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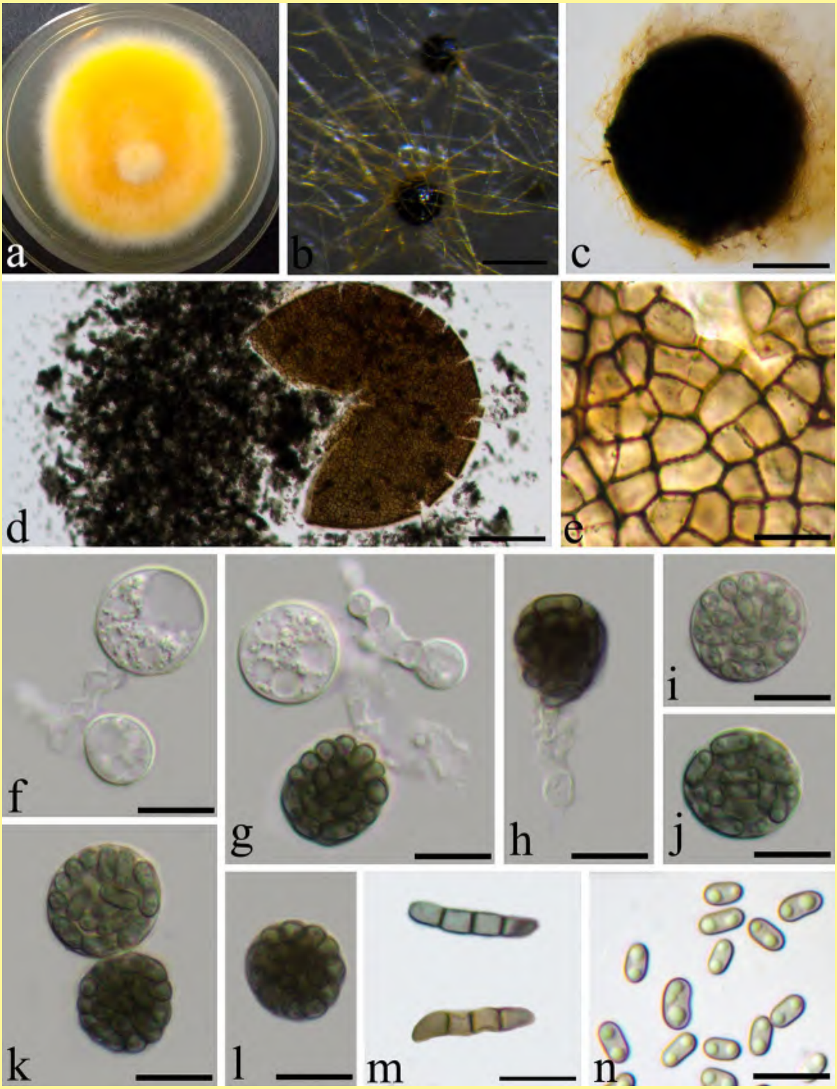

Westerdykella aquatica sp. nov.
(Song & al.— FIG. 2, p. 289)

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was issued on April 20, 2020

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Reviewers — volume one hundred thirty-five (2)

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2020 MYCOTAXON SUBMISSION PROCEDURE

Prospective MYCOTAXON authors should download the MYCOTAXON 2020 guide, review & submission forms, and MYCOTAXON sample manuscript by clicking the 'file download page' link on our INSTRUCTIONS TO AUTHORS page before preparing their manuscript. This page briefly summarizes our '4-step' submission process.

1—PEER REVIEW: Authors first contact peer reviewers (two for journal papers; three for mycobiota/fungae) before sending them formatted text & illustration files and the appropriate 2020 MYCOTAXON journal or mycota reviewer comment form. Experts return revisions & comments to BOTH the *Editor-in-Chief* <editor@mycotaxon.com> and authors. ALL co-authors MUST correct and *proof-read* their files before submitting them to the *Nomenclature Editor*.

2—NOMENCLATURAL REVIEW: Authors email all **ERROR-FREE** text & illustration files to the *Nomenclature Editor* <PennycookS@LandcareResearch.co.nz>. Place **first author surname** + **genus** + 'MYCOTAXON' on the subject line, and (required) attach a completed SUBMISSION FORM. The Nomenclature Editor will (i) immediately assign the accession number and (ii) after a few weeks return his notes and suggested revisions to the author(s) and *Editor-in-Chief*.

3—FINAL SUBMISSION: All coauthors thoroughly revise and proof-read files to prepare error-free text and images ready for immediate publication. Poorly formatted copy will be rejected or returned for revision. E-mail the final manuscript to the *Editor-in-Chief* <editor@mycotaxon.com>, adding the **accession number** to the message and **all** files, which include a (**i**) revised 2020 submission form, all (**ii**) text files and (**iii**) jpg images, and (**iv**) FN, IF, or MB identifier verifications for each new name or typification. The *Editor-in-Chief* acknowledges submissions within two weeks of final submission but requests authors to wait at least 14 days before sending a follow-up query (without attachments).

