The Phylogenetic Relationship Revealed Three New Wood-Inhabiting Fungal Species From Genus *Trechispora*

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Wood-inhabiting fungi play a significant role in wood degradation and the cycle of matter in the ecological system. In the present study, three new wood-inhabiting fungal species, Trechispora bambusicola, Trechispora fimbriata, and Trechispora fissurata spp. nov., are nested in Trechispora, which are proposed based on a combination of morphological features and molecular evidence. Sequences of internal transcribed spacer (ITS) and large subunit (nLSU) regions of the studied samples were generated, and the phylogenetic analyses were performed with maximum likelihood, maximum parsimony, and Bayesian inference methods. The phylogenetic analyses inferred from ITS showed that *T. bambusicola* was sister to *Trechispora stevensonii*, *T. fimbriata* grouped with *Trechispora nivea*, and *T. fissurata* grouped with *Trechispora echinospora*. The phylogenetic tree based on ITS + nLSU sequences demonstrated that *T. bambusicola* formed a single lineage and then grouped with *Trechispora rigida* and *T. stevensonii*. *T. fimbriata* was sister to *T. nivea*. *T. fissurata* grouped with *Trechispora thelephora*.

**Keywords:** Hydnodontaceae, phylogeny, taxonomy, wood-inhabiting fungi, Yunnan Province

INTRODUCTION

*Trechispora* P. Karst. (Hydnodontaceae, Trechisporales) was typified with *Trechispora onusta* P. Karst. (Karsten, 1890). It is characterized by the resupinate to effused basidiomata with smooth to hydnoid to poroid hymenophore, a monomitic or dimitic hyphal structure with clamped generative hyphae having typical ampullaceous septa, and short cylindric

**Abbreviations:** ITS, internal transcribed spacer; nLSU, large subunit; SWFC, herbarium of Southwest Forestry University, Kunming, China; KOH, 5% potassium hydroxide; CB, Cotton Blue; CB−, acyanophilous; 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 studied specimens, n (a/b), number of spores (a) measured from given number (b) of specimens, spore measurements do not include ornamentation; CTAB, cetyltrimethylammonium bromide; DNA, deoxyribonucleic acid; PCR, polymerase chain reaction; MP, maximum parsimony; ML, maximum likelihood; BI, Bayesian inference; TBR, tree-bisection reconnection.
basidia and smooth to verrucose or aculeate basidiospores
(Karsten, 1890; Bernicchia and Gorjón, 2010). About 49 species
are currently known in *Trechispora* worldwide (Liberta, 1966,
1973; Larsson, 1994, 1995, 1996; Ryvarden, 2002; Trichèis and
Schultheis, 2002; Miettinen and Larsson, 2006; Ordynets et al.,
2015; Xu et al., 2019) and Index Fungorum1 and MycoBank2.

Larsson (2007) addressed the classification of corticioid fungi
and revealed that *Trechispora farinacea* (Pers.) Liberta grouped
with *Trechispora hymenocystis* (Berk. and Broome) K.H. Larss.,
in which both species nested within the family Hydnodontaceae
Jülich. Based on the large subunit nuclear ribosomal RNA gene
(nLSU) datasets, Albee-Scott and Kropp (2010) supported to
transfer *Hydnodon thelephorus* (Lév.) Banker to *Trechispora as
Trechispora telephora* (Lév.) Ryvarden. The order Trechisporales
was studied employing the internal transcribed spacer (ITS) and
nLSU regions, in which it suggested that *Porpomyces* Jülich, *Sistotremastrum* J. Erikss., *Subulicystidium* Parmasto, and
*Trechispora* belonged to a highly supported clade and
*Trechispora* belongs to Hydnodontaceae and was closely related
to *Breviceillicium* K.H. Larss. and Hjortstam (Telliera et al.,
2013). A phylogenetic study of *Trechispora* was addressed and
demonstrated that *Trechispora cyathae* Ordynets, Langer and
K.H. Larss. and *Trechispora echnicristallina* Ordynets, Langer and
K.H. Larss. clustered into *Trechispora* as new members, inferred
from the combined data of the ITS and LSU datasets
(Orderynets et al., 2015). The phylogeny of Trechisporales was
inferred from a combined dataset of ITS-nLSU sequences and
showed that *Porpomyces*, *Scytinopogon*, and *Trechispora*
grouped together and nested within family Hydnodontaceae (Liu
et al., 2019). Phylogram generated from analysis of ITS sequence
dataset of *Trechispora* showed that *Trechispora echnicristallina*
telliera was sister to the clade formed by *Trechispora araneosa*
(Hohn. and Litsch.) K.H. Larss., *T. farinacea*, *T. hymenocystis*,
and *Trechispora mollusca* (Pers.) Liberta with a low support
(Phookamsak et al., 2019). The ITS + nLSU dataset comprised
22 species and revealed that *Trechispora yunnanensis* C.L. Zhao
formed a monophyletic lineage within *Trechispora* and was
closely related to *Trechispora byssinella* (Bourdot) Liberta and
*Trechispora laevis* K.H. Larss. (Xu et al., 2019).

