A Link between Respiratory Complex I and Fruiting Body Formation
Suppression of Chitin-Triggered Immunity by a New Fungal Chitin-Binding Effector Resulting from Alternative Splicing of a Chitin Deacetylase Gene

by Jesús M. Martínez-Cruz, Álvaro Polonio, Laura Ruiz-Jiménez, Alejandra Vielba-Fernández, Jesús Hierrezuelo, Diego Romero, Antonio de Vicente, Dolores Fernández-Ortuño and Alejandro Pérez-García

J. Fungi 2022, 8(10), 1022; https://doi.org/10.3390/jof8101022 (registering DOI) - 23 Sep 2022

Viewed by 49

Abstract Phytopathogenic fungi have evolved mechanisms to manipulate plant defences, such as chitin-triggered immunity, a plant defensive response based on the recognition of chitin oligomers by plant-specific receptors. To cope with chitin resistance, fungal pathogens have developed different strategies to prevent chitin recognition. such [...] Read more.

Identification of Bacillus velezensis SBB and Its Antifungal Effects against Verticillium dahliae

by Wei-Yu Wang, Wei-Liang Kong, Yang-Chun-Zi Liao and Li-Hua Zhu

J. Fungi 2022, 8(10), 1021; https://doi.org/10.3390/jof8101021 (registering DOI) - 23 Sep 2022

Viewed by 93

Abstract Traditional control methods have drawbacks in controlling Verticillium wilt diseases caused by Verticillium dahliae Kleb.; therefore, an efficient and environmentally friendly strategy for disease control must be identified and the mechanisms determined. In this study, a soil-isolated strain SBB was identified as Bacillus [...] Read more.

A Molecular Systematics and Taxonomy Research on Trechispora (Hydnodontaceae, Trechisporales): Concentrating on Three New Trechispora Species from East Asia

by Kailue Luo and Changlin Zhao

J. Fungi 2022, 8(10), 1020; https://doi.org/10.3390/jof8101020 - 27 Sep 2022

Viewed by 158

Abstract Trechispora are an important genus of wood-inhabiting fungi that have the ability to decompose rotten wood in the forest ecosystem. In this study, we reported three new species of Trechispora: T. murina, T. odoriflora, T. olivacea from a subtropical region [...] Read more.

Identification of Dermatophyte and Non-Dermatophyte Agents in Onychomycosis by PCR and DNA Sequencing—A Retrospective Comparison of Diagnostic Tools

by Isabella Pospischil, Charlotte Reinhardt, Olympia Bontems, Karine Salamin, Marina Fratti, Gabriela Blanchard, Yun-Tsun Chang, Helga Wagner, Philipp Hermann, Michel Moned, Wolfram Hoetzenecker and Emmanuelle Guerno

J. Fungi 2022, 8(10), 1019; https://doi.org/10.3390/jof8101019 - 27 Sep 2022

Viewed by 109

Abstract Rapid and reliable fungal identification is crucial to delineate infectious diseases, and to establish appropriate treatment for onychomycosis. Compared to conventional diagnostic methods, molecular techniques are faster and feature higher accuracy in fungal identification. However, in current clinical practice, molecular mycology is not [...] Read more.
A Molecular Systematics and Taxonomy Research on Trechispora (Hydnodontaceae, Trechisporales): Concentrating on Three New Trechispora Species from East Asia

Kaiyue Luo and Changlin Zhao

1 Yunnan Key Laboratory of Plateau Wetland Conservation, Restoration and Ecological Services, Southwest Forestry University, Kunming 650224, China
2 College of Biodiversity Conservation, Southwest Forestry University, Kunming 650224, China
3 Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China, Ministry of Education, Southwest Forestry University, Kunming 650224, China
4 Yunnan Key Laboratory for Fungal Diversity and Green Development, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China

Abstract: Trechispora are an important genus of wood-inhabiting fungi that have the ability to decompose rotten wood in the forest ecosystem. In this study, we reported three new species of Trechispora: T. murina, T. odontioidea, T. olivacea from a subtropical region of Yunnan Province, China. Species descriptions were based on a combination of morphological features and phylogenetic analyses of the ITS and LSU region of nuclear ribosomal DNA. Trechispora murina is characterized by the resupinate basidiomata, grandinioid hymenial surface with a greyish tint, monomitic hyphal system and ellipsoid, thick-walled, ornamented basidiospores; T. odontioidea has an odontioid hymenial surface with cylindrical to conical, blunt aculei and subglobose to globose, colorless, slightly thick-walled, ornamented basidiospores; T. olivacea has a farinaceous hymenial surface with olivaceous tint, basidia clavate and thick-walled, ornamented, broadly ellipsoid to globose basidiospores. Sequences of the ITS and nLSU rDNA markers of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony, and Bayesian inference methods. After a series of phylogenetic analyses, the 5.8S+nLSU dataset was constructed to test the phylogenetic relationship of Trechispora with other genera of Hydnodontaceae. The ITS dataset was used to evaluate the phylogenetic relationship of the three new species with other species of Trechispora. Using ITS phylogeny, the new species T. murina was retrieved as a sister to T. bambusicola with moderate supports; T. odontioidea formed a single lineage and then grouped with T. fimbriata and T. nivea; while T. olivacea formed a monophyletic lineage with T. farinacea, T. hondurensis, and T. mollis.