4—FINAL EDITORIAL REVIEW & PUBLICATION: The *Editor-in-Chief* conducts a final grammatical and scientific review and returns her editorial revisions to all expert reviewers and coauthors for final author approval. Author-approved files are placed in the publication queue.

The PDF proof and bibliographic & nomenclatural index entries are sent to all coauthors for final inspection. After PDF processing, the *Editor-in-Chief* corrects ONLY PDF editorial/conversion and index entry errors; corrections of all other errors are listed in the ERRATA of a subsequent issue for no charge. Authors will pay fees for mycobiota uploads, optional open access, and correction of major author errors to the *Business Manager* <subscriptions@mycotaxon.com> at this time.

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From the Editor-in-Chief

Collaboration & the multi-authored paper—Mycological taxonomic research is no longer a simple matter of reaching down, plucking a fungus from its substrate, seeing something REALLY different, checking the microscopical characters, reading the one or two papers ever written on aforesaid fungal family, and then writing a paper. Current fungal taxonomy encompasses a great many disciplines, including (but not limited to) microscopy, ecology, physiology, mating studies, ultrastructure, systematics, DNA extractions, sequence analyses, and evolutionary relationships. Yet we somehow expect students injected into this bewildering maelstrom of disciplines to be able (eventually) to present their research in the form of a published paper.

As only a limited number of geniuses can master all modern disciplines, there are now relatively few solo-authored papers. Most research papers are crafted by an agreeable consortium of individuals, each of whom contributes one or two expert pieces that flesh out the final manuscript. The individual who bears the greatest responsibility (and gets—however little deserved—most of the credit) is the first author. All students must oversee all stages of each manuscript submission to ensure that they master the scientific publication process. The first named author bears the responsibility for ensuring that a manuscript meets all journal requirements and seeing that all facts are coherently written and correct. Generally it is that author who discusses the research with all whose names will stand on the final publication. It is also generally the first author who gathers all contributors together to work out a complication and perfect the final text whenever an error or oversight is detected.

Nonetheless, a multi-authored paper is not a work by one author. Journals such as Mycotaxon expect all contributing authors to read and revise numerous drafts thoroughly, to check all drawings, tables, and data, and communicate with the first author throughout the research process and prior to submission. Editors expect to receive papers that have been—by *all* authors—thoroughly proofed and that contain no scientific, grammatical, or visual errors. Only through rigorous oversight by all collaborators, particularly the more experienced and knowledgeable among them, is it possible for a beginning scientist to publish in a well-established international scientific journal.

We heartily urge all of our authors to discuss their research among themselves and with their lab mates. That way lies progress!

Dear Readers (plus premature thanks to the Mycotaxon Editorial Board)—Your editors are currently swamped with submissions—the expected result of discontinuing required page charges in 2018. For sixteen years, Dr. Pennycook has tirelessly accessioned and examined manuscripts, gradually adding scientific and grammatical oversight to his already heavy nomenclatural duties. In the process, he has nomenclaturally accepted almost 2000 manuscripts, rejected ~100, and is currently reviewing 105 more. In its search for scientifically rigorous and nomenclaturally correct papers produced by dedicated authors and their expert reviewers, Mycotaxon still needs Shaun's nomenclatural knowledge because so few mycologists fully understand the rules of the International Code of Nomenclature.

Needless to say, both authors and editors are unhappy with the current lengthy time between manuscript accession and return of the nomenclatural review.

However, it now appears that all too often, author-selected experts do not devote the time needed for rigorous review, so that Dr. Pennycook frequently accessions manuscripts that require much more work. With many problems not detected by a quick scan of accessioned files, frequently only after Shaun has begun a review does he discover that the unsatisfactory files must be returned to authors for more work. Not surprisingly, this further lengthens the time between accession and nomenclatural approval.

Three months ago we decided that Shaun could work through his backlog more quickly by focusing only on nomenclature and by returning all other grammatical and scientific edits to the Editor-in-Chief (me). Unfortunately after encountering far too many scientific errors or inaccurate citations, I now must also double-check GenBank, herbarium records, and – yes – even scale bars for accuracy and consistency.

Fortunately, learning in June that your two volunteer editors needed at least one extra pair of eyes, editorial board member Else Vellinga volunteered to serve as Mycotaxon's first 'official' preliminary reader. She offered to glance through still unreviewed manuscripts to determine which authors properly implemented expert suggestions, formatted grammatically correct text files, and presented no scientific contradictions as well as flag those papers needing additional work. Dr. Vellinga surveyed several manuscripts—happily finding one in excellent shape and less happily finding several in need of considerable repair or additional research prior to nomenclatural review.

In our estimation, Else, who delivered thorough reviews forwarded to the authors, has been a rousing success. We now plan to contact other board members to help us determine which other accessions are ready for nomenclatural review, which need additional research, and which should be rejected. Authors able to make any suggested changes and return them before Shaun begins his review will not lose their place in the nomenclatural 'queue.'