During the studies on wood-inhabiting fungi in southern
China, three species of *Trechispora* could not be assigned to
any described species. Obtaining sequences from the new
taxa, the authors examine taxonomy and phylogeny of three
new species within the genus *Trechispora*, based on the ITS
and nLSU sequences.

### MATERIALS AND METHODS

**Morphology**

The studied specimens are deposited at the herbarium of
Southwest Forestry University (SWFC), Kunming, Yunnan
Province, China. Macromorphological descriptions were

1http://www.indexfungorum.org/Names/Names.asp
2https://www.mycobank.org/Biolomics.aspx?Table=Mycobank&Page=200&ViewMode=Basic
3http://lutzonilab.org/nuclear-ribosomal-dna/
4http://mafft.cbrc.jp/alignment/server/
5www.phylo.org
TABLE 1 | List of species, specimens, and GenBank accession numbers of sequences used in this study.

| Species name                  | Sample no. | GenBank accession no. | References                  |
|-------------------------------|------------|-----------------------|------------------------------|
|                               |            | ITS                   | nLSU                         |                              |
| Fibrodontia alba              | TNMF 24944 | KO928274              | KO928275                     | Yurchenko and Wu (2014)      |
| Fibrodontia gossypina         | GEL 5042   | DQ249274              | AY646100                     | Unpublished                  |
| Trechispora araneosa          | KHL 8570   | AF347084              | AF347084                     | Larsson et al. (2004)        |
| Trechispora bambusicola       | CLZhao 3302| MW544021              | MW520171                     | This study                   |
| Trechispora bambusicola       | CLZhao 3305| MW544022              | MW520172                     | This study                   |
| Trechispora bispora           | CBS 142.63 | MH858241              | MH869842                     | Yu et al. (2019)             |
| Trechispora byssinella        | UC 2023068 | KP814481              | –                            | Unpublished                  |
| Trechispora cohaerens         | TU 110332  | UDB008249             | –                            | Ordynets et al. (2015)       |
| Trechispora cohaerens         | TU 115568  | UDB016421             | –                            | Ordynets et al. (2015)       |
| Trechispora conitis           | KHL 11064  | AF347081              | AF347081                     | Larsson et al. (2004)        |
| Trechispora cyatheae          | FR-0219442 | UDB024014             | UDB024014                    | Ordynets et al. (2015)       |
| Trechispora cyatheae          | FR-0219443 | UDB024015             | UDB024015                    | Ordynets et al. (2015)       |
| Trechispora echinocristallina| FR-0219445 | UDB024018             | UDB024018                    | Ordynets et al. (2015)       |
| Trechispora echinocristallina| FR-0219448 | UDB024022             | UDB024022                    | Ordynets et al. (2015)       |
| Trechispora echinospora       | E11/37-03  | JX92845               | JX928488                     | Telleria et al. (2013)       |
| Trechispora echinospora       | E09/60-06  | JX92847               | JX928488                     | Telleria et al. (2013)       |
| Trechispora echinospora       | E11/37-05  | –                     | JX928498                     | Telleria et al. (2013)       |
| Trechispora farinacea         | KHL 8451   | AF347082              | AF347082                     | Unpublished                  |
| Trechispora farinacea         | KHL 8793   | AF347089              | AF347089                     | Larsson et al. (2004)        |
| Trechispora fissurata         | CLZhao 995 | MW544026              | MW520176                     | This study                   |
| Trechispora fissurata         | CLZhao 4571| MW544027              | MW520177                     | This study                   |
| Trechispora fimbriata         | CLZhao 4154| MW544023              | MW520173                     | This study                   |
| Trechispora fimbriata         | CLZhao 7969| MW544024              | MW520174                     | This study                   |
| Trechispora fimbriata         | CLZhao 9006| MW544025              | MW520175                     | This study                   |
| Trechispora hymenocystis      | KHL 8795   | AF347090              | AF347090                     | Unpublished                  |
| Trechispora hymenocystis      | TL 11112   | UDB000778             | UDB000778                    | Ordynets et al. (2015)       |
