



Comprehensive morphological and phylogenetic analyses of *Hymenochaetales* (*Basidiomycota*) unveil one new genus and twenty-six novel wood-inhabiting species from southwestern China

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Abstract: As part of an ongoing inventory of *Basidiomycota* in China, we examined species of the order *Hymenochaetales* collected from tropical forests. Fungi of this order cause wood rot or diseases in woody plants worldwide and recent studies have substantially contributed to improve their classification system by combining phylogenetic and morphological analysis. However, the species diversity of *Hymenochaetales* in the high-altitude forests of southwestern China is comparably understudied. We tackled this sampling gap in the present study and provide morphological descriptions, illustrations, and comprehensive notes as well as sequence and phylogenetic data for in total one new genus and 26 new species. As a result of these integrative analyses, we were able to phylogenetically resolve thirteen supported lineages in the *Hymenochaetales*. While numerous *Hymenochaetales* fungi have been documented in China, our report clearly shows that the diversity within the family *Hymenochaetales* remains largely unexplored, leaving significant potential for further discoveries in Chinese tropical forests.

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INTRODUCTION

The order *Hymenochaetales* (*Agaricomycetes*) comprises a large number of wood-inhabiting and ectomycorrhizal fungi with a large morphological variety and complexity, ranging from resupinate to pileate, stipitate and coralloid forms, and smooth to grandinioid, odontoid to hydroid, or poroid and gilled (lamellate) hymenophores (Korotkin *et al.* 2018, Zhao *et al.* 2025). Its members are involved in important roles in forest ecosystems as wood decomposers and pathogens, and are reported to form ectomycorrhizal associations, such as *Coniferiporia qilianensis*, *C. sulphurascens*, *C. uzbekistanensis*, *C. weirii*, *Fomitiporia hartigii*, *Fuscoporia coronadensis*, *Onnia circinata* and *Porodaedalea pini* (Korotkin *et al.* 2018, Dai *et al.* 2021). Moreover, some lineages of *Hymenochaetales* are used in the framework of traditional Chinese medicine (TCM) as natural remedies, such as the important genera *Inonotus* and *Sanguangporus*, which have even been shown to serve as sources for new and bioactive compounds (Sum *et al.* 2023).

The order had been initially erected and typified with

the family *Hymenochaetaceae* (and its associated genus *Hymenochaete*); however, the high degree of morphological plasticity throughout the associated families rendered a clear-cut, morphocentric taxonomic system impossible (Berkeley & Broome 1873, Larsson *et al.* 2006). Equally, initial molecular studies using ribosomal sequences proved insufficient (Larsson *et al.* 2006, Bernicchia & Gorjón 2010); however, increasing feasibility of broad scale genome sequencing campaigns have significantly improved this situation. A recent significant contribution was given by Zhao *et al.* (2025), who analysed in total 171 associated genomes and provided a robust phylogenomic framework for the first time, in which they accepted 15 families, comprising in total 65 genera with more than 1350 species (see also Léger 1998, Larsson 2007, Zhao *et al.* 2025).

Still, many geographic regions remain underexplored when it comes to *Hymenochaetales* diversity, as is for example the case for Southwestern China. This region is segregated into three provinces, one municipality and one Autonomous Region, namely Sichuan Province, Guizhou Province, Yunnan Province, Chongqing Municipality and



Xizang Autonomous Region. This vast area includes the Sichuan Basin, Yunnan-Guizhou Plateau, and the southeastern part of the Qinghai–Tibet Plateau, featuring a complex topography and considerable altitude differences. The lowest point, for example, is Hekou, in southeastern Yunnan, at an elevation of only 76 m. The highest is the peak of Mount Qomolangma, “the roof of the world”, at an elevation of 8848 m, totalling a difference in elevation as great as 8700 m (Yang *et al.* 2021). Over 17000 species of tropical, subtropical, temperate, subalpine and alpine plants have been documented in the region, together with more than 1400 species of land animals, which underscores this area as a biodiversity hotspot (Yang *et al.* 2021). In this study, we aim to complement this record by chartering the area’s diversity of *Hymenochaetales* and, in the light of these findings, evaluate the phylogenetic placement of core groups within the order to improve our understanding of their evolutionary relationships.

MATERIALS AND METHODS

Sample collection and fungarium specimen preparation

Fresh basidiomata of fungi growing on angiosperm branches were collected from Xizang Autonomous Region (Linzi) and Yunnan Province (Chuxiong, Dehong, Diqing, Puer, Wenshan, Zhaotong) China. A total of 85 specimens was studied. The samples were photographed *in situ* and detailed information including the colour, size, shape, smell, habitat, geographical location, etc. of collected fruiting bodies recorded. Macroscopic details were also recorded in the field. Photographs were taken with a Jianeng 80D camera (Tokyo, Japan). All photos were focus-stacked and merged using Helicon Focus software. All samples were dried in an electric food dehydrator at 40 °C, then sealed and stored in the fungarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China.

Morphological studies

Macromorphological descriptions were based on field notes and photos captured in both the field and laboratory and followed the colour terminology of Petersen (1996). Micromorphology was studied at magnifications 1000×, using a Nikon Eclipse 80i microscope with phase contrast illumination. Sections were mounted in 5 % KOH, 1 % Congo Red solution, 1 % phloxine B (C₂₀H₂Br₄Cl₄Na₂O₅) as well as Cotton Blue and Melzer’s reagent to observe micromorphology following the methodology described in Dong *et al.* (2025). At least 30 basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospores measurements. Hand drawings were made for the most important morphological structures to illustrate the micromorphological characters.

The following abbreviations were used: KOH = 5 % potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, CB+ = cyanophilous, IKI = Melzer’s reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation

in the L/W ratios between the specimens studied and $n = a/b$ [number of spores (a) measured from a given number (b) of specimens]. If not stated otherwise, the number of measured spores (a) was 30.

DNA extraction, PCR and sequencing

A CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, following manufacturer’s instructions. The ITS, nLSU, *tef1-α*, mt-SSU, *rpb1* and *rpb2* regions were amplified using ITS5/ITS4 (White *et al.* 1990), LR0R/LR7 (Vilgalys & Hester 1990), EF1-983F/EF1-2218R (Rehner & Samuels 1994), MS1/MS2 (White *et al.* 1990), RPB1-Af/RPB1-Cf (Matheny *et al.* 2002) and bRPB2-6F/bRPB2-7.1R (Matheny 2005) primer pairs respectively. The methodology essentially followed descriptions from Dong *et al.* (2024) and amplification programs are listed in Table 1.

The PCR products were purified and directly subjected to Sanger sequencing with a commercial supplier using a genetic analyser Applied Biosystems ABI 3730xl (Kunming Tsingke Biological Technology Limited Company, Yunnan Province, China). All newly generated sequences were deposited in GenBank (Supplementary Table S1).

Phylogenetic analyses

Phylogenetic analyses essentially followed the methodology described in Dong *et al.* (2025). Briefly, newly generated sequence data were initially subjected to a BLAST search in NCBI to obtain sequence information from related taxa in GenBank (<http://blast.ncbi.nlm.nih.gov/>). Sequence data for subsequent phylogenetic analysis was retrieved from GenBank as well (<https://www.ncbi.nlm.nih.gov/nucleotide/>). Sequences were aligned using the online version of MAFFT following the G-INS-i strategy (<http://mafft.cbrc.jp/alignment/server/large.html>, Katoh *et al.* 2019). The alignment was adjusted manually using AliView v. 1.27 (Larsson 2014). ITS, nLSU, mt-SSU, *rpb1*, *rpb2*, and *tef1-α* sequences were combined using Mesquite v. 3.51. Sequence alignments were deposited at Figshare (<https://figshare.com/>; submission doi: 10.6084/m9.figshare.29979217).

Maximum parsimony (MP), Maximum likelihood (ML), and Bayesian inference (BI) analyses were applied to the combined datasets as described in a previous study (Yang *et al.* 2025). Briefly, all characters were equally weighted and gaps were treated as missing data. The maximum parsimony analysis was conducted using PAUP v. 4.0b10 (Swofford 2002). 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 an unparametric 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. Maximum Likelihood (ML) analysis was performed using the CIPRES Science Gateway (<https://www.phylo.org/portal2/login!input.action>, Miller *et al.* 2012) using the RAXMLHPC BlackBox v. 8.2.10 (Stamatakis 2014), with settings as follows: RAXML halt bootstrapping automatically and 0.25 for

**Table 1.** Loci, primers, PCR amplification procedures, and references used in this study.

Name	Abbreviation	Primer	Direction	Sequence (5'-3')	PCR amplification procedures	References
Internal transcribed spacer region of the rDNA	ITS	ITS5	Forward	GGAAGTAAAAAGTCGTAACAAGG	94 °C 3 min; 35 cycles of 94 °C 40 s, 58 °C 45 s, 72 °C 1 min; 72 °C 10 min.	White <i>et al.</i> (1990)
Nuclear ribosomal large subunit	nLSU	ITS4	Reverse	TCCTCCGCTTATTGATATGC	94 °C 1 min; 35 cycles of 94 °C 30 s, 48 °C 1 min, 72 °C 1.5 min; 72 °C 10 min.	Vilgalys & Hester (1990)
		LR0R	Forward	ACCCGCTGAACCTTAAGC		
Mitochondrial small subunit rDNA	mt-SSU	LR7	Reverse	TACTACCACCAAGATCT	94 °C 2 min; 36 cycles of 94 °C 45 s; 52 °C 45 s; 72 °C 1 min; 72 °C 10 min.	White <i>et al.</i> (1990)
		MS1	Forward	CAGCAGTCAAGAATATTAGTCAATG		
RNA polymerase II largest subunit	<i>rpb1</i>	MS2	Reverse	GCGGATTATCGAATTTAAATAAC	94 °C 2 min; 9 cycles of 94 °C 40 s; 60 °C 40 s; 72 °C 2 min; 10 cycles of 94 °C 40 s; 94 °C 45 s; 55 °C 1.5 min; 72 °C 5 min; 37 cycles 94 °C 45 s; 72 °C 10 min	Matheny <i>et al.</i> (2002)
		RPB1-Af	Forward	GARTGYCCDGGDCAYTTYGG		
RNA polymerase II second largest subunit	<i>rpb2</i>	RPB1-Cf	Reverse	CCNGCDATNCRTRTCCAIRTA	95 °C 2.5 min; 9 cycles of 95 °C 30 s, 52 °C 1 min; 72 °C 1 min; 40 cycles of 95 °C 30 s; 72 °C 1.5 min; 40 cycles 72 °C 1.5 min; 72 °C 5 min.	Matheny (2005)
		bRPB2-6F	Forward	TGGGGYATGGTNTGYCCYGC		
Translation elongation factor 1-alpha	<i>tef1-α</i>	bRPB2-7.1R	Reverse	CCCATRGCTTGYTTRCCCAT	94 °C 2.5 min; 94 °C 45 s; 60 °C 50 s; 72 °C 2 min; 6 cycles of 94 °C 45 s; 94 °C 30 s; 55 °C 50 s; 72 °C 1.5 min; 34 cycles 94 °C 30 s; 72 °C 5 min.	Rehner & Samuels (1994)
		EF1-983F	Forward	GCYCCYGGHCAYCGTGAYTTYAT		
		EF1-2218R	Reverse	ATGACACCRACRGRACRGTYTG		



maximum hours and obtaining the best tree using ML search. Other parameters in ML analysis used default settings, and statistical support values were obtained using nonparametric bootstrapping with 1000 replicates (Felsenstein 1985). jModeltest v. 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian Inference (BI) in MrBayes v. 3.2.7a (Ronquist *et al.* 2012). The first one-fourth of all generations was discarded as burn-in and a majority rule consensus tree of all remaining trees was calculated. Resulting trees were compared and final branches were considered significantly supported if they received bootstrap values (BS) > 70 % (ML), bootstrap values (BT) > 50 % (MP), or Bayesian posterior probabilities (BPP) > 0.95 (BI). Phylogenetic trees were visualized using FigTree v. 1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree>) exported figures edited using Adobe Illustrator CS6 software (Adobe Systems, USA).

Divergence time estimation

Molecular clock analysis for the new genus *Cotylidiella* was performed using BEAST v. 2.6.0 (Bouckaert *et al.* 2019) using a combined sequence alignment (ITS+nLSU+*tef1- α* +*rpb1+rpb2*). The BEAST input files were constructed with BEAUti. The lognormal relaxed molecular clock model and the Yule speciation prior were selected to evaluate the divergence times and their corresponding credibility intervals. jModelTest (Darriba *et al.* 2012) using Akaike information criterion was used to estimate the best-fit evolutionary model for each alignment subjected to phylogenetic analysis. Three time points were set for calibration: (1) the offset age with a Gamma distribution prior (scale = 20, shape = 1) for *Agaricales*, which was set at 90 million years ago (Mya), as indicated by the minimum age of *Archaeomarasmius leggetti*, a fossil agaricoid species preserved in Dominican amber (Hibbett *et al.* 1995, 1997) and (2), an offset age of 125 Mya, representing the minimum age of *Hymenochaetaceae* using a fossil record of *Quatsinoporites cranhamii*, a poroid species collected from Apple Bay on Vancouver Island (Smith *et al.* 2004). Convergence was evaluated using Tracer v. 1.7.2 (Rambaut & Drummond 2013) in order to confirm sufficiently large ESS values (> 200). Posterior distributions of parameters were obtained using the MCMC analysis for 200 M generations with a burn-in percentage of 10 % using the program TreeAnnotator v. 2.6.5. Posterior probabilities were viewed in FigTree v. 1.4.4.

RESULTS

Phylogeny

A total collection of 85 new specimens belonging to wood-decaying fungi was examined and sequenced. From these specimens, 246 new sequences being composed of 85 ITS, 83 nLSU, 35 mt-SSU, 13 *tef1- α* , 8 *rpb1* and 22 *rpb2* sequences were generated and subjected to phylogenetic analysis (Table S1).

Phylogeny of the core *Hymenochaetales* clade based on ITS+nLSU+mt-SSU+*tef1- α* +*rpb1+rpb2* dataset

Concurrently to the morphological study, we aimed to resolve the generic affinities of our newly collected specimen in a phylogenetic inference restricted to the core group of *Hymenochaetales*. We hence selected a taxon set comprising 26 additional, complementary species (compare also with Wang *et al.* 2023) for a phylogenetic study. The final aligned dataset comprised 126 specimens representing 116 species covering the order *Hymenochaetales*, including in total six families and nine genera. Representative sequences of *Clavulinopsis wumengshanensis*, belonging to the related order of the *Agaricales* were retrieved from GenBank and used as outgroup (He *et al.* 2024, 2025). Four Markov chains were run two times from random starting trees, each for 10 M generations for the combined ITS+nLSU+mt-SSU+*tef1- α* +*rpb1+rpb2* (Fig. 1) dataset. The best model for the ITS+nLSU+mt-SSU+*tef1- α* +*rpb1+rpb2* dataset estimated and applied in the Bayesian analysis was GTR+I+G, with an average standard deviation of split frequencies = 0.295734 (BI), and the effective sample size (ESS) across the two runs double that of the average ESS (av. ESS = 230.5). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -137880.651. Bayesian and ML analysis resulted in a similar tree topologies.

Within the order, the family *Chaetoporellaceae*, *Hymenochaetaceae*, *Hyphodontiaceae*, *Peniophorellaceae*, *Schizoporaceae* and *Tubulicrinaceae* were each recovered as monophyletic lineages. The *Hymenochaetaceae* resolved in a sister relationship to the *Tubulicrinaceae*, with the former including in total 14 genera consisting of 33 species, while *Tubulicrinaceae* included one genus consisting of in total five species. *Schizoporaceae* and *Hyphodontiaceae* resolved in a sister relationship, with *Schizoporaceae* comprising three genera and 30 species, while *Hyphodontiaceae* was shown to include one genus with four species. Sequences of our new genus, *Cotylidiella*, resolved outside of the previously mentioned families with other unassigned genera (*incertae sedis*) and formed a highly supported lineage (ML-BS = 100, BPP = 1.00) that is sister to *Cotylidia pannosa* within the *Hymenochaetales*. Our newly collected and sequenced specimens robustly resolved within the genera *Hymenochaete*, *Tubulicrinis*, *Xylodon*, *Lyomyces*, *Fasciodontia*, *Hyphodontia*, *Kneiffiella*, *Peniophorella*, and *Cotylidiella gen. nov.*, which prompted us to embark on more detailed phylogenetic studies restricted to the respective genera.

Phylogeny of the core *Kneiffiella* clade based on ITS+nLSU dataset

First, we embarked on a phylogenetic analysis restricted to the genus *Kneiffiella*, with *Xylodon granuloides* as outgroup. The aligned dataset was comprised of 49 specimens representing 30 species and consisted of concatenated ITS+nLSU sequences retrieved from GenBank (Zhang *et al.* 2025). The best model for this dataset estimated and applied in the Bayesian analysis was GTR+I+G, with an average standard deviation of split frequencies = 0.006600 (BI), and the effective sample size (ESS) across the two runs double that of the average ESS (av. ESS = 458.5). The dataset comprised an aligned length of 2276 characters, of which 1314 characters were constant, 325 were variable and parsimony-uninformative, while 637 were parsimony informative. Four Markov chains were run two times from

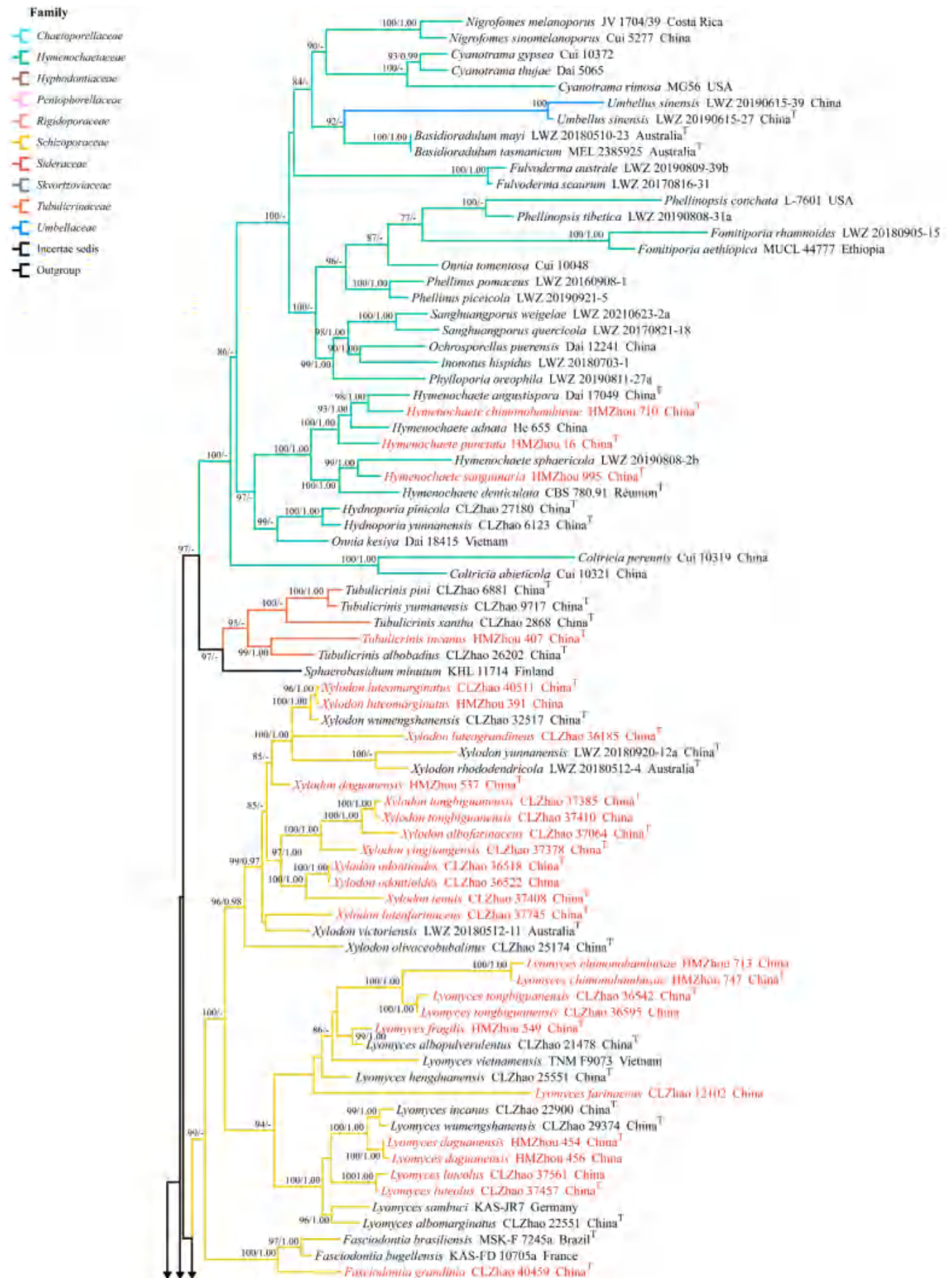


Fig. 1. Maximum likelihood phylogenetic tree of *Hymenochaetales* inferred from ITS+nLSU+mt-SSU+*tef1-α*+*rpb1*+*rpb2* sequence data. *Clavulinopsis wumengshanensis* (*Agaricales*) was used as outgroup (He et al. 2024, 2025). In total, 116 species were included in the combined analyses. Branches are labelled with Maximum likelihood bootstrap values $\geq 70\%$ and Bayesian posterior probabilities ≥ 0.95 . The newly generated sequences are in red, and ex-type strains are indicated with ^T.

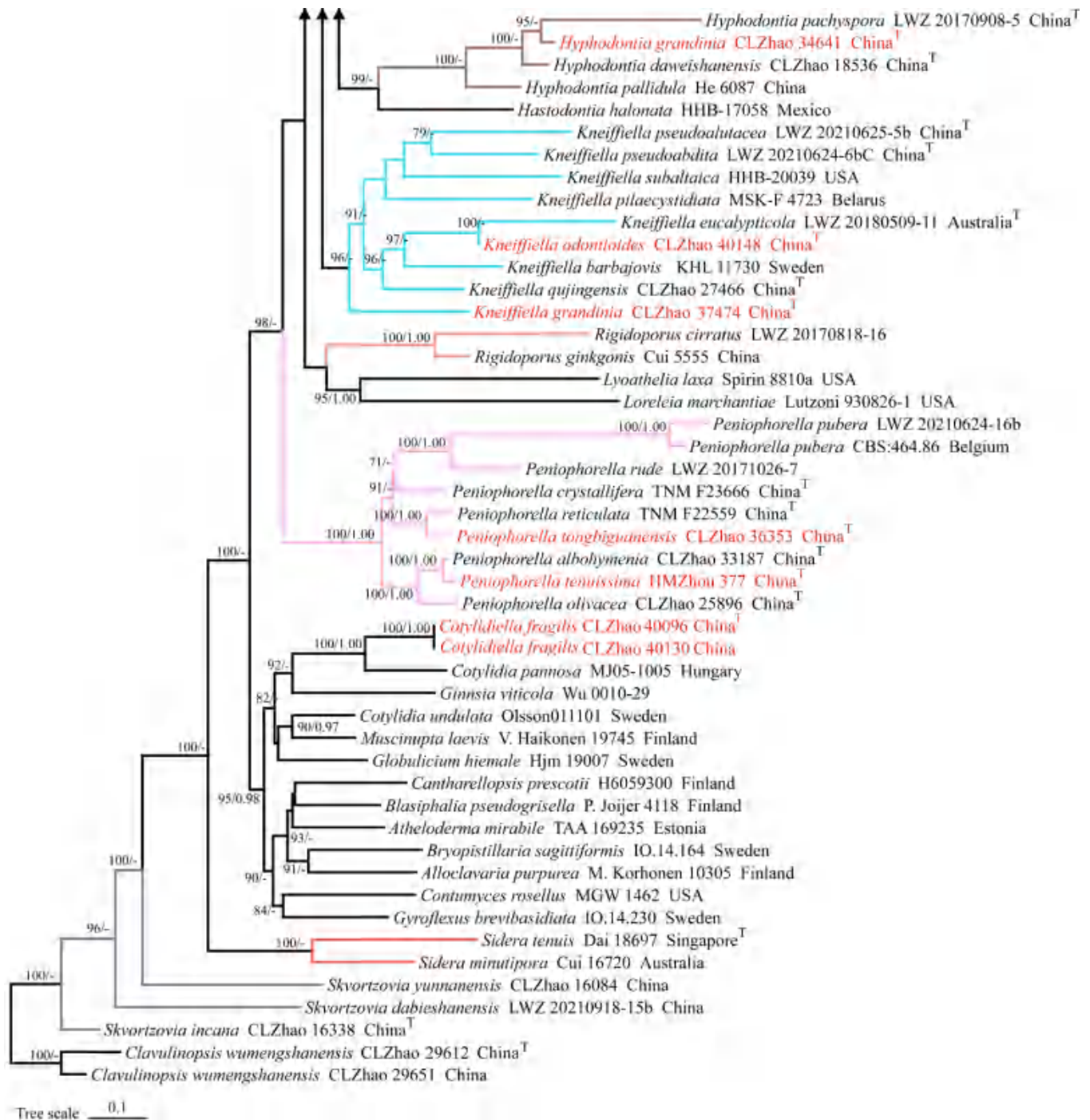


Fig. 1. (Continued).

random starting trees, each for 1.6 million generations (Fig. 2). Maximum parsimony analysis yielded a single most parsimonious tree (TL = 3319, CI = 0.4036, HI = 0.5964, RI = 0.6192, RC = 0.2909). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -17717.972. Bayesian, MP and ML analysis resulted in similar topologies. *Kneiffiella odontoides* (CLZhao 40148) resolved as a distinct lineage sister to a clade containing *K. eucalypticola*, receiving robust support (ML = 100, MP = 100, BPP = 1) and *K. grandinia*, (CLZhao 37474) resolved as a distinct lineage more basal to other *Kneiffiella* species. These results are further discussed in the taxonomic section of this paper.

Phylogeny of the core *Hymenochaete* clade based on ITS+nLSU dataset

Next, we inferred a restricted phylogeny for a combined dataset comprised of ITS+nLSU sequences for the core *Hymenochaete*, representing 245 specimens derived from 140 species. Sequences of *Hydnoporia olivacea* were retrieved from GenBank and used as an outgroup (Liu et al. 2025). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G, with an average standard deviation of split frequencies = 0.024822 (BI), and the effective sample size (ESS) across the two runs

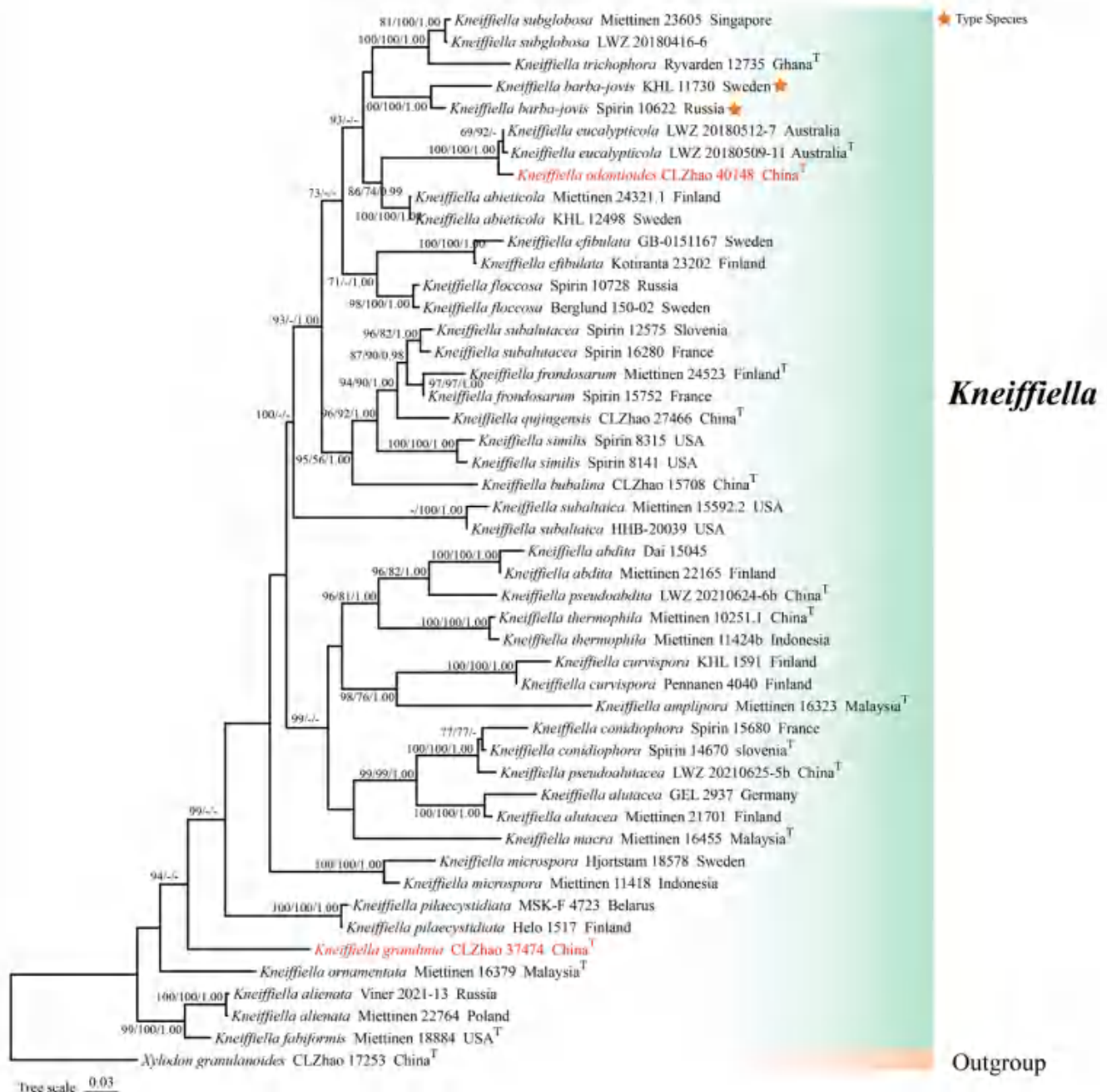


Fig. 2. Maximum likelihood phylogenetic tree of *Kneiffiella grandinia*, *K. odontoides* and related species based on ITS+nLSU sequence data. *Xylodon granulanooides* was used as outgroup. Thirty species were included in the combined analyses. Branches are labelled with Maximum likelihood bootstrap values $\geq 70\%$, maximum parsimony bootstrap values $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 . Newly generated sequences are highlighted in red, and the ex-type strains are indicated with ^T. The star indicates the generic type species.

is double that of the average ESS (av. ESS = 738). The dataset had an aligned length of 2412 characters, of which 1469 characters were constant, 146 were variable and parsimony-uninformative, while 797 were parsimony informative. Four Markov chains were run two times from random starting trees, each for 6 M generations (Fig. 3). Maximum parsimony analysis yielded a single most parsimonious tree (TL = 6659, CI = 0.2463, HI = 0.7537, RI = 0.7093, RC = 0.1747). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -33427.064. Bayesian analysis, MP and ML analysis yielded similar topologies.

Within the comprehensive phylogeny of *Hymenochaete*, our three newly sampled specimens were each placed in distinct positions: *H. chimonobambusae* (HMZhou 710) nested within an unresolved position sister to *H. subinnexa*,

H. punctata (HMZhou 16) formed a distinct lineage sister to *H. subepichlora* with robust support (ML = 99, MP = 100, BPP = 1) and *H. sanguinaria* (HMZhou 995) resolved basal to a clade containing *H. cruenta*, *H. floridea*, and *H. mougeotii* with high ML and BPP support (ML = 100, MP = -, BPP = 1). The clear phylogenetic positions of these three new species within the extensive diversity of *Hymenochaete* provide a solid basis for further discussion of their unique morphological characteristics in the taxonomic part of this study.

Phylogeny of the core *Hyphodontia* clade based on ITS+nLSU dataset

One of our newly collected specimens resolved within the genus *Hyphodontia* (Fig.1). Hence, we next examined the

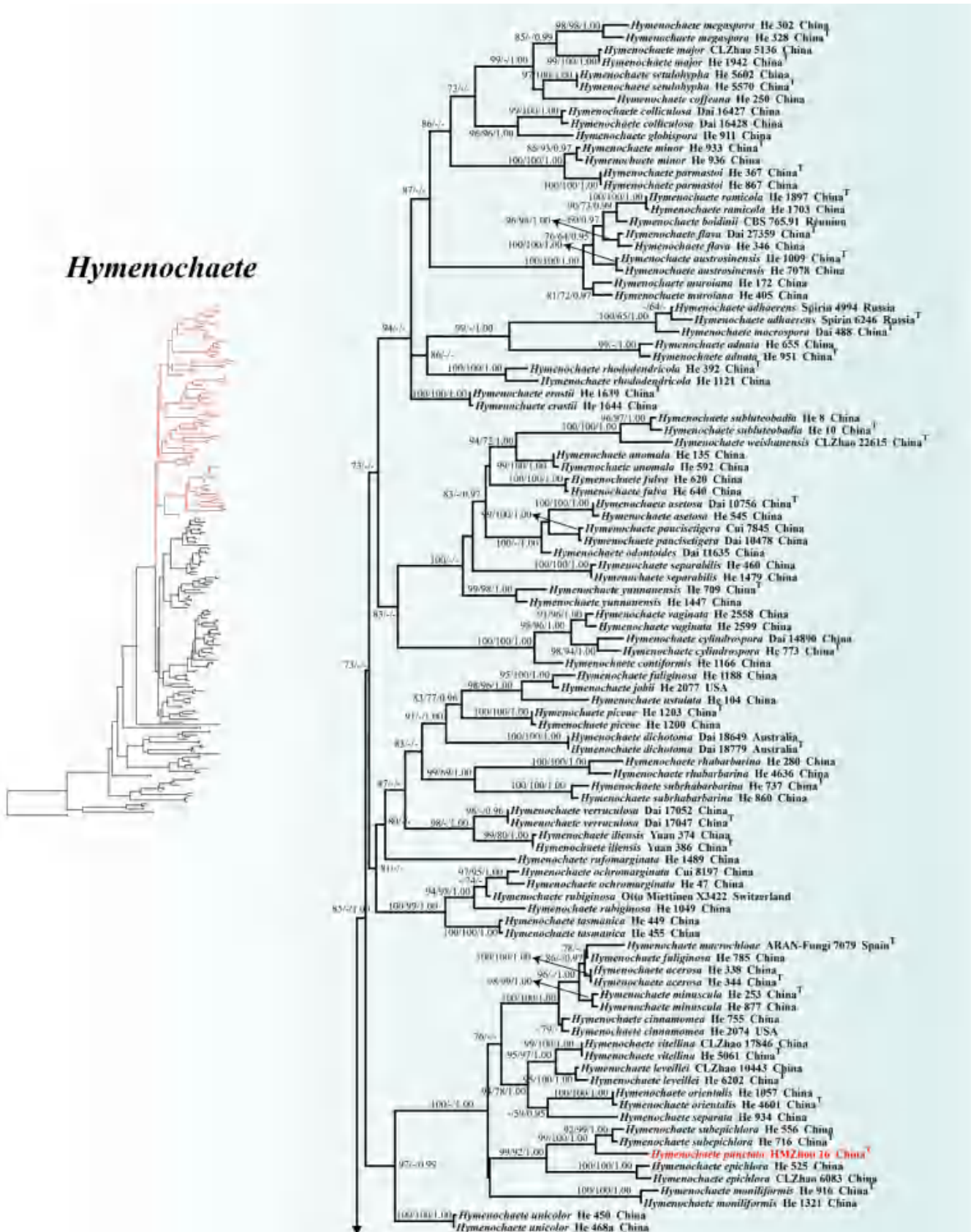


Fig. 3. Maximum likelihood phylogenetic tree of *Hymenochaete* based on ITS+nLSU sequence data. *Hydnoporia olivacea* was used as outgroup. The phylogenetic study comprised in total 140 species. Branches are labelled with Maximum likelihood bootstrap values $\geq 70\%$, Maximum parsimony bootstrap values $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 . Newly generated sequences are in red, and ex-type strains are indicated with ^T.

