Article

New Species of Talaromyces (Trichocomaceae, Eurotiales) from Southwestern China

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Abstract: Species of Talaromyces are cosmopolitan and ubiquitous, and some are of industrial and medicinal importance. Species of Talaromyces have been successively reported in China. During our examinations of samples collected from southwestern China, two new species belonging to Talaromyces sect. Talaromyces were further discovered based on phylogenetic analyses and morphological comparisons. Talaromyces ginkgonis sp. nov., isolated from a partially colonized fruit of Ginkgo biloba, differs from closely-related fungi in the combination of conidia ellipsoidal, smooth and 3.5–4 × 2–3 µm, no growth on CYA at 37 °C and sequence divergences; T. shilinensis sp. nov. is distinguished from its related allies in the combination of smooth conidia, colonies 10–11 mm diameter on CYA at 25 °C and sequence differences. Detailed descriptions and illustrations of the new taxa are given.

Keywords: DNA barcodes; fungal biodiversity; phylogeny; taxonomy

1. Introduction

Species of Talaromyces C.R. Benj. are cosmopolitan and ubiquitous, inhabiting soil, air, indoor environments, rotten food, plant debris, healthy plant as endophytes, insects, and immunodeficient humans. The beneficial and the harmful effects of Talaromyces have been well documented [1].

Seven sections have been established and widely accepted in the genus Talaromyces: Bacilliospori, Helici, Islandici, Purpurei, Subinflati, Talaromyces, and Trachyspermi [2,3]. A novel section was recently proposed as sect. Tenues [4]. A total of 171 species were compiled in the genus and listed in the latest monograph [3]. Furthermore, 26 new taxa were afterwards noted [1,4–12]. Twenty of them are from Asia: T. albisclerotius B.D. Sun et al., T. aspriconidius B.D. Sun et al., T. aureolinus L. Wang, T. bannicus L. Wang, T. brevis B.D. Sun et al., T. chongqingensis X.C. Wang & W.Y. Zhuang, T. guizhouensis B.D. Sun et al., T. gwangjuensis Hyang B. Lee & T.T.T. Nguyen, T. haitouensis L. Wang, T. koreana Hyang B. Lee, T. nanjingensis X.R. Sun et al., T. penicillioides L. Wang, T. rosarhiza H. Zhang & Y.L. Jiang, T. rufus B.D. Sun et al., T. sparsus L. Wang, T. teleomorpha Hyang B. Lee et al., T. tenuis B.D. Sun et al., T. wushanicus X.C. Wang & W.Y. Zhuang, T. yunnanensis Doilom & C.F. Liao, and T. zhenhaiensis L. Wang; five from Europe: T. calidominioluteus Houbraken & Pyrrí, T. gadinianus (C. Ramírez & A.T. Martínez) Houbraken & Socco, T. germanicus Houbraken & Pyrrí, T. pulveris Crous, and T. samsonii (Quintan.) Houbraken & Pyrrí; and one from Africa, T. afric anus Houbraken et al. Talaromyces sect. Talaromyces is the largest section and now with 84 species included.

Southwestern China shows various climates, altitudes, and vegetations, and it is rich in fungal biodiversity. Two species from soil in Chongqing were just described [1]. Along with more samples isolated from the area being examined, two additional new species belonging to Talaromyces sect. Talaromyces were further discovered based on phylogenetic analyses and morphological comparisons. Detailed descriptions and illustrations of the new taxa are provided.
2. Materials and Methods

2.1. Fungal Materials

The new species were associated with fungal (Pseudocosmospora sp.) or plant (Ginkgo biloba L.) materials collected in southwestern China (Sichuan and Yunnan provinces) during 2016–2017. Dried cultures were deposited in the Herbarium Mycologicum Academiae Sinicae (HMAS, Beijing, China), and the living ex-type strains were preserved in the China General Microbiological Culture Collection Center (CGMCC, Beijing, China).

2.2. Morphological Observations

Morphological characterization was conducted following standardized methods [13]. Four standard growth media were used: Czapek yeast autolysate agar (CYA, yeast extract Oxoid, Hampshire, UK), malt extract agar (MEA, Amresco, Solon, OH, USA), yeast extract agar (YES), and potato dextrose agar (PDA). The methods for inoculation, incubation, microscopic examinations, and digital recordings followed our previous studies [1,14–16].