We sincerely hope this will help shorten our review turn-around time and give your volunteer editors much needed assistance in their currently overwhelming editorial duties. We both dearly desire returning to a time when all submissions were so well prepared that all we need do is to rubber-stamp "approved" after the first read-through. 'Tis a consummation devoutly to be wished.

Mycotaxon 135(2) provides 22 papers and announces three mycobiota by 88 authors (from 23 countries) reviewed by 54 experts.

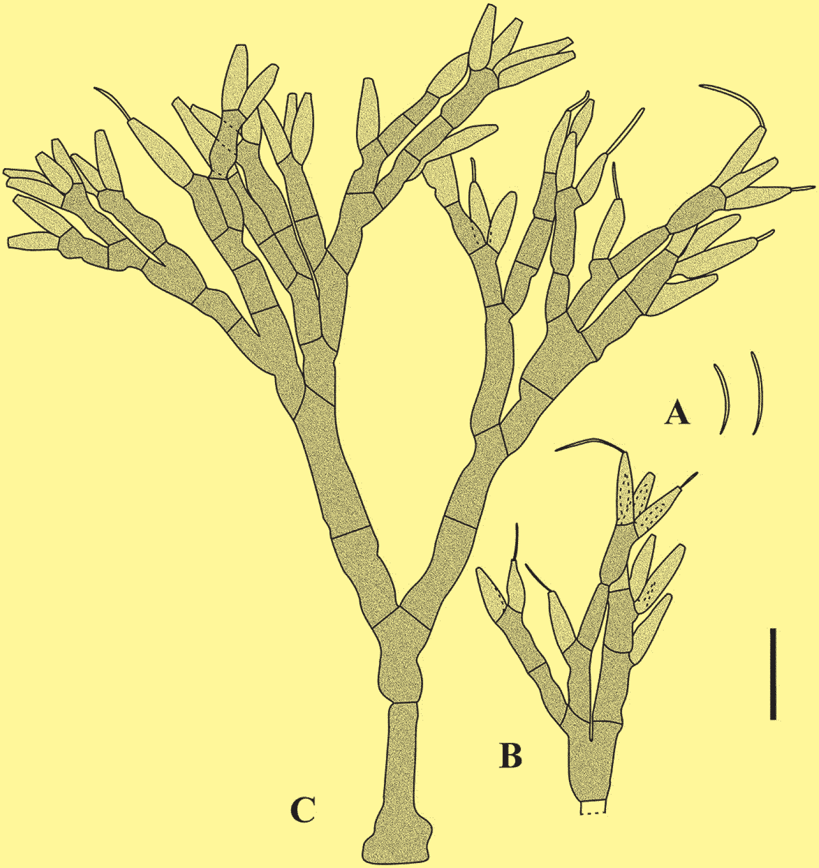
The 2020 April–June Mycotaxon sets forth one new genus (*Ramiphialis* from Brazil) and eight species new to science representing *Acarospora* & *Sarcogyne* from the US & Canada; *Armillaria, Haematomma, Vanderbylia,* and *Westerdykella* from China; *Coprinellus* from Pakistan; and *Ramiphialis* from Brazil. Authors also offer three new combinations in *Cercosporella, Ellismarsporium,* and *Microthecium.*

Range extensions are reported for [ascomycetes] the powdery mildew *Golovinomyces* (China) and truffle *Elaphomyces* (Turkey); [basidiomycetes] the agarics *Pluteus* (Europe) & *Xerula* (Argentina), secotioid *Entoloma* (Slovakia), and rust *Aecidium* (Pakistan); [lichens] the leprose *Lepraria* (Iran), assorted graphidoid & thelotremoid taxa (India), and crustose *Carbonea & Rinodina* (Poland); and [myxomycetes] the slime molds *Badhamia* & *Trichia* (Belarus).

We also offer phylogenetic explorations of *Acrospeira, Armillaria, Coprinellus, Ellismarsporium, Golovinomyces, Pluteus, Vanderbylia,* and *Westerdykella;* a key to the *Lepraria* species of Iran; reevaluation of three *Calicium* taxa proposed in 1909; and a comprehensive index of fungal names derived from te reo Māori. Finally, we announce three new www.mycotaxon.com mycobiota covering Australian marine fungi, Brazilian corticioids, and a global list of aquatic glomeromycotans.