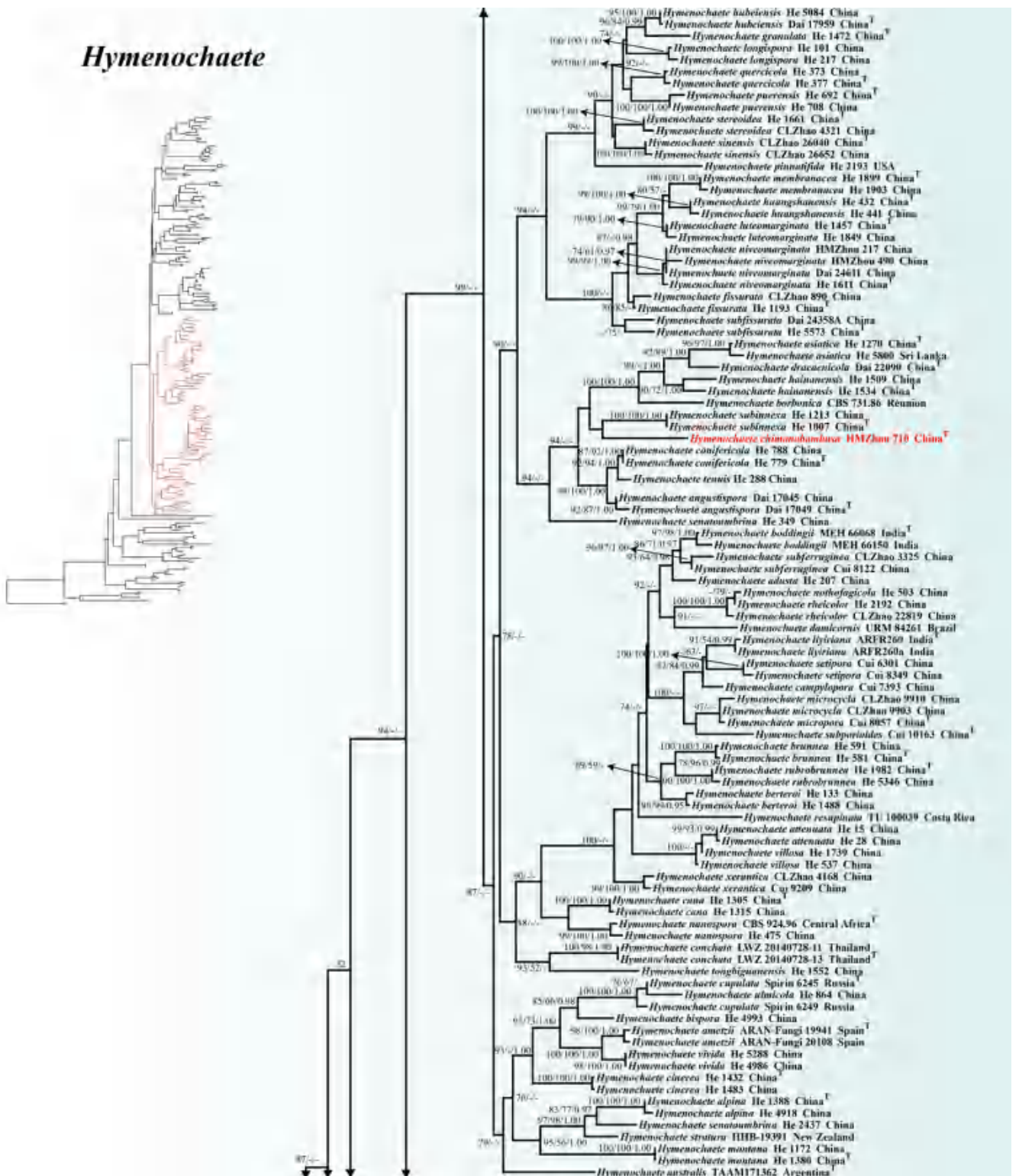


Fig. 3. (Continued).

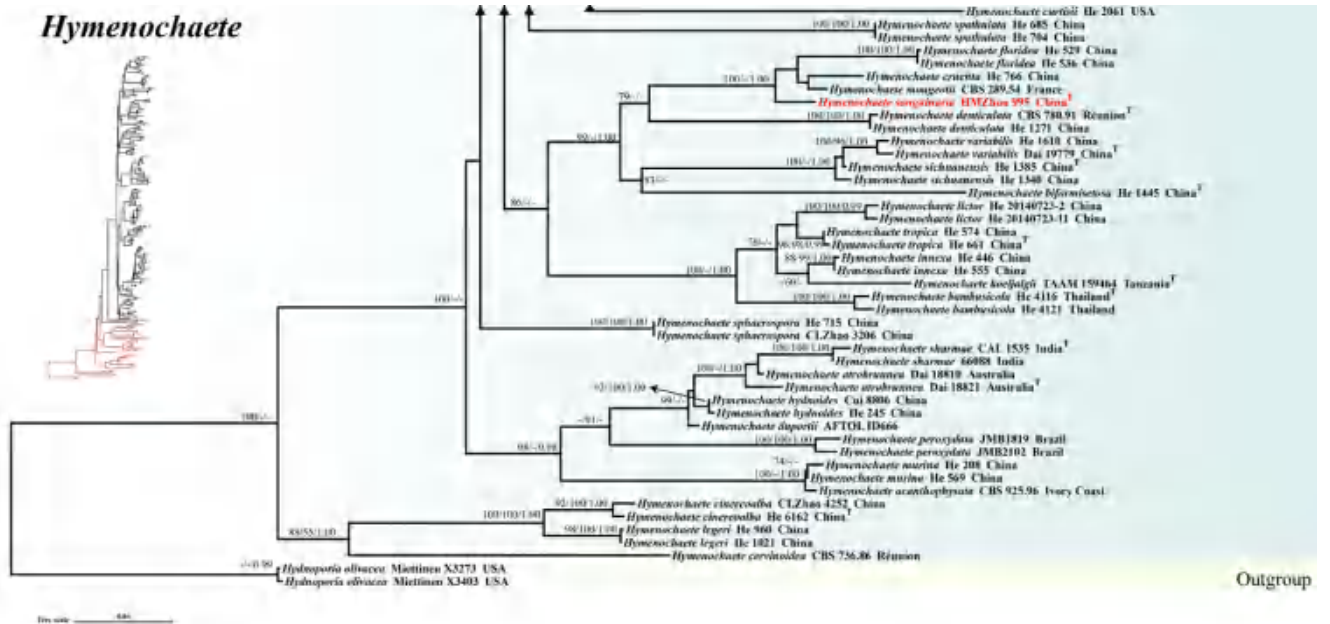


Fig. 3. (Continued).

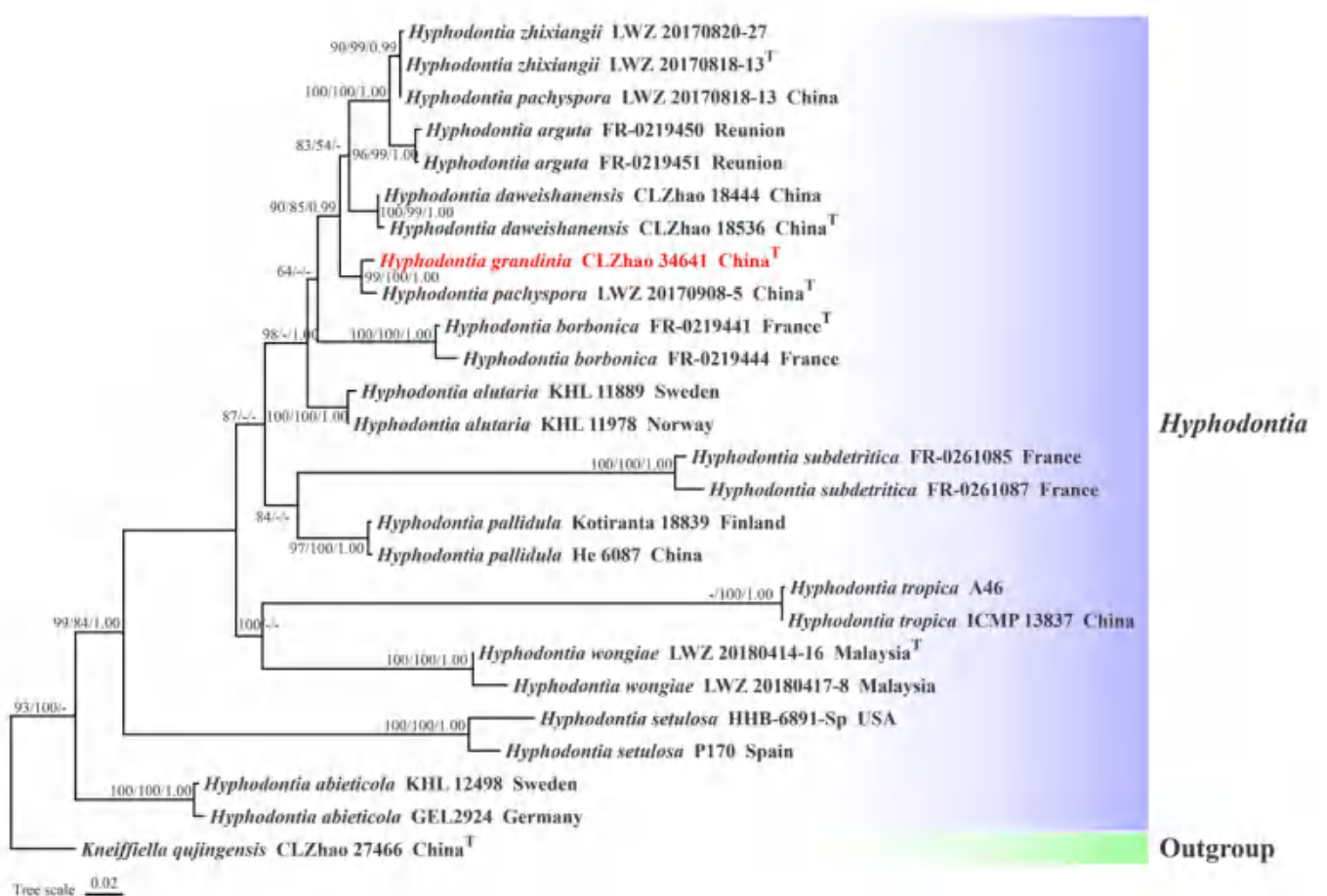


Fig. 4. Maximum likelihood phylogenetic tree of *Hyphodontia grandinia* and related species based on ITS+nLSU sequence data of *Hyphodontiaceae*. *Kneiffiella qujingensis* was used as an outgroup. Fourteen species are included in the combined analyses. Branches are labelled with maximum likelihood bootstrap values $\geq 70\%$, maximum parsimony bootstrap values $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 . The newly generated sequences are in red, and the ex-type strains are indicated with ^T.



phylogenetic relationship of this specimen in a restricted phylogenetic analysis featuring members of this genus. The subsequent combined ITS+nLSU data matrix was comprised of 26 specimens representing 14 species. Sequences of *Kneiffiella qujingensis* were retrieved from GenBank and used as outgroup (Yang et al. 2025). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was SYM+I+G, with an average standard deviation of split frequencies = 0.006012 (BI), and the effective sample size (ESS) across the two runs double that of the average ESS (av. ESS = 341). The dataset had an aligned length of 2038 characters, of which 1444 characters were constant, 172 were variable and parsimony-uninformative, while 422 were parsimony informative. Four Markov chains were run two times from random starting trees, each for 0.4 M generations (Fig. 4). Maximum parsimony analysis yielded a single most parsimonious tree (TL = 1221, CI = 0.6962, HI = 0.3038, RI = 0.7476, RC = 0.5205). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -8251.748.

Bayesian, MP and ML-based inferences resulted in similar topologies.

The phylogenetic analysis robustly placed the new species, *Hyphodontia grandinia*, within a supported clade with members of the genus *Hyphodontia*. Specifically, *H. grandinia* formed a distinct lineage sister to the known species *H. pachyspora*, with statistical support (ML = 99, MP = 100, BPP = 1). This finding is further discussed in the taxonomic section of this paper.

Phylogeny of the core *Peniophorella* clade based on ITS+nLSU dataset

The following restricted phylogenetic analysis aimed towards a more detailed resolution of our two new specimens associated with the genus *Peniophorella*. The resulting aligned dataset of combined ITS+nLSU sequences was comprised of 38 specimens representing 22 species. The best model for this dataset estimated and applied in the Bayesian

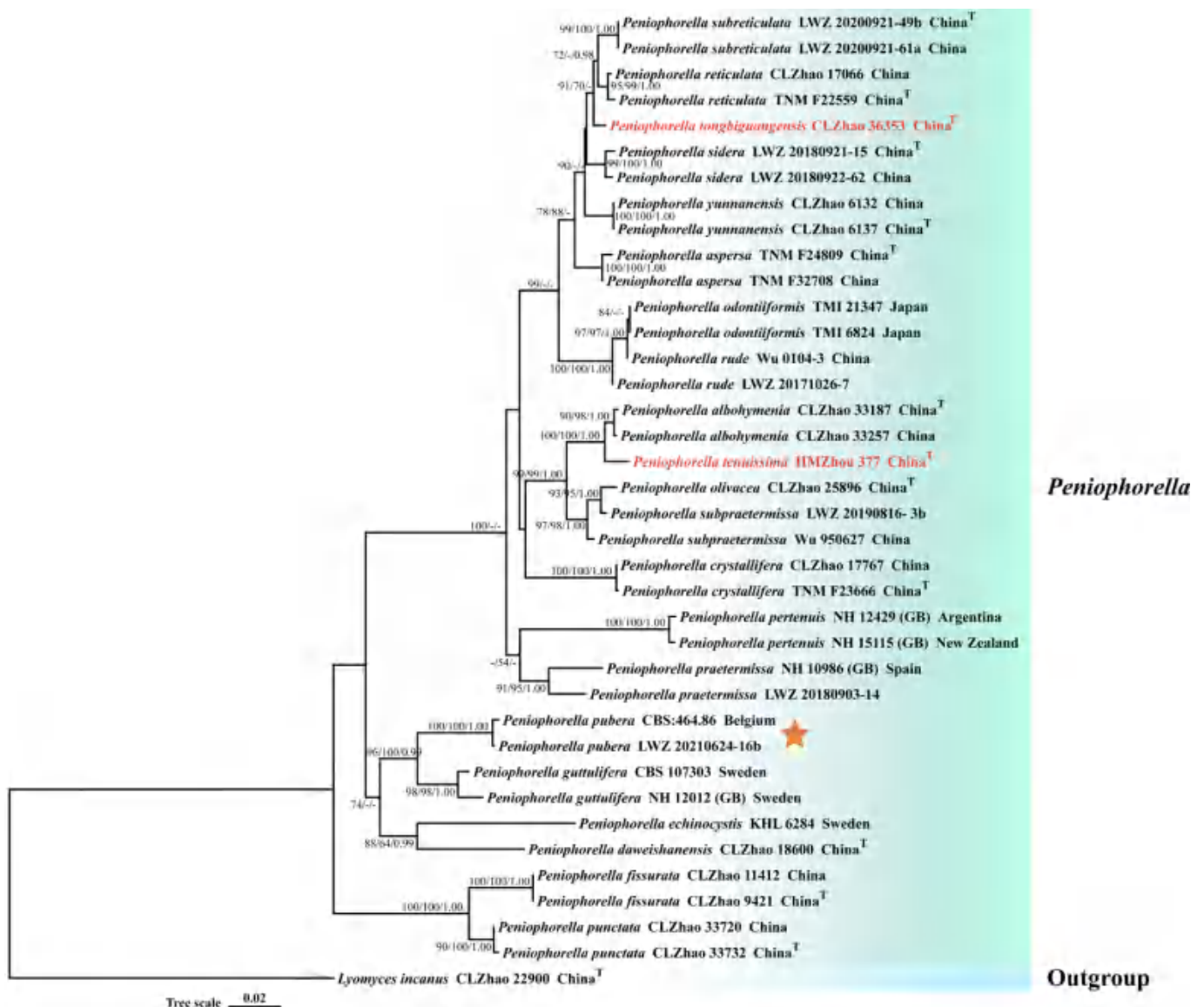


Fig. 5. Maximum likelihood phylogenetic tree of *Peniophorella tenuissima*, *P. wumengshanensis* and related species based on ITS+nLSU sequence data of *Peniophorellaceae*. *Lyomyces incanus* was used as outgroup. Twenty-two species are included in the combined analyses. Branches are labelled with Maximum likelihood bootstrap values $\geq 70\%$, maximum parsimony bootstrap values $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 . Newly generated sequences are highlighted in red, and ex-type strains are indicated with ^T. The red star indicates the generic type species.



analysis was SYM+I+G, with an average standard deviation of split frequencies = 0.006969 (BI), and the effective sample size (ESS) across the two runs double that of the average ESS (av. ESS = 208.5). The dataset had an aligned length of 1991 characters, of which 1502 characters were constant, 179 were variable and parsimony-uninformative, while 310 were parsimony informative. Sequences of *Lyomyces incanus* were retrieved from GenBank and used as an outgroup (Dong et al. 2024). Four Markov chains were run for in duplicate from random starting trees, each for 0.8 M generations (Fig. 5). Maximum parsimony analysis yielded a single most parsimonious tree (TL = 1065, CI = 0.6197, HI = 0.4618, RI = 0.7827, RC = 0.4851). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -8002.204. Bayesian, MP and ML inferences yielded similar topologies.

The two new species were each placed in distinct, supported clades: *P. tongbiguanensis* (CLZhao 36353) formed a distinct lineage sister to a clade comprising *P.*

subreticulata and *P. reticulata*. *Peniophorella tenuissima* (HMZhou 377) was resolved as sister to *P. albohymeria*, with robust support (ML = 100, MP = 100, BPP = 1). These results are further discussed in the taxonomic section of this paper.

Phylogeny of the core *Schizoporaceae* clade based on ITS+nLSU dataset

Next, we aimed to study the phylogenetic affinities of our newly collected specimens resolving with the genera *Xylodon*, *Lyomyces* and *Fasciodontia*, which are all members of the *Schizoporaceae*. The resulting dataset of combined ITS+nLSU sequences was comprised of 76 specimens representing 60 species. Sequences of *Hyphodontia daweshanensis* were retrieved from GenBank and used as an outgroup (Yang et al. 2025). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G, with an average standard deviation of split frequencies = 0.010941 (BI) and the effective sample

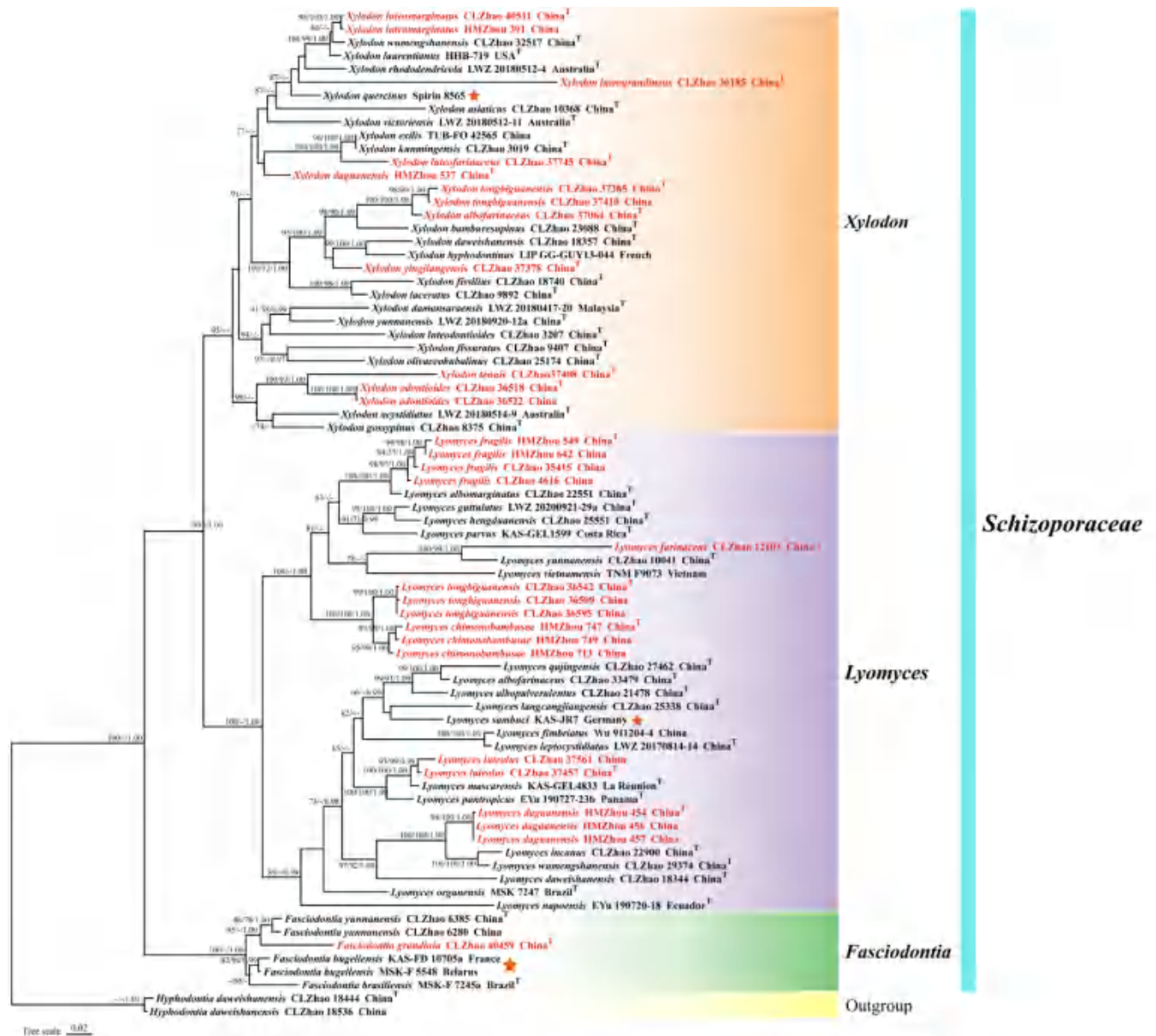


Fig. 6. Maximum likelihood phylogenetic tree of *Schizoporaceae* species based on ITS+nLSU sequence data. *Hyphodontia daweshanensis* was used as outgroup. Branches are labelled with maximum likelihood bootstrap values $\geq 70\%$, maximum parsimony bootstrap values $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 . The newly generated sequences are in red, and the ex-type strains are indicated with ^T. The red star indicates the generic type species.



★ Type Species

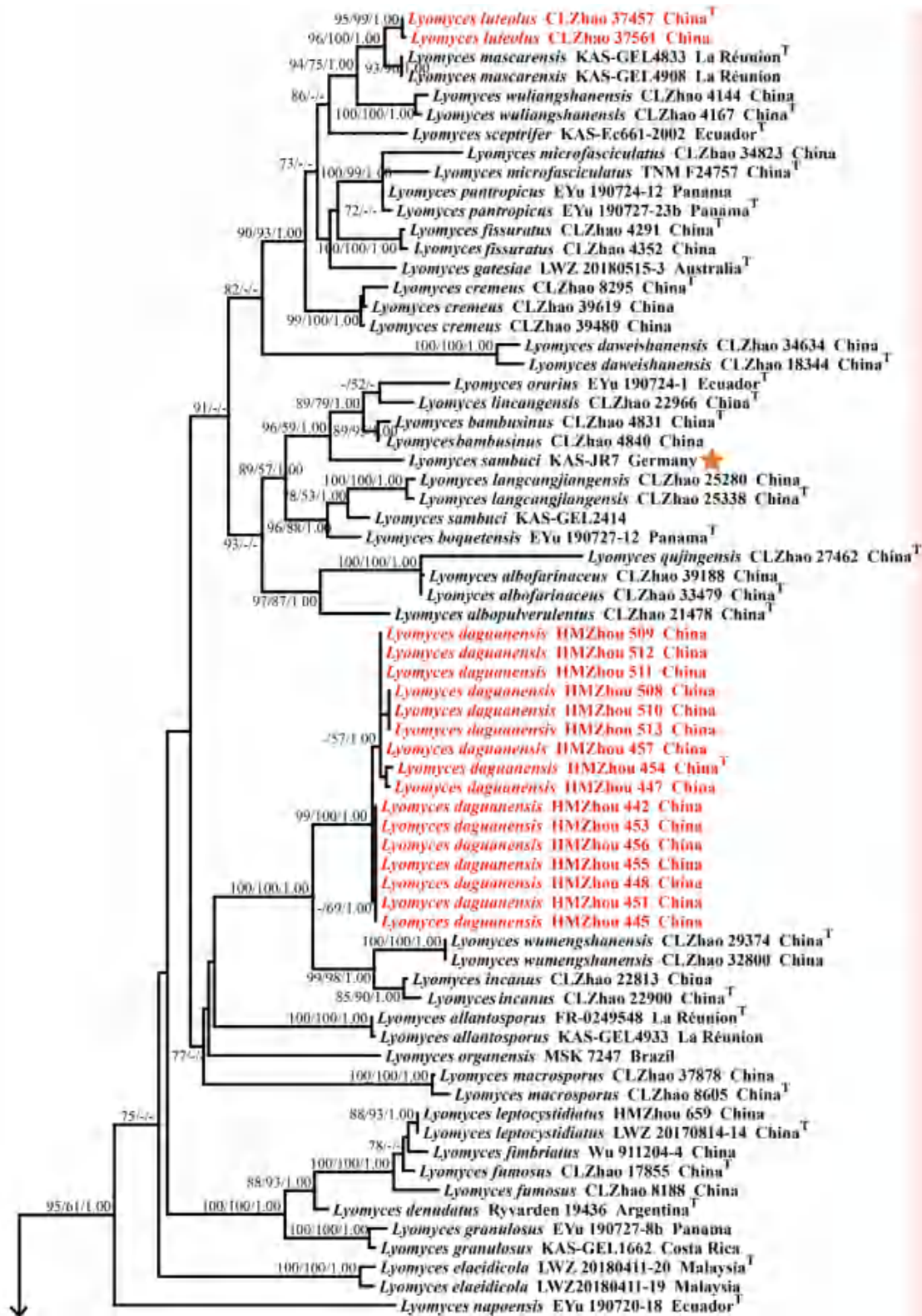


Fig. 7. Maximum likelihood phylogenetic tree of *Lyomyces* based on ITS sequence data. *Peniophorella albohymenia* was used as outgroup. Branches are labelled with Maximum likelihood bootstrap values $\geq 70\%$, Maximum parsimony bootstrap values $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 . The newly generated sequences are in red, and the ex-type strains are indicated with ^T. The star indicates the generic type species.

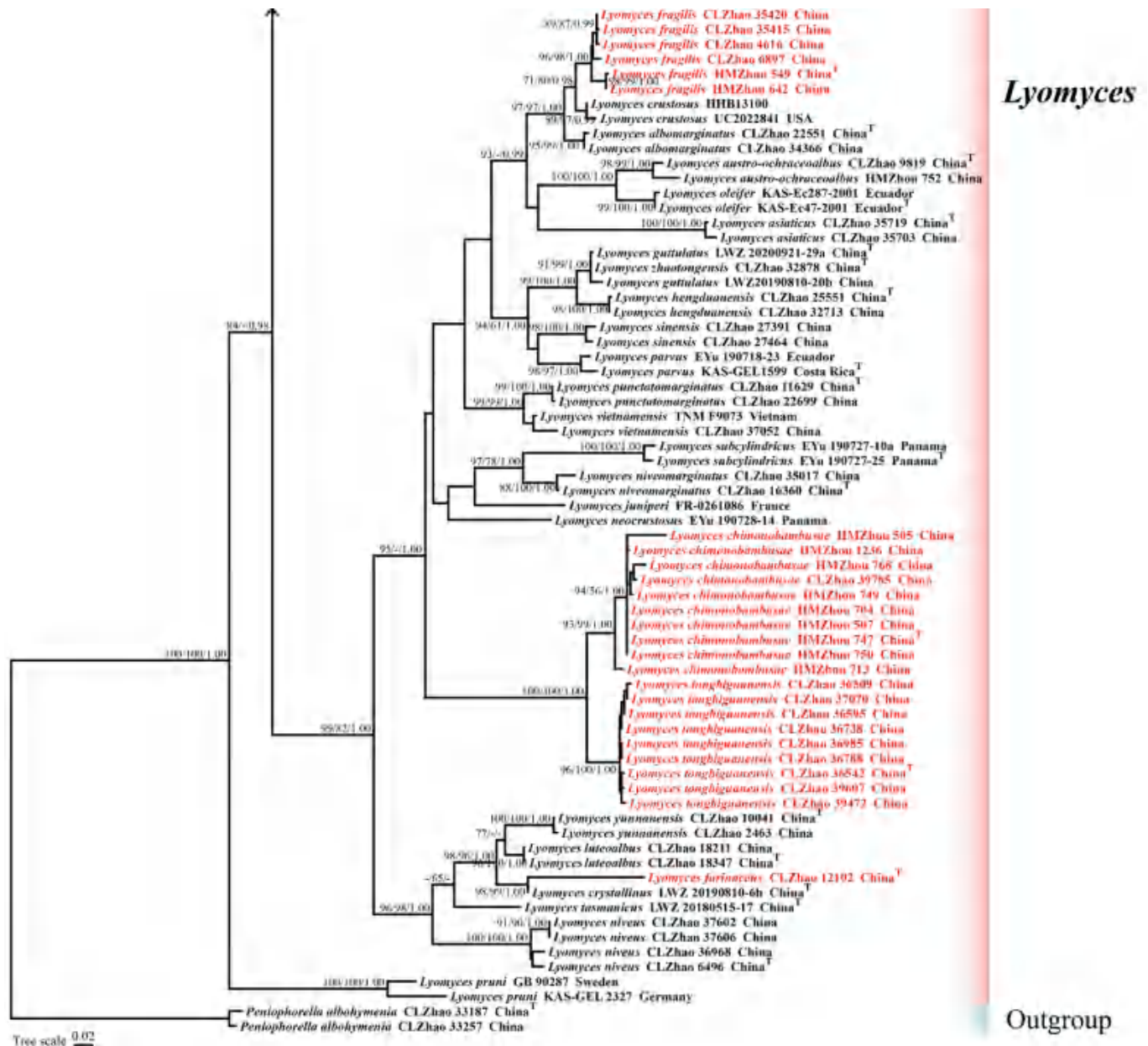


Fig. 7. (Continued).

size (ESS) across the two runs double that of the average ESS (av. ESS = 388). The dataset had an aligned length of 2095 characters, of which 1179 characters were constant, 251 were variable and parsimony-uninformative, while 665 were parsimony informative. Four Markov chains were run two times from random starting trees, each for 1 M generations (Fig. 6). Maximum parsimony analysis yielded a single most parsimonious tree (TL = 4393, CI = 0.3417, HI = 0.6583, RI = 0.6444, RC = 0.2202). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -22029.502. Bayesian, MP and ML analysis yielded similar topologies.

Within the family *Schizoporaceae*, the genera *Fasciodontia*, *Lyomyces* and *Xylodon* each resolved as monophyletic groups. *Lyomyces* and *Xylodon* were resolved as sister genera, while *Fasciodontia* formed a distinct lineage sister to the *Lyomyces*-*Xylodon* clade. All specimens (*L. chimonobambusae*, *L. daguanensis*, *L. farinaceus*, *L. fragilis*, *L. luteolus*, and *L. tongbiguanensis*; *X. albofarinaceus*, *X. luteofarinaceus*, *X. luteomarginatus*, *X. odontoides*, *X. tenuis* and *X. tongbiguanensis*) resolved in robustly (> 90 % MP-BS

> 95 % ML-BS / 1 BP) supported clades, except for *Xylodon luteograndineus*, *X. daguanensis*, *X. yingjiangensis* resolving in distinct, unsupported lineages and *Fasciodontia grandinia* receiving good MP-BS and BP values, but lacking ML-BS support (95 % MP-BS / - / 1 BP). This phylogenetic framework is further utilized in the taxonomic section of this paper to discuss morphological and taxonomic species delimitations within the family *Schizoporaceae*.

Phylogeny of the core *Lyomyces* clade based on ITS dataset

Next, we moved on to a more detailed analysis of our specimens showing phylogenetic affinities to *Lyomyces*. The resulting aligned ITS sequence dataset was comprised of 138 specimens representing 60 species. Sequences of *Peniophorella albohymenia* were retrieved from GenBank and used as an outgroup (Deng et al. 2025). The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR+I+G, with an average standard deviation

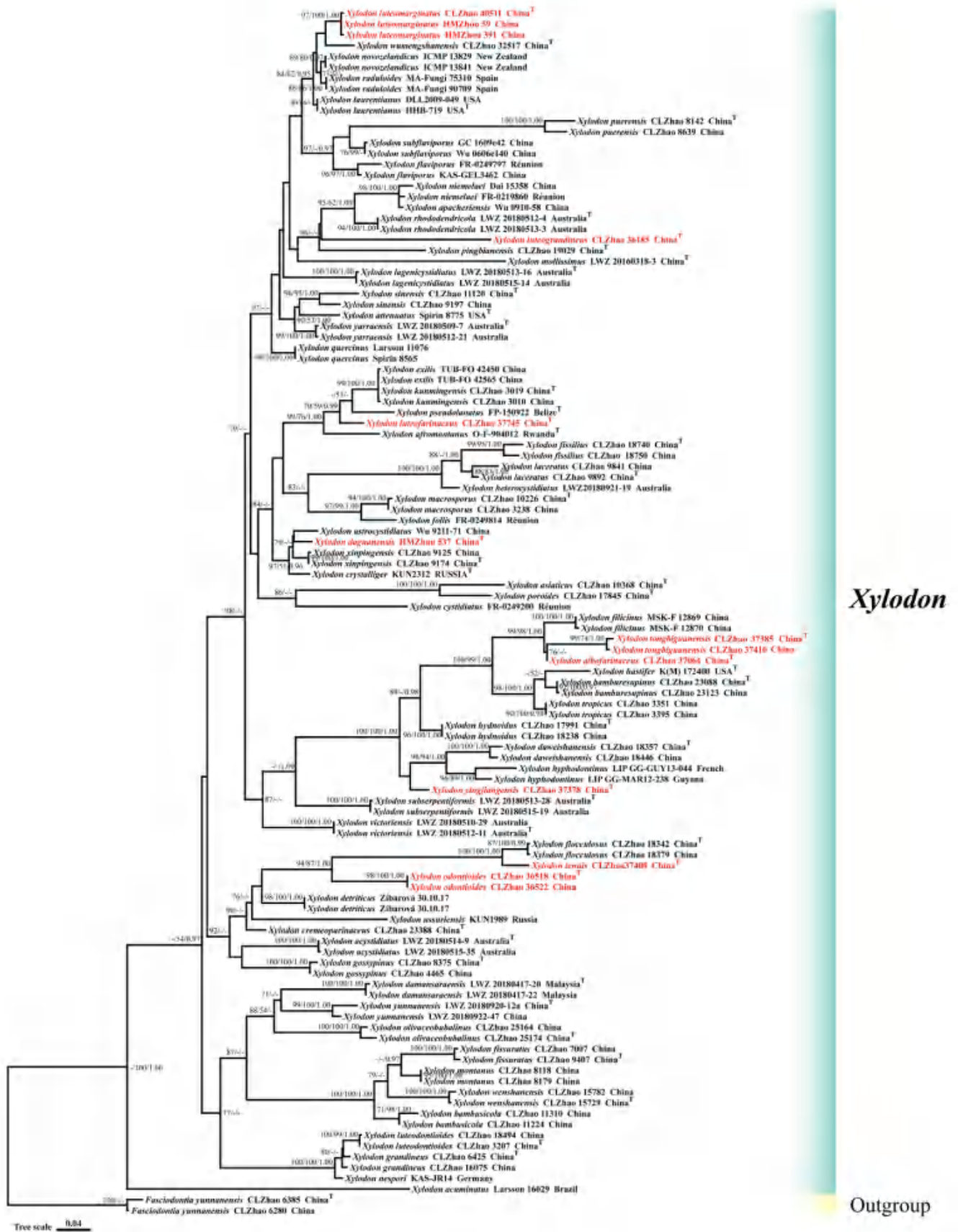


Fig. 8. Maximum likelihood phylogenetic tree of *Xylodon* based on ITS sequence data. *Fasciodontia yunnanensis* was used as outgroup. Branches are labelled with Maximum likelihood bootstrap values $\geq 70\%$, Maximum parsimony bootstrap values $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 . The newly generated sequences are in red, and the ex-type strains are indicated with †.



of split frequencies = 0.004469 (BI), and the effective sample size (ESS) across the two runs double that of the average ESS (av. ESS = 148). The dataset had an aligned length of 712 characters, of which 259 characters were constant, 63 were variable and parsimony-uninformative, while 390 were parsimony informative. Four Markov chains were run for two times from random starting trees, each for 8 M generations (Fig. 7) Maximum parsimony analysis yielded a single most parsimonious tree (TL = 2781, CI = 0.3089, HI = 0.6911, RI = 0.7950, RC = 0.2456). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -12605.785. Bayesian, MP and ML analysis resulted in similar topologies. Based on the phylogenetic analysis of the ITS dataset (138 specimens, 60 species) of the genus *Lyomyces*, our collected specimen resolved in five recognizable, supported (> 85 % MP-BP / > 85 % ML-BP / >0.95 BP) distinct clades (*L. luteolus*, *L. daguanensis*, *L. fragilis*, *L. chimonobambusae*, *L. tongbiguanensis*) and one distinct lineage, the latter which resolved sister to *L. crystallinus* with support (ML = 89, MP = 99, BPP = 1), indicative of clear species boundaries. Specifically, *L. chimonobambusae* was sister to the new species *L. tongbiguanensis*, with statistical support (ML = 100, MP = 100, BPP = 1); *L. daguanensis* grouped with a clade containing *L. incanus* and *L. wumengshanensis*, receiving robust support (ML = 100, MP = 100, BPP = 1); *L. farinaceus* was resolved as sister to the *L. yunnanensis*, with high statistical support (ML = 98, MP = 99, BPP = 1); *L. fragilis* formed a distinct lineage sister to the known species

L. albomarginatus and *L. luteolus* grouped closely with *L. mascarensis*. This phylogenetic framework provides a solid basis for discussing taxonomic relationships within the genus, which can be found in the taxonomic section of this paper.