| Trechispora incisa            | EH 24/98   | AF347085              | –                            | Unpublished                  |
| Trechispora kavinioides       | KGN 981002 | AF347086              | AF347086                     | Larsson et al. (2004)        |
| Trechispora laevis            | TU 115551  | UDB016468             | –                            | Ordynets et al. (2015)       |
| Trechispora mollusca          | DILL 2010-077| JO673209              | –                            | Ordynets et al. (2015)       |
| Trechispora mollusca          | DILL 2011-188| KJ140681              | –                            | Ordynets et al. (2015)       |
| Trechispora nivea             | MA-Fungi 76238| JX92824              | JX92825                      | Telleria et al. (2013)       |
| Trechispora nivea             | MA-Fungi 76257| JX92826              | JX92827                      | Telleria et al. (2013)       |
| Trechispora nivea             | MA-Fungi 82480| JX92829              | JX92830                      | Telleria et al. (2013)       |
| Trechispora nivea             | MA-Fungi 74044| JX92832              | JX92833                      | Telleria et al. (2013)       |
| Trechispora regularis         | KHL 10881  | AF347087              | AF347087                     | Larsson et al. (2004)        |
| Trechispora rigida            | URM 85754  | –                     | MH279999                     | Unpublished                  |
| Trechispora stevensonii       | MA-Fungi 70669| JX92841              | JX92842                      | Telleria et al. (2013)       |
| Trechispora stevensonii       | HJM 18087  | –                     | MH290761                     | Unpublished                  |
| Trechispora stevensonii       | KHL 14654  | –                     | MH290762                     | Unpublished                  |
| Trechispora stevensonii       | TU 115499  | UDB016467             | UDB016467                    | Ordynets et al. (2015)       |
| Trechispora stellulata        | UC 2022880 | KP814437              | –                            | Unpublished                  |
| Trechispora stellulata        | UC 2023099| KP814451              | –                            | Unpublished                  |
| Trechispora subsphaerocepora  | KHL 8511   | AF347080              | AF347080                     | Larsson et al. (2004)        |
| Trechispora thelephora        | URM 85757  | –                     | MH280001                     | Unpublished                  |
| Trechispora thelephora        | URM 85758  | –                     | MH280002                     | Unpublished                  |
| Trechispora yunnanensis       | CLZhao 210 | MN654918              | MN654921                     | Xu et al. (2019)             |
| Trechispora yunnanensis       | CLZhao 214 | MN654919              | MN654922                     | Xu et al. (2019)             |
| Trechispora yunnanensis       | CLZhao 215 | MN654920              | MN654923                     | Xu et al. (2019)             |
MrModeltest 2.3 (Nylander, 2004) was used to determine the best-fit evolution model (GTR + I + G) for each data set for Bayesian inference (BI) of the phylogeny. BI was calculated with MrBayes 3.1.2 (Ronquist and Huelsenbeck, 2003). Four Markov chains were run for two runs from random starting trees for 1 million generations and trees were sampled every 100 generations; the first one-fourth of generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received ML BT values > 75%, MP BT values > 75%, or Bayesian posterior probabilities (PP) > 0.95.

RESULTS

Molecular Phylogeny
In the ITS dataset, the sequences from 43 fungal specimens representing 25 species were included. The dataset had an aligned length of 1034 characters, of which 521 characters...
are constant, 86 are variable and parsimony-uninformative, and 427 are parsimony-informative. MP analysis yielded 26 equally parsimonious trees (TL = 2048, CI = 0.4561, HI = 0.5439, RI = 0.6174, RC = 0.2816). Best model for the ITS dataset estimated and applied in the Bayesian analysis: GTR + I + G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to MP analysis, with an average standard deviation of split frequencies = 0.009985 (BI).

The phylogeny (Figure 1) inferred from ITS sequences showed that *Trechispora bambusicola* was sister to *Trechispora stevensonii* (Berk. and Broome) K.H. Larss, and *Trechispora fimbriata* grouped with *Trechispora nivea*. *T. fissurata* grouped with *T. echinospora* Telleria, M. Dueñas, I. Melo, and M.P. Martin.