Keywords: fungal diversity; morphology; southwest China; subtropical region; wood-inhabiting fungi

1. Introduction

Fungi form an essential branch of the tree of life, inferred from the important relationship with animals and plants [1], and it drives the carbon cycling in forest soils, mediate mineral nutrition of plants, and alleviate carbon limitations of other soil organisms as the decomposers and mutualists of plants and animals being the fundamental ecological roles [2]. Inferred from growing on a variety of the boreal, temperate, subtropical, and tropical divers vegetation, wood-inhabiting fungi have a rich diversity [3–13]. Trechispora P. Karst. belongs to Trechisporales, a small but strongly supported order in Agaricomycotina [14,15]. Trechispora (Hydnodontaceae Jülich) typified by T. onusta P. Karst., which is characterized by resupinate to effused basidiomata; a smooth to hydnoid to poroid hymenophore; ampullaceous septa; short cylindric basidia; and smooth to verrucose or aculeate basidiospores [5,16]. Currently, MycoBank and Index Fungorum have registered 121 specific and intraspecific names in...
Trechispora. About 60 species are currently accepted in Trechispora worldwide [5,17–27], of which 18 species of the genus have been found in China [28–34].

The high phylogenetic diversity on the corticioid Agaricomycetes based on two genes, 5.8S and 28S in which nine taxa of Trechispora nested into trechisporoid clade [35]. The molecular systematics suggested that Trechispora belonged to Hydnodontaceae and was related to genera Brevicellicium K.H. Larss. & Hjortstam, Porponymes Jülich, Sistotremastrum J. Erikss., and Subulicystidium Parmasto [36], the similar morphological characters of Trechispora to these genera are basidiomata resupinate, hyphal system monomitic, cystidia absent [5,37]. The phylogeny of Trechisporales was inferred from a combined ITS-nLSU sequences, which revealed that several related genera Porponymes, Scytinopogon Singer, and Trechispora grouped closely together and nested within Hydnodontaceae [38].

Based on the ITS and nLSU datasets, the phylogenetic study of Trechispora reports two new Trechispora species: T. cyatheae Ordynets, Langer & K.H. Larss. and T. echinocristallina Ordynets, Langer & K.H. Larss., which were found in La Réunion Island [24]. Recently, a new species of Trechispora has been reported from North America and China [26,33,34]. During the investigations of the corticioid fungi, Yunnan Province, China, we collected three fungal taxa, which could not be assigned to any described species within Hydnodontaceae. We present morphological and molecular phylogenetic evidence that support them as the three new species in Trechispora.

2. Materials and Methods

2.1. Sample Collection and Herbarium Specimen Preparation

Fresh fruiting bodies of the fungi growing on fallen angiosperm branches were collected in 2019 from the Honghe and Wenshan of Yunnan Province, China. The samples were photographed in situ and macroscopic details were recorded. Field photographs were taken by a Jianeng 80D camera (Tokyo, Japan). All photographs were focus-stacked and merged using Helicon Focus Pro 7.7.5 software. Once the macroscopic details were recorded, the specimens were transported to a field station where the specimens were dried on an electronic food dryer at 45 °C. Once dried, the specimens were labeled and sealed in envelopes and plastic bags. The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

2.2. Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and laboratory. Color, texture, taste and odor of fruit bodies were mostly based on the authors’ field trip investigations. Color terminology follows Kornerup and Wanscher [39]. All materials were examined under a Nikon 80i microscope (Nikon Corporation, Tokyo, Japan). Drawings were made with the aid of a drawing tube. The measurements and drawings were made from slide preparations stained with cotton blue (0.1 mg aniline blue dissolved in 60 g pure lactic acid), Melzer’s reagent (1.5 g potassium iodide, 0.5 g crystalline iodine, 22 g chloral hydrate, aq. dest. 20 mL), and 5% potassium hydroxide. Spores were measured from the sections of the basidiomata and when presenting spore size data, 5% of the measurements excluded from each end of the range are shown in parentheses [40]. The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB = cotton clue, CB– = acyanophilous, IKI = Melzer’s reagent, IKI– = both inamyloid and indextrinoid, L = means spore length (arithmetic average for all spores), W = means spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b ((a) number of spores were measured in total, coming from (b) number of specimen).

2.3. Molecular Phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens following the manufacturer’s instructions [41]. The nuclear ribosomal ITS region was amplified with the
primers ITS5 and ITS4 [42]. The nuclear nLSU region was amplified with the primer pairs LR0R and LR7 (http://lutzonilab.org/nuclear-ribosomal-dna/, accessed on 7 June 2019). The PCR procedure used for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure used for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Kunming, Yunnan Province, China). All the newly generated sequences were deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank/, accessed on 28 November 2021) (Table 1).

Table 1. List of species, specimens, and GenBank accession numbers of sequences used in this study, the newly generated sequences are in bold fonts.