Phylogeny of the core *Xylodon* clade based on ITS dataset

In total, 13 of our described specimens showed affinities to *Xylodon*, which we aimed to resolve in greater phylogenetic detail using ITS sequences of 112 specimens representing 68 species retrieved from GenBank. Sequences of *Fasciodontia yunnanensis*, accommodated in a sister genus, were used as outgroup (Luo & Zhao 2021). The dataset had a length of 705 characters, of which 286 characters were constant, 55 were variable and parsimony-uninformative, while 364 were parsimony informative. The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR+I+G, with an average standard deviation of split frequencies = 0.020980 (BI), and the effective sample size (ESS) across the two runs double that of the average ESS (av. ESS = 203.5). Four Markov chains were run two times from random starting trees, each for 8 M generations (Fig. 8). Maximum parsimony analysis yielded a single most parsimonious tree (TL = 2852, CI = 0.2598, HI = 0.7402, RI = 0.6495, RC = 0.1687). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -11644.017. Bayesian, MP and ML analysis resulted in similar topologies.

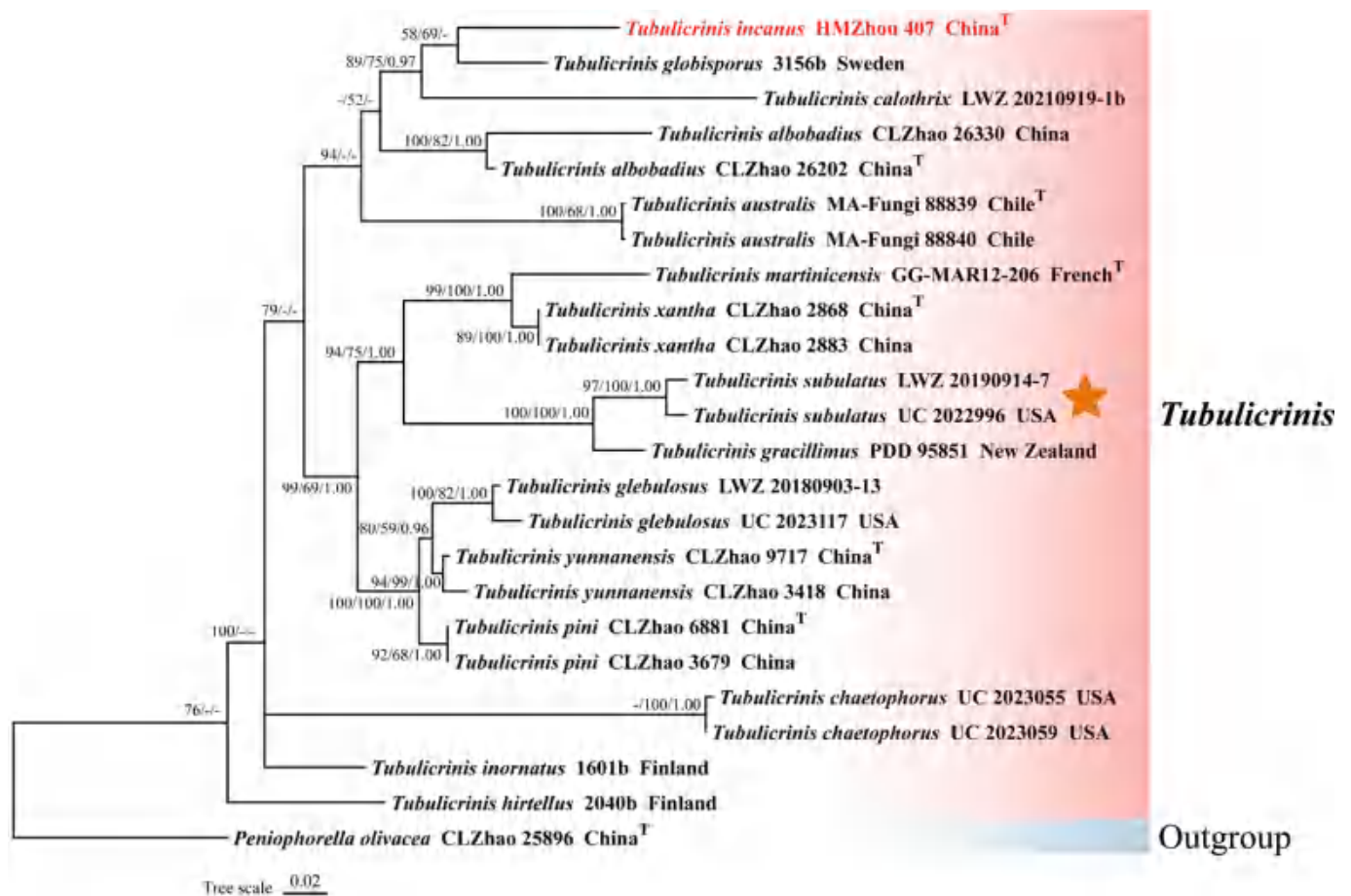


Fig. 9. Maximum likelihood phylogenetic tree of *Tubulicrinis incanus* and related species based on ITS+nLSU sequence data of *Tubulicrinaceae*. *Peniophorella olivacea* was used as outgroup. Branches are labelled with Maximum likelihood bootstrap values equal to or higher than 70 %, Maximum parsimony bootstrap values ≥ 50 % and Bayesian posterior probabilities ≥ 0.95 . The newly generated sequences are in red, and the ex-type strains are indicated with ^T. The star indicates the generic type species.



The phylogenetic reconstruction based on this dataset was resolved at species level, but showed lower resolution at its backbone. Within this framework, our specimens were placed into nine distinct positions. *Xylodon albofarinaceus* was resolved as sister to the new species *X. tongbiguanensis*. *Xylodon daguanensis* grouped with the known species *X. astrocystidiatus*. The new species *X. luteofarinaceus* formed a single branch next to a cluster comprising *X. afromontanus*, *X. exilis*, *X. kunmingensis* and *X. pseudolanatus* (ML = 70, MP = 59, BPP = 0.99). *Xylodon luteograndineus* formed a distinct lineage that was placed basal to a clade grouping *X. apacheriensis*, *X. mollissimus*, *X. niemelaei*, *X. pingbianensis* and *X. rhododendricola*. *Xylodon luteomarginatus* resolved in a sister relationship to *X. wumengshanensis*, with statistical support (ML = 97, MP = 100, BPP = 1). The new species *X.*

odontioides grouped with a clade containing *X. flocculosus* and *X. tenuis* (ML = 94, MP = 87, BPP = 1) and *X. tenuis* resolved as sister to *X. flocculosus*, with statistical support (ML = 100, MP = 100, BPP = 1). Last, *X. yingjiangensis* resolved within a clade containing *X. dawuishanensis* and *X. hyphodontinus*. These results are further discussed within the taxonomic section of this paper.

Phylogeny of the core *Tubulicrinis* clade based on ITS+nLSU dataset

Lastly, we aimed to resolve the phylogenetic placement of our specimen showing affinities to *Tubulicrinis* using concatenated ITS+nLSU sequences. The aligned dataset comprised in total 24 specimens representing 16 species.

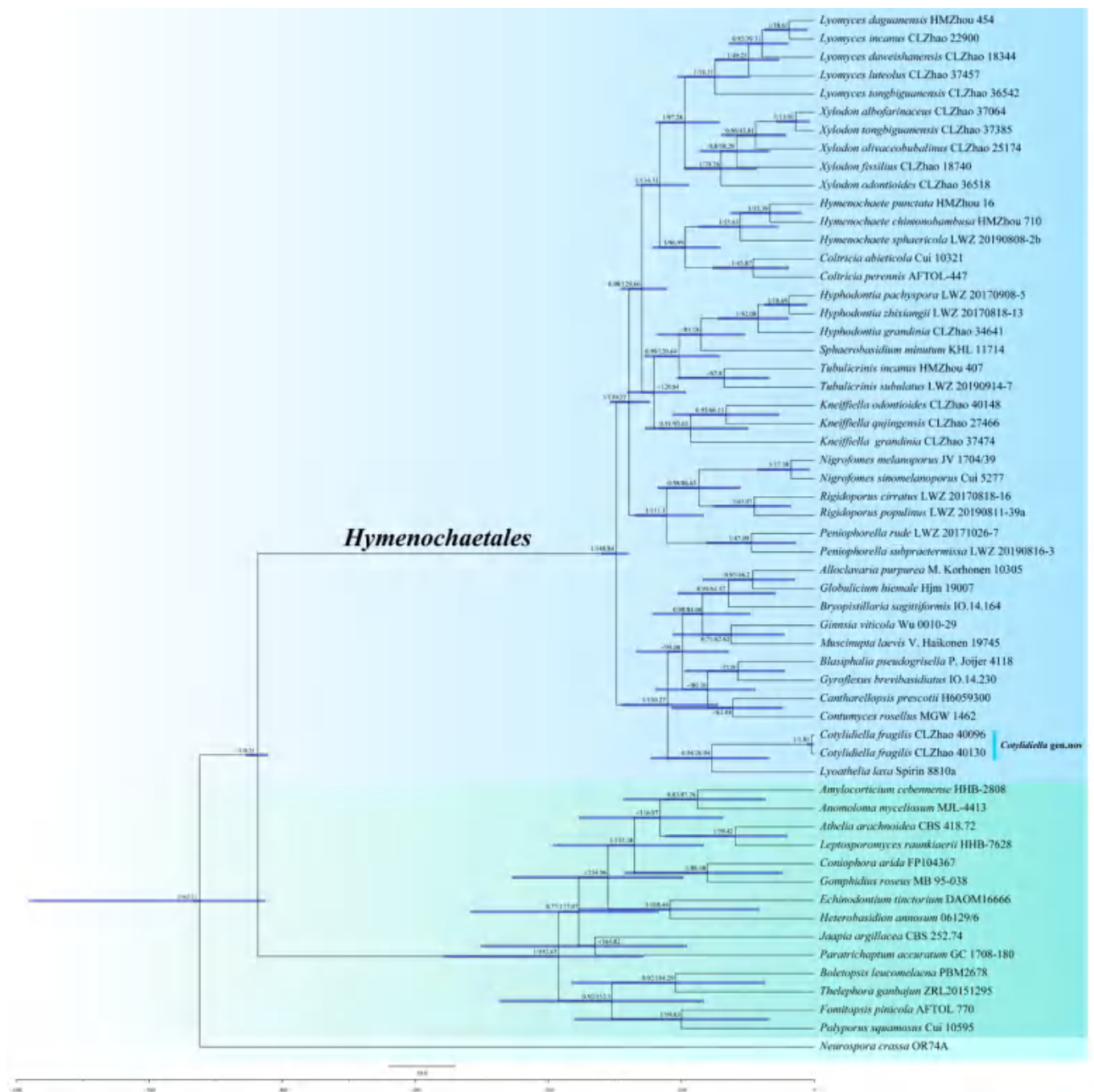


Fig. 10. Chronogram and estimated divergence times for families within *Hymenochaetales* generated by molecular clock analysis using the ITS+nLSU+*tef1- α* +*rbp1*+*rbp2* dataset. The estimated divergence times of 95 % highest posterior density were indicated as node bars for all clades. Bayesian posterior probabilities above 0.7 and mean divergence times of clades (crown ages) were labelled before and after the slashes, respectively, at the nodes.



Sequences of *Peniophorella olivacea* were retrieved from GenBank and used as an outgroup (Dong *et al.* 2024). The dataset contained in total 2086 characters, of which 1390 characters were constant, 218 were variable and parsimony-uninformative, while 478 were parsimony informative. The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G with an average standard deviation of split frequencies = 0.008895 (BI) and the effective sample size (ESS) across the two runs double that of the average ESS (av. ESS = 487.5). Four Markov chains were run two times from random starting trees, each for 0.4 M generations (Fig. 2). Maximum parsimony analysis yielded a single most parsimonious tree (TL = 1590, CI = 0.6377, HI = 0.3623, RI = 0.6193, RC = 0.3949). The maximum likelihood analysis resulted in a tree with a log-likelihood value of -9817.182. Bayesian, MP and ML analysis resulted in similar topologies.

Within our phylogenetic inference, our new species, *Tubulicrinis incanus* resolved in a distinct lineage in a sister relationship to *T. globisporus*. This finding is further discussed in the taxonomic section of this paper

The divergence time of *Cotylidiella* based on ITS+nLSU+*tef1-α+rpb1+rpb2* dataset

We further examined generic divergence times in *Hymenochaetales* including our new genus *Cotylidiella* by molecular clock analysis using the combined ITS+nLSU+*tef1-α+rpb1+rpb2* dataset, which included 57 collections, of which 42 belonged to *Hymenochaetales*, other 15 belonged to the *Agaricales*, *Amylocorticiales*, *Atheliales*, *Boletales*, *Gloeophyllales*, *Polyporales*, *Russulales*, *Thelephorales* of the *Basidiomycota* class. This dataset resulted in an alignment of 5983 characters after concatenation. GTR+I+G was determined as the best evolutionary model fit. Chain convergence was reached as indicated by the ESSs of all parameters above 897. The mean crown age of *Cotylidiella* in *Hymenochaetales* was determined as 76.94 Mya in mean, with a 95 % highest posterior density (HPD) of 33.97–122.51 Mya. This result is consistent with the divergence times of the other, associated genera.

TAXONOMY

Hymenochaetales Oberw., *Beitr. Biol. Pfl.*: **89**. 1977.

Hymenochaetales incertae sedis

Cotylidiella L. Wang & C.L. Zhao, *gen. nov.* MB 861446.

Chinese name: 小杯革菌属 (Xiao bei ge jun shu).

Etymology: The genus epithet “*Cotylidiella*” refers to the similarity of the new genus to *Cotylidia*.

Type species: *Cotylidiella fragilis* L. Wang & C.L. Zhao

Description: *Basidiomata* annual, pileate, infundibuliform, often in groups becoming confluent, stipitate, pileal surface cream at the margin, smooth to rugose, sometimes zonate, very thin; stipe tiny, eccentric to lateral, white to cream

towards base, pruinose; without odour or taste when fresh, becoming clay-buff to olivaceous buff to pinkish buff upon drying. Margin fimbriate, undulating, clay-buff. *Hyphal system* monomitic; simply septate generative hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* absent. *Basidia* clavate to subcylindrical, colourless, thin-walled, with four sterigmata and a basal simple septum; basidioles dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* subcylindrical to ellipsoid, colourless, thin-walled, smooth, with oil drops, IKI–, CB–.

Notes: Two fungal specimens from Xizang, Southwest China were found to form a distinct lineage with support within the order *Hymenochaetales* based on our ITS+nLSU+mt-SSU+*tef1-α+rpb1+rpb2* sequence data and phylogenetic analysis (Fig. 1). Morphologically, the key characters distinguishing *Cotylidia* from *Cotylidiella* are infundibuliform or spatulate, stipitate, light-coloured basidiomata and the presence of cystidia which are projecting beyond the hymenium (Kout & Zibarová 2013).

Cotylidiella fragilis L. Wang & C.L. Zhao, *sp. nov.* MB 861447. Figs 11–13.

Chinese name: 脆小杯革菌 (Cui xiao bei ge jun).

Etymology: The species epithet “*fragilis*” refers to the fragile basidiomata of the type specimen.

Description: *Basidiomata* annual, pileate, infundibuliform, often in groups becoming confluent, stipitate, pileal cream at the margin, sometimes zonate, very thin; stipe tiny, eccentric to lateral, white to cream towards base, pruinose, without odour or taste when fresh; becoming clay-buff to olivaceous buff to pinkish buff upon drying, fragile; up to 2.5 cm long, 1.5 cm wide and 500 μm thick. *Pileal surface* smooth to rugose. Margin fimbriate, undulating, clay-buff, up to 1 mm wide. *Hyphal system* monomitic; simply septate generative hyphae, colourless, thin-walled, frequently branched, interwoven, 6–8.6 μm diam., IKI–, CB–; tissue unchanged in KOH. *Cystidia* absent. *Basidia* clavate to subcylindrical, colourless, thin-walled, with four sterigmata and a basal simple septum, 53–77 × 7–10 μm; basidioles dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* subcylindrical to ellipsoid, colourless, thin-walled, smooth, with oil drops, IKI–, CB–, 10–12.5(–13) × 5–6.5 μm, L = 11.29 μm, W = 5.70 μm, Q = 1.98–2.10 (n = 60/2).



Fig. 11. Basidiomata of *Cotylidiella fragilis* CLZhao 40096 (holotype SWFC 00040096). Scale bar = 1 cm.

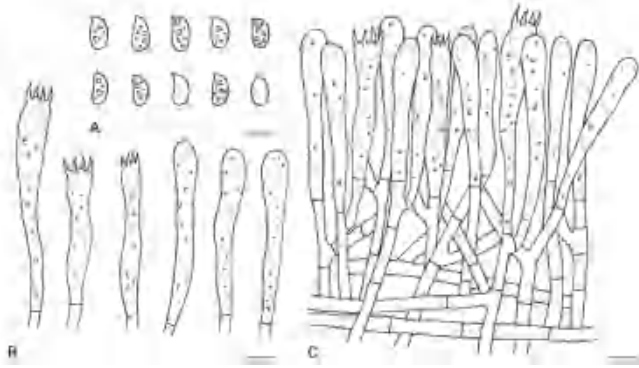


Fig. 12. Microscopic structures of *Cotyldiella fragilis* CLZhao 40096 (holotype SWFC 00040096). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** A section of the hymenium. Scale bars = 10 μ m.

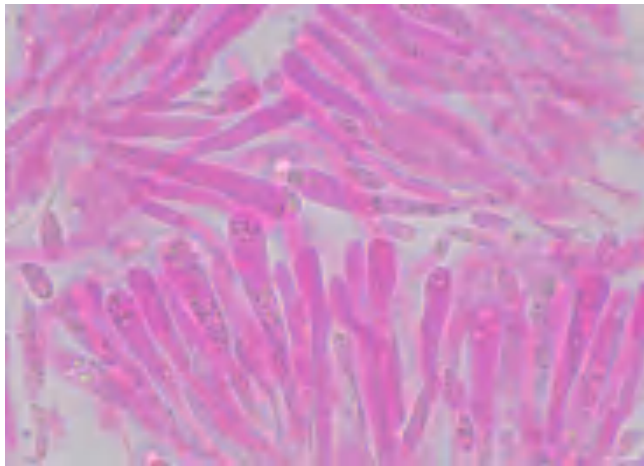


Fig. 13. Microscopic structures of *Cotyldiella fragilis* CLZhao 40096 (holotype SWFC 00040096). Scale bar = 10 μ m.

Typus: **China**, Xizang Autonomous Region, Linzhi, Sejilashan, 29°37'12"N, 94°39'1"E, 4720 m.a.s.l., on the ground, 12 Aug. 2024, C.L. Zhao, CLZhao 40096 (**holotype** SWFC 00040096).

Additional specimen examined: **China**, Xizang Autonomous Region Linzhi, Sejilashan, 29°37'12"N, 94°39'1"E, 4720 m.a.s.l., on the ground, 12 Aug. 2024, C.L. Zhao, CLZhao 40130 (SWFC 00040130).

Notes: Our new specimen (CLZhao 40096) resolved in a sister relationship to *C. pannosa* in our combined ITS+nLSU+mt-SSU+*tef1-a+rpb1+rpb2* phylogenetic analysis (Fig. 1). However, morphologically, *C. pannosa* can be distinguished from this new taxon by its infundibuliform basidiomata with bright red orange pileal surface, present tubular hymenial cystidia and smaller basidiospores (8–10 × 4–4.6 μ m vs 10–12.5 × 5–6.5 μ m, Kout & Zibarová 2013). Thus, we accommodate this specimen under the new epithet *C. fragilis*.

Chaetoporellaceae Jülich, *Biblioth. Mycol.* **85**: 359. 1982.

Kneiffiella P. Karst., *Bidr. Känn. Finl. Nat. Folk* **48**: 371. 1889.

Notes: *Kneiffiella* was established by Petter Karsten (1889), with *Kneiffiella barba-jovis* as the type species, which

nowadays comprises 42 accepted species (Viner *et al.* 2024). The typical feature of this genus is the structure of the hymenophore surface, which can range between smooth, floccose, tuberculate, grandinoid, coralloid, odontoid or irpicoid basidiomata; whitish, creamish, yellowish, gray, buff, brown or ochraceous, a monomitic to pseudodimitic hyphal system; and cylindrical, ellipsoid or allantoid basidiospores (Hjortstam & Ryvarden 2002, Viner *et al.* 2024). The genus *Kneiffiella* is not uniform in terms of morphology, as pruinose to hydroid or even poroid basidiomata have been reported (Viner *et al.* 2024). Recent molecular studies including long stretches of four unlinked loci (mt-SSU, *rpb1*, *rpb2*, and *tef1- α* ; Viner *et al.* 2024, Yang *et al.* 2025) have further challenged a traditional morphocentric taxonomy. Based on these new results, Veiner and colleagues segregated the new genus *Egonia* from *Kneiffiella* and concurrently described 13 new species, proposed one new combination, and presented a taxonomic key for the remaining 29 recognized species for the latter (Viner *et al.* 2024). Here, we describe two new species with the epithets *Kneiffiella grandinia* and *K. odontoides* based on morphological and molecular data.

Kneiffiella grandinia L. Wang & C.L. Zhao, *sp. nov.* MB 861448. Figs 14–16.

Chinese name: 小齿革克氏菌 (Xiao chi ge ke shi jun).

Etymology: The species epithet “*grandinia*” refers to its grandinoid hymenial surface.

Description: *Basidiomata* annual, resupinate, closely adnate, ceraceous, without odour or taste when fresh, up to 8 cm long,



Fig. 14. **A, B.** Basidiomata of *Kneiffiella grandinia* CLZhao 37474 (holotype SWFC 00037474). Scale bars: A = 1 cm; B = 2 mm.

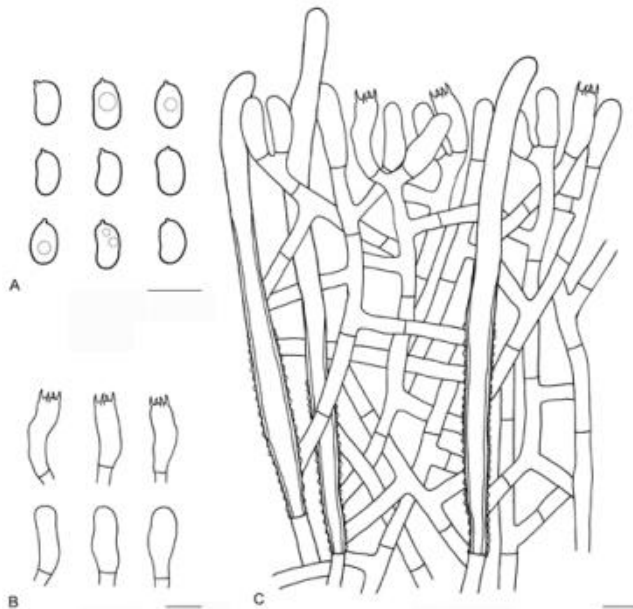


Fig. 15. Microscopic structures of *Kneiffiella grandinia* CLZhao 37474 (holotype SWFC 00037474). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** A section of the hymenium. Scale bars = 10 μ m.

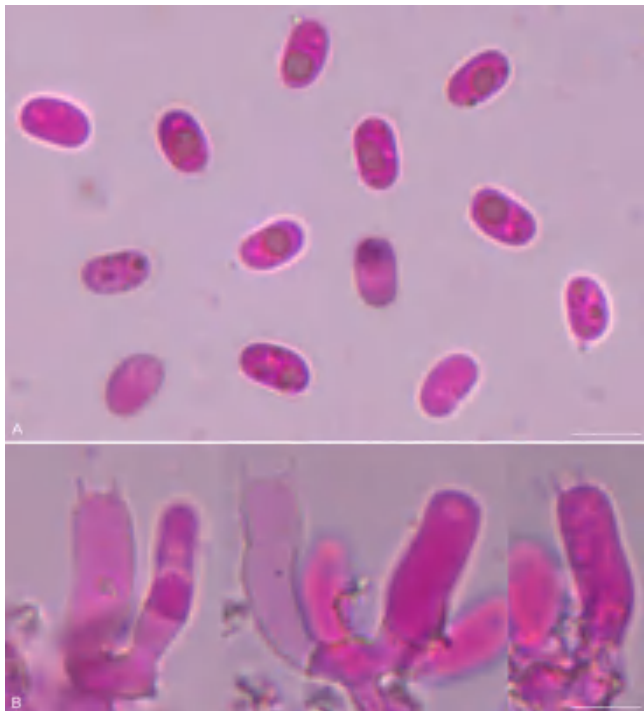


Fig. 16. Microscopic structures of *Kneiffiella grandinia* CLZhao 37474 (holotype SWFC 00037474). **A.** Basidiospores. **B.** Basidia and basidioles. Scale bars = 10 μ m.

3 cm wide and 600 μ m thick. *Hymenial surface* grandinoid, white when fresh, white to cream when dry. Sterile margin white, up to 1 mm wide. *Hyphal system* monomitic; simply septate generative hyphae, colourless, thin-walled, frequently branched, interwoven, 3–6 μ m diam., IKI–, CB–; tissue unchanged in KOH. *Cystidia* absent. Basidia cylindrical, colourless, thin-walled, with four sterigmata and a basal simple septum, 17–22 \times 5.5–6.5 μ m; basidioles dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* subcylindrical to ellipsoid, colourless, thin-walled, smooth, usually with one or more oil drops, IKI–, CB–, (6–)6.5–8(–9) \times (3–)3.5–5(–5.5) μ m, L = 7.39 μ m, W = 4.34 μ m, Q = 1.71 (n = 30/1).

Typus: **China**, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36" E, 1000 m.a.s.l., on dead bamboo, 3 Jul. 2024, C.L. Zhao, CLZhao 37474 (**holotype** SWFC 00037474).

Notes: Our newly reported specimen (CLZhao 37474) resolved within *Kneiffiella* in our combined ITS+nLSU phylogenetic analysis (Fig. 2). Morphologically, *K. barba-jovis* differs from *K. grandinia* sp. nov. by its cream hymenophore with long aculeie, generative hyphae with clamp connections and subglobose basidiospores (4.5–5.5 \times 3.5–4.5 μ m vs 6.5–8 \times 3.5–5 μ m, Viner et al. 2024). *Kneiffiella ornamentata* differs from *K. grandinia* sp. nov. by its grainy crust of crystal cystidia and smaller ellipsoid basidiospores (4.3–5.3 \times 3–4 μ m vs 6.5–8 \times 3.5–5 μ m, Viner et al. 2024).

Kneiffiella odontoides L. Wang & C.L. Zhao, sp. nov. MB 859932. Figs 17–19.

Chinese name: 钝齿革克氏菌 (Dun chi ge ke shi jun).

Etymology: The species epithet “odontoides” refers to its odontoid basidiomata.

Description: *Basidiomata* annual, resupinate, closely adnate, at first minutely floccose or furaceous, then odontoid with small (usually less than 1 mm long) conical aculei, white to cream when fresh, cream to slightly buff upon drying, without odour or taste when fresh, up to 10 cm long, 3 cm wide, and 600 μ m thick. Sterile margin thinning out, white to cream, up to 1 mm. *Hyphal system* monomitic, colourless, thin- to thick-walled, smooth, frequently branched, interwoven, 3–5 μ m



Fig. 17. **A, B.** Basidiomata of *Kneiffiella odontoides* CLZhao 40148 (holotype SWFC 00040148). Scale bars: A = 1 cm; B = 2 mm.

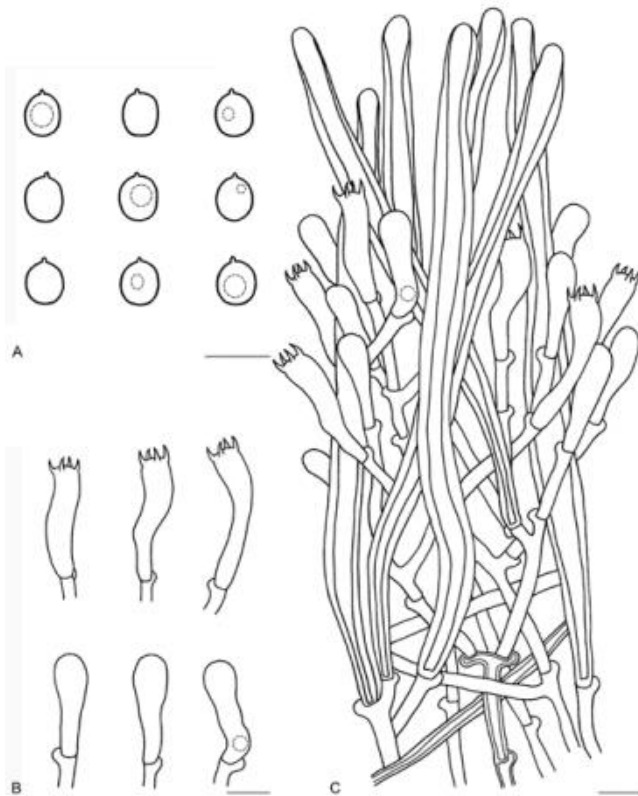


Fig. 18. Microscopic structures of *Kneiffiella odontioides* CLZhao 40148 (holotype SWFC 00040148). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** A section of the hymenium. Scale bars = 10 μ m.

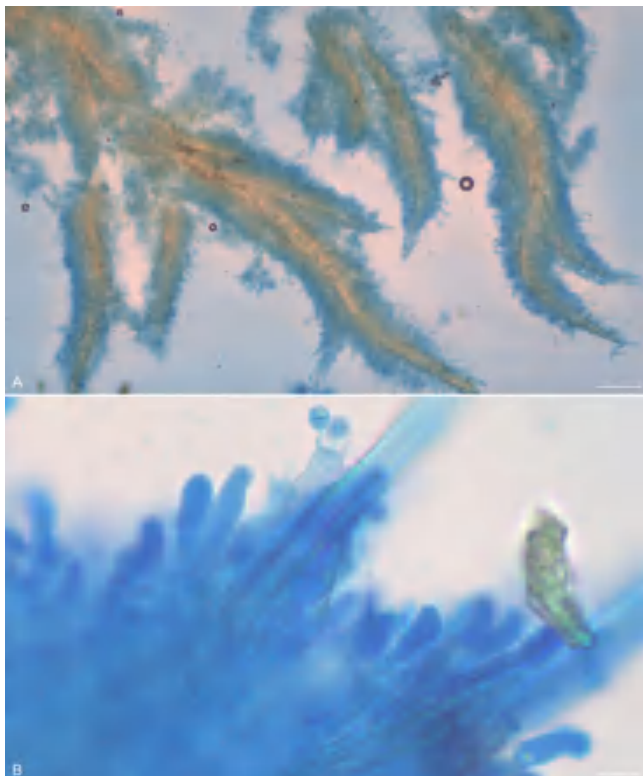


Fig. 19. Microscopic structures of *Kneiffiella odontioides* CLZhao 40148 (holotype SWFC 00040148). **A.** A section of the hymenium (40 \times microscope). **B.** A section of the hymenium (100 \times microscope). Scale bars = 10 μ m.

diam. generative hyphae with clamp connections, IKI–, CB–; tissue unchanged in KOH. *Cystidia* absent. *Basidia* clavate, slightly flexuous, with four sterigmata and a basal clamp connection, 28–35 \times 5.5–7.5 μ m; basidioles numerous, in

shape similar to basidia but smaller. *Basidiospores* globose, colourless, thin-walled, smooth, some with oil droplets, IKI–, CB–, (5.5–)6–8(–8.5) \times 5.5–7(–7.5) μ m, L = 6.83 μ m, W = 6.10 μ m, Q = 1.12 (n = 30/1).

Typus: **China**, Xizang Autonomous Region: Linzhi, Sejilashan, 29°37'12"N, 94°39'1"E, 4720 m.a.s.l., on fallen angiosperm branch, 12 Aug. 2024, C.L. Zhao, CLZhao 40148 (**holotype** SWFC 00040148).

Notes: The combined ITS+nLSU phylogenetic analysis (Fig. 2) revealed that our new species *Kneiffiella odontioides* sp. nov. (CLZhao 40148) resolved in a sister relationship to *K. pseudoabdita*. The key characters distinguishing *K. pseudoabdita* from *K. odontioides* are its poroid hymenophore and ellipsoid, thick-walled basidiospores (Liu *et al.* 2024).

Hymenochaetaceae Donk, *Bull. Bot. Gard. Buitenzorg.* **17:** 474. 1948.

Hymenochaete Lév., *Ann. Sci. Nat., Bot.*, sér. 3 **5:** 150. 1846.