In the ITS + nLSU dataset, it included sequences from 49 fungal specimens representing 27 species. The dataset had an aligned length of 2256 characters, of which 1387 characters are constant, 188 are variable and parsimony-uninformative, and 681 are parsimony-informative. MP analysis yielded 100 equally parsimonious trees (TL = 2811, CI = 0.4963, HI = 0.5037, RI = 0.6409, RC = 0.3180). Best model for the ITS dataset estimated and applied in the Bayesian analysis: GTR + I + G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to MP analysis, with an average standard deviation of split frequencies = 0.009991 (BI).

The phylogenetic tree (Figure 2) inferred from ITS + nLSU sequences demonstrated 27 species of *Trechispora* and revealed that *T. bambusicola* formed a single lineage and then grouped with *Trechispora rigidia* (Berk.) K.H. Larss. and *T. stevensonii*. **FIGURE 1** Maximum Parsimony strict consensus tree illustrating the phylogeny of three new species and related species in *Trechispora* based on ITS + nLSU sequences. Branches are labeled with maximum likelihood bootstrap values > 70%, parsimony bootstrap proportion values > 50%, and Bayesian posterior probabilities > 0.95, respectively.
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T. fimbriata was sister to T. nivea. T. fissurata grouped with T. thelephora (Lév.) Ryvarden.

**Taxonomy**

*Trechispora bambusicola* C.L. Zhao, sp. nov.

*MycoBank no.*: MB 838612 (Figures 3, 4).

_Holotype_—China, Yunnan Province, Pu’er, Laiyanghe National Forest Park, on dead bamboo, 30 September 2017, CLZhao 3305 (SWFC).

_Etymology_—*Bambusicola* (Lat.): referring to occurrence on bamboo stump.

**Basidiomata**

Annual, adnate, soft, and fragile, without odor or taste when fresh, becoming granulose upon drying, up to 15 cm long and 5 cm wide, 50–300 µm thick. Hymenial surface odontoid, aculei cylindrical to conical, blunt, 0.3–0.5 mm long, white to cream when fresh, turn to cream to buff upon drying. Margin white to cream.

**Hyphal structure**

Monomitic, generative hyphae with clamp connections, hyaline, thick-walled, up to 0.7 µm, richly branched, 2–3 µm in diameter, IKI−, CB−; hyphae unchanged in KOH.

**Hymenium**

Cystidia and cystidioides absent; basidia shortly cylindrical to subclavate with median constriction, with 4 sterigmata and a basal clamp connection, 9–13 × 2.5–5 µm, basidioles dominant, in shape similar to basidia, but slightly smaller.

**Basidiospores**

Ellipsoid, hyaline, thick-walled, ornamented, sparse aculei, sharp, IKI−, CB−, (2.6−)2.9–3.5(−3.9) × 2–2.7 µm, $L = 3.18$ µm, $W = 2.41$ µm, $Q = 1.26–1.38$ (n = 60/2).

**Type of rot**

White rot.

*Additional specimen examined*

CHINA, Yunnan Province, Pu’er, Laiyanghe National Forestry Park, on dead bamboo, 30 September 2017, CLZhao 3302 (SWFC).

*Trechispora fimbriata* C.L. Zhao, sp. nov.

*MycoBank no.*: MB 838613 (Figures 5, 6).

_Holotype_—China, Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, on the angiosperm trunk, October 5, 2017, CLZhao 4154 (SWFC).

_Etymology_—*Fimbriata* (Lat.): refers to the fimbriate margin of the basidiomata.

**Basidiomata**

Annual, adnate, without odor or taste when fresh, becoming fragile upon drying, up to 10 cm long and 3 cm wide, 100–200 µm thick. Hymenial surface hydnoid, with aculei, cylindrical, blunt, 0.4–0.7 mm long, white to pink when fresh, turn to pink to buff upon drying. Margin white to cream, thinning out, fimbriate.

**Hyphal system**

Monomitic, generative hyphae with clamp connections, hyaline, thick-walled, up to 0.6 µm, branched, 2–4 µm in diameter, IKI−, CB−; hyphae unchanged in KOH.