Best wishes for excellent health and with warm regards,

Lorelei L. Norvell (*Editor-in-Chief*)
8 July 2020



Ramiphialis ronuroensis sp. nov.
(Barbosa & al.— Fig. 2, p. 296)
Patricia Oliveira Fiuza, *artist*

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Vanderbylia cinnamomea sp. nov. from southwestern China

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Abstract—*Vanderbylia cinnamomea* is proposed as a new wood-inhabiting polypore species based on morphological characters supported by phylogenetic analysis. The species is characterized by an annual, pileate basidiocarp, a brown to black pileal surface, an olivaceous buff to smoke grey pore surface, a dimitic hyphal system with clamped generative hyphae, and subglobose to amygdaliform, hyaline, thick-walled, smooth, dextrinoid, and cyanophilous basidiospores. ITS+nLSU sequence analyses place *V. cinnamomea* in *Vanderbylia* within a subclade with a high support (100% BS, 100% BP, 1.00 BPP) sister to a subclade comprising *V. fraxinea* and *V. robiniophila*.

Key words—*Perenniporia*, *Polyporaceae*, *Polyporales*, taxonomy, Yunnan Province

Introduction

Vanderbylia D.A. Reid (*Polyporaceae*, *Polyporales*) is typified by *V. vicina* (Lloyd) D.A. Reid (Reid 1973). Ryvarden & Johansen (1980) reduced the genus to a synonym under *Perenniporia* Murrill for a long time, but recent phylogenetic research of a combined sequence dataset of the internal transcribed spacer (ITS) and the large subunit nuclear ribosomal RNA gene (nLSU) supports *Vanderbylia* as an independent genus (Robledo &

al. 2009, Zhao & al. 2013, Cui & al. 2019). Morphologically *Vanderbylia* is characterized by pileate basidiocarps, a dimitic hyphal system with clamped generative hyphae and variably dextrinoid skeletal hyphae, and subglobose to amygdaliform, non-truncate and variably dextrinoid basidiospores (Reid 1973, Zhao & Cui 2013). Currently, nine species are accepted in *Vanderbylia* worldwide: *V. borneensis* Corner, *V. delavayi* (Pat.) B.K. Cui & Y.C. Dai, *V. devians* (Bres.) D.A. Reid, *V. fraxinea* (Bull.) D.A. Reid, *V. nigroapplanata* (Van der Byl) D.A. Reid, *V. robiniophila* (Murrill) B.K. Cui & Y.C. Dai, *V. subincarnata* Corner, *V. ungulata* D.A. Reid, and *V. vicina* (Bresadola 1920, Reid 1975, Corner 1987, Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Ryvarden & Melo 2014, Cui & al. 2019).

Robledo & al. (2009), who revealed the relationship between *Perenniporia* and *Perenniporiella* Decock & Ryvarden, grouped two *Vanderbylia* species together—the generic type *V. vicina* and *V. fraxinea*. In their phylogenetic overview of *Perenniporia* s.l., Zhao & al. (2013) and revealed that *Vanderbylia fraxinea*, *V. robiniophila,* and *V. vicina* form a single lineage. Subsequently, Cui & al. (2019) investigated the species diversity, taxonomy, and phylogeny of *Polyporaceae* in China and proposed two new combinations, *Vanderbylia delavayi* and *V. robiniophila*.

During investigations on wood-inhabiting fungi in Yunnan Province, an additional taxon was found that could not be assigned to any described species. In examining the taxonomy and phylogeny of this new species, we employed a two-gene molecular phylogenetic approach using internal transcribed spacer (ITS) and long subunit (nLSU) plus an expanded sampling of *Vanderbylia* isolates that support the existence of a new species, *Vanderbylia cinnamomea.*

Materials & methods

The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, P.R. China (SWFC). Macromorphological descriptions are based on field notes. Color terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens and observed under light microscopy following Dai (2012). The following abbreviations are used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, 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 = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

We extracted genomic DNA from dried specimens using Magen Biotech HiPure Fungal DNA Mini Kit II according to the manufacturer's instructions with some

Table 1. Species, specimens, and sequences used in this study.
(New sequences in **bold**).

Species name	Sample no.	GenBank no.		References
		ITS	nLSU	
Donkioporia expansa	MUCL 35116	FJ411104	FJ393872	Robledo & al. (2009)
Pyrofomes demidoffii	MUCL 41034	FJ411105	FJ393873	Robledo & al. (2009)
Vanderbylia cinnamomea	**CLZhao 8952 T**	MT372778	MT372788	Present study
	CLZhao 8959	MT372779	MT372789	Present study
	CLZhao 8961	MT372780	MT372790	Present study
	CLZhao 8962	MT372781	MT372791	Present study
	CLZhao 8963	MT372782	MT372792	Present study
	CLZhao 9001	MT372783	MT372793	Present study
V. fraxinea	DP 83	AM269789	AM269853	Robledo & al. (2009)
	Cui 7154	HQ654095	HQ654110	Zhao & al. (2013)
	Cui 8871	JF706329	JF706345	Zhao & al. (2013)
V. robiniophila	Cui 5644	HQ876609	JF706342	Zhao & al. (2013)
	Cui 7144	HQ876608	JF706341	Zhao & al. (2013)
	Cui 9174	HQ876610	JF706343	Zhao & al. (2013)
V. vicina	MUCL 44779	FJ411095	AF518666	Robledo & al. (2009)