Notes: *Hymenochaete* was proposed by L veill  (1846) mainly to accommodate a specimen featuring setae in the hymenium, with *H. rubiginosa* as the type species (Dai 2010, Parmasto *et al.* 2014). *Hymenochaete* is characterized by its annual to perennial, resupinate, effused-reflexed to pileate basidiomata with smooth, tuberculate, lamellate, poroid or hydroid hymenial surface; a simply septate monomitic or dimitic hyphal system; the presence of setae, and hyaline, thin-walled, ellipsoid, oblong-ellipsoid to cylindrical basidiospores (L ger 1998, Parmasto 2001, He & Dai 2012, Li *et al.* 2024b). Species in this genus are mostly found to grow on various dead angiosperm and gymnosperm wood and rarely on living trees. They can cause a white rot and form basidiomata with a xanthochroic brown colouration (He *et al.* 2024). Recently, a comprehensive taxonomic and multi locus phylogenetic study on corticioid and hydroid *Hymenochaetaceae* was carried out, in which 44 new species were described. The study recognized 249 species in *Hymenochaete* and *Hydnoporia* and provided an annotated checklist covering the whole globe (Liu *et al.* 2025). Taxa of *Hymenochaete* are divided into many supported phylogenetic clades, but species within each clade do not have uniform morphological characteristics. Main differences include the colour of basidiomata, type of hymenophore, shape of basidiospores, and size of setae and basidiospores (Liu *et al.* 2025). To date, *Hymenochaete* comprises 400 specific and infraspecific names, and the actual number of the species is 260 (Liu *et al.* 2025). Here, we describe three new species viz. *Hymenochaete chimonobambusa*, *H. punctata* and *H. sanguinaria*.

Hymenochaete chimonobambusae L. Wang & C.L. Zhao, **sp. nov.** MB 859933. Figs 20–22.

Chinese name: 筇竹锈革菌 (Qiong zhu xiu ge jun).

Etymology: The species epithet “*chimonobambusae*” refers to the type specimen growing on the host of *Chimonobambusa tumidissinoda*.



Fig. 20. A, B. Basidiomata of *Hymenochaete chimonobambusae* HMZhou 710 (holotype SWFC 00100710). Scale bars: A = 1 cm; B = 2 mm.

Description: *Basidiomata* annual, resupinate, closely adnate, inseparable from substrate, leathery, without odour or taste when fresh, up to 8 cm long, 2 cm wide, and 400 μm thick. *Hymenial surface* tuberculate, honey yellow to aurantium when fresh, aurantium to coconut brown upon drying, cracked. Sterile margin narrow, buff yellow, up to 1 mm wide. *Hyphal system* monomitic; colourless to yellowish, thin- to thick-walled, frequently branched, interwoven, simply septate generative hyphae 1–2.5 μm diam., IKI–, CB–; tissue unchanged in KOH. *Setae* abundant, mostly subulate, thick-walled with a wide lumen, yellowish to reddish brown, with obtuse to acute tips, projecting above the hymenium, 30–42.5 \times 5.5–9.5 μm . *Simple hyphidia* occasionally present, colourless, thin-walled, 9–22 \times 1.5–3 μm . *Basidia* subclavate, slightly flexuous, with four sterigmata and a basal simple septum, 8–12 \times 2–4 μm ; basidioles numerous, in shape similar to basidia, but smaller. *Basidiospores* oblong ellipsoid,

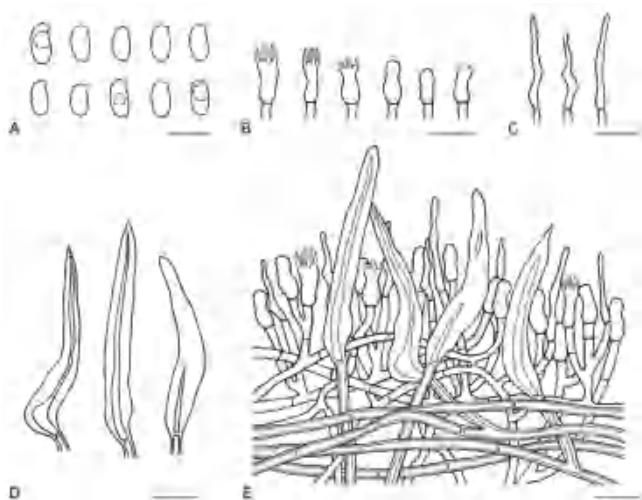


Fig. 21. Microscopic structures of *Hymenochaete chimonobambusae* HMZhou 710 (holotype SWFC 00100710). A. Basidiospores. B. Basidia and basidioles. C. Hyphidia. D. Setae. E. A section of the hymenium. Scale bars: A = 5 μm ; B–E = 10 μm .

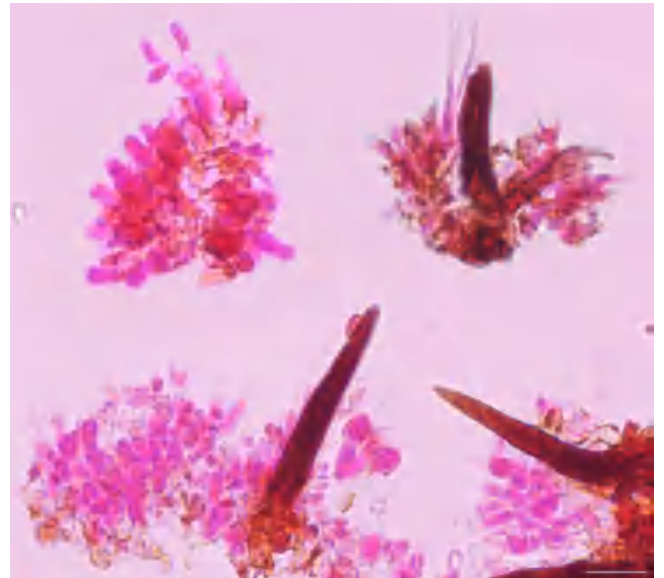


Fig. 22. Microscopic structures of *Hymenochaete chimonobambusae* HMZhou 710 (holotype SWFC 00100710). Scale bar = 10 μm .

colourless, thin-walled, smooth, some with an oil droplet, IKI–, CB–, (3–)3.5–4.5 \times 1.5–2.5 μm , L = 3.82 μm , W = 1.93 μm , Q = 1.98 (n = 30/1).

Typus: **China**, Yunnan Province, Zhaotong, Yongshan County, Xisha Village, Wumengshan National Nature Reserve, 28°18'01"N, 103°58'12"E, 1812 m.a.s.l., on dead *Chimonobambusa tumidissinoda*, 19 Aug. 2024, H.M. Zhou, HMZhou 710 (**holotype** SWFC 00100710).

Notes: The combined ITS+nLSU sequences of our new species resolved in a sister relationship to *H. subinnexa* in *Hymenochaete* in the phylogenetic inference (Fig. 3). *Hymenochaete chimonobambusae* (HMZhou 710) differs from *H. subinnexa* by its brownish to cinnamon hymenophore and bigger, oblong-ellipsoid basidiospores (6–7.8 \times 2.8–3.1 μm vs 3.5–4.5 \times 1.5–2.5 μm ; Liu et al. 2025).

Hymenochaete punctata L. Wang & C.L. Zhao, **sp. nov.** MB 859934. Figs 23–25.

Chinese name: 斑点锈革菌 (Ban dian xiu ge jun).

Etymology: The species epithet “*punctata*” refers to the punctate hymenial surface of the type specimen.

Description: *Basidiomata* annual, resupinate, closely adnate, inseparable from substrate, leathery, without odour or taste when fresh, up to 5 cm long, 2 cm wide, and 300 μm thick. *Hymenial surface* smooth, orange yellow to orange when fresh, orange to clay-buff upon drying. Sterile margin thinning out, orange yellow, up to 1 mm wide. *Hyphal system* monomitic; yellowish, thin- to thick-walled, frequently branched, interwoven simply septate generative hyphae 2.5–4 μm diam., IKI–, CB–; tissue unchanged in KOH. *Cystidia* tubular, slightly sinuous, colourless, thin-walled, 20.5–39 \times 4.5–8 μm . *Setae* abundant, mostly subulate, thick-walled with a wide lumen, yellowish to reddish brown, with obtuse to acute tips, projecting above the hymenium, 63–115 \times 5–11.5 μm . *Basidia* subclavate, slightly flexuous, with four sterigmata and a basal simple septum, 11–22 \times 4–6 μm ;



Fig. 23. A, B. Basidiomata of *Hymenochaete punctata* HMZhou 16 (holotype SWFC 00100016). Scale bars: A = 1 cm; B = 2 mm.

basidiospores numerous, in shape similar to basidia, but smaller. *Basidiospores* ellipsoid, colourless, thin-walled, smooth, some with oil droplets, IKI–, CB–, $4.5\text{--}5.5\text{--}(6) \times 2.5\text{--}3.5 \mu\text{m}$, $L = 5.18 \mu\text{m}$, $W = 3.03 \mu\text{m}$, $Q = 1.71$ ($n = 30/1$).

Typus: China, Yunnan Province, Zhaotong, Zhaoyang District, Yongfeng Town, $27^{\circ}15'36''\text{N}$, $103^{\circ}38'24''\text{E}$, 2018 m.a.s.l., on fallen angiosperm branch, 16 Aug. 2024, *H.M. Zhou*, HMZhou 16 (**holotype** SWFC 00100016).

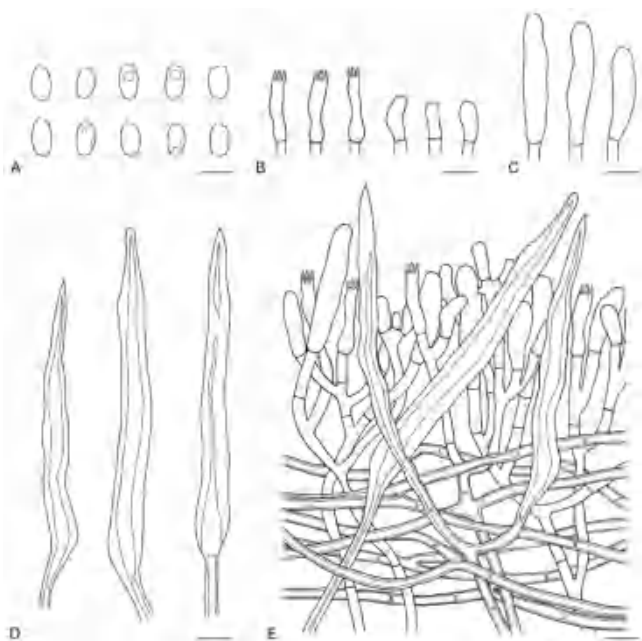


Fig. 24. Microscopic structures of *Hymenochaete punctata* HMZhou 16 (holotype SWFC 00100016). **A.** Basidiospores. **B.** Basidia and basidiospores. **C.** Cystidia. **D.** Setae. **E.** A section of the hymenium. Scale bars: A = 5 μm ; B–E = 10 μm .

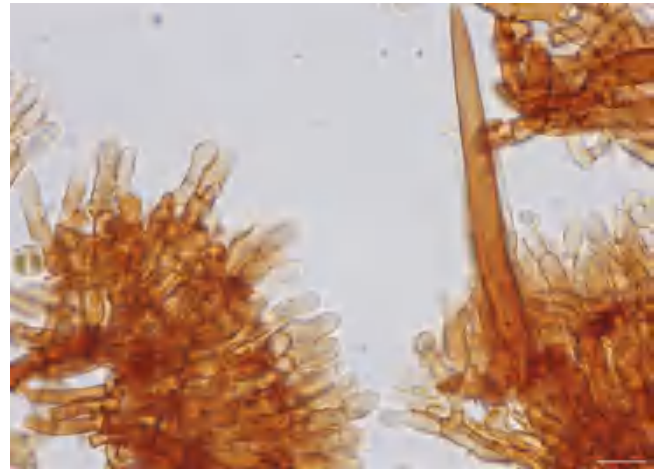


Fig. 25. Microscopic structures of *Hymenochaete punctata* HMZhou 16 (holotype SWFC 00100016). Scale bar = 10 μm .

Notes: The combined ITS+nLSU sequences of our new species *Hymenochaete punctata* (specimen HMZhou 16) resolved in a sister relationship to *H. subepichlora* within *Hymenochaete* in our phylogenetic study (Fig. 3). Key characters distinguishing *H. subepichlora* from *H. punctata* are its clay buff to cinnamon hymenophore surface and setae, which can be up to $145 \times 7 \mu\text{m}$ in size (Liu *et al.* 2025).

Hymenochaete sanguinaria L. Wang & C.L. Zhao, *sp. nov.* MB 859935. Figs 26–28.

Chinese name: 深红锈革菌 (Shen hong xiu ge jun).

Etymology: The species epithet “*sanguinaria*” refers to the species having a blood red hymenial surface.



Fig. 26. A, B. Basidiomata of *Hymenochaete sanguinaria* HMZhou 995 (holotype SWFC 00100995). Scale bars: A = 1 cm; B = 2 mm.

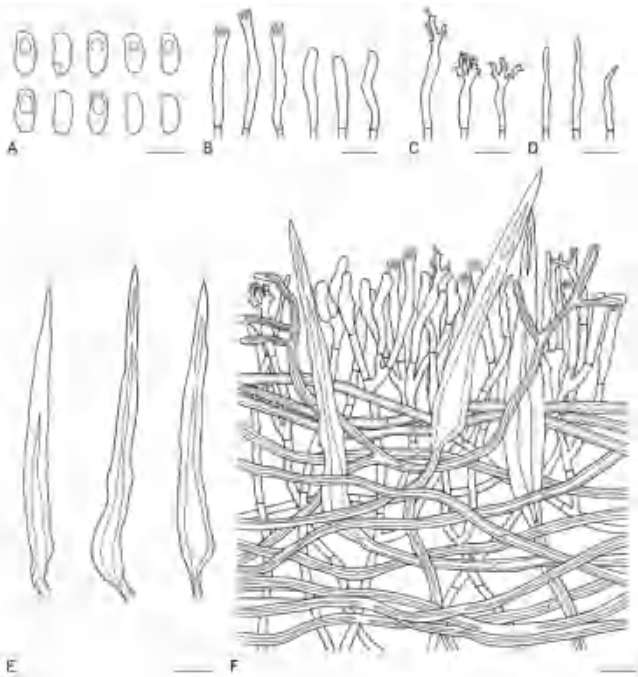


Fig. 27. Microscopic structures of *Hymenochaete sanguinaria* HMZhou 995 (holotype SWFC 00100995). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Dendrohyphidia. **D.** Hyphidia. **E.** Setae. **F.** A section of the hymenium. Scale bars: A = 5 μ m; B–F = 10 μ m.

Description: *Basidiomata* annual, effused-reflexed with slightly elevated margins, adnate, detachable, leathery, without odour or taste when fresh, up to 12 cm long, 2 cm wide, and 500 μ m thick. *Hymenial surface* smooth, blood red when fresh, blood red to brownish red upon drying, cracked. Sterile margin thinning out, yellowish brown, up to 1 mm wide. *Hyphal system* monomitic; simply septated, colourless to yellowish, thin- to thick-walled, frequently branched, interwoven generative hyphae, 1.5–3.5 μ m diam., IKI–, CB–; tissue unchanged in KOH. *Setae* abundant, mostly subulate, thick-walled with a wide lumen, yellowish to reddish brown, with obtuse to acute tips, projecting above the hymenium, 58–90 \times 6–12 μ m. *Dendrohyphidia* numerous, colourless, thin-walled, irregularly and strongly branched, 20–37 \times 2–4 μ m. Simple hyphidia occasionally present, colourless, thin-walled, 18.5–27 \times 1.5–3.5 μ m. *Basidia* cylindrical, slightly flexuous, with four sterigmata and a basal simple septum, 17–32.5 \times 2.5–4 μ m; basidioles numerous, in shape similar to basidia, but smaller. *Basidiospores* narrowly ellipsoid, colourless, thin-walled, smooth, some with an oil droplet, IKI–, CB–, 5–6.5 \times 2–3 μ m, L = 5.83 μ m, W = 2.49 μ m, Q = 2.34 (n = 30/1).

Typus: **China**, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Xiaocaoba Ecotourism Scenic Sport, 28°8'10"N, 103°58'2"E, 1253 m.a.s.l., on fallen angiosperm trunk, 15 Oct. 2024, *H.M. Zhou*, HMZhou 995 (**holotype** SWFC 00100995).

Notes: Our new species (specimen HMZhou 995) nested within *Hymenochaete* in our phylogenetic inference using combined ITS+nLSU data (Fig. 3) and clustered together with *H. floridea*, *H. cruenta* and *H. mougeotii*. Key characters distinguishing *H. floridea* from *H. sanguinaria* are its larger, cylindrical to ellipsoid basidiospores (6–7 \times 2.5–2.8 μ m vs 5–6.5 \times 2–3 μ m, Berkeley & Broome 1873), while *H.*

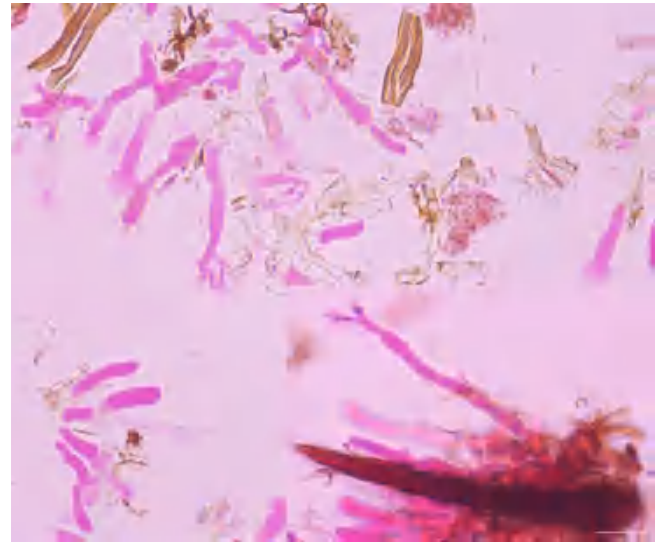


Fig. 28. Microscopic structures of *Hymenochaete sanguinaria* HMZhou 995 (holotype SWFC 00100995). Scale bar = 20 μ m.

cruenta can be distinguished from *H. sanguinaria* by its brown hymenial surface and cylindrical, slightly curved basidiospores (6–8 \times 2–2.5 μ m vs 5–6.5 \times 2–3 μ m, Donk 1959) and *H. mougeotii* differs from *H. sanguinaria* by its membranaceous basidiomata and subcylindrical to ellipsoid basidiospores (6–8 \times 2.5–3.5 μ m vs 5–6.5 \times 2–3 μ m, Donk 1959).

Hyphodontiaceae Xue W. Wang & L.W. Zhou, *J. Fungi* 7(no. 478): 24. 2021.

Hyphodontia J. Erikss., *Symb. Bot. Upsal.* 16(no. 1): 101. 1958.

Notes: The genus *Hyphodontia* was proposed by Eriksson (1958) with *H. pallidula* as the type species (Kotiranta & Saarenoksa 2000). Species in this widespread genus commonly occur in temperate to tropical areas causing white rot (Bernicchia & Gorjón 2010, Yang et al. 2025). Members of *Hyphodontia* are characterized by its grandinoid, odontoid or poroid, whitish to yellowish, buff, tawny olive or buckthorn brown hymenophore. Their hyphal system has been shown to be monomitic to pseudodimitic and generative hyphae occur with clamp connections. Moreover, species possess one or two types of cystidia: lagenocystidia and capitate cystidia, while basidia are clavate, capitate, subcylindrical or utriform, with four sterigmata. Basidiospores are reported to be ellipsoid, cylindrical, ovoid or subglobose, smooth, thin-walled or slightly thick-walled (Wang et al. 2021, 2023). The family *Hyphodontiaceae* was only recently erected based on *Hyphodontia*, which was delimited from *Hyphodontia sensu lato*, based on molecular evidence which concurrently confirmed the *Hyphodontiaceae* as an independent monotypic family in *Hymenochaetales*. As a consequence, the morphological circumscription of *Hyphodontia* has been narrowed down. Based on MycoBank and Index Fungorum entries (accessed on 4 January 2026), *Hyphodontia* is associated with 182 specific and infraspecific names, and the actual number of the described species is only 39 (Yang et al. 2025). Here, we report on a new species which we accommodate as *Hyphodontia grandinia*.



Hyphodontia grandinia L. Wang & C.L. Zhao, *sp. nov.* MB 859936. Figs 29–31.

Chinese name: 小齿丝齿菌 (Xiao chi si chi jun).

Etymology: The species epithet “*grandinia*” refers to its grandinoid basidiomata.

Description: *Basidiomata* annual, resupinate, closely adnate, membranaceous, cracking with age, without odour or taste when fresh, up to 10 cm long, 3 cm wide, and 600 μm thick. *Hymenophore* grandinoid, cream when fresh, cream to buff upon drying. Sterile margin narrow, white to cream, up to 1 mm. *Hyphal system* monomitic; colourless, thin- to thick-walled, smooth, frequently branched, interwoven generative hyphae 2.5–4 μm diam. with clamp connections, IKI–, CB–; tissue unchanged in KOH. Presence of numerous crystals



Fig. 29. A, B. Basidiomata of *Hyphodontia grandinia* CLZhao 34641 (holotype SWFC 00034641). Scale bars: A = 1 cm; B = 2 mm.

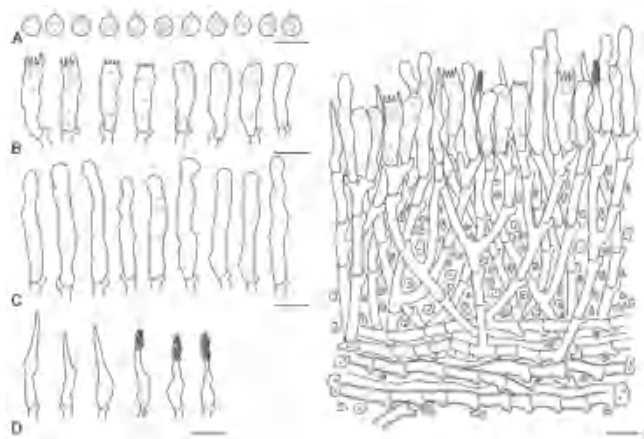


Fig. 30. Microscopic structures of *Hyphodontia grandinia* CLZhao 34641 (holotype SWFC 00034641). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Capitata cystidia. **D.** Lagenocystidia. **E.** A section of the hymenium. Scale bars = 10 μm .

among hyphae. *Cystidia* of two kinds: 1) capitate, slightly flexuous, colourless, thin-walled, smooth, 26.5–40 \times 4.5–7 μm ; 2) lagenocystidia, slightly flexuous, colourless, thin-walled, with broad bases and tapering tips, incrustation on

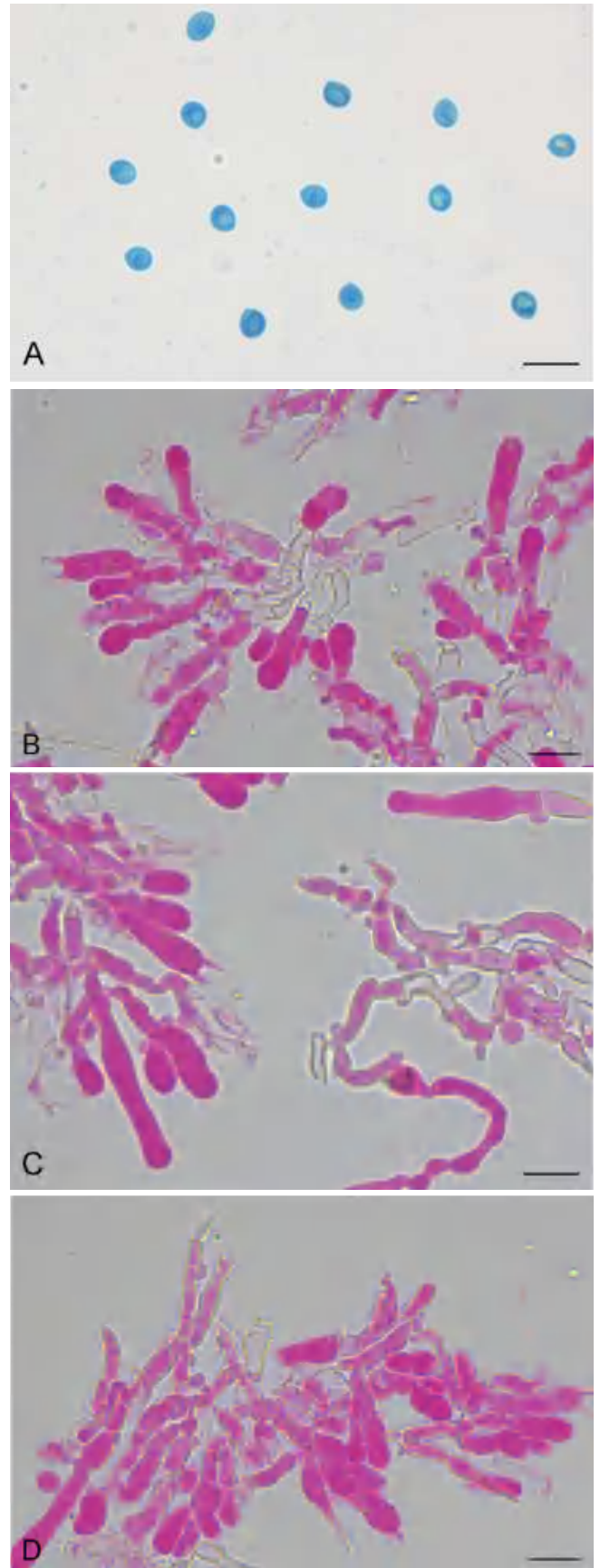


Fig. 31. Microscopic structures of *Hyphodontia grandinia* CLZhao 34641 (holotype SWFC 00034641). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Capitata cystidia. **D.** Lagenocystidia. Scale bars = 10 μm .



cystidia that partly dissolve in KOH, $17\text{--}25.5 \times 3\text{--}5.5 \mu\text{m}$. *Basidia* short cylindrical to clavate, slightly flexuous, with a basal clamp connection and four sterigmata, some with oil droplets, $15\text{--}31 \times 4\text{--}6.5 \mu\text{m}$; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* subglobose, colourless, thin-walled, smooth, some with oil droplets, IKI–, CB–, $5\text{--}6.5 \times 4.5\text{--}6(\text{--}6.5) \mu\text{m}$, $L = 5.79 \mu\text{m}$, $W = 5.24 \mu\text{m}$, $Q = 1.11$ ($n = 30/1$).

Typus: **China**, Yunnan Province, Diqing, Weixi County, Weideng Town, Songpo Village, $27^{\circ}5'23''\text{N}$, $99^{\circ}10'12''\text{E}$, 1400 m.a.s.l., on fallen angiosperm branch, 13 Oct. 2023, C.L. Zhao, CLZhao 34641 (**holotype** SWFC 00034641).

Notes: Our new species (specimen CLZhao 34641) was shown to group within *Hyphodontia* in a sister relationship to *H. pachyspora* in our combined ITS+nLSU phylogenetic inference (Fig. 4). However, *H. pachyspora* differs from *H. grandinia* by its smaller, light-buff hymenophore and thick-walled basidiospores ($4.7\text{--}5.5 \times 4.2\text{--}5.1 \mu\text{m}$ vs $5\text{--}6.5 \times 4.5\text{--}6 \mu\text{m}$, Wang *et al.* 2021).

Peniophorellaceae L.W. Zhou *et al.*, *Mycosphere* **14**: 476. 2023.

Peniophorella P. Karst., *Bidrag Kännedom Finlands Natur Folk.* **48**: 427. 1889.

Notes: *Peniophorella* was introduced as a monotypic genus with *P. pubera* as its type. The genus is characterized by its smooth to tuberculate, white to yellowish hymenophores, its monomitic hyphal system featuring generative hyphae with clamp connections and metuloids, gloecystidia or leptocystidia. Moreover, echinulate cells and its basidia are narrowly to broadly clavate, while basidiospores are hyaline and ellipsoid, cylindrical or allantoid in shape (Hallenberg *et al.* 2007, Bernicchia & Gorjón 2010, Guan *et al.* 2020). After a long time of systematic oblivion, Larsson (2007) resurrected *Peniophorella* from *Hyphoderma* in *Hymenochaetales*, based on molecular phylogenetic data. During the revision of the order *Polyporales* at family level, Justo *et al.* (2017) transferred 20 species to *Peniophorella* and accommodated the genus in the *Hyphodermataceae* (*Hymenochaetales*). At the family level, *Peniophorella* occupies an independent phylogenetic position from other known genera and families in *Hymenochaetales*. However, the estimated divergence time of this genus (82.43 Mya) is in the ranges of other families in *Basidiomycota* (27–178 Mya, He *et al.* 2019, 2024), which lead Wang *et al.* (2023) to erect the *Peniophorellaceae* based on a combined dataset of nSSU, ITS, nLSU, *tef1- α* , *rpb1* and *rpb2* regions (Wang *et al.* 2023). For now, according to MycoBank and Index Fungorum (accessed on 4 January 2026), a total of 42 species are accepted in *Peniophorella* (Deng *et al.* 2025).

Peniophorella tenuissima L. Wang & C.L. Zhao, *sp. nov.* MB 859937. Figs 32–34.

Chinese name: 薄小隔孢伏革菌 (Bao xiao ge bao fu ge jun).

Etymology: The species epithet “*tenuissima*” refers to its very thin basidiomata.

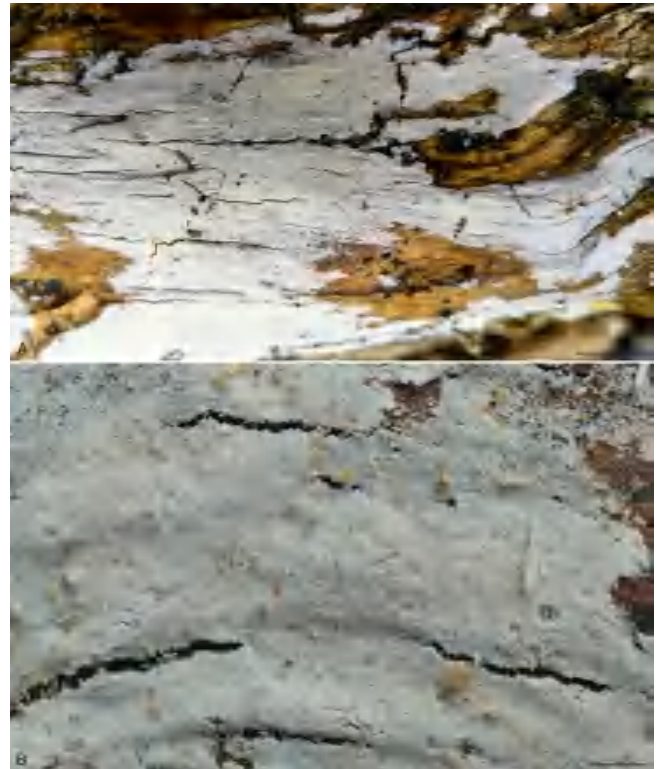


Fig. 32. A, B. Basidiomata of *Peniophorella tenuissima* HMZhou 377 (holotype SWFC 00100377). Scale bars: A = 1 cm; B = 2 mm.

Description: *Basidiomata* annual, resupinate, closely adnate, farinaceous, without odour or taste when fresh, up to 15 cm long, 6 cm wide and 300 μm thick. *Hymenophore* smooth, white when fresh, white to buff when dry. Sterile margin thin, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, frequently branched, smooth, interwoven, 4–6 μm diam. generative hyphae with clamp connections, IKI–, CB–; tissue unchanged in KOH. *Cystidia*

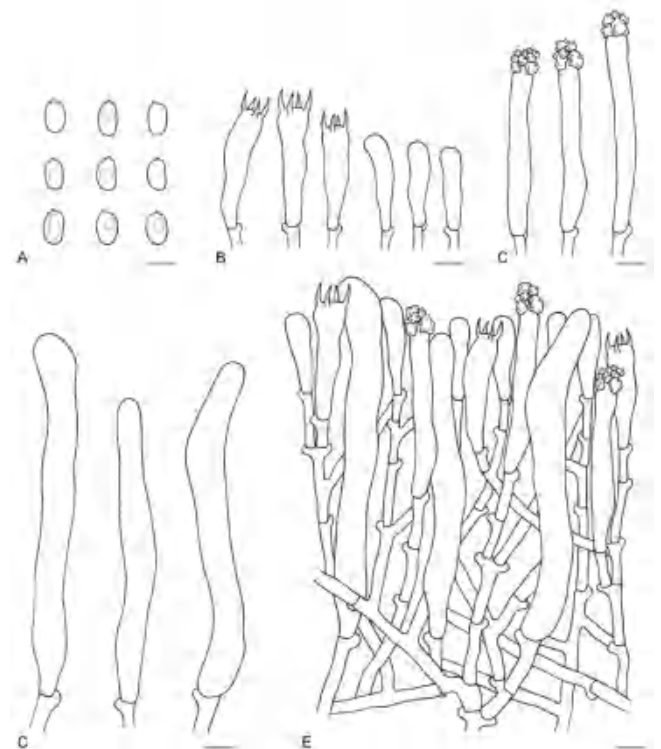


Fig. 33. Microscopic structures of *Peniophorella tenuissima* HMZhou 377 (holotype SWFC 00100377). A. Basidiospores. B. Basidia and basidioles. C. Asterocystidia. D. Gloecystidia. E. A section of the hymenium. Scale bars = 10 μm .