<table>
<thead>
<tr>
<th>Species Name</th>
<th>Specimen No.</th>
<th>GenBank Accession No.</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brevicellicium exile</td>
<td>H (Spirin 8370)</td>
<td>MT002322 MT002338</td>
<td>[43]</td>
</tr>
<tr>
<td>B. olivascens</td>
<td>KHL 8571</td>
<td>HE963792 HE963793</td>
<td>[36]</td>
</tr>
<tr>
<td>Dextrinocystis calaminola</td>
<td>He 5700</td>
<td>MK204534 MK204547</td>
<td>[38]</td>
</tr>
<tr>
<td>Fibrodontia alba</td>
<td>TNMF 24944</td>
<td>NR153983 NG064014</td>
<td>[24]</td>
</tr>
<tr>
<td>E. brevidens</td>
<td>Wu 9807-16</td>
<td>KC928276 KC928277</td>
<td>[44]</td>
</tr>
<tr>
<td>Litschauerella gladola</td>
<td>He 3171</td>
<td>MK204555 MK204556</td>
<td>[38]</td>
</tr>
<tr>
<td>Laelia cystiata</td>
<td>JHP 0945</td>
<td>MW371211 Unpublished</td>
<td></td>
</tr>
<tr>
<td>Porphyropsicus mucidus</td>
<td>Dai 12692</td>
<td>KT157833 KT157838</td>
<td>[45]</td>
</tr>
<tr>
<td>P. submicidus</td>
<td>Cui 5183</td>
<td>KT132143 KT132145</td>
<td>[45]</td>
</tr>
<tr>
<td>Scytinopogon pallescens</td>
<td>He 5192</td>
<td>MK204553</td>
<td>[38]</td>
</tr>
<tr>
<td>S. havencampii</td>
<td>DED 8300</td>
<td>KT253946 KT253947</td>
<td>[46]</td>
</tr>
<tr>
<td>Sistotremastrum guttuliferum</td>
<td>He 3338</td>
<td>MK204540 MK204552</td>
<td>[46]</td>
</tr>
<tr>
<td>S. niveocremeum</td>
<td>CBS 42854</td>
<td>MH857381 MH868921</td>
<td>[47]</td>
</tr>
<tr>
<td>S. succinum</td>
<td>H (Miettinen14550)</td>
<td>MT075860 MT002336</td>
<td>[43]</td>
</tr>
<tr>
<td>Sphaerobasidium minutum</td>
<td>KHL 11714</td>
<td>DQ873652 DQ873653</td>
<td>[48]</td>
</tr>
<tr>
<td>Subulicystidium brachisporum</td>
<td>KASL 1584b</td>
<td>MH041544 MH041610</td>
<td>[49]</td>
</tr>
<tr>
<td>S. coelum</td>
<td>KHL 11200</td>
<td>MN207036 MN207024</td>
<td>[50]</td>
</tr>
<tr>
<td>S. longisporum</td>
<td>Ordnets 00146</td>
<td>MN207039 MN207032</td>
<td>[50]</td>
</tr>
<tr>
<td>S. meridense</td>
<td>Hjm 16400</td>
<td>MH041538 MH041604</td>
<td>[49]</td>
</tr>
<tr>
<td>Trechispora amantiathina</td>
<td>CBS 202.54</td>
<td>MH857292</td>
<td>[47]</td>
</tr>
<tr>
<td>T. aranosa</td>
<td>KHL 8570</td>
<td>AF347084</td>
<td>[35]</td>
</tr>
<tr>
<td>T. bambusicola</td>
<td>CLZhao 3305</td>
<td>MW544022 MW520172</td>
<td>[33]</td>
</tr>
<tr>
<td>T. bipora</td>
<td>CBS 142.63</td>
<td>MH858241</td>
<td>[47]</td>
</tr>
<tr>
<td>T. hypsaella</td>
<td>UC 203068</td>
<td>KP814481 Unpublished</td>
<td></td>
</tr>
<tr>
<td>T. clancularis</td>
<td>FRDBI 4426619</td>
<td>MW487976</td>
<td>Unpublished</td>
</tr>
<tr>
<td>T. coloarenis</td>
<td>HHB 19445</td>
<td>MW740327 Unpublished</td>
<td></td>
</tr>
<tr>
<td>T. cuposa</td>
<td>AMO 453</td>
<td>MN701018 Unpublished</td>
<td>[27]</td>
</tr>
<tr>
<td>T. confinis</td>
<td>KHL 1197</td>
<td>AY463473 AY586719</td>
<td>[35]</td>
</tr>
<tr>
<td>T. davenishanos</td>
<td>CLZhao 18255</td>
<td>MW302338</td>
<td>[34]</td>
</tr>
<tr>
<td>T. echinospora</td>
<td>MA Fungi 82486</td>
<td>JX392853</td>
<td>[36]</td>
</tr>
<tr>
<td>T. farinacea</td>
<td>MA Fungi 79474</td>
<td>JX392855 JX392856</td>
<td>[36]</td>
</tr>
<tr>
<td>T. fimbriata</td>
<td>CLZhao 9006</td>
<td>MW544025 MW520175</td>
<td>[33]</td>
</tr>
<tr>
<td>T. fissurata</td>
<td>CLZhao 4571</td>
<td>MW544027</td>
<td>[33]</td>
</tr>
<tr>
<td>T. gelatinosa</td>
<td>AMO 1139</td>
<td>MN701021 Unpublished</td>
<td>[27]</td>
</tr>
<tr>
<td>T. havencampii</td>
<td>DED 8300</td>
<td>NR154418</td>
<td>[46]</td>
</tr>
<tr>
<td>T. hondurensis</td>
<td>HONDURAS 19-F016</td>
<td>MT571523 MT635404</td>
<td>Unpublished</td>
</tr>
<tr>
<td>T. hymenocytis</td>
<td>KHL 8795</td>
<td>AF347090 Unpublished</td>
<td>[35]</td>
</tr>
<tr>
<td>T. incisa</td>
<td>GB 0090648</td>
<td>KU747095 Unpublished</td>
<td></td>
</tr>
<tr>
<td>T. incisitata</td>
<td>UC 202088</td>
<td>KP814425 Unpublished</td>
<td></td>
</tr>
<tr>
<td>T. kaviinoides</td>
<td>KGN 981002</td>
<td>AF347086 Unpublished</td>
<td>[35]</td>
</tr>
<tr>
<td>T. mollis</td>
<td>URM 85884</td>
<td>MK516945 Unpublished</td>
<td>[26]</td>
</tr>
<tr>
<td>T. mollusca</td>
<td>CBS 43948</td>
<td>MH856428</td>
<td>[47]</td>
</tr>
<tr>
<td>T. murina</td>
<td>CLZhao 11736</td>
<td>OL615003</td>
<td>Present study</td>
</tr>
<tr>
<td>T. murina</td>
<td>CLZhao 11752</td>
<td>OL615004 OL615009</td>
<td>Present study</td>
</tr>
<tr>
<td>T. nitea</td>
<td>MA Fungi 74044</td>
<td>JX392832</td>
<td>[36]</td>
</tr>
<tr>
<td>T. odontotioides</td>
<td>CLZhao 17890</td>
<td>ON417458</td>
<td>Present study</td>
</tr>
<tr>
<td>T. olistivacea</td>
<td>CLZhao 17826</td>
<td>ON417457</td>
<td>Present study</td>
</tr>
</tbody>
</table>
Table 1. Cont.