**Hymenium**

Cystidia and cystidioides absent; basidia shortly cylindrical with median constriction, with 4–6 sterigmata and a basal clamp connection, 7–11.5 × 3.5–5 µm, basidioles dominant, in shape similar to basidia, but slightly smaller.

**Basidiospores**

Ellipsoid, hyaline, thick-walled, ornamented, sparse aculei, sharp, IKI−, CB−, (2.5−)3.6(−3.8) × 2.4–3.2 µm, $L = 3.25$ µm, $W = 2.63$ µm, $Q = 1.17–1.38$ (n = 90/3).

**Type of rot**

White rot.
FIGURE 4 | Microscopic structures of *Trechispora bambusicola* (drawn from the holotype): (A) Section of hymenium. (B) Basidiospores. (C) Basidia and basidioles. Bars: (A,C) 10 µm; (B) 5 µm.

Additional specimens examined
China, Yunnan Province, Yuxi, Xinping County, Mopanshan National Forestry Park, on living tree of angiosperm, August 9, 2018, CLZhao 7969 (SWFC); on angiosperm trunk, October 15, 2018, CLZhao 9006 (SWFC).

*Trechispora fissurata* C.L. Zhao, sp. nov.
*MycoBank no.: MB 838614* (Figures 7, 8).

Holotype—China, Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, October 6, 2017, CLZhao 4571 (SWFC).

Etymology—*Fissurata* (Lat.): refers to the cracking fissures on hymenial surface.

**Basidiomata**
Annual, adnate, without odor or taste when fresh, becoming cracking upon drying, up to 8 cm long and 4.5 cm wide, 400–800 µm thick. Hymenial surface hydnoid, with aculei, cylindrical to conical, sharp, 0.5–0.9 mm long, cream to straw yellow when fresh, turn to cream to yellow upon drying. Margin cream to yellow.

**Hyphal system**
Monomitic, generative hyphae with clamp connections, hyaline, thick-walled, up to 0.8 µm, branched, 2.5–5 µm in diameter, IKI−, CB−; hyphae unchanged in KOH.

**Hymenium**
Cystidia and cystidioles absent; basidia shortly clavate to tubular, with 4-sterigmata and a basal clamp connection, 8–10.5 × 2.5–4.5 µm, basidioles dominant, in shape similar to basidia, but slightly smaller.
Basidiospores
Ellipsoid, hyaline, thick-walled, ornamented, dense aculei, sharp, IKI −, CB −, (3−)3.3−4(−4.3) × (2.5−)2.8−3.5(−3.9) µm, L = 3.67 µm, W = 3.19 µm, Q = 1.13−1.17 (n = 60/2).

Type of rot
White rot.

Additional specimen examined
CHINA, Yunnan Province, Yuxi, Xinpeng County, Mopanshan Forestry Park, on the fallen angiosperm branch, January 17, 2017, CLZhao 995 (SWFC).

DISCUSSION
Phylogenetically, Phookamsak et al. (2019) introduced the phylogram generated from BI analysis of ITS sequence dataset of Trechispora sequences and included most taxa in this genus, in which it implied the phylogenetic relationship among species of Trechispora. In the present study, based on the ITS sequences (Figure 1), T. bambusicola was sister to T. stevensonii (Berk. and Broome) K.H. Larss; T. fimbriata grouped with T. nivea; T. fissurata grouped with T. echinospora Telleria, M. Dueñas, I. Melo, and M.P. Martín. Further ITS + nLSU dataset (Figure 2) revealed that T. bambusicola formed a single lineage and then grouped with T. rigida and T. stevensonii; T. fimbriata was sister to T. nivea; T. fissurata grouped with T. thelephora. However, T. rigida differs in its dirty white to buff hymenophore (Larsson, 1996). T. stevensonii is separated from T. bambusicola by the smooth to hydnoid hymenophore and larger basidiospores (4−4.5 × 3−3.5 µm; Larsson, 1995). T. nivea differs from T. fimbriata by the white to light ochraceous hymenial surface (Persoon, 1794). T. echinospora differs from T. fissurata by the farinaceous to grandinioid hymenophore and larger, globose basidiospores (3.3−4 × 2.8−3.5 µm; Phookamsak et al., 2019) and T. thelephora differs in its pileate to stipitate
with light yellow brown surface and larger (4–5 × 3.4–4.5 μm; Albee-Scott and Kropp, 2010).