modifications. A small piece (about 30 mg) of dried fungal material was ground to powder with liquid nitrogen, transferred to a 1.5 mL centrifuge tube, suspended in 0.4 mL of lysis buffer, and incubated in a 65 °C water bath for 60 min. After the addition of 0.4 mL phenol-chloroform (24:1) to each tube, the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL supernatant was transferred to a new tube and mixed with 0.45 mL binding buffer. That mixture was transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 30 s. After washing twice with 0.5 mL washing buffer, the AC was transferred to a clean centrifuge tube, and 0.1 mL elution buffer was added to the middle of adsorbed film to elute the genomic DNA. The ITS region was amplified with primer pairs ITS5 and ITS4 (White & al. 1990). Nuclear LSU region was amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi). The PCR procedure for ITS was optimized as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR condition for nLSU was as follow: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. The six new sequences from specimens of *Vanderbylia cinnamomea* were aligned with additional *Vanderbylia* sequences downloaded from GenBank (Table 1).

Sequences were aligned in MAFFT 7 (http://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy, and manually adjusted in BioEdit (Hall 1999).

Alignment datasets were deposited in TreeBase (submission ID 24081). GenBank sequences of *Donkioporia expansa* (Desm.) Kotl. & Pouzar and *Pyrofomes demidoffii* (Lév.) Kotl. & Pouzar obtained from GenBank were used as an outgroup to root trees following Zhao & al. (2013) in the ITS+nLSU analysis.

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

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 with a general time reversible (GTR+I+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 2 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 greater than or equal to 80% (maximum likelihood, BL), 50% (maximum parsimony, BP), and 0.95 (Bayesian posterior probabilities, BPP) were considered as significantly supported.

Phylogenetic results

The ITS dataset included sequences from 15 fungal specimens or isolates representing 6 species. The dataset had an aligned length of 1844 characters, of which 1690 characters were constant, 65 were variable and parsimony-uninformative, and 89 were parsimony-informative. Maximum parsimony analysis yielded 6 equally parsimonious trees (TL = 178, CI = 0.921, HI = 0.787, RI = 0.944, RC = 0.870). Best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian and ML analyses produced a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.001512 (BI).

The phylogeny (Fig. 1) inferred from ITS+nLSU sequences obtained for related taxa of *Vanderbylia* support the new species as independent in one sub-clade and sister to the /fraxinea-robinophila subclade.

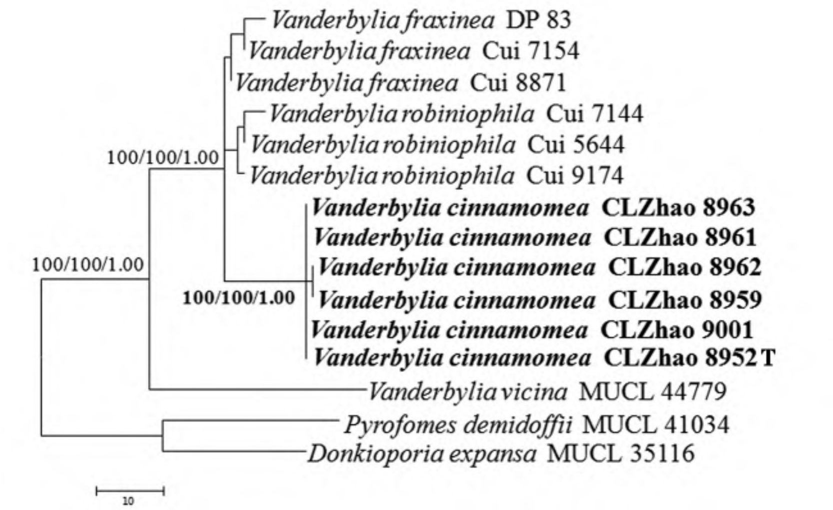

Fig. 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Vanderbylia cinnamomea* and related species in *Vanderbylia* based on ITS+nLSU sequence analyses. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.

Taxonomy

Vanderbylia cinnamomea C.L. Zhao, **sp. nov.** Figs 2–4

MB 831788

Differs from *Vanderbylia vicina* by its annual basidiocarps and its smaller basidiospores.

Type: China. Yunnan Province: Kunming, Tanhuasi Park, on living tree of *Cinnamomum camphora* (L.) J. Presl (*Lauraceae*), 13 October 2018, CL Zhao 8952 (**Holotype**, SWFC 008952; GenBank MT372778, MT372788).

Etymology: The specific epithet *cinnamomea* (Lat.) refers to the host of *Cinnamomum camphora*.

Basidiomata annual, pileate, imbricate, without odor or taste and corky when fresh, becoming hard corky upon drying. Pilei dimidiate, projecting ≤10 cm, 18 cm wide, 4.5 cm thick at centre. Pileal surface pale brown to brown when fresh and brown to black from the base upon drying, smooth, gently concentrically sulcate, glabrous. Pore surface pure buff to olivaceous buff when fresh, olivaceous buff to smoke grey upon drying; pores round, 5–7 per mm; dissepiments thick, entire. Sterile margin narrow, buff, ≤0.5

mm wide. Context cream, cottony, ≤4 cm thick. Tubes concolorous with pore surface, ≤5 mm long.

