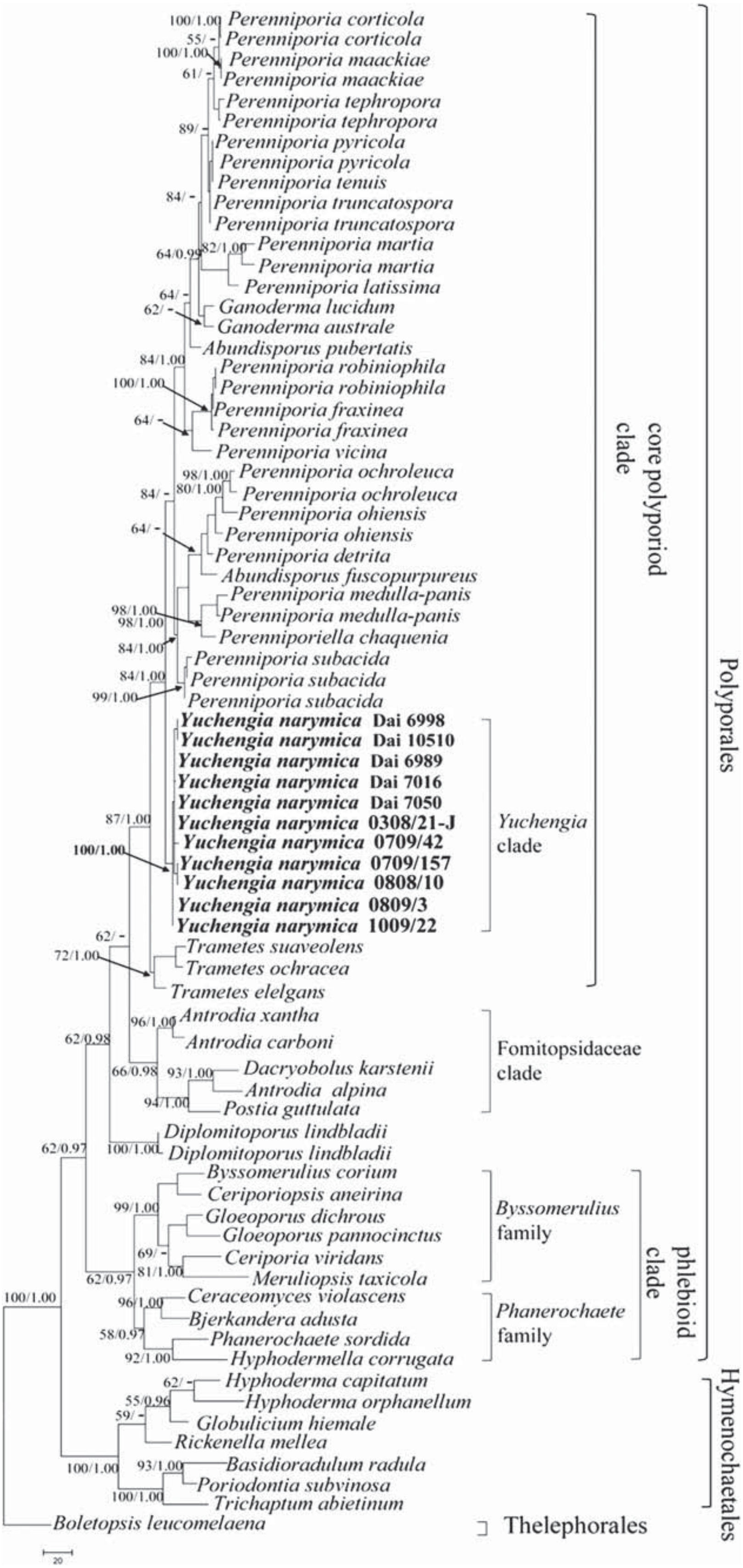

Figure 3. Strict consensus tree illustrating the phylogeny of *Yuchengia* and *Perenniporia* generated by Maximum Parsimony and Bayesian analysis based on a combined ITS + nLSU sequences dataset. Parsimony bootstrap proportions (before the slash sign) higher than 50% and Bayesian posterior probabilities (after the slash sign) larger than 0.95 are indicated along branches.

Table 2. List of characters of *Yuchengia narymica* comb. nov. from different regions.