2.3. Molecular Experiments

DNA was extracted from the cultures grown on PDA for 7 days, using the Plant Genomic DNA Kit (DP305, TIANGEN Biotech, Beijing, China). Polymerase chain reaction (PCR) amplifications of the internal transcribed spacer (ITS), beta-tubulin (BenA), calmodulin (CaM), and RNA polymerase II second largest subunit (RPB2) gene regions were conducted with routine methods [1,14–16]. The products were purified and subjected to sequencing on an ABI 3730 DNA Sequencer (Applied Biosystems, Bedford, MA, USA). Although the ITS region is proposed as the universal DNA barcode for fungi, it is not sufficient to distinguish species of Talaromyces. The ITS sequences provided in this study might be helpful for other researchers in case of need.

2.4. Phylogenetic Analyses

The forward and the reverse sequences newly generated in this study were assembled using Seqman v. 7.1.0 (DNASTAR Inc., Madison, WI, USA). The assembled sequences were deposited in GenBank. Sequences used for phylogenetic analyses were listed in Table 1. Sequences of each of the three separate datasets (BenA, CaM, and RPB2) and those that were combined were aligned using MAFFT v. 7.221 [17], and then manually edited in BioEdit v. 7.1.10 [18] and MEGA v. 6.0.6 [19]. Maximum Likelihood (ML) analyses were determined using RAxML-HPC2 [20] on XSEDE 8.2.12 on CIPRES Science Gateway v. 3.3 [21] with the default GTRCAT model. Bayesian Inference (BI) analyses were performed with MrBayes v. 3.2.5 [22]. Appropriate nucleotide substitution models and parameters were determined by Modeltest v. 3.7 [23]. The consensus trees were viewed in FigTree v. 1.3.1 (http://tree.bio.ed.ac.uk/software/%20figtree/ accessed on 1 September 2015). The type species T. trachyspermus of Talaromyces sect. Trachyspermum served as an outgroup.

Table 1. Fungal species and sequences used in phylogenetic analyses of Talaromyces sect. Talaromyces.

| Species          | Strain      | Locality             | Substrate                  | ITS       | BenA      | CaM      | RPB2      |
|------------------|-------------|----------------------|----------------------------|-----------|-----------|-----------|-----------|
| T. aculeatus     | CBS 289.48 T| USA                  | textile                    | KF741995  | KF741929  | KF741975  | MH793099  |
| (Raper & Fennell)Samson et al., 2011 |             |                      |                            |           |           |           |           |
| T. adpressus     | CGMCC 3.18211 T | China: Beijing      | indoor air                 | KU866657  | KU866844  | KU866741  | KU867001  |
| A.J. Chen et al., 2016 |             |                      |                            |           |           |           |           |
| T. alveolaris    | CBS 142379 T | USA                  | human bronchoalveolar lavage | LT558969  | LT559086  | LT795596  | LT795597  |
| Guevara-Suarez et al., 2017 |             |                      |                            |           |           |           |           |
| T. amazonensis   | CBS 140373 T | Colombia             | leaf litter                | KX011509  | KX011490  | KX011502  | MN969186  |
| N. Yilmaz et al., 2016 |             |                      |                            |           |           |           |           |
Table 1. Cont.