Hyphal structure dimitic; generative hyphae with clamp connections, strongly dextrinoid, CB+; tissues unchanging in KOH.

Context generative hyphae infrequent, hyaline, thin-walled, unbranched, 2–3 µm in diam; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, branched, interwoven, 4.5–5.5 µm in diam.

Tubes generative hyphae infrequent, hyaline, thin-walled, unbranched, 1.5–2.5 µm in diam; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, branched, interwoven, 4–5 µm in diam. Presence of arboriform hyphae, thick-walled to almost solid, with few branches and short, lateral or terminal processes, tortuous, 25–40 × 2–6 µm. Cystidia and cystidioles not seen; basidia clavate, with 4 sterigmata and a basal clamp connection, 20–24 × 6–9.5 µm; basidioles dominant, clavate-shaped to pear-shaped.

Basidiospores subglobose to amygdaliform, hyaline, thick-walled, smooth, strongly dextrinoid, cyanophilous, 5–6(–6.5) × 4–5(–5.5) µm, L = 5.67 µm, W = 4.73 µm, Q = 1.17–1.21 (n = 180/6).

Type of rot: white.

Additional specimens examined: **CHINA. Yunnan province. Kunming:** Tanhuasi Park, on living tree of *Cinnamomum camphora,* 15 October 2018, CLZhao 8959 (SWFC 008959; GenBank MT372779, MT372789); CLZhao 8961 (SWFC 008961; GenBank MT372780, MT372790); CLZhao 8962 (SWFC 008962, GenBank MT372781, MT372791); CLZhao 8963 (SWFC 008963; GenBank MT372782, MT372792); CLZhao 9001 (SWFC 009001; GenBank MT372783, MT372793).

Discussion

We describe here a new species *Vanderbylia cinnamomea* based on phylogenetic analyses and morphological characters.

Phylogenetically, *Vanderbylia cinnamomea* grouped with species *V. fraxinea, V. robiniophila,* and *V. vicina* in the rDNA-based phylogeny (Fig. 1). Morphologically *V. fraxinea* differs in its perennial basidiocarps and larger basidiospores (6–8 × 5–6.5 µm, Ryvarden & Melo 2014), while *Vanderbylia robiniophila* is distinguished by its growth on *Robinia* L., its white to pale brown pore surface, and its larger basidiospores (5–8 × 5–7 µm, Gilbertson & Ryvarden 1987; Núñez & Ryvarden 2001); *Vanderbylia vicina* differs in its perennial basidiocarps and larger basidiospores (8–8.9 × 6.9–7.5 µm, Reid 1973).

Four species are morphologically similar to *Vanderbylia cinnamomea: V. borneensis*, *V. devians*, *V. subincarnata,* and *V. ungulata*. *Vanderbylia*