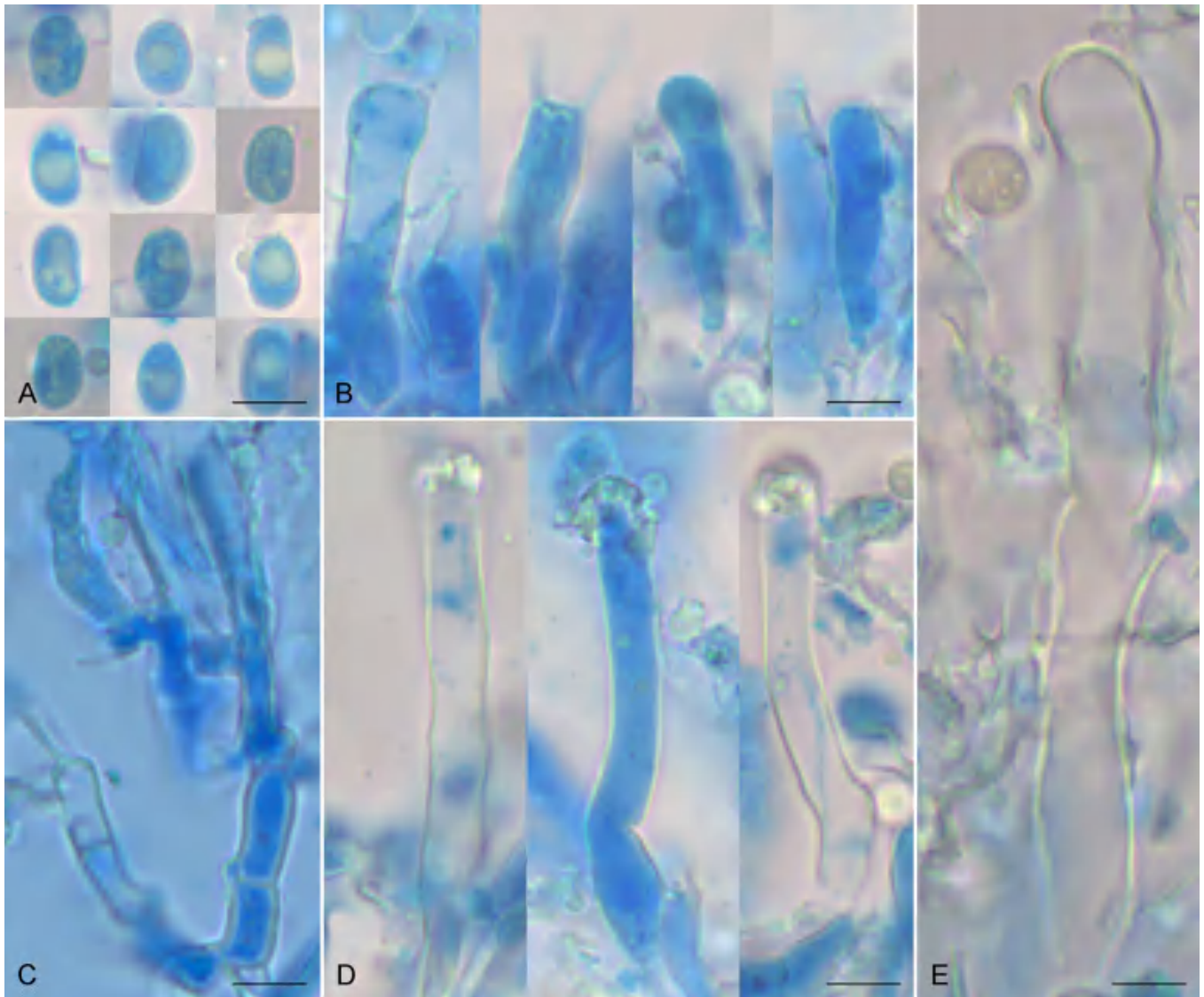


Fig. 34. Microscopic structures of *Peniophorella tenuissima* HMZhou 377 (holotype SWFC 00100377). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Generative hyphae with clamp connections. **D.** Asterocystidia. **E.** Gloeocystidia. Scale bars = 10 µm.

of two kinds: 1) colourless, thin-walled, with the apical part encrusted asterocystidia, $65\text{--}85 \times 7\text{--}8$ µm; 2) subcylindrical to subclavate, slightly sinuous, colourless, thin-walled, mostly embedded gloeocystidia, $80\text{--}105 \times 11.5\text{--}16$ µm. *Basidia* clavate, colourless, thin-walled, with four sterigmata and a basal clamp connection, $40\text{--}48 \times 7\text{--}10.5$ µm; basidioles dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, colourless, smooth, thin-walled, with oil drops, IKI–, CB–, $8\text{--}11.5(–12) \times (5\text{--})5.5\text{--}7.5$ µm, $L = 9.58$ µm, $W = 6.45$ µm, $Q = 1.49$ ($n = 30/1$).

Typus: **China**, Yunnan Province, Zhaotong, Yiliang County, Xiaocao Dam, Wumengshan Nature Reserve, $28^{\circ}8'10''\text{N}$, $103^{\circ}58'2''\text{E}$, 1180 m.a.s.l., on fallen angiosperm trunk, 19 Aug. 2024, *H.M. Zhou*, HMZhou 377 (**holotype** SWFC 00100377).

Notes: Our new species *Peniophorella tenuissima* (HMZhou 377) was shown to cluster within *Peniophorella* and grouped with *P. albohymenia* in our phylogenetic inference based on combined ITS+nLSU data. However, *P. albohymenia* can be delimited from *P. tenuissima* by its membranaceous basidiomata and the presence of in total four cystidia types, namely stephanocystidia, fusiform cystidia, cylindrical cystidia and capitate cystidia (Deng et al. 2025).

Peniophorella tongbiguanensis L. Wang & C.L. Zhao, *sp. nov.* MB 859939. Figs 35–37.

Chinese name: 铜壁关小隔孢伏革菌 (Tong bi guan xiao ge bao fu ge jun).

Etymology: The species epithet “*tongbiguanensis*” refers to the locality (Tongbiguan Provincial Nature Reserve) of the type specimen.

Description: *Basidiomata* annual, resupinate, closely adnate, farinaceous, without odour or taste when fresh, up to 4 cm long, 1 cm wide and 0.2 mm thick. *Hymenial surface* smooth, white when fresh, white to cream when dry. Sterile margin white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, frequently branched, interwoven, 2–4 µm diam. generative hyphae with clamp connections, IKI–, CB–; tissue unchanged in KOH. *Cystidia* of two kinds: 1) colourless, thin-walled moniliform cystidia, with a variable number of constrictions, $28\text{--}41 \times 6\text{--}9$ µm; 2) colourless, thin-walled, abundantly covered by coarse crystals encrusted cystidia, $27\text{--}40 \times 3\text{--}4$ µm. *Basidia* clavate, colourless, thin-walled, with four sterigmata and a basal clamp connection, $18\text{--}35 \times 7\text{--}8.5$ µm; basidioles dominant, in shape similar to



basidia, but slightly smaller. *Basidiospores* oblong-ellipsoid, colourless, smooth, thin-walled, occasionally with oil drops, IKI–, CB–, 11–13.5(–14) × (5–)5.5–7(–7.5) μm, L = 12.34 μm, W = 6.13 μm, Q = 2.01 (n = 30/1).



Fig. 35. A, B. Basidiomata of *Peniophorella tongbiguanensis* CLZhao 36353 (holotype SWFC 00036353). Scale bars: A = 1 cm; B = 2 mm.

Typus: China, Yunnan Province, Dehong, Mang City, Mengga Town, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on fallen angiosperm branches, 29 Jun. 2024, C.L. Zhao, CLZhao 36353 (**holotype** SWFC 00036353).

Notes: Our new species *Peniophorella tongbiguanensis* (CLZhao 36353) clustered within *Peniophorella*, and grouped with *P. reticulata* and *P. subreticulata* in our phylogenetic inference using ITS+nLSU data (Fig. 5). However, *P. reticulata* can be delimited from *P. tongbiguanensis* by its odontoid basidiomata and the presence of peg-like hyphal structures in the subhymenium. *P. subreticulata* differs from *P. tongbiguanensis* by its grandinoid to odontoid hymenophore and fusoid to subcylindrical leptocystidia (Yurchenko *et al.* 2020b, Liu *et al.* 2024).

Schizoporaceae Jülich, *Biblioth. Mycol.* **85**: 389. 1982. [1981].

Fasciodontia Yurchenko & Riebesehl, *Mycol. Progr.* **19**: 178. 2020.

Notes: The genus *Fasciodontia* was initially introduced by Yurchenko *et al.* (2020a) based on a molecular and phylogenetic analysis of ITS+nLSU sequence data to accommodate *F. bugellensis* and *F. brasiliensis*, which

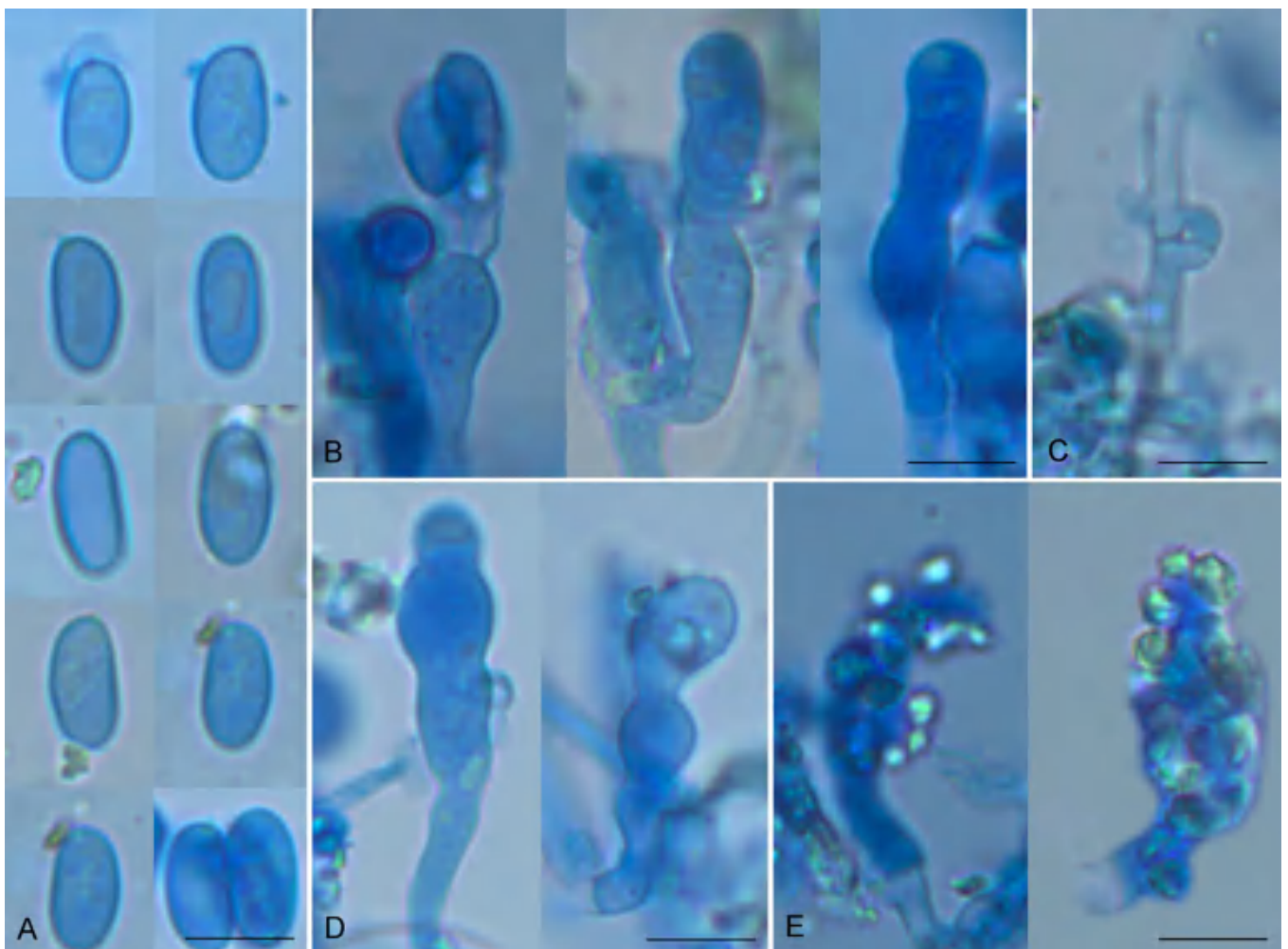


Fig. 36. Microscopic structures of *Peniophorella tongbiguanensis* CLZhao 36353 (holotype SWFC 00036353). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Moniliform cystidia. **D.** Encrusted cystidia. **E.** A section of the hymenium. Scale bars = 10 μm.

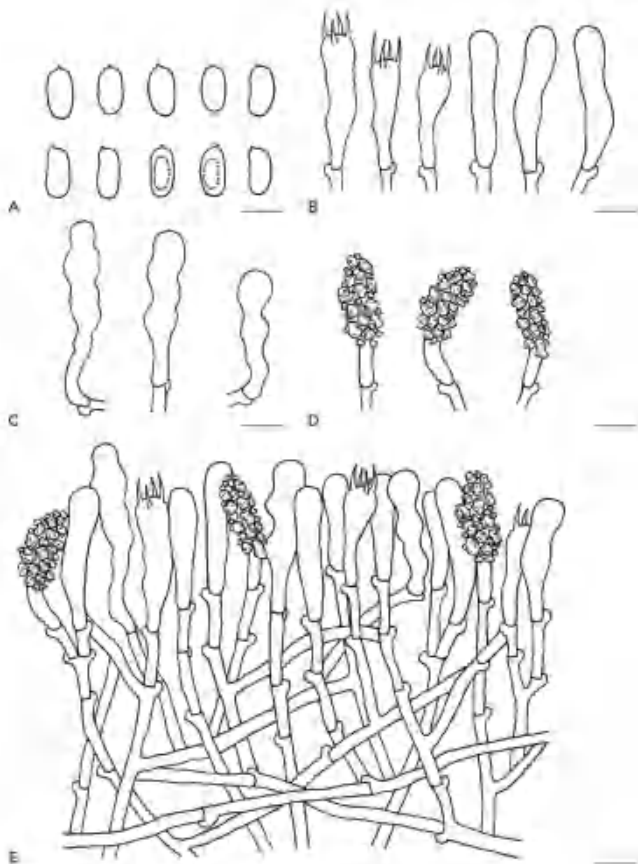


Fig. 37 Sections of hymenium of *Peniophorella tongbiguanensis* CLZhao 36353 (holotype SWFC 00036353). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Generative hyphae with clamp connections. **D.** Moniliform cystidia. **E.** Encrusted cystidia. Scale bars = 10 μ m.

appeared delimited from the genera *Lyomyces* and *Xylodon*. Later, a third species *F. yunnanensis* was described, and the position of the genus within the family *Schizoporaceae* confirmed (Luo & Zhao 2021, Index Fungorum 2025). The genus is characterized by resupinate to effused basidiomata with minutely odontoid hymenophores, sterile (except for the bases) aculei, consisting of projecting hyphae, a turning, pseudodimitic hyphal system bearing clamp connections showing a slightly yellowish colour reaction in KOH, with moderately CB+, IKI-. Moreover, cystidia are cylindrical to slightly moniliform and capitate, while basidia are utriform to subcylindrical with two slight constrictions. Basidiospores are ellipsoid, colourless, smooth, slightly thick-walled to thick-walled, and show a slight to moderate CB+ reaction (Yurchenko *et al.* 2020a, Luo & Zhao 2021). In this study, we introduce a novel wood-inhabiting fungal species, *Fasciodontia grandinia*, from China based on ITS+nLSU sequence data and morphological characteristics (Fig. 6).

Fasciodontia grandinia L. Wang & C.L. Zhao, *sp. nov.* MB 859940. Figs 38–40.

Chinese name: 小齿束齿菌 (Xiao chi shu chi jun).

Etymology: The species epithet “*grandinia*” refers to its grandinoid hymenophore surface.

Description: *Basidiomata* annual, resupinate, closely adnate, membranaceous, cracked with age, without odour or taste



Fig. 38. A, B. Basidiomata of *Fasciodontia grandinia* CLZhao 40459 (holotype SWFC 00040459). Scale bars: A = 1 cm; B = 2 mm.

when fresh, up to 12 cm long, 4.5 cm wide and 600 μ m thick. *Hymenophore* minutely grandinoid, aculei 50–100 μ m long, 8–10 aculei/mm, white when fresh, white to cream upon drying. Sterile margin narrow, white to cream, up to 1 mm. *Hyphal system* pseudodimitic; generative hyphae with clamp connections, colourless, thin- to slightly thick-walled, smooth, branched, interwoven, 3–5.5 μ m diam., crystals present in moderate amounts among hyphae, IKI-, CB+; tissue unchanged in KOH. *Cystidia* capitate, slightly flexuous, colourless, thin-walled, smooth, 24–35.5 \times 6–7 μ m. *Basidia* clavate, slightly flexuous, with a basal clamp connection and four sterigmata, 21–38 \times 5.5–7 μ m; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid, colourless, thin-walled, smooth, IKI-, CB-, 7–8.5(–9) \times 4.5–6(–6.5) μ m, L = 8.02 μ m, W = 5.42 μ m, Q = 1.48 (n = 30/1).

Typus: **China**, Yunnan Province, Zhaotong, Yiliang, Wumengshan National Nature Reserve, 27°46'12"N, 104°15'02" E, 1900 m.a.s.l., on fallen angiosperm branch, 14 Oct. 2024, C.L. Zhao, CLZhao 40459 (**holotype** SWFC 00040459).

Notes: Sequences of our new species showed affinities to *Fasciodontia* and resolved in a sister relationship to *F. yunnanensis* in our phylogenetic inference using ITS+nLSU data (Fig. 6). Key characters distinguishing *Fasciodontia grandinia* *sp. nov.* from *F. yunnanensis* are the minutely grandinoid hymenophore (8–10 aculei/mm) and thin-walled, bigger ellipsoid basidiospores (7–8.5 \times 4.5–6 μ m). On the other hand, *F. yunnanensis* differs by its minutely odontoid hymenial surface (aculei 50–100 μ m long, 10–13 aculei/mm), and thick-walled, smaller ellipsoid basidiospores (3.1–5.7 \times 2.1–4.1 μ m, Luo & Zhao 2021).

Lyomyces P. Karst., *Rev. Mycol.*, Toulouse **3**(no. 9): 23.

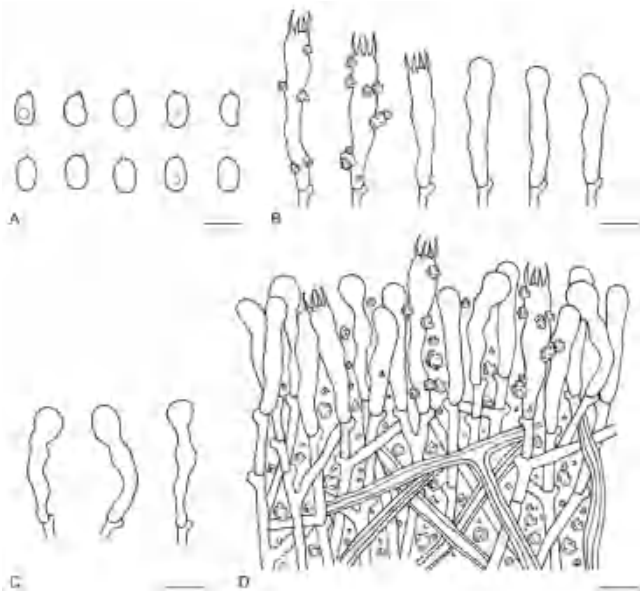


Fig. 39. Microscopic structures of *Fasciodontia grandinia* CLZhao 40459 (holotype SWFC 00040459). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Capitulate cystidia. **D.** A section of the hymenium. Scale bars = 10 μm .

1881.

Notes: The genus *Lyomyces* was initially described by Karsten (1881), based on *L. serus* as type species, which is now accommodated under the name *L. sambuci* (Karsten 1881, Bernicchia & Gorjón 2010, Yurchenko & Wu 2013, 2016). *Lyomyces* comprises corticioid fungi characterised by thin, effused, membranaceous basidiomata that appear fragile in a dry state. The hymenial surface is predominantly white or whitish, and the hyphal system is monomitic. Subicular hyphae are thin- or somewhat thick-walled, while the cystidia

are thin-walled with tapering, cylindrical, subcapitate, or capitate apical parts. Basidia are utriform, and basidiospores colourless with thin to thick, smooth, or occasionally minutely warted walls (Bernicchia & Gorjón 2010, Yurchenko *et al.* 2024a). Species of *Lyomyces* are saprobes that inhabit decaying angiosperm and gymnosperm wood and bark, and a number of *Lyomyces* species display a notable tolerance to drying and can even be found on dead branches on living trees (Guan *et al.* 2023, Yuan *et al.* 2024, Yurchenko *et al.* 2024a). Riebesehl & Langer (2017) divided *Hyphodontia s. l.* into six genera, viz., *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lagarobasidium*, *Lyomyces*, and *Xylodon*, and proposed 35 new combinations, including 14 *Lyomyces* species. Later, Riebesehl *et al.* (2019) subsequently clarified the generic concept and the phylogeny of *Lyomyces*, in which *L. sambuci* resolved sister to *L. crustosus*. This arrangement is confirmed in recently published phylogenies (Yurchenko *et al.* 2024a). Here in this study, six novel wood-inhabiting fungal species, viz. *L. chimonobambusae*, *L. daguanensis*, *L. farinaceous*, *L. fragilis*, *L. luteoluswere*, and *L. tongbiguanensis* are introduced from Yunnan Province based on phylogenetic and morphological characteristics (Figs 6, 7).

Lyomyces chimonobambusae L. Wang & C.L. Zhao, *sp. nov.* MB 859941. Figs 41–43.

Chinese name: 筇竹疏伏革菌 (Qiong zhu shu fu ge jun).

Etymology: The species epithet “*chimonobambusae*” refers to the type specimen growing on *Chimonobambusa tumidissinoda*.

Description: *Basidiomata* annual, resupinate, closely adnate,

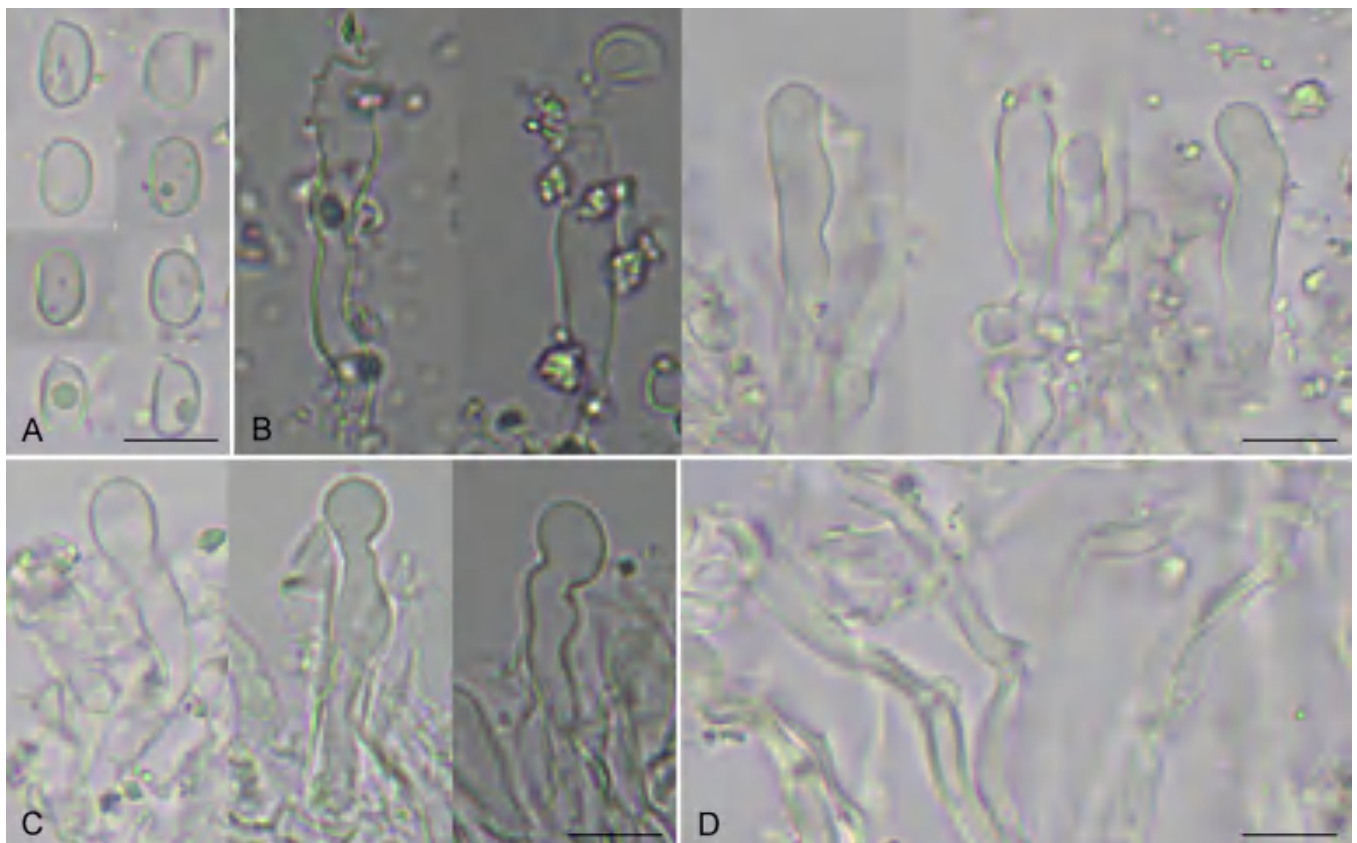


Fig. 40. Microscopic structures of *Fasciodontia grandinia* CLZhao 40459 (holotype SWFC 00040459). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Capitulate cystidia. **D.** A section of generative hyphae with clamp connections. Scale bars = 10 μm .



Fig. 41. A, B. Basidiomata of *Lyomyces chimonobambus* HMZhou 747 (holotype SWFC 00100747). Scale bars: A = 1 cm; B = 2 mm.

inseparable from substrate, membranaceous, without odour or taste when fresh, up to 5 cm long, 2 cm wide, and 300 μm thick. *Hymenial surface* slightly grandinioid, white when fresh, white to cream upon drying, cracked. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin- to thick-walled, smooth, frequently branched, interwoven, 2–4.5 μm diam. generative hyphae with clamp connections, crystals present in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* of two types: (1) fusiform, tapering, colourless, thin-walled, smooth, 17–40 \times 7–9 μm ; (2) fusoid to subcylindrical, colourless, thin-walled, smooth, 12.5–20.5 \times 7–10 μm . *Basidia* subcylindrical, slightly flexuous, with a basal clamp connection and four sterigmata, 20–30.5 \times 7–9 μm ; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid,

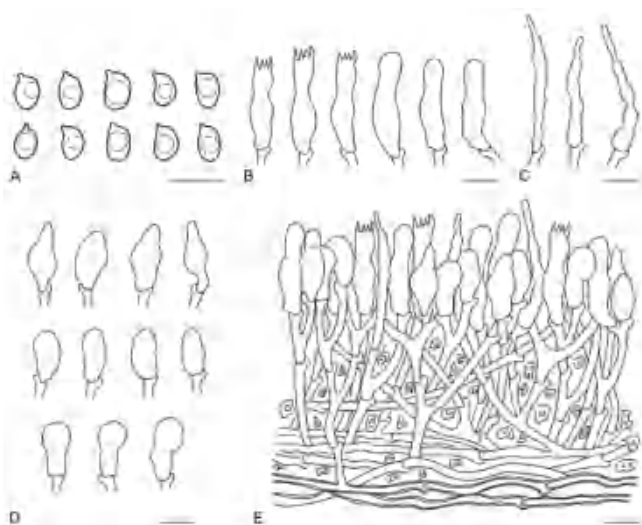


Fig. 42. Microscopic structures of *Lyomyces chimonobambus* HMZhou 747 (holotype SWFC 00100747). A. Basidiospores. B. Basidia and basidioles. C. Tapering cystidia. D. Fusoid to subcylindrical cystidia. E. A section of the hymenium. Scale bars = 10 μm .

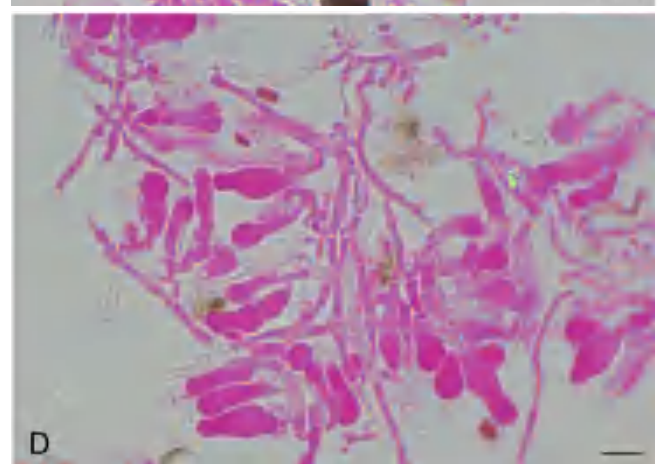
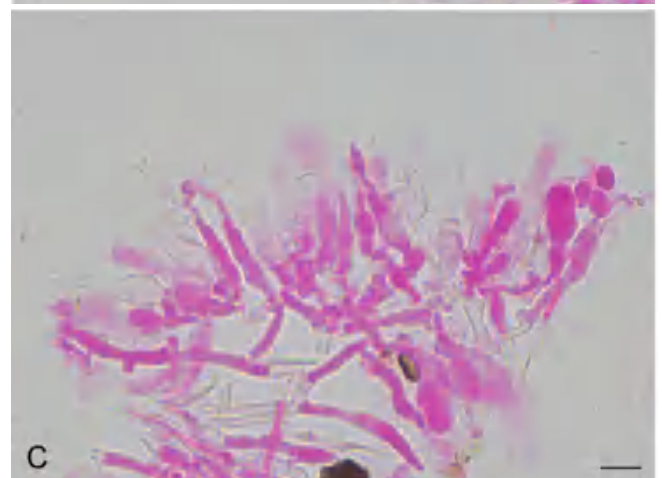
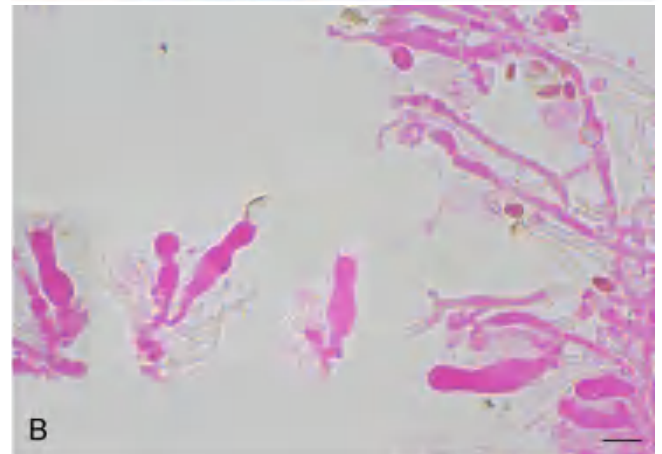
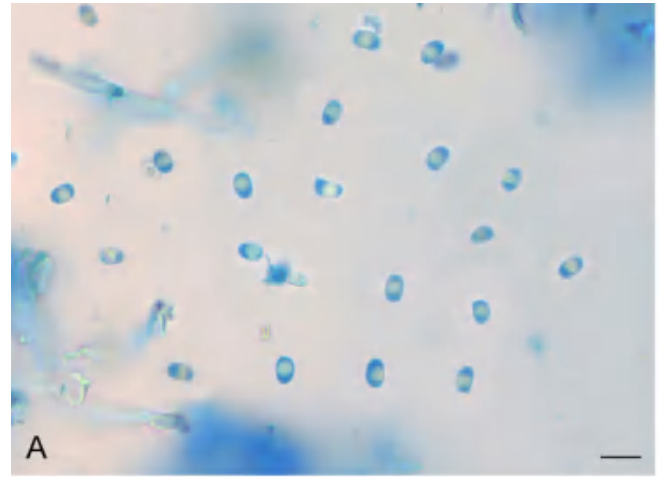


Fig. 43. Microscopic structures of *Lyomyces chimonobambus* HMZhou 747 (holotype SWFC 00100747). A. Basidiospores. B. Basidia and basidioles. C. Tapering cystidia. D. Fusoid to subcylindrical cystidia. Scale bars = 10 μm .



colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, (5–)6–7.5 × (3.5–)4–5.5 μm, L = 6.66 μm, W = 4.74 μm, Q = 1.378–1.493 (n = 150/5).

Typus: **China**, Yunnan Province, Zhaotong, Yongshan County, Xisha Village, Wumengshan National Nature Reserve, 28°18'01"N, 103°58'12"E, 1812 m.a.s.l., on dead *Chimonobambusa tumidissinoda*, 13 Oct. 2024, *H.M. Zhou*, HMZhou 747 (**holotype** SWFC 00100747).

Additional specimens examined: **China**, Yunnan Province, Zhaotong, Dagan County, Tianxing Town, Wumengshan National Nature Reserve, 27°49'48"N, 103°59'24"E, 1800 m.a.s.l., on dead bamboo, 20 Aug. 2024, *H.M. Zhou*, HMZhou 505 (SWFC 00100505), HMZhou 507 (SWFC 00100507); Yongshan County, Xisha Village, Wumengshan National Nature Reserve, 28°18'01"N, 103°58'12"E, 1812 m.a.s.l., on dead *Chimonobambusa tumidissinoda*, 13 Oct. 2024, *H.M. Zhou*, HMZhou 704 (SWFC 00100704), HMZhou 749 (SWFC 00100749), HMZhou 750 (SWFC 00100750), HMZhou 768 (SWFC 00100768); on fallen angiosperm branch, 13 Oct. 2024, HMZhou 713 (SWFC 00100713); Yongshan County, Tuanjie Village, Wumengshan National Nature Reserve, 28°12'00"N, 103°51'01"E, 1800 m.a.s.l., on dead *Chimonobambusa tumidissinoda*, 4 Sep. 2024, *H.M. Zhou*, HMZhou 1236 (SWFC 00101236); Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l. on dead bamboo, 3 Jul. 2024, *C.L. Zhao*, CLZhao 39785 (SWFC 00039785).

Notes: Our phylogenetic analysis (Fig. 1) confirmed the affinities of our new species *Lyomyces chimonobambus* to *Lyomyces*. It resolved sister to *L. tongbiguanensis*, from which it can be distinguished by its smooth hymenophore and smaller, ellipsoid to drop-shaped basidiospores (4.5–6 × 2.5–3.5 μm).



Fig. 44. A, B. Basidiomata of *Lyomyces daguanensis* HMZhou 454 (holotype SWFC 00100454). Scale bars: A = 1 cm; B = 2 mm.

Lyomyces daguanensis L. Wang & C.L. Zhao, **sp. nov.** MB 859942. Figs 44–46.

Chinese name: 大关疏伏革菌 (Da guan shu fu ge jun).

Etymology: The species epithet “*dakuanensis*” refers to the collection site (Daguan County) of the type specimen.

Description: *Basidiomata* annual, resupinate, closely adnate, inseparable from substrate, membranaceous, without odour or taste when fresh, up to 3 cm long, 2 cm wide, and 500 μm thick. *Hymenial surface* tuberculate, white when fresh, white to cream upon drying, cracked upon drying. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, smooth, frequently branched, interwoven generative hyphae 2–3.5 μm diam. with clamp connections, with crystals present in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* of two shapes: (1) capitate, colourless, thin-walled, smooth, 11–19 × 4.5–8 μm; (2) subclavate to fusiform, tapering, colourless, thin-walled, smooth, 10.5–25 × 4.55–7.5 μm. *Basidia* subclavate, slightly flexuous, with a basal clamp connection and four sterigmata, 11.5–20 × 4–6.5 μm; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* subcylindrical, colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, 5.5–7.5(–8) × (2.5–)3–3.5(–4) μm, L = 6.44 μm, W = 3.39 μm, Q = 1.579–1.902 (n = 150/5).

Typus: **China**, Yunnan Province, Zhaotong, Dagan County, Tianxing Town, Wumengshan National Nature Reserve, 27°49'48"N, 103°58'48"E, 1800 m.a.s.l., on dead bamboo, 19 Aug. 2024, *H.M. Zhou*, HMZhou 454 (**holotype** SWFC 00100454).

Additional specimens examined: **China**, Yunnan Province, Zhaotong, Dagan County, Tianxing Town, Wumengshan National Nature Reserve, 27°49'48"N, 103°58'48"E, 1800 m.a.s.l., on dead bamboo, 19 Aug. 2024, *H.M. Zhou*, HMZhou 442 (SWFC 00100442), HMZhou 445 (SWFC 00100445), HMZhou 447 (SWFC 00100447), HMZhou 448 (SWFC

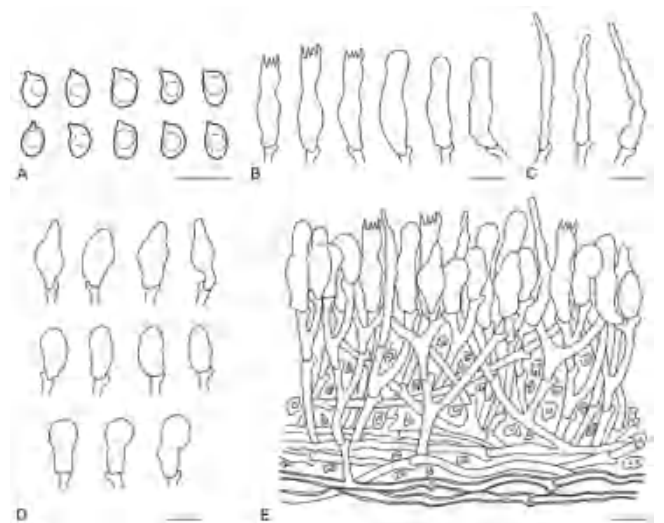


Fig. 45. Microscopic structures of *Lyomyces daguanensis* HMZhou 454 (holotype SWFC 00100454). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Clavate to capitate cystidia. **D.** Subclavate to fusiform cystidia. **E.** A section of the hymenium. Scale bars = 10 μm.