| Species                | Strain     | Locality         | Substrate                  | ITS           | BenA       | CaM         | RPB2        |
|------------------------|------------|------------------|----------------------------|---------------|------------|-------------|-------------|
| T. amestolkiae N. Yilmaz et al., 2012 | CBS 132696 T | South Africa     | house dust                 | JX315660      | JX315623   | KF741937    | JX315698    |
| T. angeliæ S.H. Yu et al., 2013 | KACC 46611 T | South Korea      | dried root of Angelica gigas | KF183638      | KF183640   | KJ885259    | KX961275    |
| T. annesophiae Houbraken 2017 | CBS 142939 T | Netherlands      | soil                       | MF574592      | MF590098   | MF590104    | MN969199    |
| T. apiiculatus Samson et al., 2011 | CBS 312.59 T | Japan            | soil                       | JN899375      | KF741916   | KF741950    | KM023287    |
| T. argentinensis Jurjević & S.W. Peterson 2019 | NRRL 28750 T | Ghana            | soil                       | MH793045      | MH792917   | MH792981    | MH793108    |
| T. aspronidius B.D. Sun et al., 2020 | CBS 141835 T | China: Yunnan    | soil                       | MN864274      | MN863343   | MN863320    | MN863332    |
| T. aurantiacus (J.H. Mill. et al.) Samson et al., 2011 | CBS 314.59 T | USA              | soil                       | JN899380      | KF741917   | KF741951    | KX961285    |
| T. aurulinus L. Wang 2021 | CGMCC 3.15865 T | China: Yunnan    | soil                       | MK837953      | MK837937   | MK837945    | MK837961    |
| T. australis Visagie et al., 2015 | CBS 137102 T | Australia        | soil under pasture          | KF741991      | KF741922   | KF741971    | KX961284    |
| T. bannicus L. Wang 2021 | CGMCC 3.15862 T | China: Yunnan    | soil                       | MK837955      | MK837939   | MK837947    | MK837963    |
| T. beijingensis A.J. Chen et al., 2016 | CGMCC 3.18200 T | China: Beijing   | indoor air                 | KU866649      | KU866837   | KU866733    | KU866993    |
| T. bries B.D. Sun et al., 2020 | CBS 141833 T | China: Beijing   | soil                       | MN864269      | MN863338   | MN863315    | MN863328    |
| T. calidicanius (J.L. Chen) Samson et al., 2011 | CBS 112002 T | China: Taiwan    | soil                       | JN899319      | HQ156944   | KF741934    | KM023311    |
| T. californicus Jurjević & S.W. Peterson 2019 | NRRL 58168 T | USA              | air                        | MH793056      | MH792928   | MH792992    | MH793119    |
| T. cnidi S.H. Yu et al., 2013 | KACC 46617 T | South Korea      | dried roots of Cnidium     | KF183639      | KF183641   | KJ885266    | KM023299    |
| T. coprophilus Guevara-Suarez et al., 2020 | CBS 142756 T | Spain            | herbivore dung              | LT899794      | LT898319   | LT899776    | LT899812    |
| T. cucurbitiradicus L. Su & Y.C. Niu 2018 | ACCC 39155 T | China: Beijing   | endophyte from root of Cucurbita moschata | KY053254      | KY053228   | KY053246    | n.a.        |
| T. derxii Takada & Udagawa 1988 | CBS 412.89 T | Japan            | cultivated soil            | JN899327      | JX494306   | KF741959    | KM023282    |
| T. dimorphus X.Z. Jiang & L. Wang 2018 | CGMCC 3.15692 T | China: Hainan    | forest soil                 | KY007095      | KY007111   | KY007103    | KY112593    |
| T. domesticus Jurjević & S.W. Peterson 2019 | NRRL 58121 T | USA              | floor swab                 | MH793055      | MH792927   | MH792991    | MH793118    |
| T. duclauxii (Delacr.) Samson et al., 2011 | CBS 322.48 T | France           | canvas                     | JN899342      | JX091384   | KF741955    | JN121491    |
| T. eucolorcarpius Yaguchi et al., 1999 | CBM PF1203 T | Japan            | soil                       | AB176617      | KJ865733   | KJ885271    | KM023303    |
| T. flavovirens (Duriel & Mont.) Visagie et al., 2012 | CBS 102801 T | Spain            | unknown                    | JN899392      | JX091376   | KF741933    | KX961283    |
Table 1. Cont.