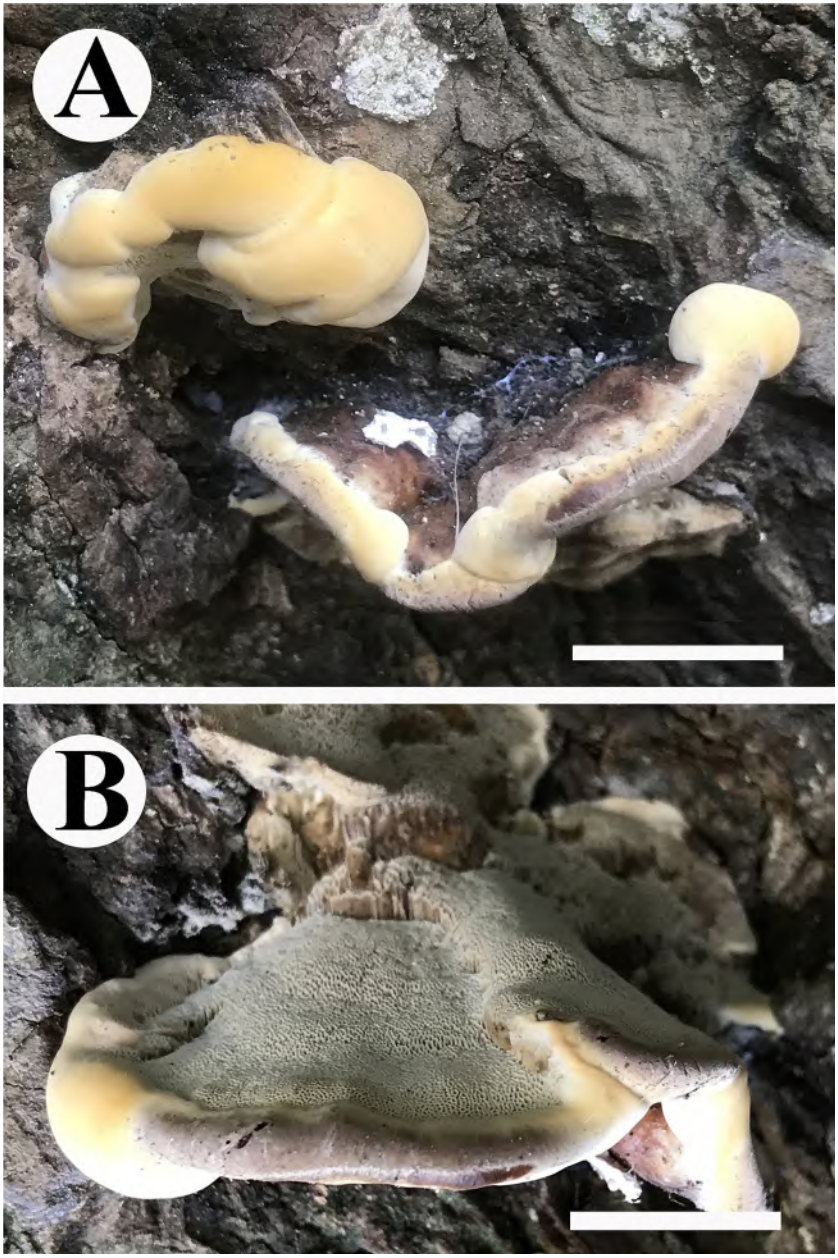

Fig. 2. *Vanderbylia cinnamomea* (holotype, SWFC 008952).
Basidiocarps. Scale bars = 5 cm.

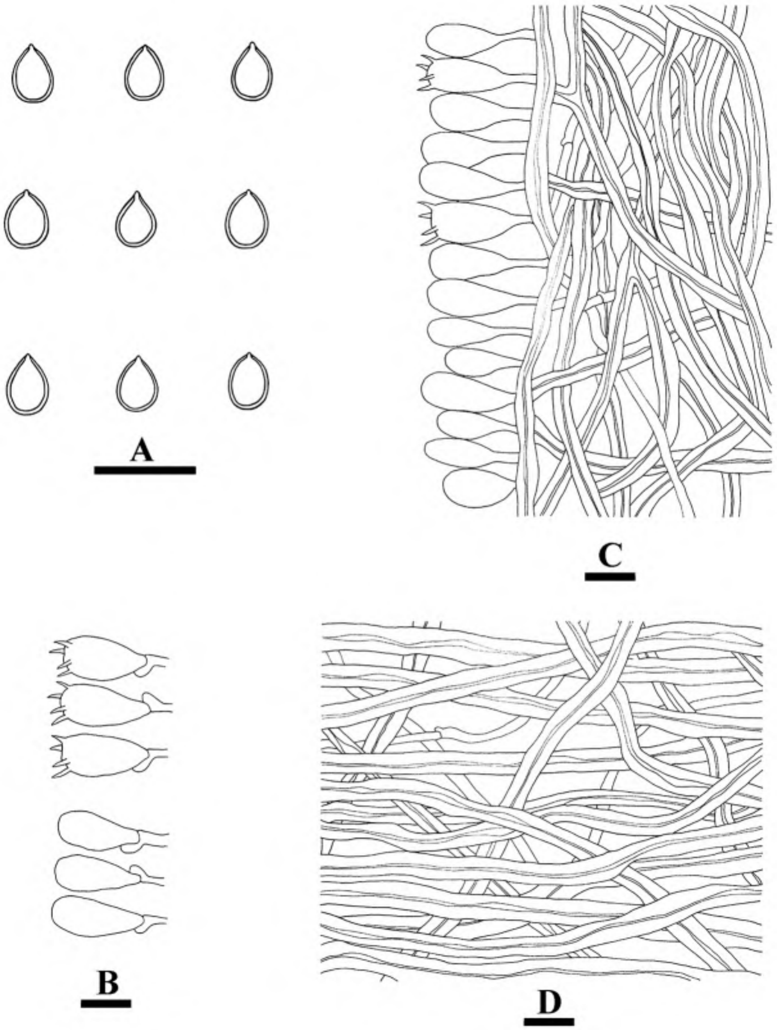

Fig. 3. *Vanderbylia cinnamomea* (holotype, SWFC 008952).
A. Basidiospores; B. Basidia and basidioles; C. Hyphae from trama; D. Hyphae from context.
Scale bars = 10 µm.