In the present study, three new species, *Trechispora bambusicola*, *T. fimbriata*, and *T. fissurata* spp. nov. are found from rotten wood. Morphologically, *T. bambusicola* is similar to *T. cyatheae* Ordynets, Langer and K.H. Larss. by sharing the characteristics of soft and fragile basidiomata. However, *T. cyatheae* differs from *T. bambusicola* by having farinaceous to granulose crystals (Bernicchia and Gorjón, 2010); *T. fimbriata* by the white to ochraceous hymenial surface and thinner-walled generative hyphae encrusted with granular crystals (Bernicchia and Gorjón, 2010); *T. fissurata* by the slightly cyanophilous and larger basidiospores (4–5 × 3.5–4.5 μm; Larsson, 1996).

Currently, eight species of *Trechispora* have been reported from China (Dai, 2011; Xu et al., 2019), *Trechispora alnicola*, *T. cohaerens*, *T. farinacea*, *T. microspora*, *T. nivea*, *T. polygonospora* Ryvarden, *T. subphaeospora* (Litsch.) Liberta, and *T. yunnanensis*, and one species of *T. yunnanensis* was found in Yunnan Province of China and it differs from three new species by having a smooth to farinaceous hymenial surface and larger basidiospores (7–8.5 × 5–5.5 μm; Xu et al., 2019). Three new taxa do not closely group together in phylogenetic trees, and morphologically, *T. bambusicola* differs from *T. fimbriata* and *T. fissurata* by having granulose basidiomata with cream to buff hymenial surface and growth on dead bamboo. *T. fimbriata* differs in its fimbriate margin of the basidiomata with pink to buff hymenial surface.

In addition, the ectomycorrhizal fungi (EcM) play an important role in ecosystems based on their mutualistic association with many groups of plants (Heijden et al., 2015). Vanegas-León et al. (2019) discovered the Trechisporales basidiomes and root colonization from *T. thelephora* basidiome. In the present study, *T. fissurata* was sister to *T. thelephora* based on ITS + nLSU phylogenetic analysis (Figure 2), which implied that both species have close evolutionary relationship. However, *T. fissurata* grows on deeply decayed wood, and *T. thelephora* is a soil-inhabiting fungus. Therefore, future investigations in both inhabiting types are needed to determine whether the natural selection or other factors pushes the different direction on inhabiting soil/wood among *Trechispora*.

In the habitat and distribution, Hibbett et al. (2014) revealed that most species of *Trechispora* is considered as soil-inhabiting. Later, some species were found on deeply decayed wood fungi (Bernicchia and Gorjón, 2010; Dai, 2011). However, some species in *Trechispora* are a typical feature of ectomycorrhizal fungi as frequently forming basidiomes on soil (Dunham et al., 2007; Vanegas-León et al., 2019). In the neotropical and subtropical region, the ectomycorrhizal basidiomes are found; however, the researches on the new taxa related to wood-decaying fungi of *Trechispora* from China are poorly reported. Further studies may focus on the relationships between...
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Three Potential New Ectomycorrhizal Species

FIGURE 8 | Microscopic structures of *Trechispora fissurata* (drawn from the holotype). (A) Basidiospores. (B) Basidia and basidioles. (C) Section of hymenium. Bars: (A) 5 µm; (B, C) 10 µm.

the plants and species from *Trechispora* and try to better understand the evolutionary directions between soil-inhabiting and decayed wood fungi of *Trechispora*; many fungal studies on phylogeny and application were from these areas, which will be useful to push future researches for the genus *Trechispora* (Dai, 2011; Cui et al., 2019; Shen et al., 2019; Zhu et al., 2019; Richter et al., 2019; Angelini et al., 2020; Bao et al., 2020).

**DISCLOSURE**

All the experiments undertaken in this study comply with the current laws of the People's Republic of China.

**DATA AVAILABILITY STATEMENT**

The data presented in the study are deposited in the https://www.ncbi.nlm.nih.gov/GenBank and https://www.mycobank.org/page/Home/MycoBank repository accession number of GenBank (ITS MW544021-MW544027 and nLSU MW520171-MW520177) and MycoBank (MB 838612-MB 838614).

**AUTHOR CONTRIBUTIONS**

C-LZ collected the species. WZ performed the molecular phylogenetic analyses. Both authors were responsible for the morphological analysis and description of the collections, planned, organized, and evaluated critically the experimental parts, wrote the manuscript, contributed to the article, and approved the submitted version.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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