| Species | Strain   | Locality      | Substrate              | ITS           | BenA        | CaM        | RPB2          |
|---------|----------|---------------|------------------------|---------------|-------------|------------|---------------|
| T. flavus (Klöcker) Stolk & Samson 1972 | CBS 310.38 T | New Zealand | unknown               | JN899360      | JX494302   | KF741949   | JF417426      |
| T. francae N. Yilmaz et al., 2016 | CBS 113134 T | Colombia     | leaf litter            | KX011510      | KX011489   | KX011501   | MN969188      |
| T. funiculosus (Thom) Samson et al., 2011 | CBS 272.86 T | India         | Lagenaria vulgaris     | JN899377      | MN969408   | KF741945   | KM023293      |
| T. fuscoiridis Visagie et al., 2015 | CBS 193.69 T | Netherlands  | soil                   | KF741979      | KF741912   | KF741942   | MN969156      |
| T. fusiformis A.J. Chen et al., 2016 | CGMCC 3.18210 T | China: Beijing | indoor air             | KU866656      | KU866843   | KU866740   | KU867000      |
| T. galapagensis Samson & Mahoney 1977 | CBS 751.74 T | Ecuador      | soil under Maytenus obvata | JN899358      | JX091388   | KF741966   | KX961280      |
| T. ginkgonis X.C. Wang & W.Y. Zhuang sp. nov. | 10725 T | China: Sichuan | rotten fruit of Ginkgo biloba | OL638158      | OL689844   | OL689846   | OL689848      |
| T. haistowensis L. Wang 2022 | CGMCC 3.16101 T | China: Jiangsu | riverside soil         | MZ045695      | MZ054634   | MZ054637   | MZ054631      |
| T. indigoticus Takada & Udagawa 1993 | CBS 100534 T | Japan       | soil                   | JN899331      | JX494308   | KF741931   | KX961278      |
| T. intermedium (Apinis) Stolk & Samson 1972 | CBS 152.65 T | UK          | swamp soil             | JN899332      | JX091387   | KJ885290   | KX961282      |
| T. kabadanensis Houbraken et al., 2016 | CBS 139564 T | Iran         | hypersaline soil       | KP851981      | KP851986   | KP851995   | MN969190      |
| T. kendrickii Visagie et al., 2015 | CBS 136666 T | Canada      | forest soil            | KF741987      | KF741921   | KF741967   | MN969158      |
| T. lentulas X.Z. Jiang & L. Wang 2018 | CGMCC 3.15689 T | China: Shandong | soil                  | KY007088      | KY007104   | KY007096   | KY112586      |
| T. liani (Kamyschko) N. Yilmaz et al., 2014 | CBS 225.66 T | China       | soil                   | JN899395      | JX091380   | KJ885257   | KX961277      |
| T. louisianensis Jurjevič & S.W. Peterson 2019 | NRRL 35823 T | USA         | air                    | MH793052      | MH792924   | MH792988   | MH793115      |
| T. macrosporus (Stolk & Samson) Frisvad et al., 1990 | CBS 317.63 T | South Africa | apple juice            | JN899333      | JX091382   | KF741952   | KM023292      |
| T. mae X.Z. Jiang & L. Wang 2018 | CGMCC 3.15690 T | China: Shanghai | forest soil            | KY007090      | KY007106   | KY007098   | KY112588      |
| T. malicola Jurjevič & S.W. Peterson 2019 | NRRL 3724 T | Italy       | rhizosphere of an apple tree | MH909513      | MH909406   | MH909459   | MH909567      |
| T. mangshanicus X.C. Wang & W.Y. Zhuang 2016 | CGMCC 3.18013 T | China: Hunan | soil                   | KX447531      | KX447530   | KX447528   | KX447527      |
| T. marneffei (Segretain et al.) Samson et al., 2011 | CBS 388.87 T | Vietnam     | Rhizomys sinensis      | JN899344      | JX091389   | KF741958   | KM023283      |
| T. muroii Yaguchi et al., 1994 | CBS 756.96 T | China: Taiwan | soil                   | MN431394      | KJ865727   | KJ885274   | KX961276      |
| T. mycothecae R.N. Barbosa et al., 2018 | CBS 142494 T | Brazil      | nest of Melipona scutellaris | MF278326      | LT855561   | LT855564   | LT855567      |
### Table 1. Cont.