<table>
<thead>
<tr>
<th>Species Name</th>
<th>Specimen No.</th>
<th>GenBank Accession No.</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>T. pallescens</td>
<td>FLOR 56186</td>
<td>MK458766</td>
<td>Unpublished</td>
</tr>
<tr>
<td>T. papillosa</td>
<td>AMO 713</td>
<td>MN701022</td>
<td>[27]</td>
</tr>
<tr>
<td>T. regularis</td>
<td>KHL 10881</td>
<td>AF347087</td>
<td>[35]</td>
</tr>
<tr>
<td>T. rigida</td>
<td>URM 85754</td>
<td>MT406381</td>
<td>[26]</td>
</tr>
<tr>
<td>T. stellulata</td>
<td>UC 2023096</td>
<td>KP814450</td>
<td>Unpublished</td>
</tr>
<tr>
<td>T. stevensontii</td>
<td>MA Fungi 70669</td>
<td>JX392541</td>
<td>[36]</td>
</tr>
<tr>
<td>T. subsphaerospora</td>
<td>KHL 8511</td>
<td>AF347080</td>
<td>[35]</td>
</tr>
<tr>
<td>T. termotrophila</td>
<td>AMO 1169</td>
<td>MN701028</td>
<td>[27]</td>
</tr>
<tr>
<td>T. thelephora</td>
<td>1820 AMV</td>
<td>KP937369</td>
<td>[51]</td>
</tr>
<tr>
<td>T. torrendii</td>
<td>URM 85886</td>
<td>MK515148</td>
<td>[26]</td>
</tr>
<tr>
<td>T. xantha</td>
<td>CLZhao 17781</td>
<td>MW302340</td>
<td>[34]</td>
</tr>
<tr>
<td>T. yunnanensis</td>
<td>CLZhao 215</td>
<td>MN654923</td>
<td>[31]</td>
</tr>
<tr>
<td>Tubulicium raphidisporum</td>
<td>He 3191</td>
<td>MK204537</td>
<td>[38]</td>
</tr>
<tr>
<td>T. vermiferum</td>
<td>KHL 8714</td>
<td>—</td>
<td>AY463477</td>
</tr>
</tbody>
</table>

The sequences and alignment were adjusted manually using AliView version 1.27 [52]. The datasets were aligned with Mesquite version 3.51. The 5.8S+nLSU sequences dataset was used to know the phylogenetic relationship of the three new species in *Trechispora* and related genera, and the ITS dataset was used to evaluate the phylogenetic relationships of the new species with known species of the genus. Sequences of *Porpomyces mucidus* (Pers.) that Jülč and *P. submucidus* F. Wu & C.L. Zhao retrieved from GenBank were used as the outgroup for the 5.8S+nLSU analysis (Figure 1) [34], and sequences of *Fibrodontia alba* that Yurchenko & Sheng H. Wu and *F. brevidens* (Pat.) Hjortstam & Ryvarden retrieved from GenBank were used as the outgroup for the ITS analysis (Figure 2) [24,34].

![Figure 1](image-url)  
*Figure 1.* Maximum parsimony strict consensus tree illustrating the phylogeny of *Trechispora* and related genera in Trechisporales based on 5.8S+nLSU sequences. The genera represented by each color are indicated in the upper left of the phylogenetic tree. Branches are labelled with maximum likelihood bootstrap value $\geq 70\%$, parsimony bootstrap value $\geq 50\%$, and Bayesian posterior probabilities $\geq 0.95$, respectively.
Figure 2. Maximum parsimony strict consensus tree illustrating the phylogeny of three new species and related species in *Trechispora* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap value $\geq 70\%$, parsimony bootstrap value $\geq 50\%$, and Bayesian posterior probabilities $\geq 0.95$, respectively. The new species are in bold.