00100448), HMZhou 451 (SWFC 00100451), HMZhou 453 (SWFC 00100453), HMZhou 455 (SWFC 00100455), HMZhou 456 (SWFC 00100456), HMZhou 457 (SWFC 00100457), HMZhou 508 (SWFC 00100508), HMZhou 509 (SWFC 00100509), HMZhou 510 (SWFC 00100510), HMZhou 511 (SWFC 00100511), HMZhou 512 (SWFC 00100512), HMZhou 513 (SWFC 00100513).

Notes: Our phylogenetic analysis confirmed the affinities of our new species to *Lyomyces* (Fig. 1), in which it clustered with *L. wumengshanensis* and *L. incanus* (Fig. 7). Key characters distinguishing *L. wumengshanensis* from *L. daguanensis* are its cream, coriaceous hymenophore and ellipsoid to broad ellipsoid basidiospores ($4\text{--}6 \times 3\text{--}5 \mu\text{m}$, Yuan *et al.* 2024), while *L. incanus* differs from *L. daguanensis* by its furfuraceous basidiomata with incanus, smooth hymenial surface, and ellipsoid basidiospores ($5\text{--}6.5 \times 4\text{--}5 \mu\text{m}$, Dong *et al.* 2024).

Lyomyces farinaceus L. Wang & C.L. Zhao, *sp. nov.* MB 859944. Figs 47–49.

Chinese name: 粉末状疏伏革菌 (Fen zhuang shu fu ge jun).

Etymology: The species epithet “*farinaceus*” refers to its farinaceous hymenial surface.

Description: *Basidiomata* annual, resupinate, closely adnate, inseparable from substrate, farinaceous, without odour or taste when fresh, up to 8 cm long, 2 cm wide, and 500 μm thick. *Hymenial surface* grandinoid, cream when fresh, cream to buff upon drying, occasionally cracked upon drying. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, smooth, frequently branched, interwoven generative hyphae 2–3.5 μm diam., with clamp connections and crystals present in moderate amounts among hyphae; IKI–, CB–; tissue unchanged in KOH. *Cystidia* of three types: (1) fusiform, tapering, slightly flexuous, colourless, thin-walled, smooth, $17\text{--}22.5 \times 2.5\text{--}4 \mu\text{m}$; (2) capitate, colourless, thin-walled, smooth, $14\text{--}20.5 \times 5.5\text{--}7 \mu\text{m}$; (3) cylindrical with a wider base and a clavate apex, colourless, thin-walled, smooth, $22\text{--}26.5 \times 4.5\text{--}6 \mu\text{m}$. *Basidia* subclavate, slightly flexuous, with a basal clamp connection and four sterigmata, $17.5\text{--}21 \times 3.5\text{--}6 \mu\text{m}$; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* subcylindrical, colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, $6\text{--}7(\text{--}7.5) \times 3\text{--}4 \mu\text{m}$, $L = 6.49 \mu\text{m}$, $W = 3.41 \mu\text{m}$, $Q = 1.905$ ($n = 30/1$).

Typus: **China**, Yunnan Province, Wenshan, Laojunshan Nature Reserve, $23^{\circ}18'36''\text{N}$, $103^{\circ}59'24''\text{E}$, 2000 m.a.s.l., on fallen angiosperm branch, 23 Jan. 2019, C.L. Zhao, CLZhao 12102 (**holotype** SWFC 00012102).

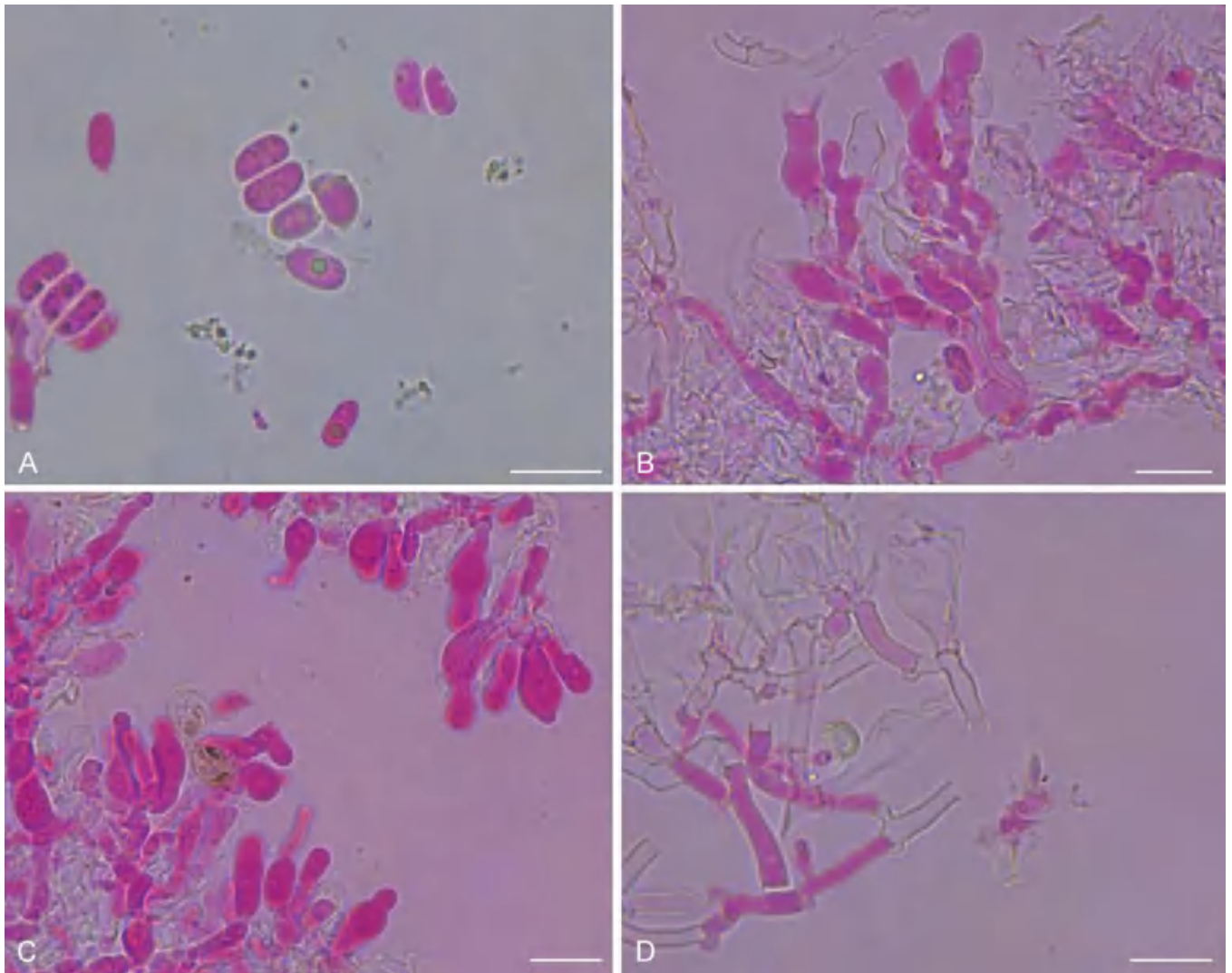


Fig. 46. Microscopic structures of *Lyomyces daguanensis* HMZhou 454 (holotype SWFC 00100454). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Cystidia of several types. **D.** A section of generative hyphae. Scale bars = 10 μm .



Fig. 47. A, B. Basidiomata of *Lyomyces farinaceus* CLZhao 12102 (holotype SWFC 00012102). Scale bars: A = 1 cm; B = 2 mm.

Notes: Sequences of our new species confirmed its affinities to *Lyomyces* (Fig. 1) and resolved sister to *L. crystallinus* (Fig. 7) in our phylogenetic studies. The key characters distinguishing *L. crystallinus* from *L. farinaceus* are its smooth

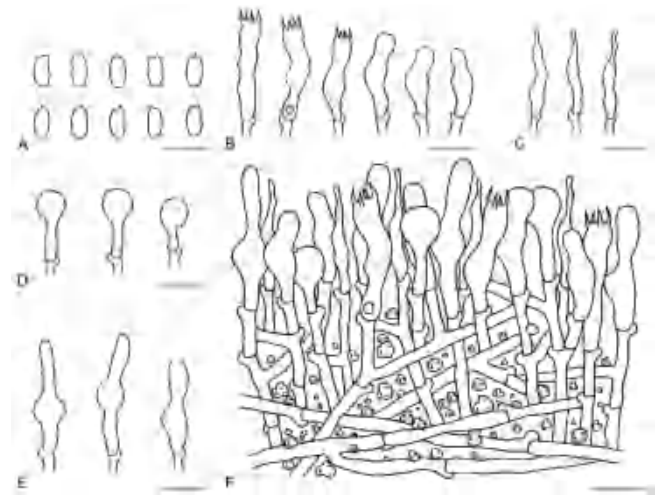


Fig. 48. Microscopic structures of *Lyomyces farinaceus* CLZhao 12102 (holotype SWFC 00012102). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Fusiform cystidia. **D.** Capitulate cystidia. **E.** Cystidia of cylindrical with a wider base and a clavate round apex. **F.** A section of the hymenium. Scale bars = 10 μ m.

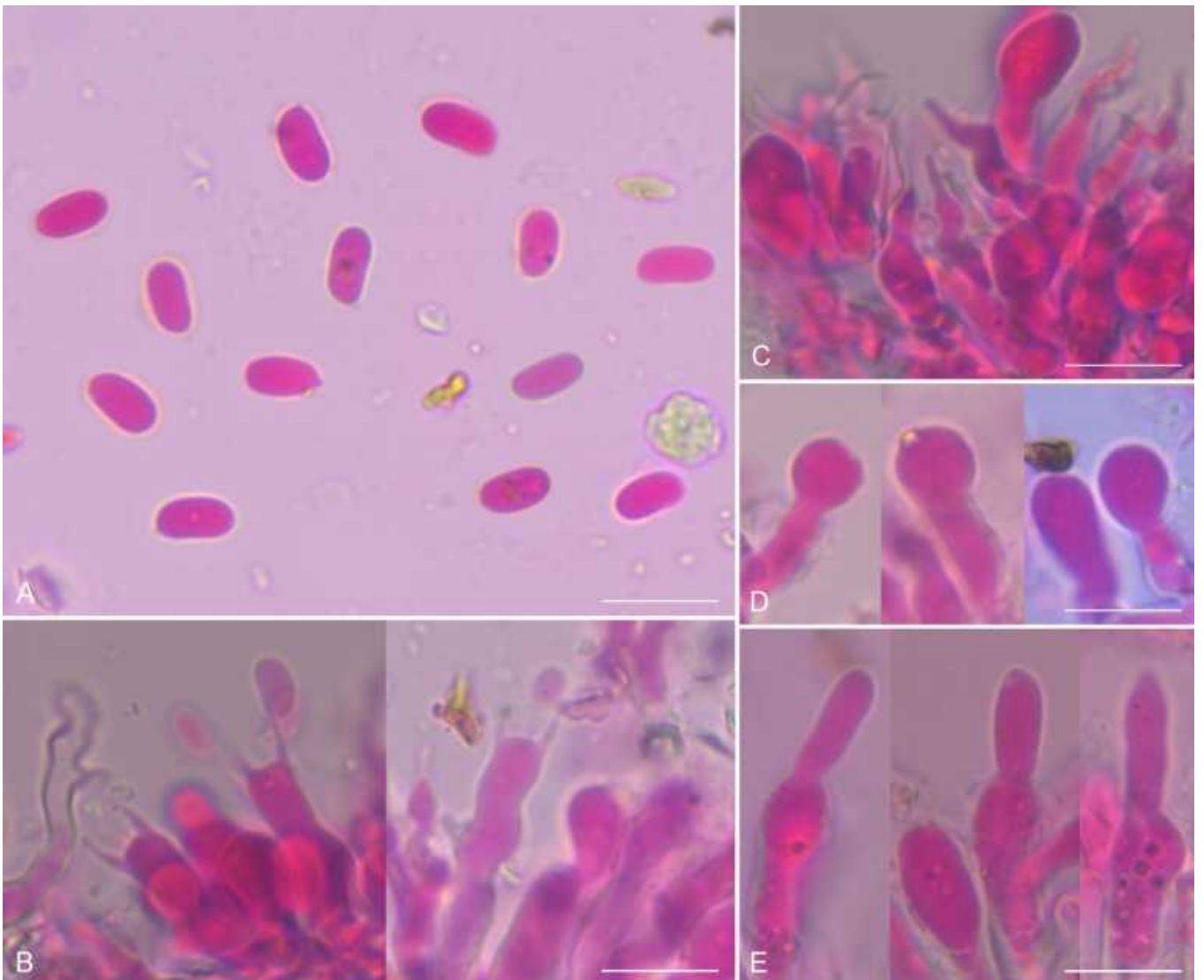


Fig. 49. Microscopic structures of *Lyomyces farinaceus* CLZhao 12102 (holotype SWFC 00012102). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Fusiform cystidia. **D.** Capitulate cystidia. **E.** Cystidia of cylindrical with a wider base and a clavate round apex. Scale bars = 10 μ m.



to slightly grandinioid, cream to pale buff hymenophore and smaller, ellipsoid basidiospores (5.1–6.5 × 3.1–3.4 μm, Liu *et al.* 2024).

Lyomyces fragilis L. Wang & C.L. Zhao, *sp. nov.* MB 859945. Figs 50–52.

Chinese name: 脆疏伏革菌 (Cui shu fu ge jun).

Etymology: The species epithet “*fragilis*” refers to its fragile basidiomata.

Description: *Basidiomata* annual, resupinate, closely adnate, fragile, inseparable from substrate, coriaceous, without odour or taste when fresh, up to 6 cm long, 4 cm wide, and 400 μm thick. *Hymenial surface* smooth, white to cream when fresh, cream to slightly buff upon drying; occasionally cracked when fresh and densely cracked upon drying. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin- to thick-walled, smooth, frequently branched, interwoven generative hyphae 2–3.5 μm diam. with clamp connections and crystals in dense amounts among hyphae, IKI–, CB–; tissues unchanged in KOH. *Cystidia* of three types: (1) fusiform, tapering, colourless, thin-walled, smooth, 24.5–30 × 2.5–4 μm; (2) cylindrical with a wider base and a capitate apex, colourless, thin-walled, smooth, 9–14 × 3–4.5 μm; (3) capitate, colourless, thin-walled, smooth, 9.5–18 × 3.5–6 μm. *Basidia* subclavate, slightly flexuous, with a basal clamp connection and four sterigmata, 15.5–21.5 × 3.5–5.5 μm; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid, colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, (4–)4.5–5.5 × 2.5–3.5 μm, L = 4.88 μm, W = 2.98 μm, Q = 1.625–1.783 (n = 120/4).



Fig. 50. A, B. Basidiomata of *Lyomyces fragilis* HMZhou 549 (holotype SWFC 00100549). Scale bars: A = 1 cm; B = 2 mm.

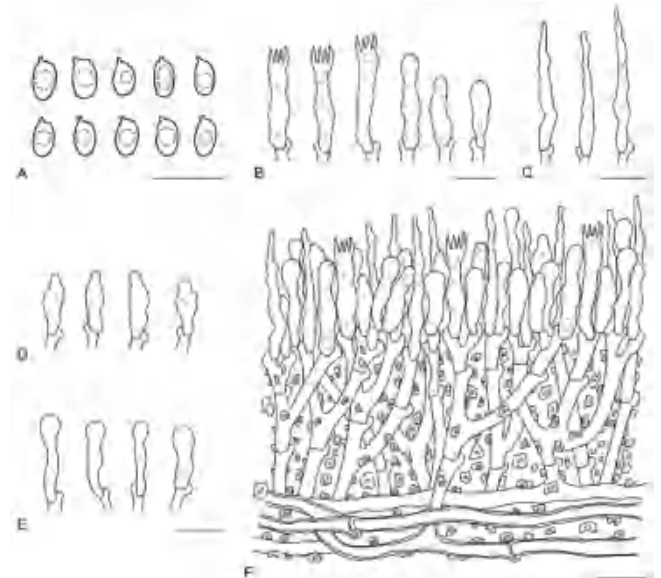


Fig. 51. Microscopic structures of *Lyomyces fragilis* HMZhou 549 (holotype SWFC 00100549). A. Basidiospores. B. Basidia and basidioles. C. Fusiform cystidia. D. Cylindrical with a wider base and a capitate apex cystidia. E. Capitate cystidia. F. A section of the hymenium. Scale bars = 10 μm.

Typus: **China**, Yunnan Province, Zhaotong, Dagan County, Mugan Town, Wumengshan National Nature Reserve, 28°8'24"N, 103°58'11"E, 1780 m.a.s.l., on fallen angiosperm branch, 12 Oct. 2024, H.M. Zhou, HMZhou 549 (**holotype** SWFC 00100549).

Additional specimens examined: **China**, Yunnan Province, Zhaotong, Dagan County, Mugan Town, Wumengshan National Nature Reserve, 28°8'24"N, 103°58'11"E, 1780 m.a.s.l., on fallen angiosperm branch, 12 Oct. 2024, H.M. Zhou, HMZhou 624 (SWFC 00100624); Puer, Jingdong County, Wuliangshan National Nature Reserve, 23°34'11"N, 100°13'12"E, 3380 m.a.s.l., on fallen angiosperm branch, C.L. Zhao, 6 Oct. 2017, CLZhao 4616 (SWFC 00004616); Chuxiong, Zixishan National Forest Park, 24°40'48"N, 106°36'02"E, 1900 m.a.s.l., on fallen angiosperm branch, 30 Jun. 2018, C.L. Zhao, CLZhao 6897 (SWFC 00006897); Zhaotong, Dagan County, Wumengshan National Nature Reserve, 28°8'24"N, 103°58'11"E, 1780 m.a.s.l., on fallen angiosperm branch, 6 Nov. 2023, C.L. Zhao, CLZhao 35415 (SWFC 00035415), CLZhao 35420 (SWFC 00035420).

Notes: Our phylogenetic analysis confirmed the affinities of our new species to *Lyomyces* (Fig. 1), where it resolved in a sister relationship to *L. crustosus* (Fig. 7). Key characters to distinguish *L. crustosus* from *L. fragilis* are its pale yellowish white hymenial surface and subulate or fusoid, sinuous leptocystidia (see also Maekawa 1994).

Lyomyces luteolus L. Wang & C.L. Zhao, *sp. nov.* MB 859946. Figs 53–55.

Chinese name: 浅黄疏伏革菌 (Qian huang shu fu ge jun).

Etymology: The species epithet “*luteolus*” refers to its cream to buff hymenial surface.

Description: *Basidiomata* annual, resupinate, closely adnate, inseparable from substrate, coriaceous, without odour or

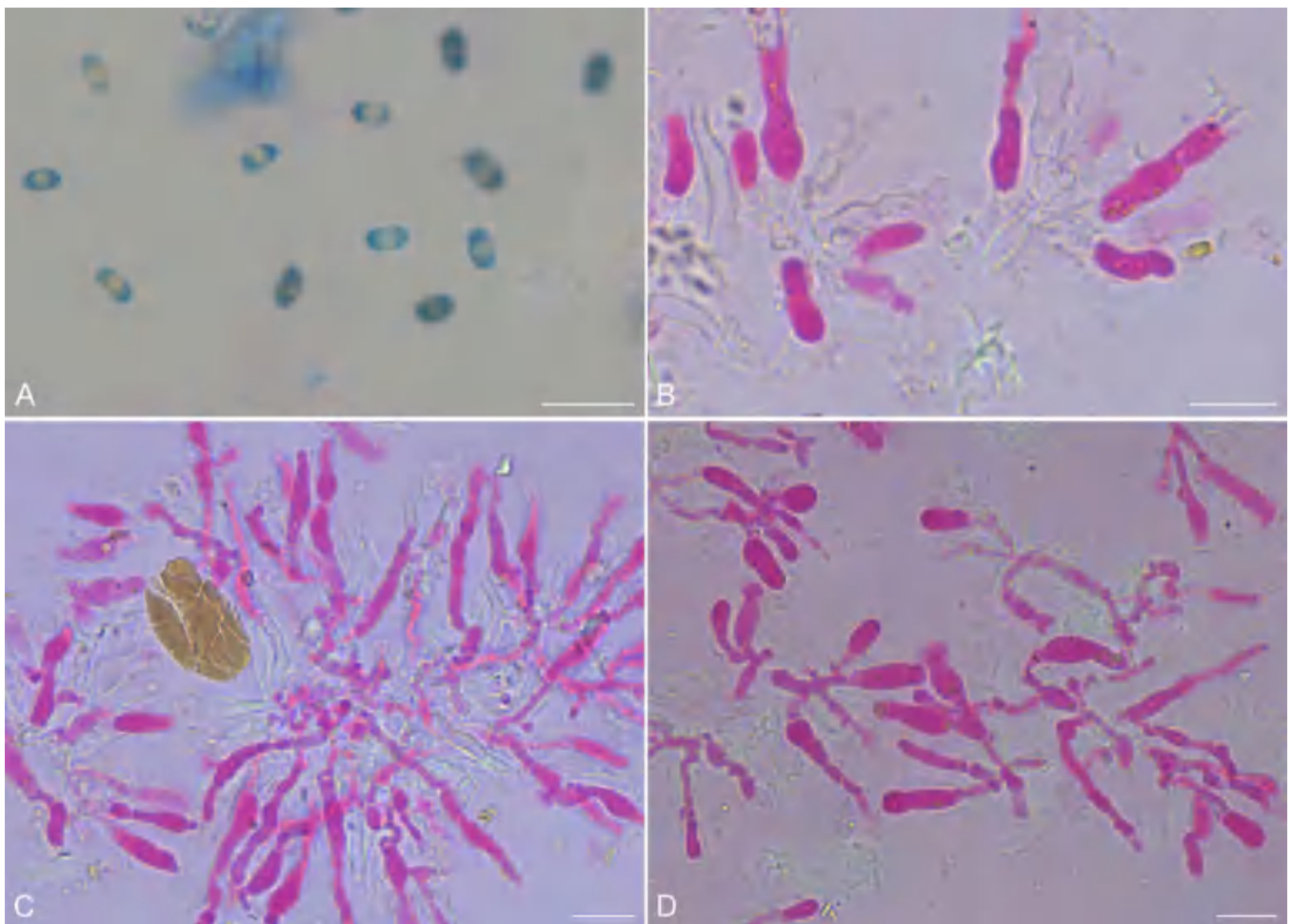


Fig. 52. Microscopic structures of *Lyomyces fragilis* HMZhou 549 (holotype SWFC 00100549). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Fusiform cystidia. **D.** Capitatae cystidia. Scale bars = 10 μ m.

taste when fresh, up to 4 cm long, 2 cm wide, and 500 μ m thick. *Hymenial surface* smooth, white to cream when fresh, cream to buff upon drying. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, smooth, frequently branched, interwoven generative hyphae 2.5–5.5 μ m diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* subcylindrical to subclavate, colourless, thin-walled, smooth, 18.5–31 \times 4–8.5 μ m. *Basidia* subclavate, slightly flexuous, with a basal clamp connection and four sterigmata, 28–48.5 \times 5–8.5 μ m; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid, colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, 6–8 \times 4.5–6 μ m, L = 6.97 μ m, W = 5.108 μ m, Q = 1.330–1.365 (n = 60/2).

Typus: **China**, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on dead bamboo, 3 Jul. 2024, C.L. Zhao, CLZhao 37457 (**holotype** SWFC 00037457).

Additional specimen examined: **China**, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on dead bamboo, 3 Jul. 2024, C.L. Zhao, CLZhao 37561 (SWFC 00037561).

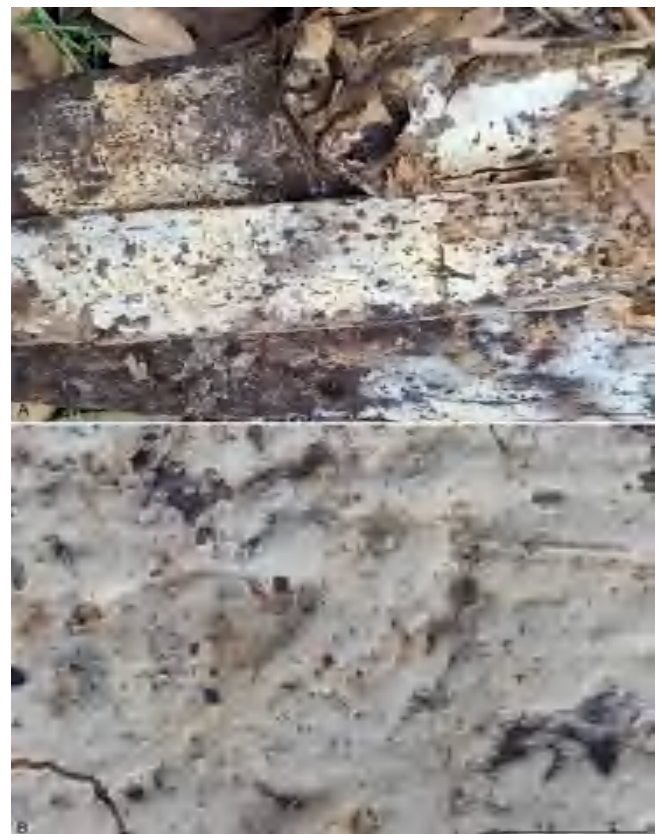


Fig. 53. **A, B.** Basidiomata of *Lyomyces luteolus* CLZhao 37457 (holotype SWFC 00037457). Scale bars: A = 1 cm; B = 2 mm.



Notes: Our phylogenetic analysis confirmed the generic affinities of our new species *Lyomyces luteolus* (Fig. 1), in which it was shown to resolve in a sister relationship to *L. mascarensis* (Fig. 7). However, *L. mascarensis* differs from *L. luteolus* by its cream to brownish hymenophore and smaller, ellipsoid basidiospores ($4.5\text{--}6 \times 3.3\text{--}4 \mu\text{m}$, Yurchenko et al. 2017).

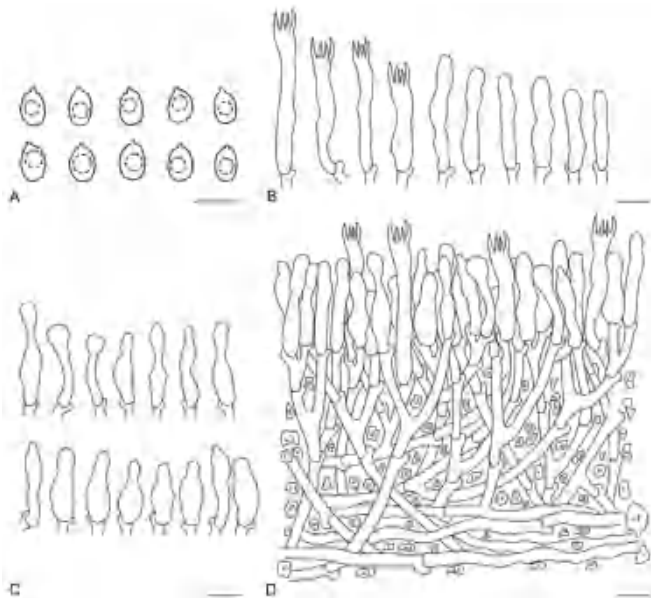


Fig. 54. Microscopic structures of *Lyomyces luteolus* CLZhao 37457 (holotype SWFC 00037457). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Cystidia. **D.** A section of the hymenium. Scale bars = 10 μm .

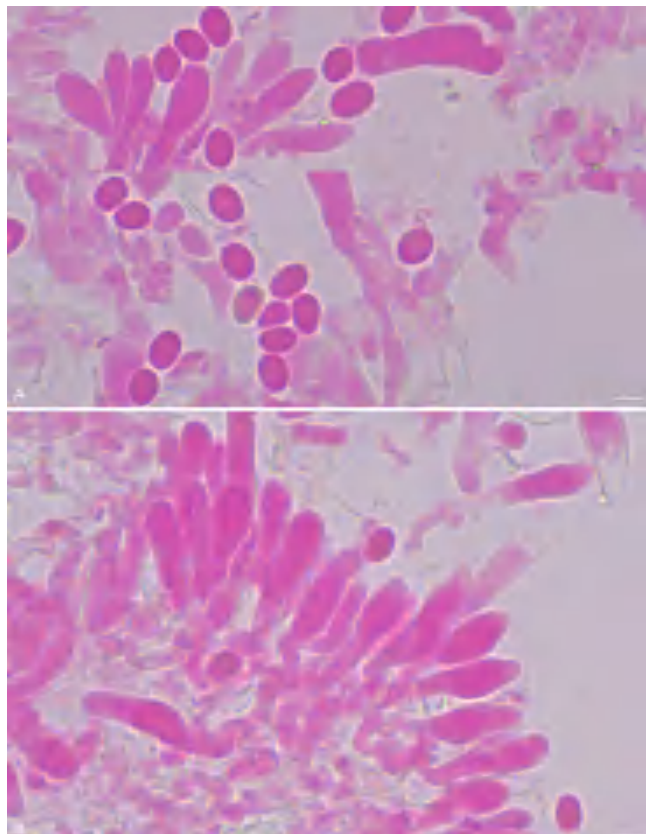


Fig. 55. **A, B.** Microscopic structures of *Lyomyces luteolus* CLZhao 37457 (holotype SWFC 00037457). **A.** Basidiospores. **B.** A section of the hymenium. Scale bars = 10 μm .

Lyomyces tongbiguanensis L. Wang & C.L. Zhao, *sp. nov.* MB 859947. Figs 56–58.

Chinese name: 铜壁关疏伏革菌 (Tong bi guan shu fu ge jun).

Etymology: The species epithet “*tongbiguanensis*” refers to the collection site (Tongbiguan Provincial Nature Reserve) of the type specimen.

Description: *Basidiomata* annual, resupinate, closely adnate, inseparable from substrate, membranaceous, without odour or taste when fresh, up to 12 cm long, 2 cm wide, and 600 μm thick. *Hymenial surface* smooth, white when fresh, white to cream upon drying, occasionally cracked when fresh and



Fig. 56. **A, B.** Basidiomata of *Lyomyces tongbiguanensis* CLZhao 36542 (holotype SWFC 00036542). Scale bars: **A** = 1 cm; **B** = 2 mm.

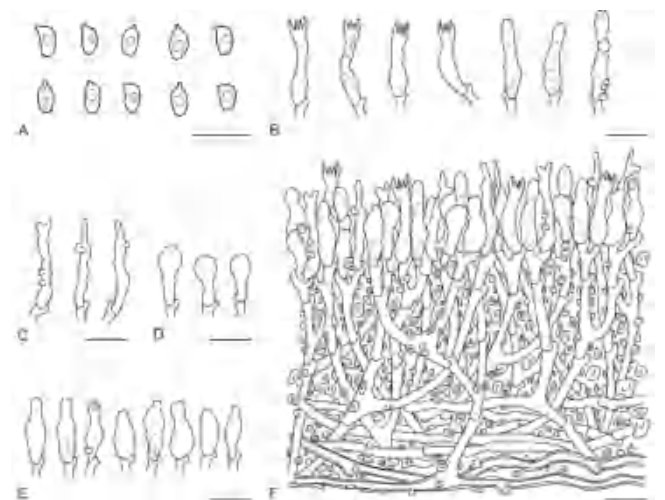


Fig. 57. Microscopic structures of *Lyomyces tongbiguanensis* CLZhao 36542 (holotype SWFC 00036542). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Fusiform cystidia. **D.** Capitulate cystidia. **E.** Subclavate to subcylindrical cystidia. **F.** A section of the hymenium. Scale bars = 10 μm .



densely cracked upon drying. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin- to thick-walled, smooth, frequently branched, interwoven generative hyphae 2–3 µm diam. with clamp connections and crystals in dense amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. Cystidia of three types: (1) fusiform, tapering, colourless, thin-walled, smooth, 16.5–24 × 2.5–5 µm; (2) capitate, colourless, thin-walled, smooth, 11.5–20.5 × 3.5–5.5 µm; (3) subclavate to subcylindrical, colourless, thin-walled, smooth, 9.5–19 × 4.5–6 µm. *Basidia* subclavate, slightly flexuous, with a basal clamp connection and four sterigmata, 13–22.5 × 3.5–6.5 µm; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid to drop-shaped, colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, (4–)4.5–6 × 2.5–3.5(–4) µm, L = 5.15 µm, W = 3.09 µm, Q = 1.621–1.687 (n = 150/3).

Typus: **China**, Yunnan Province, Dehong, Mang City, Mengga Town, Tongbiguan Provincial Nature Reserve, 24°16'12"N, 98°27'36"E, 1100 m.a.s.l., on fallen angiosperm branch, 29 Jun. 2024, C.L. Zhao, CLZhao 36542 (**holotype** SWFC 00036542).

Additional specimens examined: **China**, Yunnan Province, Dehong, Mang City, Mengga Town, Tongbiguan Provincial Nature Reserve, 24°16'12"N, 98°27'36"E, 1100 m.a.s.l., on fallen angiosperm branch, 29 Jun. 2024, C.L. Zhao, CLZhao 36509 (SWFC 00036509), CLZhao 36595 (SWFC 00036595); 30 Jun. 2024, CLZhao 36738 (SWFC 00036738), CLZhao 36788 (SWFC 00036788), CLZhao 36985 (SWFC 00036985), CLZhao 37070 (SWFC 00037070); 8 Jul. 2024, CLZhao 39472 (SWFC 00039472), CLZhao 39607 (SWFC 00039607).

Notes: Our phylogenetic inference (Fig. 1) confirmed the generic affinities of our new species *Lyomyces tongbiguanensis*, and it was shown to resolve sister to *L.*

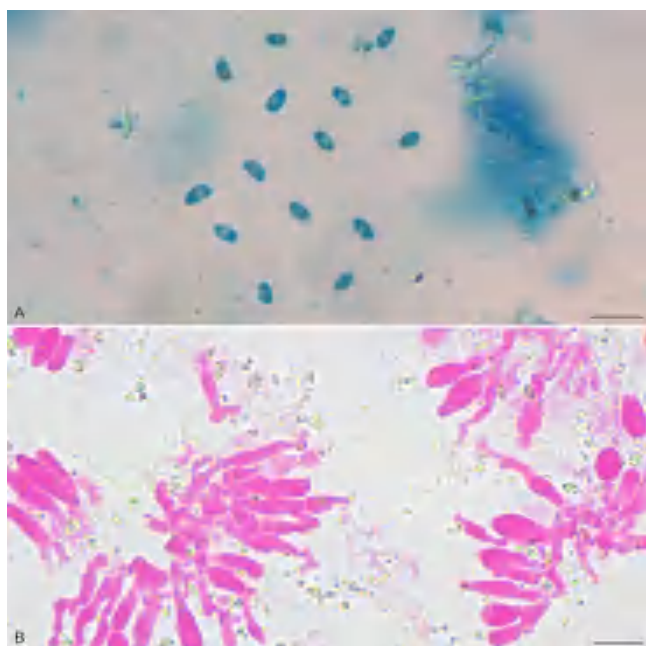


Fig. 58. **A, B.** Microscopic structures of *Lyomyces tongbiguanensis* CLZhao 36542 (holotype SWFC 00036542). **A.** Basidiospores. **B.** A section of the hymenium. Scale bars = 10 µm.

chimonobambus (Fig. 7). Key characters distinguishing *L. chimonobambus* from *L. tongbiguanensis* by its bigger basidiospores (6–7.5 × 4–5.5 µm).