| Species                  | Strain          | Locality         | Substrate                          | ITS     | BenA     | CaM     | RPB2     |
|--------------------------|-----------------|------------------|------------------------------------|---------|----------|---------|----------|
| *T. nanjingensis* X.R. Sun et al., 2022 | CCTCC.M 2012167 T | China: Jiangsu | rhizosphere soil of Pinus massoniana | MW130720 | MW147759 | MW147760 | MW147762 |
| *T. neofusisporus* L. Wang 2016 | CGMCC 3.15415 T   | China: Tibet     | leaf sample                        | KP765385 | KP765381 | KP765383 | MN969165 |
| *T. oumae-annae* Visagie et al., 2014 | CBS 138208 T   | South Africa     | house dust                         | KJ775720 | KJ775213 | KJ775425 | KX961281 |
| *T. panamensis* (Samson et al.) Samson et al., 2011 | CBS 128.89 T | Panama           | soil                               | JN899362 | HQ156948 | KF741936 | KM023284 |
| *T. penicillioides* L. Wang 2021 | CGMCC 3.15822 T   | China: Guizhou   | soil                               | MK837956 | MK837940 | MK837948 | MK837964 |
| *T. pinophilus* (Hedgc.) Samson et al., 2011 | CBS 631.66 T | France           | PVC                                | JN899382 | JX091381 | KF741964 | KM023291 |
| *T. pratenensis* Jurjević & S.W. Peterson 2019 | NRRL 62170 T      | USA              | effluent of water treatment plant  | MH793075 | MH792948 | MH793012 | MH793139 |
| *T. primulatus* (Pitt) Samson et al., 2011 | CBS 321.48 T | USA              | unknown                            | JN899317 | JX494305 | KF741954 | KM023294 |
| *T. pseudofuniculosus* Guevara-Suarez et al., 2020 | CBS 143041 T      | Spain            | herbivore dung                     | LT899796 | LT898323 | LT899778 | LT899814 |
| *T. purgamentorum* N. Yilmaz et al., 2016 | CBS 113145 T      | Colombia         | leaf litter                        | KX011504 | KX011487 | KX011500 | MN969189 |
| *T. purpureogenus* (Stoll) Samson et al., 2011 | CBS 286.36 T | unknown          | unknown                            | JN899372 | JX315639 | KF741947 | JX315709 |
| *T. qii* L. Wang 2016 | CGMCC 3.15414 T | China: Tibet    | leaf sample                        | KP765384 | KP765380 | KP765382 | MN969164 |
| *T. rapidus* Guevara-Suarez et al., 2017 | CBS 142382 T | USA             | human bronchoalveolar lavage       | LT558970 | LT559087 | LT795600 | LT795601 |
| *T. rosarhiza* H. Zhang & Y.L. Jiang 2021 | GUCC 190040.1 T | China: Guizhou  | endophyte of Rosa roxburghii      | MZ221603 | MZ333143 | MZ333137 | MZ333141 |
| *T. ruber* (Stoll) N. Yilmaz et al., 2012 | CBS 132704 T | UK              | aircraft fuel tank                 | JX315662 | JX315629 | KF741938 | JX315700 |
| *T. rubicundus* (J.H. Mill. et al.) Samson et al., 2011 | CBS 342.59 T | USA             | soil                              | JN899384 | JX494309 | KF741956 | KM023296 |
| *T. rufus* B.D. Sun et al., 2020 | CBS 141834 T | China: Yunnan   | soil                              | MN864272 | MN863341 | MN863318 | MN863331 |
| *T. sayulitensis* Visagie et al., 2014 | CBS 138204 T | Mexico          | house dust                        | KJ775713 | KJ775206 | KJ775422 | MN969146 |
| *T. shilinensis* X.C. Wang & W.Y. Zhuang sp. nov. | XCW_SN259 T | China: Yunnan  | associated with Pseudocosmospora sp. | OL638159 | OL689845 | OL689847 | OL689849 |
| *T. siamensis* (Manoch & C. Ramírez) Samson et al., 2011 | CBS 475.88 T | Thailand        | forest soil                       | JN899385 | JX091379 | KF741960 | KM023279 |
| *T. soli* Jurjević & S.W. Peterson 2019 | NRRL 62165 T | USA            | soil                              | MH793074 | MH792947 | MH793011 | MH793138 |
| *T. sparsus* L. Wang 2021 | CGMCC 3.16003 T | China: Beijing | soil                              | MT077182 | MT083924 | MT083925 | MT083926 |
Table 1. Cont.