Specimens	Locality	Basidiospores (µm)	Average	Q	Pores mm^{-1}
PRM 811202 (Type)	Russia	(4.1–)4.1–5.0(–5.1) × (3.0–)3.1–4.0(–4.0)	4.8 × 3.6	1.33	4–5
Vlasák 9010/32-Vam	Slovakia	(4.1–)4.2–5.0(–5.1) × (3.1–)3.1–4.0(–4.1)	4.7 × 3.6	1.31	5–6
Vlasák 9810/12	Slovakia	(4.1–)4.2–5.0(–5.0) × (3.0–)3.0–3.9(–4.0)	4.8 × 3.7	1.30	5–6
Vlasák 0308/21-J	USA	(4.1–)4.3–5.0(–5.1) × (3.0–)3.1–4.0(–4.0)	4.8 × 3.4	1.41	4–5
Vlasák 0709/42	USA	(4.0–)4.1–5.1(–5.2) × (3.0–)3.0–4.0(–4.0)	4.8 × 3.5	1.37	4–5
Vlasák 0709/157	USA	(4.0–)4.4–5.0(–5.1) × (3.0–)3.1–4.0(–4.1)	4.8 × 3.6	1.31	3–5
Vlasák 0808/10	USA	(4.1–)4.4–5.0(–5.2) × (3.0–)3.0–4.0(–4.1)	4.8 × 3.5	1.37	3–4
Vlasák 0809/3	USA	(4.0–)4.1–5.0(–5.1) × (3.0–)3.1–3.9(–4.0)	4.7 × 3.5	1.34	3–5
Vlasák 1009/22	USA	(4.1–)4.2–5.0(–5.1) × (3.0–)3.1–4.0(–4.0)	4.8 × 3.6	1.31	3–4
Dai 6989	China	(4.0–)4.1–5.0(–5.1) × (3.0–)3.1–4.0(–4.3)	4.5 × 3.6	1.24	4–5
Dai 7016	China	(4.1–)4.2–5.2(–5.9) × (3.0–)3.1–4.0	4.9 × 3.7	1.32	4–5
Dai 6998	China	(4.2–)4.3–5.1(–5.2) × (3.1–)3.2–4.0	4.8 × 3.7	1.30	3–4
Dai 10510	China	(4.0–)4.2–5.1(–5.2) × (3.0–)3.2–4.0(–4.2)	4.8 × 3.8	1.26	4–5
Dai 7050	China	(4.5–)4.6–5.3(–5.7) × (3.2–)3.5–4.0(–4.2)	5.0 × 3.9	1.28	3–5

basidiospores that are cyanophilous and negative in Melzer's reagent. The combination of the above characters makes it distinct from *Perenniporia*.

Perenniporia amylodextrinoidea Gilb. & Ryvarden may be confused with *Yuchengia narymica*, both having amyloid skeletal hyphae, however, the former species differs in its truncate and dextrinoid basidiospores (Gilbertson and Ryvarden 1987). *Perenniporia hattorii* Y. C. Dai & B. K. Cui also has amyloid skeletal hyphae, but differs from *Y. narymica* in having truncate, amyloid, and larger basidiospores (9.8–12.7 × 5.8–7.2 µm, Dai et al. 2011). *Perenniporia medulla-panis* (Jacq.) Donk resembles *Y. narymica* by having resupinate basidiocarps and similar pores, but it differs in its white pore surface, branched skeletal hyphae and truncate, dextrinoid basidiospores (Decock and Stalpers 2006).

Perenniporia subacida (Peck) Donk is similar to *Yuchengia narymica*, and both have unbranched skeletal hyphae and non-truncate, non-dextrinoid basidiospores; However, *P. subacida* is distinguished from *Y. narymica* by having distinctly perennial basidiocarps with ivory to yellowish pore surface and a trimitic hyphal system with skeletal hyphae which are strongly dextrinoid, cyanophilous and not dissolving in KOH (Núñez and Ryvarden 2001, Decock and Stalpers 2006). Phylogenetically, *P. subacida* is clustered within the *Perenniporia* s.l. clade, while *Y. narymica* forms a monophyletic clade sister to the *Perenniporia* s.l. clade.

Pseudopiptoporus Ryvarden, typified by *Pseudopiptoporus devians* (Bres.) Ryvarden is a genus which also has amyloid skeletal hyphae. It differs from *Yuchengia narymica* by having pileate basidiocarps, a monomitic hyphal system in trama, and pale straw-coloured and dextrinoid basidiospores (Ryvarden and Johansen 1980, Decock and Ryvarden 2003).

Several species of *Antrodia* P. Karst., such as *A. carbonica* (Overh.) Ryvarden & Gilb. or *A. xantha* (Fr.) Ryvarden have amyloid skeletal hyphae, but these species have thin-walled and acyanophilous basidiospores and cause a brown rot (Gilbertson and Ryvarden 1987, Núñez and Ryvarden 2001) in which features they differ from *Y. narymica*.

In this study, the phylogeny of *Yuchengia* and *Perenniporia* were reconstructed based on nLSU (Fig. 2) and combined ITS + nLSU (Fig. 3) sequences. In both analyses (Fig. 2, 3), *Yuchengia narymica* formed a well-supported monophyletic lineage (100% BP, 1.00 BBP) distinct from the *Perenniporia* lineage. The tree based on ITS + nLSU analysis demonstrates that *Yuchengia narymica* belongs to the core polyporiod clade (Fig. 3). Thus, a new genus *Yuchengia* is proposed to accommodate *Perenniporia narymica* as *Yuchengia narymica.*

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