Xylodon (Pers.) Gray, *A natural arrangement of British plants* (London) 1: 649. 1821.

Notes: *Xylodon* is a large genus of corticoid fungi with a cosmopolitan distribution, which is known from almost all types of biomes where wooden plant debris occurs, which includes humid to semi-arid climates, the seashore as well as the upper limit of wooden vegetation in altitudinal gradients (Yurchenko *et al.* 2024b). The genus is typified with *X. quercinus* and characterised by resupinate or effused basidiomata with a smooth, tuberculate, grandinoid, odontoid, coralloid, irpicoid or poroid hymenophore, a monomitic or dimitic hyphal system with clamped generative hyphae and different shapes of cystidia. Moreover, basidia are utriform or subutriform and basidiospores occur in cylindrical, ellipsoid to globose shape (Gray 1821, Bernicchia & Gorjón 2010, Cho *et al.* 2021, Yuan & Zhao 2024). Basidiomata of *Xylodon* appear on living parts of trees and non-woody plant remains, and cause a white rot (Kotiranta & Saarenoksa 2000, Viner *et al.* 2018, 2021, Yurchenko *et al.* 2024b). *Lyomyces* and *Xylodon* are two closely related genera with unclear molecular and morphological borders, which were treated in *Hyphodontia* for a couple of decades until Hjortstam & Ryvarden (2007, 2009) resurrected them (Yurchenko *et al.* 2017, Viner *et al.* 2021). All published results so far indicate that the relationship within *Xylodon* and allied genera cannot be resolved when using ribosomal DNA sequences as sole source for phylogenetic information (Viner *et al.* 2021). Similarly, it is hard to distinguish *Xylodon* from yet another genus, *Schizopera* when using morphology and phylogenetics. Consequently, Riebesehl & Langer (2017) proposed to accommodate *Schizopera* within *Xylodon*. Later phylogenies inferred from ITS+nLSU regions of *Xylodon* and related genera suggested that the two genera *Lagarobasidium* and *Xylodon* are congeneric, which led to the transfer of the three *Lagarobasidium* species to *Xylodon* (Viner *et al.* 2018). The genera *Odontopsis* and *Palifer* were synonymized with *Xylodon* in a similar fashion based on phylogenetic analyses of 28S and ITS data by Riebesehl *et al.* (2019). Inspiringly, new species have been described in recent years at an accelerated pace, which can be attributed to the increasing availability of large amounts of sequences for comparison taxon samples and the fact that multiple DNA loci are available (Luo *et al.* 2022, Yurchenko *et al.* 2024b, Yuan & Zhao 2024). However, as its generic borders are notoriously difficult to delimitate, only time will tell if this reflects its true biodiversity or an artificially inflated species number. To date, 245 specific and infraspecific names are registered for *Xylodon*, and the actual number of species is 164 (Zhang *et al.* 2025). During investigations on wood-inhabiting fungi in the Yunnan Province of China, we found in total nine new species *viz.* *X. albofarinaceus*, *X. daguanensis*, *X. luteofarinaceus*, *X. luteograndineus*, *X. luteomarginatus*, *X. odontoides*, *X. tenuis*, *X. tongbiguanensis*, and *X. yingjiangensis* that we describe in this study.

Xylodon albofarinaceus L. Wang & C.L. Zhao, **sp. nov.** MB 859948. Figs 59–61.



Fig. 59. A, B. Basidiomata of *Xylodon albofarinaceus* CLZhao 37064 (holotype SWFC 00037064). Scale bars: A = 1 cm; B = 2 mm.

Chinese name: 白粉末木齿菌 (Bai fen mo mu chi jun).

Etymology: The species epithet “*albofarinaceus*” refers to its white basidiomata with farinaceous hymenial surface.

Description: *Basidiomata* annual, resupinate, adnate, farinaceous, without odour or taste when fresh, up to 10 cm long, 2 cm wide, and 400 μ m thick. *Hymenial surface* grandinoid, white when fresh, white to cream upon drying. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, slightly thick-walled, smooth, frequently branched, interwoven generative hyphae 2–3.5 μ m diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* capitata, colourless, thin-walled, smooth,

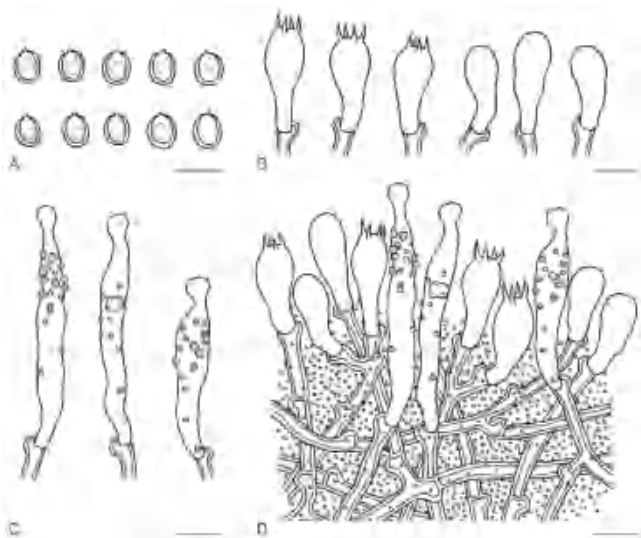


Fig. 60. Microscopic structures of *Xylodon albofarinaceus* CLZhao 37064 (holotype SWFC 00037064). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Capitata cystidia. **D.** A section of the hymenium. Scale bars = 10 μ m.

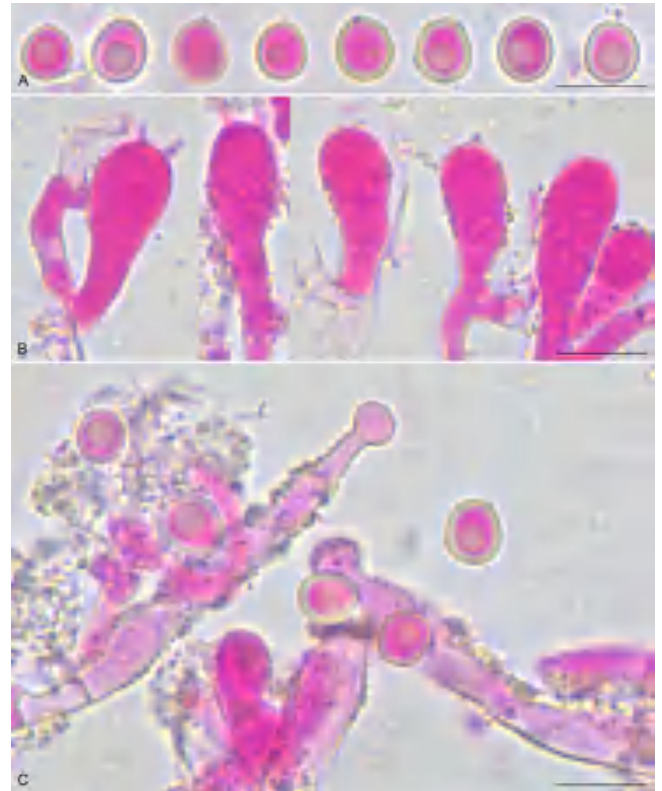


Fig. 61. Microscopic structures of *Xylodon albofarinaceus* CLZhao 37064 (holotype SWFC 00037064). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Capitata cystidia. Scale bars = 10 μ m.

38–51.5 \times 5.5–7.5 μ m. *Basidia* clavate, with a basal clamp connection and four sterigmata, 18–22.5 \times 8–9.5 μ m; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* subglobose, colourless, thick-walled, smooth, with oil droplets, IKI–, CB–, (5–)5.5–7.5 \times (4.5–)5–6.5 μ m, $L = 6.47 \mu$ m, $W = 5.71 \mu$ m, $Q = 1.135$ ($n = 30/1$).

Typus: **China**, Yunnan Province, Dehong, Mang City, Mengga Town, Sanxiandong Park, 24°13'48"N, 95°28'48" E, 1100 m.a.s.l., on fallen angiosperm branch, 30 Jun. 2024, C.L. Zhao, CLZhao 37064 (**holotype** SWFC 00037064).

Notes: Our new species *Xylodon albofarinaceus* resolved sister to *X. tongbiguanensis* in our ITS-sequence based phylogenetic analysis (Fig. 8). *Xylodon tongbiguanensis* can be distinguished from *X. albofarinaceus* by its odontoid, cream hymenial surface and broadly ellipsoid basidiospores (6–7.5 \times 5–6.5 μ m).

Xylodon daguanensis L. Wang & C.L. Zhao, **sp. nov.** MB 859949. Figs 62–64.

Chinese name: 大关木齿菌 (Da guan mu chi jun).

Etymology: The species epithet “*dakuanensis*” refers to the collection site (Dakuan County) of the type specimen.

Description: *Basidiomata* annual, resupinate, adnate, inseparable from substrate, coriaceous, without odour or taste when fresh, up to 4 cm long, 3 cm wide, and 500 μ m thick. *Hymenial surface* grandinoid, white when fresh, white to cream and cracked upon drying. Sterile margin thinning out, white to cream, up to 1 mm wide. *Hyphal*



system monomitic; colourless, slightly thick-walled, smooth, frequently branched, interwoven generative hyphae 3–5.5 μm diam. with clamp connections and crystals in moderate



Fig. 62. A, B. Basidiomata of *Xylodon daguanensis* HMZhou 537 (holotype SWFC 00100537). Scale bars: A = 1 cm; B = 2 mm.

amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* of two types: (1) capitate, colourless, thin-walled, smooth, 19.5–43 \times 5–7.5 μm ; (2) fusiform, tapering, slightly flexuous, colourless, thin-walled, smooth, 28.5–41.5 \times 3.5–7.5 μm . *Basidia* subcylindrical, slightly flexuous, with a

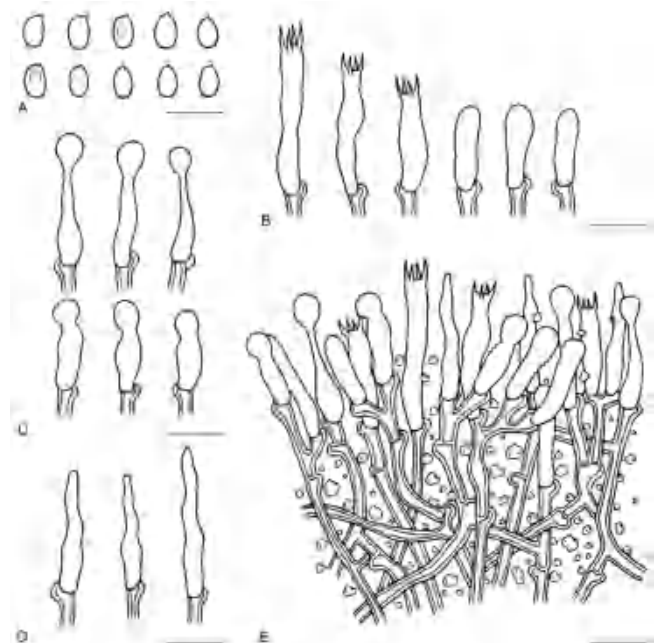


Fig. 63. Microscopic structures of *Xylodon daguanensis* HMZhou 537 (holotype SWFC 00100537). A. Basidiospores. B. Basidia and basidioles. C. Capitate cystidia. D. Fusiform cystidia. E. A section of the hymenium. Scale bars = 10 μm .

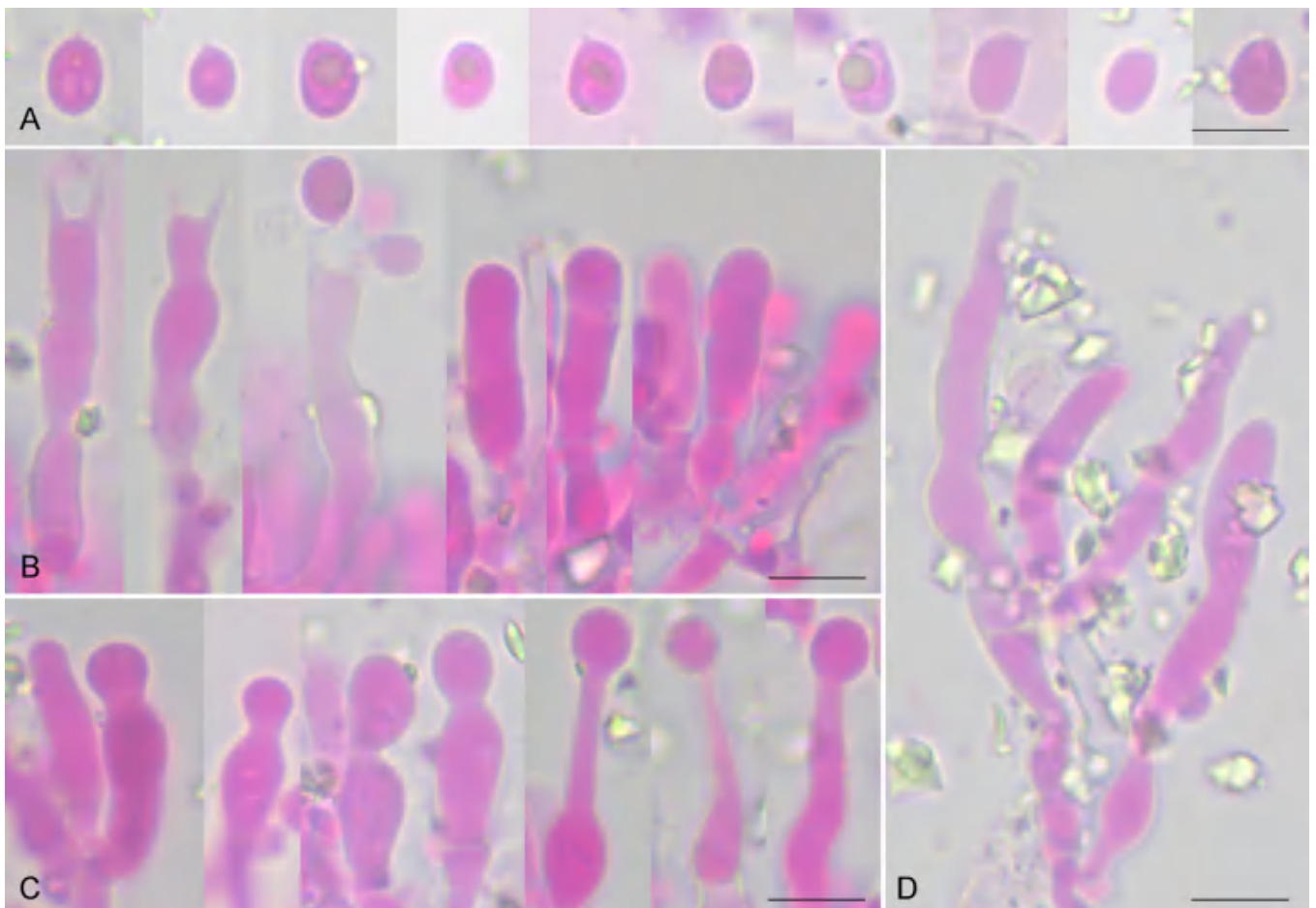


Fig. 64. Microscopic structures of *Xylodon daguanensis* HMZhou 537 (holotype SWFC 00100537). A. Basidiospores. B. Basidia and basidioles. C. Capitate cystidia. D. Fusiform cystidia. Scale bars = 10 μm .



basal clamp connection and four sterigmata, $25\text{--}32 \times 6\text{--}6.5 \mu\text{m}$; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid to broad ellipsoid, colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, $(6\text{--})6.5\text{--}8.5 \times (4\text{--})4.5\text{--}6.5 \mu\text{m}$, $L = 7.35 \mu\text{m}$, $W = 5.24 \mu\text{m}$, $Q = 1.403$ ($n = 30/1$).

Typus: **China**, Yunnan Province, Zhaotong, Dagan County, Tianxing Town, Wumengshan National Nature Reserve, $27^{\circ}49'48''\text{N}$, $103^{\circ}58'48''\text{E}$, 1800 m.a.s.l. on fallen angiosperm branch, 20 Aug. 2024, *H.M. Zhou*, HMZhou 537 (**holotype** SWFC 00100537).

Notes: Phylogenetic analysis of a multi-locus data set (Fig. 1) confirmed the generic affinities of our new species *Xylodon daguanensis* (HMZhou 537), which subsequently resolved sister to *X. astrocystidiatus* in an ITS-based phylogeny. Our new species differs from this taxon by its soft-membranaceous hymenophore and smaller basidiospores ($5\text{--}6 \times 3.7\text{--}4.2 \mu\text{m}$ vs $6.5\text{--}8.5 \times 4.5\text{--}6.5 \mu\text{m}$, Riebesehl & Langer 2017).

Xylodon luteofarinaceus L. Wang & C.L. Zhao, *sp. nov.* MB 859950. Figs 65–67.

Chinese name: 黄粉末木齿菌 (Huang fen mo mu chi jun).

Etymology: The species epithet “*luteofarinaceus*” refers to its flavescent basidiomata with a farinaceous hymenophore surface.

Description: *Basidiomata* annual, resupinate, adnate, inseparable from substrate, membranaceous, without odour or taste when fresh, up to 7 cm long, 2 cm wide, and 400 μm thick. *Hymenial surface* farinaceous, cream to buff when fresh, buff to olivaceous buff upon drying. Sterile margin thinning out, buff, up to 1 mm wide. *Hyphal system*



Fig. 65. A, B. Basidiomata of *Xylodon luteofarinaceus* CLZhao 37745 (holotype SWFC 00037745). Scale bars: A = 1 cm; B = 2 mm.

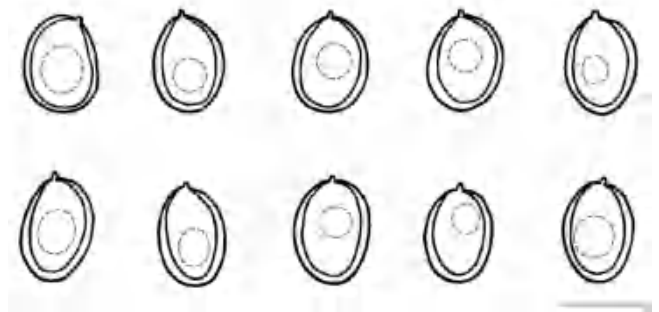


Fig. 66. Basidiospores structures of *Xylodon luteofarinaceus* CLZhao 37745 (holotype SWFC 00037745). Scale bar = 5 μm .

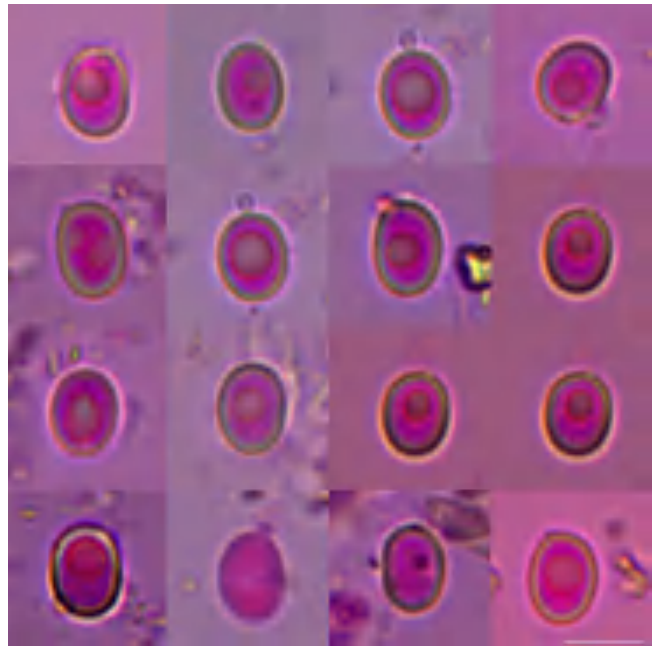


Fig. 67. Basidiospores of *Xylodon luteofarinaceus* CLZhao 37745 (holotype SWFC 00037745). Scale bar = 5 μm .

monomitic; colourless, thin- to slightly thick-walled, smooth, frequently branched, interwoven generative hyphae $2\text{--}3.5 \mu\text{m}$ diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissues unchanged in KOH. *Basidiospores* broadly ellipsoid, colourless, slightly thick-walled, smooth, with an oil droplet mostly, IKI–, CB–, $(4.5\text{--})5\text{--}6.5 \times 3.5\text{--}4.5 \mu\text{m}$, $L = 5.53 \mu\text{m}$, $W = 4.09 \mu\text{m}$, $Q = 1.351$ ($n = 30/1$).

Typus: **China**, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, $24^{\circ}42'35''\text{N}$, $97^{\circ}51'36''\text{E}$, 1000 m.a.s.l., on dead bamboo, 4 Jul. 2024, *C.L. Zhao*, CLZhao 37745 (**holotype** SWFC 00037745).

Notes: Our multi-locus phylogenetic analysis (Fig. 1) confirmed the generic affinities of our new species *Xylodon luteofarinaceus* (CLZhao 37745). When using ITS sequences alone, our species formed a clade with *X. exilis*, *X. kunmingensis* and *X. pseudolanatus* (Fig. 8). Key characters distinguishing *X. exilis* from *X. luteofarinaceus* are its odontoid hymenial surface and its narrowly ellipsoid basidiospores ($5.5\text{--}6 \times 2.5\text{--}3 \mu\text{m}$, Riebesehl *et al.* 2019). *Xylodon kunmingensis* can be distinguished by its odontoid hymenophore with cream to buff surface and oblong-ellipsoid basidiospores ($5\text{--}5.8 \times 2.8\text{--}3.5 \mu\text{m}$, Shi *et al.* 2019), while



X. pseudolanatus differs by cream, odontoid hymenophores (Riebesehl et al. 2019).

Xylodon luteograndineus L. Wang & C.L. Zhao, *sp. nov.*
MB 859952. Figs 68–70.

Chinese name: 黄小齿木齿菌 (Huang xiao chi mu chi jun).



Fig. 68. A, B. Basidiomata of *Xylodon luteograndineus* CLZhao 36185 (holotype SWFC 00036185). Scale bars: A = 1 cm; B = 2 mm.

Etymology: The species epithet “*luteograndineus*” refers to its flavescent hymenophore surface with a grandinoid hymenophore.

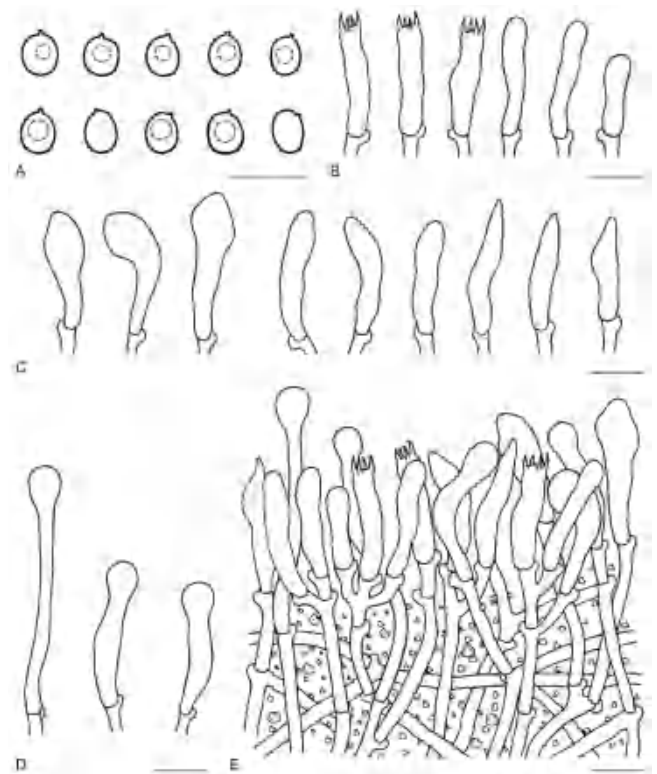


Fig. 69. Microscopic structures of *Xylodon luteograndineus* CLZhao 36185 (holotype SWFC 00036185). A. Basidiospores. B. Basidia and basidioles. C. Clavate cystidia. D. Capitulate cystidia. E. A section of the hymenium. Scale bars = 10 μ m.

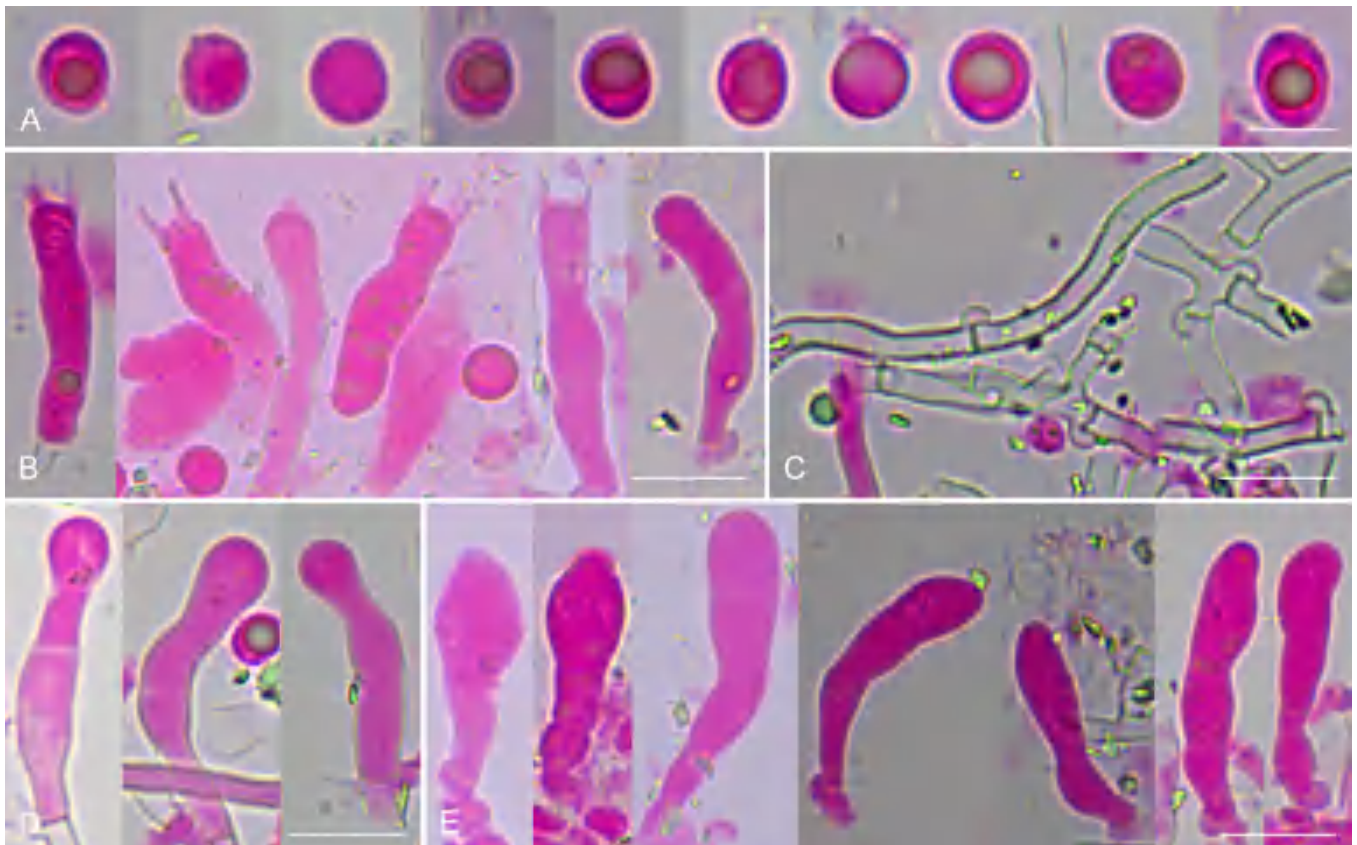


Fig. 70. Microscopic structures of *Xylodon luteograndineus* CLZhao 36185 (holotype SWFC 00036185). A. Basidiospores. B. Basidia and basidioles. C. Generative hyphae with clamp connections. D. Capitulate cystidia. E. Clavate cystidia. Scale bars: A = 5 μ m; B–E = 10 μ m.



Description: *Basidiomata* annual, resupinate, adnate, inseparable from substrate, membranaceous, without odour or taste when fresh, up to 6 cm long, 2 cm wide, and 400 μm thick. *Hymenial surface* grandinoid, cream when fresh, cream to buff upon drying. Sterile margin thinning out, cream, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, smooth, frequently branched, interwoven generative hyphae 2.5–4.5 μm diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* of two types: (1) capitate, thin-walled, smooth, 21–46 \times 4.5–6.5 μm ; (2) subclavate, slightly flexuous, thin-walled, smooth, 13.5–31 \times 3.5–8.5 μm . *Basidia* cylindrical, slightly flexuous, with a basal clamp connection and four sterigmata, 20–25.5 \times 3.5–5.5 μm ; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* broad ellipsoid, colourless, thin-walled, smooth, mostly with an oil droplet, IKI–, CB–, 4–5.5(–6) \times 3.5–4.5 μm , L = 4.90 μm , W = 3.97 μm , Q = 1.234 (n = 30/1).

Typus: **China**, Yunnan Province, Zhaotong, Yiliang County, Wumengshan National Nature Reserve, 28°8'10"N, 103°58'2"E, 1180 m.a.s.l., on angiosperm trunk, 23 Jun. 2024, C.L. Zhao, CLZhao 36185 (**holotype** SWFC 00036185).

Notes: The phylogenetic position of our new species *Xylodon luteograndineus* could not be resolved in our ITS-based phylogenetic inference (Fig. 8), however it formed a distant, single branch that somewhat showed affinities to *X. pingbianensis*, from which it can be distinguished by its cinnamon-buff hymenophore surface and tubular cystidia (Dong et al. 2024). Another related clade is comprised of the species *X. apacheriensis*, *X. niemelaei*, and *X. rhododendricola*. These species can be distinguished from *Xylodon luteograndineus* by its soft-fibrous, pore surface cream hymenophore and bigger basidiospores (5–6.5 \times 4–5.5 μm vs 4–5.5 \times 3.5–4.5 μm ; *X. apacheriensis*, Hjortstam & Ryvarden 2009), poroid, cream hymenophore and subulate leptocystidia (*X. niemelaei*, Hjortstam & Ryvarden 2009), odontoid, cream to buff hymenophore and bigger basidiospores (4.8–6.5 \times 3.8–5.1 μm vs 4–5.5 \times 3.5–4.5 μm ; *X. rhododendricola*, Wang et al. 2021).

Xylodon luteomarginatus L. Wang & C.L. Zhao, **sp. nov.** MB 859953. Figs 71–73.

Chinese name: 黄边缘木齿菌 (Huang bian yuan mu chi jun).

Etymology: The species epithet “*luteomarginatus*” refers to the flavescent margin of its basidiomata.

Description: *Basidiomata* annual, resupinate, adnate, inseparable from substrate, coriaceous, without odour or taste when fresh, up to 7 cm long, 3 cm wide, and 400 μm thick. *Hymenial surface* poroid, laceratus, cream to pinkish buff when fresh, pinkish buff to cinnamon-buff upon drying. Sterile margin thinning out, flavescent, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin- to slightly thick-walled, smooth, frequently branched, interwoven generative hyphae 4–5.5 μm diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissues unchanged in KOH. *Cystidia* of two types: (1) schizopapillate, colourless, thin-walled, smooth, 21.5–25.5 \times 5.5–7 μm ; (2)



Fig. 71. A, B. Basidiomata of *Xylodon luteomarginatus* CLZhao 40511 (holotype SWFC 00040511). Scale bars: A = 1 cm; B = 2 mm.

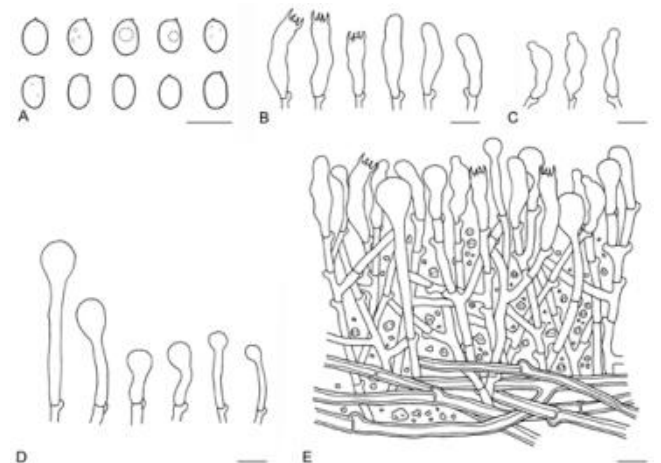


Fig. 72. Microscopic structures of *Xylodon luteomarginatus* CLZhao 40511 (holotype SWFC 00040511). A. Basidiospores. B. Basidia and basidioles. C. Schizopapillate cystidia. D. Capitate cystidia. E. A section of the hymenium. Scale bars = 10 μm .

capitate, colourless, thin-walled, smooth, 16.5–55 \times 5–13 μm . *Basidia* subclavate to subcylindrical, slightly flexuous, with a basal clamp connection and four sterigmata, 20–29 \times 5–6.5 μm ; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid, colourless, thin-walled, smooth, with oil droplets, IKI–, CB–, 6–8.5 \times (3–)4–5.5(–6) μm , L = 7.23 μm , W = 4.61 μm , Q = 1.490–1.567 (n = 90/3).

Typus: **China**, Yunnan Province, Zhaotong, Yiliang County, Wumengshan National Nature Reserve, 28°8'10"N, 103°58'2"E, 1180 m.a.s.l., on fallen angiosperm trunk, 15 Oct. 2024, C.L. Zhao, CLZhao 40511 (**holotype** SWFC 00040511).

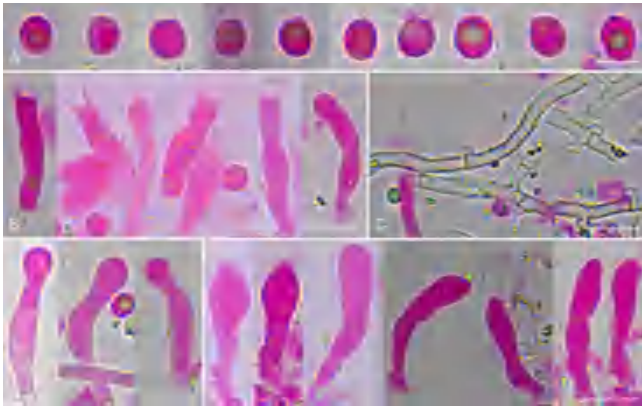


Fig. 73. Microscopic structures of *Xylodon luteomarginatus* CLZhao 40511 (holotype SWFC 00040511). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Schizopapillate cystidia. **D.** Capitate cystidia. **E.** Generative hyphae with clamp connections. Scale bars = 10 μ m.

Additional specimens examined: **China**, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, 28°18'01"N, 103°58'12"E, 1900 m.a.s.l., on fallen angiosperm trunk, 17 Aug. 2024, H.M. Zhou, HMZhou 59 (SWFC 00100059); Dagan County, Tianxing Town, Wumengshan National Nature Reserve, 27°49'48"N, 103°58'48"E, 1800 m.a.s.l., on dead bamboo, 19 Aug. 2024, H.M. Zhou, HMZhou 391 (SWFC 00100391).

Notes: Our new species *Xylodon luteomarginatus* resolved in a sister relationship to *X. wumengshanensis* within *Xylodon* in our phylogenetic analysis using ITS sequences alone (Fig. 8). However, *X. wumengshanensis* can be morphologically distinguished from *X. luteomarginatus* by its grandinoid hymenophore surface and smaller basidiospores (5–6.5 \times 4–5.5 μ m, Yuan & Zhao 2024).