The three combined datasets were analyzed using maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI), according to Zhao and Wu [41]. Maximum parsimony analyses were constructed using PAUP* version 4.0b10 [53]. All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates [54]. Descriptive tree statistics—tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI)—were calculated for each maximum parsimonious tree generated. Multiple sequence alignment was also analyzed using ML in RAxML-HPC2 through the Cipres Science Gateway [55]. Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 [56] was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI), which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites [57]. A total of 4 Markov chains were run, each consisting of 1.6 million generations, with random starting trees for 5.8S+nLSU (Figure 1) and 1.2 million generations for ITS (Figure 2) with trees and parameters sampled every 1000 generations. The first one-fourth of all generations were discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received a maximum likelihood bootstrap value (BS) $\geq 70\%$, maximum parsimony bootstrap value (BT) $\geq 70\%$, or Bayesian posterior probabilities (BPP) $\geq 0.95$.

3. Results
3.1. Molecular Phylogeny

The 5.8S+nLSU dataset (Figure 1) included sequences from 30 fungal samples representing 30 species. The dataset had an aligned length of 1508 characters, of which 1141 characters are constant, 104 are variable and parsimony uninformative, and 263 are parsimony informative. Maximum parsimony analysis yielded 54 equally parsimonious
trees (TL = 986, CI = 0.5172, HI = 0.4828, RI = 0.5211, and RC = 0.2695). The best model was GTR+I+G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1)). Bayesian and ML analyses showed a topology similar to that of MP analysis with split frequencies equal to 0.022581 (BI), and the effective sample size (ESS) across the two runs is double of the average ESS (avg ESS) = 869.5.

The 5.8S+nLSU rDNA gene regions (Figure 1) include ten genera within Trechisporales, Brevicellicium, Dextrinocystis Gilb. & M. Blackw., Litschauerella Oberw., Luellia K.H. Larss. & Hjortstam, Scytinopogon, Sistotremastrum J. Erikss., Sphaerobasidium Parmasto, Tubulicium Oberw., and Trechispora, shows that all related genera cluster into Trechisporales and the three new species grouped into Trechispora.

The ITS-alone dataset (Figure 2) included sequences from 42 fungal specimens representing 41 species. The dataset had an aligned length of 580 characters, of which 178 characters are constant, 61 are variable and parsimony-uninformative, and 341 are parsimony-informative. Maximum parsimony analysis yielded 584 equally parsimonious trees (TL = 2802, CI = 0.3123, HI = 0.6877, RI = 0.2519, and RC = 0.0787). Best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR+I+G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian and ML analyses resulted in a topology similar to that of MP analysis with split frequencies equal to 0.025000 (BI), and the effective sample size (ESS) across the two runs is double of the average ESS (avg ESS) = 621.5.

The phylogram inferred from the ITS dataset (Figure 2) indicated that the three new species grouped into Trechispora, in which the new species T. murina was sister to T. bambusicola with higher supports (96% BS, 92% BP, and 1.00 BPP); T. odontioidea formed a unique position within the clade of T. fimbriata C.L. Zhao and T. nivea (Pers.) K.H. Larss; while T. olivacea shared a clade formed by the members of T. farinacea (Pers.) Liberta, T. hondurensis Schoutteten & Haelew., and T. mollis.

3.2. Taxonomy

**Trechispora murina** K.Y. Luo & C.L. Zhao, sp. nov. Figures 3 and 4.

![Figure 3](image3.png)

**Figure 3.** Basidiomata of *Trechispora murina* (holotype CLZhao 11752): the front of the basidiomata (A), characteristic hymenophore (B). Bars: (A) = 5 mm and (B) = 1 mm.
Figure 4. Microscopic structures of *Trechispora murina* (holotype CLZhao 11752): basidiospores (A), a cross-section of basidiomata (B), basidia and basidioles (C). Bars: (A) = 5 µm, (B,C) = 10 µm.

MycoBank no.: 842491.

**Holotype**—China, Yunnan Province, Wenshan, Funing County, Guying Village, GPS coordinates 23°44′ N, 105°56′ E, altitude 750 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 20 January 2019, CLZhao 11752 (SWFC).

**Etymology**—*murina* (Lat.): Referring to the furry mouse-like hymenial surface.

**Basidiomata**—Annual, resupinate, thin, growing adnate but easily separable, up to 15 cm long, 3 cm wide, 100–500 µm thick. Hymenial surface grandinioid, pale greyish to grey when fresh, turn to greyish upon drying. Sterile margin concolorous with a hymenial surface, up to 2 mm wide.

**Hyphal system**—Monomitic; generative hyphae with clamp connections; colorless; thick-walled with a wide to lumen; richly branched; interwoven; encrusted; 2–3.5 µm in diameter; IKI–, CB–; tissues unchanged in KOH.

**Hymenium**—Cystidia and cystidioles absent; basidia more or less clavate, with four sterigmata and a basal clamp connection, 10.0–14.0 × 3.5–4.5 µm; basidioles dominant; basidioles in shape similar to basidia, but slightly smaller.

**Spores**—Basidiospores ellipsoid, colorless, thick-walled, ornamented, IKI–, CB–, (2.5–) 3–4 × (2–) 2.5–3 µm, L = 3.42 µm, W = 2.87 µm, Q = 1.17–1.20 (n = 60/2).