| Species                  | Strain     | Locality             | Substrate              | ITS          | BenA         | CaM          | RPB2        |
|--------------------------|------------|----------------------|------------------------|--------------|--------------|--------------|-------------|
| *T. stellenboschensis*   | CBS 135665 T | South Africa         | soil                   | JX091471     | JX091605     | JX140683     | MN969157    |
| *T. stipitatus* (Thom)   | CBS 375.48 T | USA                  | rotting wood           | JN899348     | KM111288     | KF741957     | KM023280    |
| *T. stollii* N. Yilmaz et al., 2012 | CBS 408.93 T | Netherlands          | AIDS patient           | JX315674     | JX315633     | JX315646     | JX315712    |
| *T. stratoconidium*      | CBS 550.89 T | Cuba                 | leaf litter of *Pachyanthus poirettii* | MN431418     | MN969441     | MN969360     | MT156347    |
| *T. thailandensis*       | CBS 133147 T | Thailand             | forest soil            | JX898041     | JX494294     | KF741940     | KM023307    |
| *T. tumuli* Jurjević & S.W. Peterson 2019 | NRRL 62151 T | USA                  | soil from prairie      | MH793071     | MH792944     | MH793008     | MH793135    |
| *T. verekampii* Visagie et al., 2015 | CBS 500.78 T | Columbia             | soil                   | KF741984     | KF741918     | KF741961     | KX961279    |
| *T. verruculosus* (Peyronel) Samson et al., 2011 | NRRL 1050 T | USA                  | soil                   | KF741994     | KF741928     | KF741944     | KM023306    |
| *T. versatilis* Bridge & Buddie 2013 | IMI 134755 T | UK                   | unknown                | MN431395     | MN969412     | MN969319     | MN969161    |
| *T. viridis* (Stolk & G.F. Orr) Arx 1987 | CBS 114.72 T | Australia            | soil                   | AF285782     | JX494310     | KF741935     | JN121430    |
| *T. viridus* Samson et al., 2011 | CBS 252.87 T | Australia            | soil                   | JN899314     | JX091385     | KF741943     | JF417422    |
| *T. wushanicus* X.C. Wang & W.Y. Zhuang 2021 | CGMCC 3.20481 T | China: Chongqing     | soil                   | MZ356356     | MZ361347     | MZ361354     | MZ361361    |
| *T. xishaensis* X.C. Wang & W.Y. Zhuang 2021 | CGMCC 3.17995 T | China: Hainan        | soil                   | KU644580     | KU644581     | KU644582     | MZ361364    |
| *T. yunnanensis* Doilom & C.F. Liao 2020 | KUMCC 18-0208 T | China: Yunnan        | rhizosphere soil       | MT152339     | MT161683     | MT178251     | n.a.        |
| *T. zhenhaiensis* L. Wang 2022 | CGMCC 3.16102 T | China: Zhejiang      | mudflat soil           | MZ045697     | MZ054636     | MZ054639     | MZ054633    |
| *T. trachyspermus* (Shear) Stolk & Samson 1973 | CBS 373.48 T | USA                  | unknown                | JN899354     | KF114803     | KJ885281     | JF417432    |

GenBank accession numbers in bold indicating the newly generated sequences. Full names of the culture collection centers: ACCC (Agricultural Culture Collection of China); CBS (Centraalbureau voor Schimmelcultures, now Westerdijk Fungal Biodiversity Institute); CCTCC (China Center for Type Culture Collection); CGMCC (China General Microbiological Culture Collection); GUCC (Culture Collection at Department of Plant Pathology, Agriculture College, Guizhou University); IMI (CABI Bioscience); KACC (Korean Agricultural Culture Collection); KUMCC (Kunming Institute of Botany Culture Collection); NRRL (USDA-ARS Culture Collection).

3. Results

3.1. Phylogenetic Analysis

To infer the phylogeny of Talaromyces sect. *Talaromyces* and to determine the positions of the new species, three separate datasets (BenA, CaM and RPB2) and those that were combined were compiled and analyzed. Detailed characteristics of the datasets are listed in Table 2.
Table 2. Detailed characteristics of datasets of *Talaromyces* sect. *Talaromyces*.

| Gene Fragment | No. of Seq. | Length of Alignment (bp) | No. of Variable Sites | No. of Parsimony-Informative Sites | Model for BI |
|---------------|-------------|--------------------------|-----------------------|-----------------------------------|--------------|
| BenA          | 87          | 643                      | 246                   | 200                               | K81uf + I + G |
| CaM           | 87          | 581                      | 305                   | 260                               | SYM + I + G  |
| RPB2          | 85          | 978                      | 359                   | 319                               | TVM + I + G  |
| BenA + CaM + RPB2 | 87          | 2202                     | 910                   | 779                               | GTR + I + G  |

Full names of the used models: GTR + I + G (General Time Reversible model with unequal base frequencies with Invariable sites and Gamma distribution); K81uf + I + G (Kimura 3-parameter model with unequal base frequencies with Invariable sites and Gamma distribution); SYM + I + G (Symmetrical model with Invariable sites and Gamma distribution); TVM + I + G (Transversion model with Invariable sites and Gamma distribution).