Fig. 74. A, B. Basidiomata of *Xylodon odontoioides* CLZhao 36518 (holotype SWFC 00036518). Scale bars: A = 1 cm; B = 2 mm.

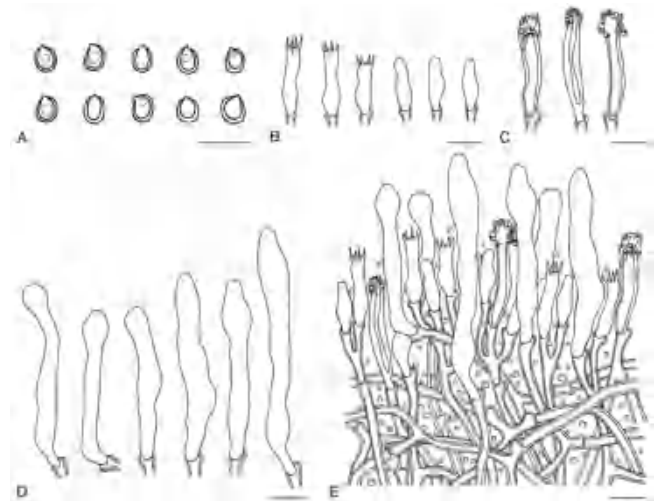


Fig. 75. Microscopic structures of *Xylodon odontoioides* CLZhao 36518 (holotype SWFC 00036518). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Asterocystidia. **D.** Subclavate to capitate cystidia. **E.** A section of the hymenium. Scale bars = 10 μ m.

Xylodon odontoioides L. Wang & C.L. Zhao, *sp. nov.* MB 859954. Figs 74–76.

Chinese name: 钝齿木齿菌 (Dun chi mu chi jun).

Etymology: The species epithet “*odontoioides*” refers to its odontoid hymenial surface.

Description: *Basidiomata* annual, resupinate, adnate, coriaceous, without odour or taste when fresh, up to 4 cm long, 3 cm wide, and 600 μ m thick. *Hymenial surface* odontoid, white to cream when fresh, cream upon drying. Sterile margin thinning out, white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, smooth, frequently branched, interwoven generative hyphae 2–5 μ m diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* of two types: (1) apically encrusted, flexuous, colourless, slightly thin-walled, smooth asterocystidia, 29–37 \times 5–7.5 μ m; (2) subclavate to capitate, colourless, thin-walled, smooth, 24.5–71.5 \times 6.5–9.5 μ m. *Basidia* subclavate, slightly flexuous, with a basal clamp connection and four sterigmata, 15–20.5 \times 4–5.5 μ m; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid, colourless, thick-walled, smooth, with oil droplets, IKI–, CB–, (4–)4.5–5.5(–6) \times (3–)3.5–4.5(–5) μ m, L = 4.93 μ m, W = 3.87 μ m, Q = 1.27–1.29 (n = 60/2).

Typus: **China**, Yunnan Province, Dehong, Mang City, Mengga Town, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on fallen angiosperm branch, 29 Jun. 2024, C.L. Zhao, CLZhao 36518 (**holotype** SWFC 00036518).

Additional specimen examined: **China**, Yunnan Province, Dehong, Mang City, Mengga Town, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on fallen angiosperm branch, 29 Jun. 2024, C.L. Zhao, CLZhao 36522 (SWFC 00036522).

Notes: Our new species was shown to form a distinct lineage split from a cluster formed by *X. flocculosus* and *X. tenuis*

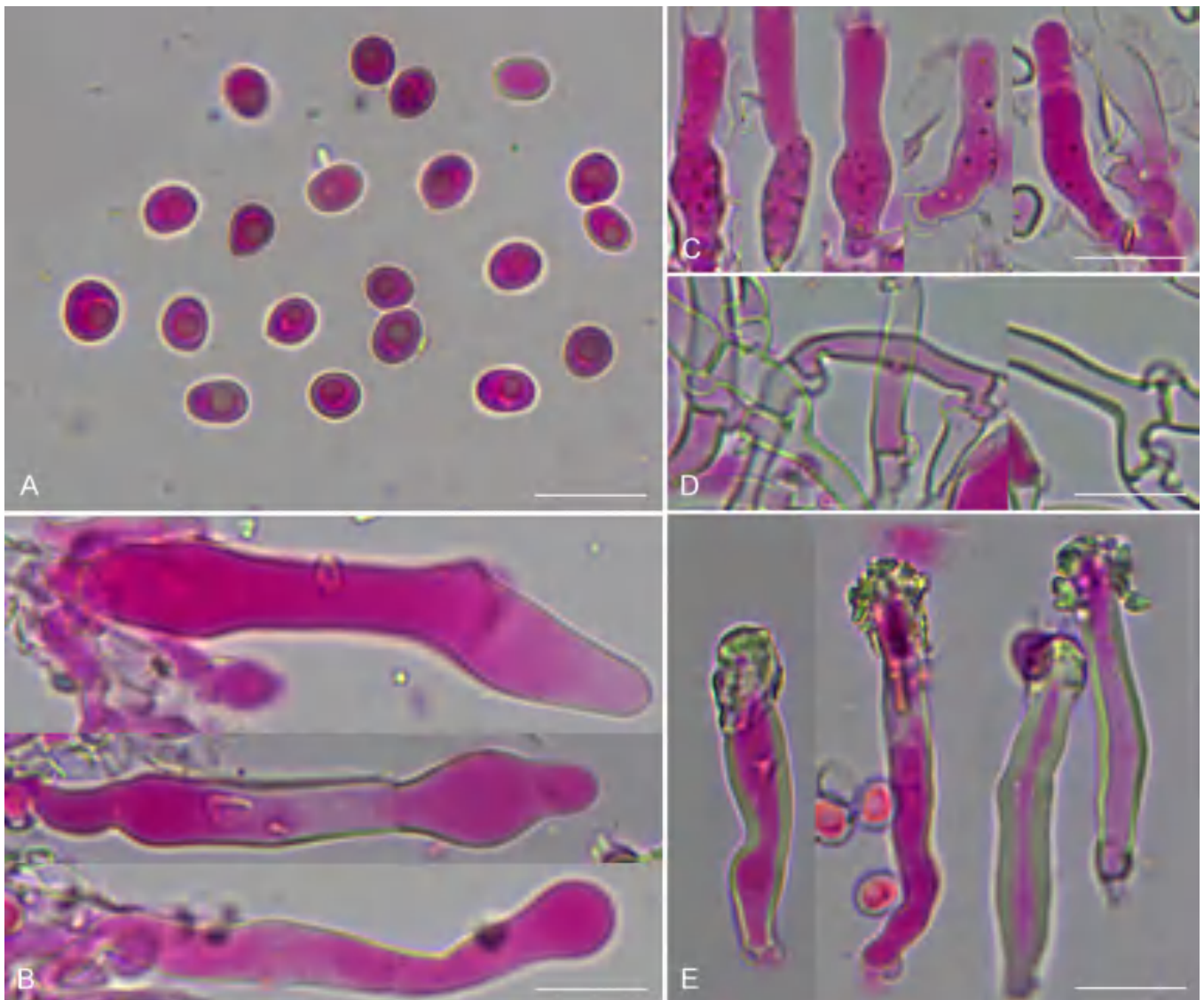


Fig. 76. Microscopic structures of *Xylodon odontioides* CLZhao 36518 (holotype SWFC 00036518). **A.** Basidiospores. **B.** Subclavate to capitate cystidia. **C.** Basidia and basidioles. **D.** Generative hyphae with clamp connections. **E.** Asterocystidia. Scale bars = 10 µm.

species in our phylogenetic analysis (Fig. 8). Key characters distinguishing *X. flocculosus* from *X. odontioides* are its cottony hymenophore (Qu & Zhao 2022) and *X. tenuis* differs by its thin and reticulate hymenial surface and smaller ellipsoid basidiospores ($4\text{--}5 \times 3\text{--}4 \mu\text{m}$ vs $4.5\text{--}5.5 \times 3.5\text{--}4.5 \mu\text{m}$, Hjortstam & Ryvarden 2007).

Xylodon tenuis L. Wang & C.L. Zhao, *sp. nov.* MB 859955. Figs 77–79.

Chinese name: 薄木齿菌 (Bo mu chi jun).

Etymology: The species epithet “*tenuis*” refers to its thin basidiomata.

Description: *Basidiomata* annual, resupinate, adnate, thin, membranaceous, without odour or taste when fresh, up to 6 cm long, 2 cm wide, and 200 µm thick. *Hymenial surface* reticulate, cream when fresh, cream to straw yellow upon drying. Sterile margin thinning out, cream to straw yellow, up to 1 mm wide. *Hyphal system* monomitic; colourless, slightly thick-walled, smooth, frequently branched, interwoven generative hyphae 2–4 µm diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–;



Fig. 77. **A, B.** Basidiomata of *Xylodon tenuis* CLZhao 37408 (holotype SWFC 00037408). Scale bars: A = 1 cm; B = 2 mm.

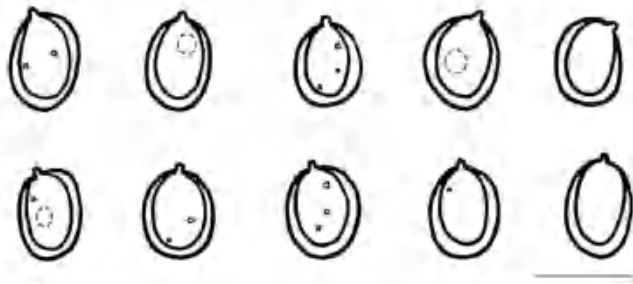


Fig. 78. Basidiospores structures of *Xylodon tenuis* CLZhao 37408 (holotype SWFC 00037408). Scale bar = 5 μ m.

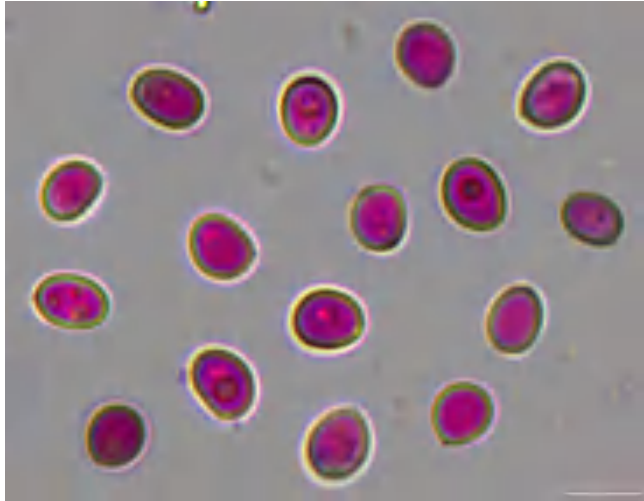


Fig. 79. Basidiospores of *Xylodon tenuis* CLZhao 37408 (holotype SWFC 00037408). Scale bar = 5 μ m.

tissues unchanged in KOH. *Basidiospores* broad ellipsoid, colourless, thick-walled, smooth, with oil droplets, IKI–, CB–, 4–5(–5.5) \times (2.5–)3–4 μ m, L = 4.53 μ m, W = 3.48 μ m, Q = 1.304 (n = 30/1).

Typus: China, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1050 m.a.s.l., on dead bamboo, 3 Jul. 2024, C.L. Zhao, CLZhao 37408 (**holotype** SWFC 00037408).

Notes: Our new species resolved in a sister relationship with *X. flocculosus* in our ITS-based phylogenetic inference (Fig. 8). However, *X. flocculosus* can be distinguished from *X. tenuis* by its cottony and odontoid hymenial surface and the presence of cystidia (Qu & Zhao 2022).

Xylodon tongbiguanensis L. Wang & C.L. Zhao, *sp. nov.* MB 859957. Figs 80–82.

Chinese name: 铜壁关木齿菌 (Tong bi guan mu chi jun).

Etymology: The species epithet “*tongbiguanensis*” refers to the collection site (Tongbiguan Provincial Nature Reserve) of the type specimen.

Description: *Basidiomata* annual, resupinate, adnate, inseparable from substrate, membranaceous, without odour or taste when fresh, up to 10 cm long, 2 cm wide, and 600 μ m thick. *Hymenial surface* odontoid, white to cream when fresh, cream upon drying. Sterile margin thinning out, white



Fig. 80. A, B. Basidiomata of *Xylodon tongbiguanensis* CLZhao 37385 (holotype SWFC 00037385). Scale bars: A = 1 cm; B = 2 mm.

to cream, up to 1 mm wide. *Hyphal system* monomitic; colourless, slightly thick-walled, smooth, frequently branched, interwoven generative hyphae 3.5–5.5 μ m diam. with clamp connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* and *cystidioles* absent. *Aculei* peg-like, conical or subcylindrical, apically entirely or slightly penicillate. *Basidia* subclavate to subcylindrical, with a basal clamp connection and four sterigmata, 23–31.5 \times 5–7 μ m; *basidioles* numerous, in shape similar to basidia but smaller. *Basidiospores* broadly ellipsoid, colourless, thin-walled, smooth, IKI–, CB–, 6–7.5(–8) \times 5–6.5 μ m, L = 6.86 μ m, W = 5.91 μ m, Q = 1.164–1.988 (n = 60/2).

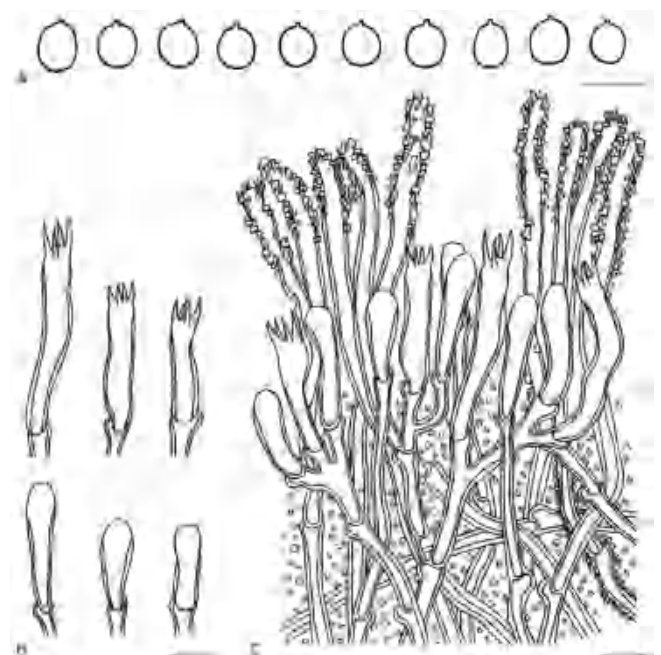


Fig. 81. Microscopic structures of *Xylodon tongbiguanensis* CLZhao 37385 (holotype SWFC 00037385) **A.** Basidiospores. **B.** Basidia and basidioles. **C.** A section of the hymenium. Scale bars = 10 μ m.



Typus: China, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on dead bamboo, 3 Jul. 2024, C.L. Zhao, CLZhao 37385 (**holotype** SWFC 00037385).

Additional specimen examined: China, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on dead bamboo, 3 Jul. 2024, C.L. Zhao, CLZhao 37410 (SWFC 00037410).

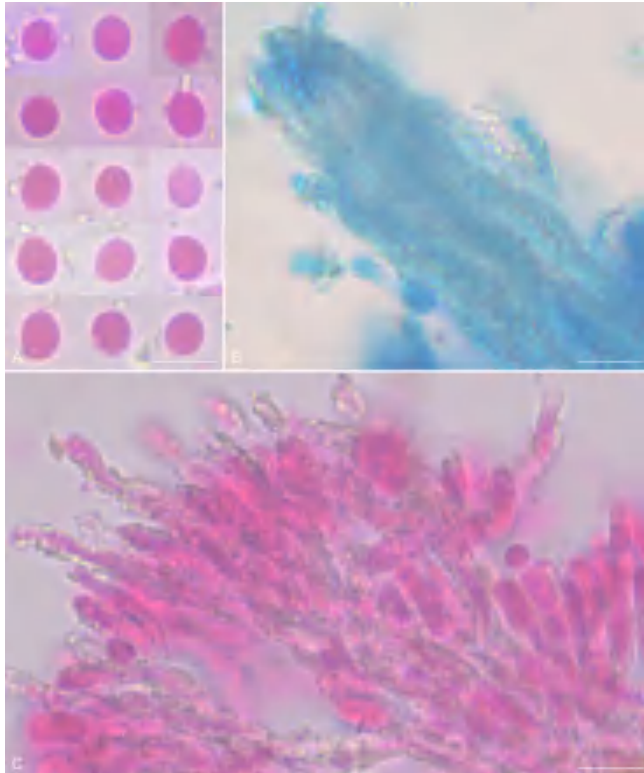


Fig. 82. Microscopic structures of *Xylodon tongbiguanensis* CLZhao 37385 (holotype SWFC 00037385). **A.** Basidiospores. **B.** A section of the aculei pegs (40× microscope). **C.** A section of the hymenium. Scale bars = 10 µm.

Notes: Our phylogenetic analysis (Fig. 8) revealed affinities of our new species *Xylodon tongbiguanensis* to *X. albofarinaceus*. However, *X. albofarinaceus* can be distinguished from *X. tongbiguanensis* by its white, farinaceous hymenophore and smaller, subglobose basidiospores (5.5–7.5 × 5–6.5 µm).

Xylodon yingjiangensis L. Wang & C.L. Zhao, *sp. nov.* MB 859958. Figs 83–85.

Chinese name: 盈江木齿菌 (Ying jiang mu chi jun).

Etymology: The species epithet “*yingjiangensis*” refers to the collection site (Yingjiang County) of the type specimen.

Description: *Basidiomata* annual, resupinate, adnate, inseparable from substrate, coriaceous, without odour or taste when fresh, up to 10 cm long, 2 cm wide, and 600 µm thick. *Hymenial surface* odontoid, white to cream when fresh, cream to buff upon drying. Sterile margin thinning out, white to cream, up to 1 mm wide. *Hyphal system* monomitic; colourless, slightly thick-walled, smooth, frequently branched, interwoven generative hyphae 2–4 µm diam. with clamp



Fig. 83. A, B. Basidiomata of *Xylodon yingjiangensis* CLZhao 37378 (holotype SWFC 00037378). Scale bars: A = 1 cm; B = 2 mm.

connections and crystals in moderate amounts among hyphae, IKI–, CB–; tissue unchanged in KOH. *Cystidia* of three types: (1) fusiform, tapering, slightly flexuous, colourless, thin-walled, smooth, 11–23.5 × 4.5–6 µm; (2) cylindrical, colourless, thin-walled, smooth, 28.5–35.5 × 5–7 µm; (3) capitate, colourless, thin-walled, smooth, 12–23 × 5–6 µm. *Basidia* subclavate to subcylindrical, slightly flexuous, with a basal clamp connection and four sterigmata, 16–20.5 × 4–5 µm; basidioles numerous, in shape similar to basidia but smaller. *Basidiospores* subglobose, colourless, thin-walled, smooth, IKI–, CB–, 4–5(–5.5) × 3.5–5 µm, L = 4.66 µm, W = 4.27 µm, Q = 1.089 (n = 30/1).

Typus: China, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°42'35"N, 97°51'36"E, 1000 m.a.s.l., on fallen angiosperm branch, 3 Jul. 2024, C.L. Zhao, CLZhao 37378 (**holotype** SWFC 00037378).

Notes: Our new species *Xylodon yingjiangensis* was shown to occupy a basal lineage to a cluster formed by *X. daweishanensis* and *X. hyphodontinus* in our phylogenetic analysis (Fig. 8). Key characters distinguishing *X. daweishanensis* from *X. yingjiangensis* are its asterocystidia and smaller, broad ellipsoid basidiospores (3–4 × 2.5–3.5 µm, Guan *et al.* 2023), while *X. hyphodontinus* differs in its odontoid, light ochraceous basidiomata and the absence of cystidia (Riebesehl *et al.* 2019).

Tubulicrinaceae Jülich, *Biblioth. Mycol.* **85**: 392. 1982. [1981]

Tubulicrinis Donk, *Fungus* (Wageningen) **26**(1–4): 13. 1956.

Notes: The genus *Tubulicrinis* Donk (1956) is characterized by resupinate basidiomata, firmly adnate, smooth, pruinose

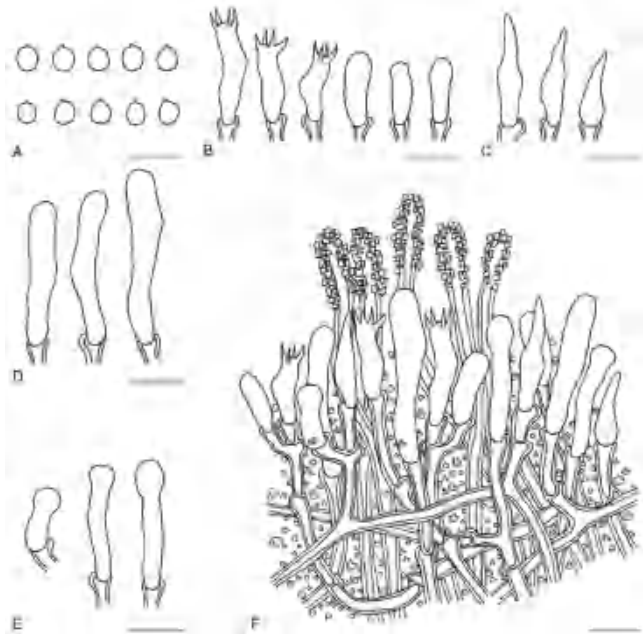


Fig. 84. Microscopic structures of *Xylodon yingjiangensis* CLZhao 37378 (holotype SWFC 00037378). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Fusiform cystidia. **D.** Cylindrical cystidia; **E.** Capitulate cystidia. **F.** A section of the basidiomata. Scale bars = 10 μ m.

to porulose, white, cream to pale ochraceous hymenophores, a monomitic hyphal system, generative hyphae with clamp connections and cylindrical or conical cystidia, generally bi- or multi-radicale with capitate or subulate apex. Its basidia are clavate and basidiospores are thin-walled, smooth, cylindrical to allantoid or globose to ellipsoid and are both IKI and CB negative (IKI⁻, CB⁻), (Bernicchia & Gorjón 2010). The genus is typified with *T. glebulosus* (Fr.) Donk. and first recognized in the hymenochaetoid clade, before it was later placed in the order *Hymenochaetales* (Larsson 2007). Published phylogenies based on both nuclear DNA and

protein-encoding gene regions support the independence of *Tubulicrinis*, including the generic type *T. glebulosus*, from other known families and genera in *Hymenochaetales* (He et al. 2020, Wang et al. 2023). Based on MycoBank entries and Index Fungorum (accessed on 4 January 2026), in total 61 specific and infraspecific names are registered for *Tubulicrinis*, and the actual number of species is 46, of which four new species, viz. *T. albobadius*, *T. pini*, *T. xantha* and *T. yunnanensis* were published in the past five years from Yunnan Province, China, alone (Dai et al. 2025).

Tubulicrinis incanus L. Wang & C.L. Zhao, *sp. nov.* MB 861449. Figs 86–88.

Chinese name: 白筒毛革菌 (Bai tong mao ge jun).

Etymology: The species epithet “*incanus*” referring to the incanus hymenial surface of the type specimen.

Description: *Basidiomata* annual, resupinate, closely adnate, farinaceous, without odour or taste when fresh, becoming pruinose upon drying, up to 10 cm long, 2 cm wide and 500 μ m thick. *Hymenial surface* smooth, white when fresh, white to cream when dry. Sterile margin white, up to 1 mm wide. *Hyphal system* monomitic; colourless, thin-walled, frequently branched, interwoven generative hyphae 1.5–3 μ m diam. with clamp connections, IKI⁻, CB⁻; tissue unchanged in KOH. *Lyocystidia* numerous, projecting, cylindrical to slightly sinuous, bi-rooted, dissolving in KOH, capillary lumen ending gradually, thin-walled, 84–112 \times 9–15 μ m. *Basidia* clavate, colourless, thin-walled, with short and blunt four sterigmata and a basal clamp connection, 17–19 \times 6–8 μ m; basidioles dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* cylindrical, colourless, thin-walled, smooth, with oil drops, IKI⁻, CB⁻, 8.5–10.5(–11) \times 3–4(–4.5) μ m, L = 9.46 μ m, W = 3.65 μ m, Q = 2.59 (n = 30/1).

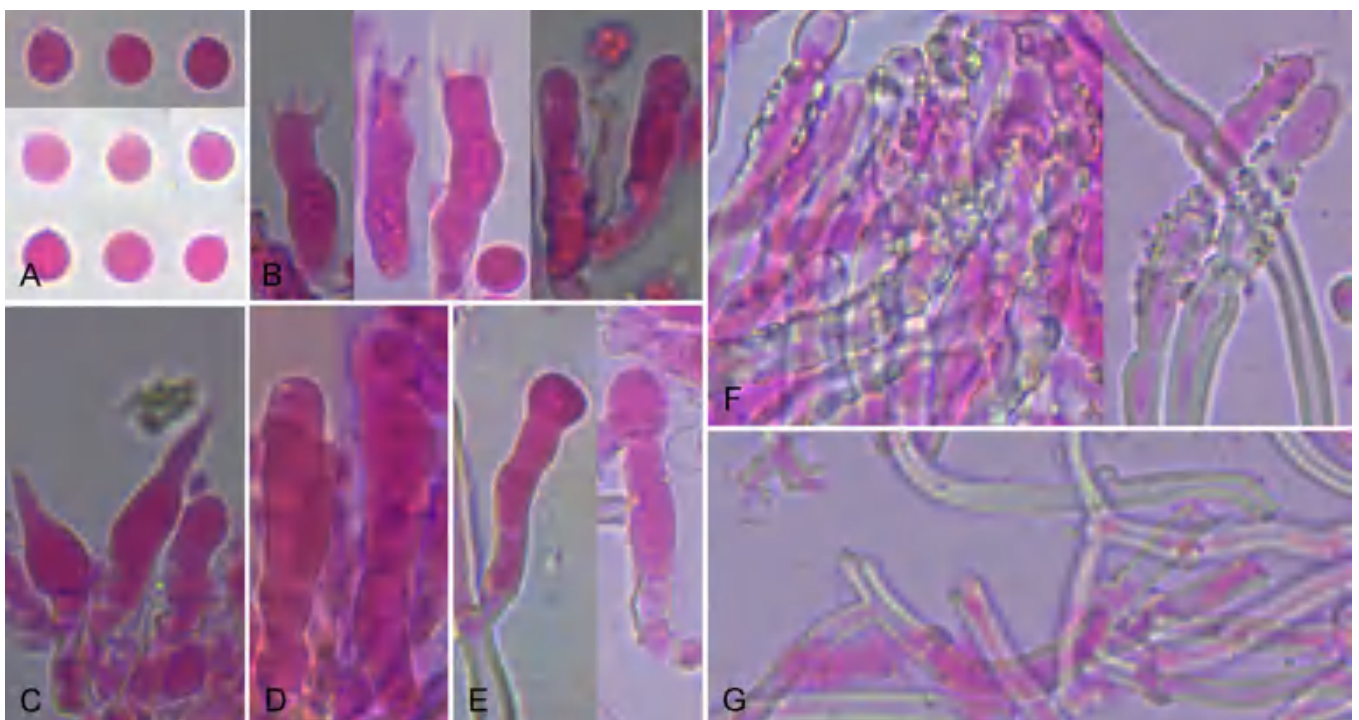


Fig. 85. Microscopic structures of *Xylodon yingjiangensis* CLZhao 37378 (holotype SWFC 00037378). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Fusiform cystidia. **D.** Cylindrical cystidia. **E.** Capitulate cystidia. **F.** The tip of the hyphae. **G.** Generative hyphae with clamp connections. Scale bars = 10 μ m.



Fig. 86. **A, B.** Basidiomata of *Tubulicrinis incanus* HMZhou 407 (holotype SWFC 00100407). Scale bars: A = 1 cm; B = 2 mm.

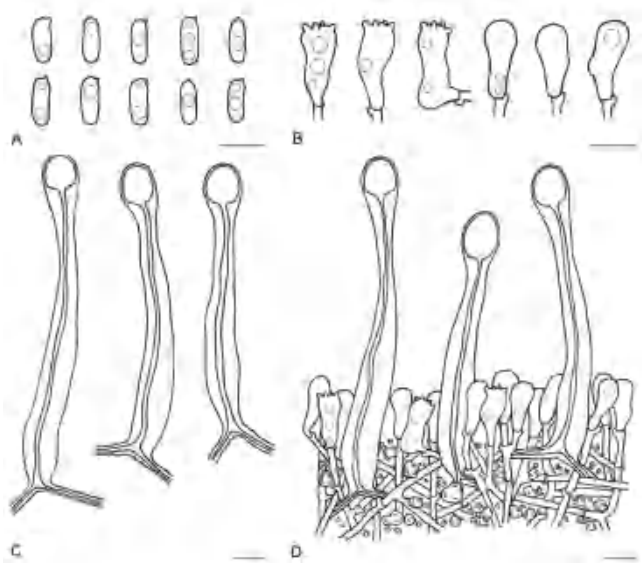


Fig. 87. Microscopic structures of *Tubulicrinis incanus* HMZhou 407 (holotype SWFC 00100407). **A.** Basidiospores. **B.** Basidia and basidioles. **C.** Lycocystidia. **D.** A section of the hymenium. Scale bars = 10 μ m.

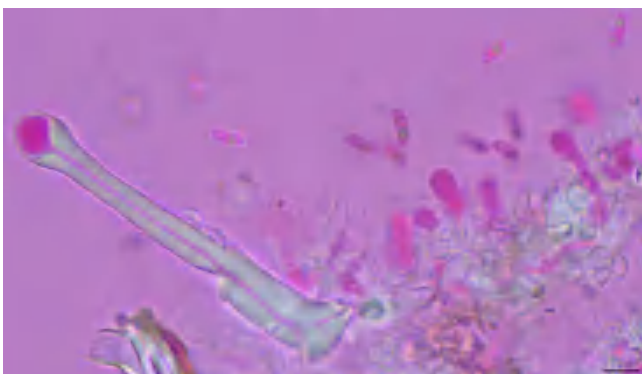


Fig. 88. A section of the hymenium of *Tubulicrinis incanus* HMZhou 407 (holotype SWFC 00100407). Scale bars = 10 μ m.

Typus: **China**, Yunnan Province, Zhaotong, Dagan County, Tianxing Town, Wumengshan National Nature Reserve, 28°8'10"N, 103°58'2"E, 1180 m.a.s.l., on fallen branches of *Vitis*, 20 Aug. 2024, *H.M. Zhou*, HMZhou 407 (**holotype** SWFC 00100407).

Notes: Our phylogenetic inference using concatenated ITS+nLSU sequences (Fig. 9) revealed that our new species *Tubulicrinis incanus* resolved sister to *T. globisporus* within *Tubulicrinis*. However, morphologically, *T. globisporus* differs from *T. incanus* by its porulose and discontinuous, whitish hymenial surface of basidiomata and subglobose basidiospores (Hjortstam & Larsson 1978).

DISCUSSION

Approximately 1300 species are currently accommodated in *Hymenochaetales* (<https://www.catalogueoflife.org>), which renders it among the largest orders of mushroom-forming fungi (Wang *et al.* 2023), with 1162016 observations recorded in the GBIF database (<https://www.gbif.org/>) worldwide. Still, we encountered specimen in southwestern China that could not be assigned to any of the described species which now lead us to describe in total one new genus, *Cotylidiella*, and 26 new species. All of the 26 wood-inhabiting fungal species were shown to belong to the *Hymenochaetales*, of which 16 were assigned to genera of the *Schizoporaceae* (*Fasciodontia*, *Lyomyces*, *Xylodon*), three to *Hymenochaete*, and seven were shown to belong to five other genera. The number of different species of *Schizoporaceae* and *Hymenochaete* seems to be exceptionally high in southwestern China, consistent with previous surveys in this region (Yuan *et al.* 2024, Liu *et al.* 2025), which suggests a degree of endemism for these fungi. This finding is consistent with the idea that regions in southwestern China (particularly the Hengduan Mountains) act as a biodiversity hotspot for wood-inhabiting fungi and potentially even as an evolutionary reservoir for *Schizoporaceae* and *Hymenochaete* lineages.

The present phylogenetic analysis of the *Lyomyces* revealed that the genus formed a monophyletic clade (Fig. 1), which is in accordance with previous studies (Yuan *et al.* 2024, Yurchenko *et al.* 2024a). A similar pattern was observed for species in the other two genera of the family *Schizoporaceae* – *Fasciodontia* and *Xylodon*. Each species formed a distinct lineage even though individual samples originated from different latitudes, altitudes, forest types and temperature zones. The three genera occupied an independent phylogenetic position within the *Hymenochaetales*, supporting its recognition at the family level, which is in accordance with previous reports (Larsson *et al.* 2006, Wang *et al.* 2023).

Species of *Lyomyces* comprise diverse basidiomata types (*viz.*, farinaceous, coriaceous, and membranaceous basidiomata) and smooth to grandinoid hymenophores (Yuan *et al.* 2024, Yurchenko *et al.* 2024a), although the hymenial surface is predominantly cream or whitish (Bernicchia & Gorjón 2010). Notably, it is difficult to distinguish species of *Lyomyces* if solely relying on their morphology, and the constant addition of new species renders the few available morphological characters used to distinguish species within morpho-ecological types ineffective (Jerusalem *et al.* 2025).



This is not uncommon in fungal taxonomy, as morphometric taxonomic systems are frequently described insufficient. Hence, so-called polyphasic approaches augment morphological analysis by DNA sequencing, which allows for a more easy and unequivocal species delimitation and recognition (Larsson *et al.* 2006, Yang *et al.* 2025).

Cotylidiella fragilis formed a distinct lineage with *Cotylidia pannosa*. Divergence times were estimated from ITS+nLSU+*tef1-α*+*rpb1*+*rpb2* sequences representing all the main lineages in *Hymenochaetales*. Previously, time ranges for *Basidiomycota* inferred by Zhao *et al.* (2017), resulted in an estimated phylum divergence at ca 530 Mya, while subphyla were estimated to have emerged at 406–490 Mya, most classes at 245–393 Mya and orders at 120–290 Mya. In the present study, the divergence time of the new genus *Cotylidiella* was estimated with 76.94 Mya (PP = 0.94), which is consistent with the segregation of other genera (49–135 Mya) in the *Hymenochaetales* when using molecular clock dating analyses (Zhao *et al.* 2025). Therefore, we propose to accept *Cotylidiella* as an independent genus in *Hymenochaetales*.

Hymenochaete resolved into many supported clades in our phylogenetic analysis of ITS+nLSU data, however species within each clade lacked consistent morphological traits, i.e. showing considerable variations in basidioma colour, hymenophore type, basidiospore shape, and setae/basidiospore size, which contradicts traditional classification principles for this genus but aligns well with recent findings of other studies (Liu *et al.* 2025). Presently, it cannot be ruled out that macroscopic characteristics of *Hymenochaete* are influenced by external factors (host/substrate specificity, latitude, altitude, forest type, temperature, and humidity), genetic variation or if they merely represent intrageneric variation. It is important to verify these findings with more phylogenetically informative markers, such as proteinogenic – or housekeeping genes, which might foster a revision of the genus in the future.

Indeed, with rapid development of genome sequencing technologies offering superior resolution, it is to be expected that phylogenomic approaches can be utilized to resolve these issues in the future (Varga *et al.* 2019, Strasser & Monaghan 2022, Nagy *et al.* 2026). Our phylogenetic frameworks as well as descriptions of the extant biodiversity represents an important cornerstone of such research at the order level in the future.

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SUPPLEMENTARY MATERIAL

Table S1. GenBank accession numbers of the strains included in the phylogenetic analyses.