**Additional specimen examined (paratype)**—China, Yunnan Province, Wenshan, Funing County, Guying Village, GPS coordinates 23°39′ N, 105°59′ E, altitude 1400 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 20 January 2019, CLZhao 11736 (SWFC).


MycoBank no.: 844493.

**Holotype**—China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve. GPS coordinates: 23°420′ N, 103°300′ E; altitude: 1500 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 1 August 2019, CLZhao 17890 (SWFC).

**Etymology**—*odontioidea* (Lat.): Referring to the odontioid hymenophore.

**Basidiomata**—Annual, adnate, thin, up to 11 cm long, 2.5 cm wide, 50–200 µm thick. Hymenial surface odontioid, aculei cylindrical to conical, blunt, 0.3–0.6 mm long, pale buff when fresh, turn to buff upon drying. Sterile margin indistinct, cream to buff, 0.5–1 mm wide.

**Hyphal system**—Monomitic; generative hyphae with clamp connections; colorless, thin- to thick-walled; frequently branched; interwoven; 2–3.5 µm in diameter; ampullate hyphae frequently present; IKI–, CB–; tissues unchanged in KOH.
Hymenium—Cystidia and cystidioles absent; basidia clavate, with four sterigmata and a basal clamp connection, 8.0–12.0 × 2.5–4 µm; basidioles dominant, in shape similar to basidia, but smaller.

Spores—Basidiospores subglobose to globose, colorless, slightly thick-walled, ornamented, IKI−, CB−, 2–3 × 1.5–2.5 µm, L = 2.53 µm, W = 2.00 µm, Q = 1.27 (n = 30/1).


---

**Figure 5.** Basidiomata of *Trechispora odontioidea* (holotype CLZhao 17890): the front of the basidiomata (A), characteristic hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

**Figure 6.** Microscopic structures of *Trechispora odontioidea* (holotype CLZhao 17890): basidiospores (A), basidia and basidioles (B), a cross section of basidiomata (C). Bars: (A) = 5 µm, (B,C) = 10 µm.
Figure 7. Basidiomata of *Trechispora olivacea* (holotype CLZhao 17826): the front of the basidiomata (A), characteristic hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

Figure 8. Microscopic structures of *Trechispora olivacea* (holotype CLZhao 17826): basidiospores (A), basidia and basidioles (B), a cross-section of basidiomata (C). Bars: (A) = 5 μm, (B,C) = 10 μm.
Mycobank no.: 844494.

**Holotype**—China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve. GPS coordinates: 23°420’ N, 103°300’ E; altitude: 1500 m asl., on fallen angiosperm branches, leg. C.L. Zhao, 1 August 2019, CLZhao 17826 (SWFC).

**Etymology**—*olivacea* (Lat.): Referring to the olivaceous hymenial surface.

**Basidiomata**—Annual, resupinate, thin, very hard to separate from substrate, up to 11 cm long, 2.5 cm wide, 30–80 µm thick. Hymenial surface farinaceous, pale white to slightly olivaceous when fresh, turn to olivaceous upon drying. Sterile margin indistinct, slightly olivaceous, 0.2–0.5 mm wide.

**Hyphal system**—Monomitic; generative hyphae with clamp connections; colorless; thin- to thick-walled; occasionally branched; interwoven; 1.5–3.0 µm in diameter; ampullate hyphae present; IKI–, CB–; tissues unchanged in KOH.

**Hymenium**—Cystidia and cystidioles absent; basidia clavate, with four sterigmata and a basal clamp connection, 10.0–12.0 × 4.5–5.5 µm; basidia dominant, with the shape similar to basidia, but smaller.

**Spores**—Basidiospores broadly ellipsoid to globose, colorless, thick-walled, ornamented, IKI–, CB–, 2.5–4 × 1.5–2.5 µm, L = 3.30 µm, W = 2.65 µm, Q = 1.25 (n = 30/1).

4. Discussion

The classification of corticioid fungi revealed that two taxa of *Trechispora farinacea* and *T. hymenocystis* nested into *Trechispora* located in Hydnodontaceae (Trechisporales) [15]. In the present study (Figure 2), *Trechispora murina*, *T. odontioidea*, and *T. olivacea* are nested into *Trechispora*, in which *T. murina* was sister to *T. bambusicola*; *T. odontioidea* formed a monophyletic lineage and then grouped with *T. fimbriata* and *T. nivea*; while *T. olivacea* formed a monophyletic lineage and then grouped with *T. farinacea*, *T. hondurensis*, and *T. mollis*. However, *T. bambusicola* is morphologically distinguishable from *T. murina* by having the odontioid hymenophore with cream to buff the hymenial surface [33]. *Trechispora fimbriata* is distinguishable from *T. odontioidea* by having the hydnoid hymenial surface and longer basidiospores (3–3.6 × 2.4–3.2 µm) [33]. *T. nivea* differs from *T. odontioidea* by its thin-walled, larger basidiospores (3.5–4 × 2.5–3 µm) [5]. *Trechispora farinacea* is distinguishable from *T. olivacea* by its smooth to grandinioid or odontioid hymenophore with whitish to ochraceous hymenial surface and larger basidiospores (4–5 × 3.5–4 µm) [5]. *T. hondurensis* is separated from *T. olivacea* by having a hydnoid to partly irpicoid hymenial surface and thin-walled, wider basidiospores (3.6–3.8 × 2.7–2.9 µm) [58]; *T. mollis* is distinguishable from *T. olivacea* because it has white-yellow to pale yellow hydnoid hymenial surface, and wider ampullate septa at generative hyphae (reaching 8 µm in width) [26].