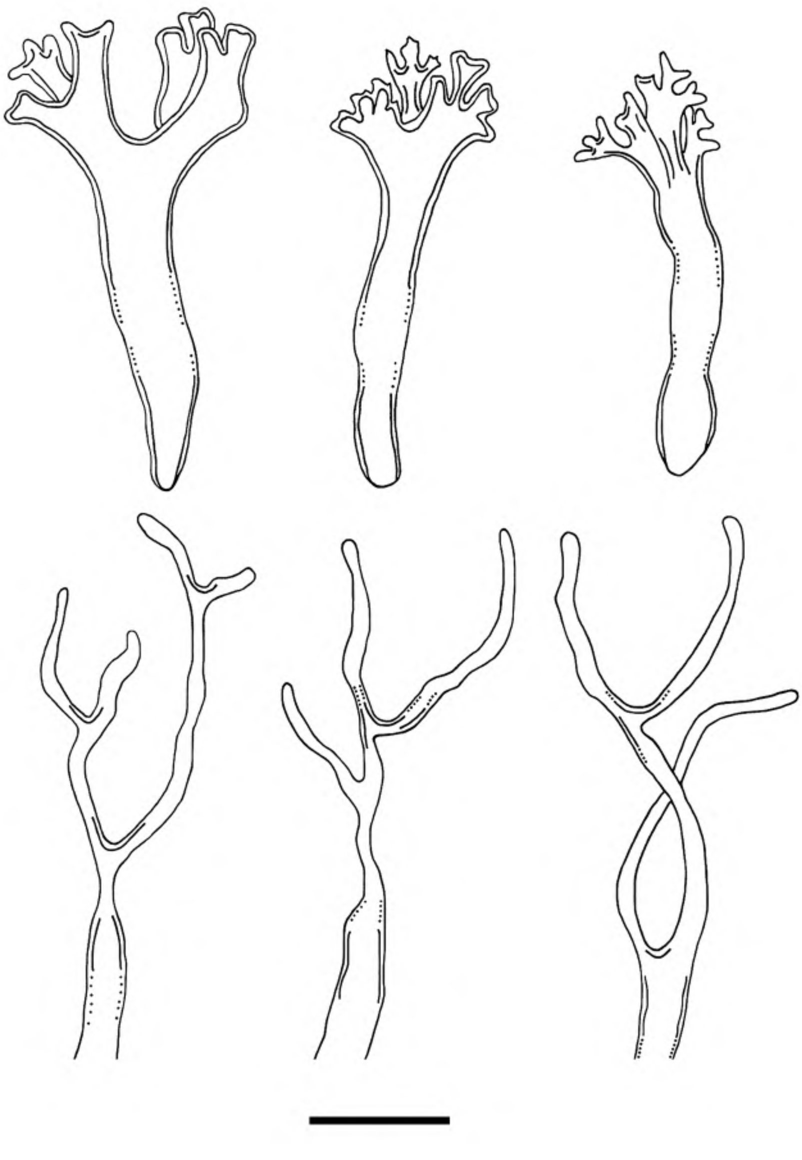

Fig. 4. *Vanderbylia cinnamomea* (holotype, SWFC 008952).
Arboriform hyphae. Scale bar = 10 µm.

borneensis differs from *V. cinnamomea* in its smaller pores (8–10 per mm) and the presence of skeletal hyphal endings in the dissepiments (Corner 1987); *V. devians* is distinguished by its substipitate basidiocarps with alutaceous to isabelline pore surface and larger pores (3–4 per mm, Bresadola 1920); *V. subincarnata* is diagnosed by its pinkish pore surface and smaller pores (7–10 per mm, Corner 1987); and *V. ungulata* has ungulate basidiocarps with an ochraceous pore surface and hyaline to yellow basidiospores (Ryvarden & Johansen 1980).

When Decock & Ryvarden (1999) examined the holotype of *Polyporus delavayi* Pat., they proposed that it be transferred to *Perenniporia* based on its strongly dextrinoid, cyanophilous skeletal hyphae and dextrinoid, thick-walled basidiospores; they also examined the type specimen of *Perenniporia formosana* T.T. Chang and synonymized it under *P. delavayi* (Pat.) Decock & Ryvarden. Cui & al. (2019) subsequently transferred *Polyporus delavayi* to *Vanderbylia* based on molecular data and morphological characters on finding *P. delavayi* nested within the *Vanderbylia* lineage and manifesting morphological features consistent with the concept of *Vanderbylia*. Morphologically, *V. delavayi* differs from *V. cinnamomea* by its dirty greyish orange to greyish brown pore surface, larger pores (4–5 per mm), and larger basidiospores (5.7–7 × 4.7–5.9 µm, Decock & Ryvarden 1999).

Wood-rotting basidiomycetes have been extensively studied (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014), but Chinese wood-rotting fungi diversity is still not well known, especially in the subtropics and tropics. The new species *Vanderbylia cinnamomea* is from the Chinese subtropics, where many new taxa in *Polyporales* have been described (Cui & al. 2007, 2011; Cui & Dai 2008; Du & Cui 2009; Li & Cui 2010; He & Li 2011; Jia & Cui 2011; Yu & al. 2013; Yang & He 2014; Chen & al. 2015; Zhao & Wu 2017; Shen & al. 2018; Zhao & Ma 2019). We anticipate that more new polypore taxa will be found in China after further investigations and molecular analyses.

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