Morphologically, *Trechispora murina* is similar to *T. farinacea*, *T. rigida*, *T. subsphaerospora* (Litsch.) Liberta, and *T. torrendii* Chikowski & K.H. Larss. Based on the character of the grandinioid hymenial surface. However, *Trechispora farinacea* is separated from *T. murina* by having a whitish to ochraceous hymenial surface and larger, subglobose to broadly ellipsoid basidiospores (4–5 × 3.5–4 µm) [5]. *Trechispora rigida* differs from *T. murina* due to the presence of its dirty white to buff hymenophore [59] and having larger basidiospores (4.5–5.5 × 4 µm) [27]. *Trechispora subsphaerospora* differs from *T. murina* by having smooth basidiospores [34]. *Trechispora torrendii* differs in its pale yellow to yellow hymenophore [26] and has globose to subglobose basidiospores (2.8–3.5 × 3–3.5 µm) [27].

*Trechispora murina* is similar to *T. canariensis* Ryvarden & Liberta, *T. fastidiosa* (Pers.) Liberta, *T. praefocata* (Bourdot & Galzin) Liberta, *T. stevensonii* (Berk. & Broome) K.H. Larss., and *T. yunnanensis* C.L. Zhao due to the presence of the ellipsoid, ornamented basidiospores. However, *Trechispora canariensis* differs from *T. murina* because it has arachnoid to pelliculose hymenial surface and thin-walled, larger basidiospores (5–7 × 3–3.5 µm) [5]. *Trechispora fastidiosa* is separated from *T. murina* by having a membranaceous, whitish to cream hymenial surface and larger basidiospores (6–7 × 4.5–5.5 µm) [5]. *Trechispora praefocata* differs by having the farinaceous to arachnoid hymenial surface and larger basidiospores (5–6.5 × 4–5.5 µm) [5]. *Trechispora stevensonii* differs from *T. murina* by its
hydroid hymenophore and larger basidiospores (4–4.5 × 3–3.5 µm) [5]. *Trechispora yunnanensis* is separated from *T. murina* by having the farinaceous hymenial surface and larger basidiospores (7–8.5 × 5–5.5 µm) [31].

*Trechispora odontioidea* is similar to *T. bambusicola* C.L. Zhao and *T. nivea* in having an odontioid hymenial surface. However, *Trechispora bambusicola* differs from *T. odontioidea* because it has granulose basidiomata, and the absence of the ampullaceous septa [33]. *Trechispora nivea* differs from *T. odontioidea* due to the presence of white to ochraceous basidiomata and broadly ellipsoid to subglobose, thin-walled, larger basidiospores (3.5–4 × 2.5–3 µm) [5].

*Trechispora odontioidea* resembles *T. clancularis* (Park.-Rhodes) K.H. Larss., *T. cyatheae* Ordynets, Langer & K.H. Larss., *T. hymenocystis* (Berk. & Broome) K.H. Larsson, *T. invistitata* (H.S. Jacks.) Liberta, and *T. torrendii* Chikowski & K.H. Larss. due to the presence of ornamented or aculeate basidiospores. However, *Trechispora clancularis* is distinguishable from *T. odontioidea* due to the presence of its poroid to irpicoid hymenial surface and subglobose to ovoid, larger basidiospores (6–6.5 × 5–6 µm) [5]. *Trechispora cyatheae* differs from *T. odontioidea* in having a farinaceous to grandinoid hymenial surface, and broadly elliptical to slightly lacrymiform and adaxial side convex or straight, longer basidiospores (3–3.5 × 2–3 µm) [24]. *Trechispora hymenocystis* is distinguishable from *T. odontioidea* by its poroid basidiomata and broadly ellipsoid to ellipsoidal, larger basidiospores (4.5–5.5 × 3.5–4.5 µm) [19]. *Trechispora invistitata* differs from *T. odontioidea* because it has a smooth to porulose, farinaceous to granulose hymenial surface and ellipsoid to ovate, larger basidiospores (4.5–5.5 × 3–4 µm) [5]. *Trechispora torrendii* differs from *T. odontioidea* because it has a farinose to grandinoid hymenial hyphal system, and larger basidiospores (3.2–3.5 × 2.8–3.2 µm) [26].

*Trechispora olivacea* is similar to *T. caucasica* (Parmasto) Liberta, *T. dimitica* Hallenb., *T. gelatinosa* Meiras-Ottoni & Gibertoni, *T. verruculosa* (G. Cunn.) K.H. Larss., and *T. yunnanensis* C.L. Zhao due to the presence of a farinaceous hymenial surface. However, *Trechispora caucasica* differs from *T. olivacea* by having a white to greyish hymenial surface and narrowly ellipsoid to reniform with a median constriction, larger basidiospores (5–5.5 × 4.4–5 µm) [5].

*Trechispora dimitica* differs from *T. olivacea* in its white to pale greyish hymenial surface, dimitic hyphal system, and shorter basidia (7–10 × 4.5–5.5 µm) [5]. *Trechispora gelatinosa* is distinguishable from *T. olivacea* by its coralloid basidiomata and wider basidiospores (3.2–4.5 × 2.5–3.5 µm) [27]. *Trechispora verruculosa* differs from *T. olivacea* because it has granulose to hydnoid with small cylindrical aculei, white to yellowish to ochraceous hymenial surface and larger basidiospores (4.5–5.5 × 3.5–4.5 µm) [5].

*Trechispora yunnanensis* can be delimited from *T. olivacea* by its larger basidiospores (7–8.5 × 5–5.5 µm) [31].

*Trechispora olivacea* resembles *T. hypogeton* (Maas Geest.) Hjortstam & K.H. Larss., *T. nivea*, *T. rigida*, and *T. thelephora* (Lév.) Ryvarden in having broadly ellipsoid to globose, ornamented basidiospores. However, *Trechispora hypogeton* is distinguishable from *T. olivacea* by its stipitate basidiomata and wider basidiospores (3.8–4.3 × 2.7–3.1 µm) [26].

*Trechispora nivea* differs from *T. olivacea* by the presence of an odontioid hymenial surface with white to pale ochraceous and wider basidiospores (3.5–4 × 2.5–3 µm) [5]. *Trechispora rigida* differs from *T. olivacea* due to the presence of a colliculose hymenial surface and larger basidiospores (4.5–5.5 × 4 µm) [26]. *Trechispora thelephora* differs from *T. olivacea* because it has a stipitate basidiomata and larger basidiospores (4.0–5.0 × 3.4–4.5 µm) [26].

Wood-rotting fungi are an extensively studied group of Basidiomycota [12,13,60–66] and the three taxa of *Trechispora* are a typical example group of wood-rotting fungi [15,33–35,67]. Based on our present morphology and phylogeny focusing on *Trechispora*, all taxa in this genus can be separated from the three new species.

**Key to 21 accepted species of Trechispora in China**

1. Basidiospores smooth
   1. Basidiospores aculeate, verrucose or ornamented
   2. Ampullate hyphae > 5 µm in width, basidiospores angular ————*T. subsphaerospora*
   2. Ampullate hyphae < 5 µm in width, basidiospores ellipsoid ————*T. cohaerens*
   3. Basidiospores thick-walled

   3. Basidiospores thin-walled ————*T. vanduzeei*
4. Hymenial surface tuberculate ———————————————————— *T. daweishanensis*
4′ Hymenial surface smooth ———————————————————— *T. xantha*
5. Hyphal system dimitic ———————————————————— *T. dimictica*
5′ Hyphal system monomitic ———————————————————— 6
6. Hyphae without ampullate septa ———————————————————— 7
6′ Hyphae with ampullate septa ———————————————————— 12
7. Basidiospores thin-walled, ovoid to subglobose ———————————————————— *T. suberea*
7′ Basidiospores thick-walled, ellipsoid ———————————————————— 8
8. Basidiospores > 7 µm in length ———————————————————— *T. yunnanensis*
8′ Basidiospores < 7 µm in length ———————————————————— 9
9. Basidiomata margin greyish ———————————————————— *T. murina*
9′ Basidiomata margin white to cream ———————————————————— 10
10. Hymenial surface odontioid ———————————————————— *T. bambusicola*
10′ Hymenial surface hydnoid ———————————————————— 11
11. Hymenophore with blunt aculei ———————————————————— *T. fimbriata*
11′ Hymenophore with sharp aculei ———————————————————— *T. fissurata*
12. Sphaerocysts present, hyphae inflated ———————————————————— *T. hymenocystis*
12′ Sphaerocysts absent, hyphae uninflated ———————————————————— 13
13. Ampullate septa > 6 µm in width ———————————————————— 14
13′ Ampullate septa < 6 µm in width ———————————————————— 15
14. Basidiospores sparsely verrucose ———————————————————— *T. polygonospora*
14′ Basidiospores densely aculeate ———————————————————— *T. mollusca*
15. Subhymenium with short-celled hyphae ———————————————————— 16
15′ Subhymenium with long-celled hyphae ———————————————————— 17
16. Basidiome thin, ochraceous ———————————————————— 18
16′ Basidiome thick, dirty white to buff ———————————————————— *T. rigida*
17. Basidiospores thin-walled ———————————————————— 19
17′ Basidiospores thick-walled ———————————————————— 19
18. Hymenophore with hydnoid ———————————————————— *T. nivea*
18′ Hymenophore without hydnoid ———————————————————— *T. microspora*
19. Basidiospores > 5 µm in length ———————————————————— *T. praefocata*
19′ Basidiospores < 5 µm in length ———————————————————— 20
20. Hymenial surface farinaceous with olivaceous ———————————————————— *T. olivacea*
20′ Hymenial surface odontioid with buff ———————————————————— *T. odontioidea*

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

**Funding:** The research was supported by the National Natural Science Foundation of China (Project No. 32170004, U2102220), Yunnan Fundamental Research Project (Grant No. 202001AS070043), the High-level Talents Program of Yunnan Province (YNQR-QNRC-2018-111), and the Opening Foundation of Yunnan Key Laboratory of Plateau Wetland Conservation, Restoration and Ecological Services (202105AG070002).

**Institutional Review Board Statement:** Not applicable.

**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** Publicly available datasets were analyzed in this study. This data can be found here: [https://www.ncbi.nlm.nih.gov/], accessed on 28 November 2021; [https://www.mycobank.org/page/Simple%20names%20search].

**Conflicts of Interest:** The authors declare no conflict of interest.