In the BenA phylogeny (Figure S1), the strain 10725 was clustered with *T. aspriconidius*, *T. calidicanius*, *T. duclauxii*, *T. flavus*, *T. haitouensis*, and *T. marneffei*; and XCW_SN259 was grouped with *T. kabodanensis* and *T. primulinus*. In the CaM tree (Figure S2), 10725 showed as a distinct lineage, while XCW_SN259 was a sister taxon of *T. primulinus*. In the RPB2 phylogeny (Figure S3), the position of 10725 was similar to that shown in the BenA phylogeny with relatively weak supports, while the sister relationship between *T. primulinus* and XCW_SN259 was confirmed as that in the CaM phylogeny. In the phylogenetic tree of the combined three-gene dataset (Figure 1), the position of 10725 was identical with the BenA and RPB2 trees and that of XCW_SN259 was consistent in all the trees (Figures 1 and S1–S3).

3.2. Taxonomy

*Talaromyces ginkgonis* X.C. Wang & W.Y. Zhuang, sp. nov. Figure 2 Fungal Names: FN570954

Etymology: The specific epithet refers to the substrate of the fungus in *Talaromyces* sect. *Talaromyces*

Typification: CHINA. Sichuan Province, Chengdu City, Dujiangyan City, Mount Qingcheng, 30°54′8″ N 103°33′40″ E, on a partially colonized fruit of *Ginkgo biloba* L., 22 August 2016, Xin-Cun Wang 10725, cultured by Xin-Cun Wang (holotype HMAS 247853, ex-type strain CGMCC 3.20698)

DNA barcodes: ITS OL638158, BenA OL689844, CaM OL689846, RPB2 OL689848

Colony diam., 7 days, 25 °C (unless stated otherwise): CYA 9–13 mm; CYA 37 °C no growth; MEA 19–21 mm; YES 12–13 mm; PDA 15–27 mm

Colony characteristics: On CYA 25 °C, 7 days: Colonies nearly circular, plain; margins moderately wide, fimbriate; mycelia colorless; texture velutinous; sporulation moderately dense; conidia *en masse* greyish green; soluble pigments absent; exudates absent; reverse greenish white.

On MEA 25 °C, 7 days: Colonies nearly circular, plain; margins wide, fimbriate; mycelia white; texture velutinous; sporulation dense; conidia *en masse* vivid green; soluble pigments absent; exudates absent; reverse buff but pink at centers and white at margins.

On YES 25 °C, 7 days: Colonies irregular, plain; margins narrow, fimbriate; mycelia white; texture velutinous; sporulation dense; conidia *en masse* bluish green; soluble pigments absent; exudates absent; reverse buff at centers, green at periphery, and white at margins.

On PDA 25 °C, 7 days: Colonies nearly circular to irregular, plain; margins wide, irregular; mycelia white; texture velutinous; sporulation dense; conidia *en masse* yellowish green to vivid green; soluble pigments absent; exudates absent; reverse usually pink at centers, green to buff at periphery, and white at margins.

Micromorphology: Conidiophores biverticillate, rarely terverticillate; stipes smooth-walled, 150–360 × 2.0–3.0 µm; metulae 3–5, 11.0–22.5 × 2.0–3.5 µm; phialides aceros, tapering into very thin neck, 3–5 per metula, 12.0–15.0 × 2.0–3.0 µm; conidia ellipsoidal to fusiform, smooth, 3.5–4.0 × 2.0–3.0 µm
Figure 1. ML phylogeny of *Talaromyces* sect. *Talaromyces* inferred from the combined (BenA + CaM + RPB2) dataset. Bootstrap values $\geq 70\%$ (left) or posterior probability values $\geq 0.95$ (right) are indicated at nodes. Asterisk denotes 100% bootstrap or 1.00 posterior probability.
Figure 2. Colonial and microscopic morphology of *Talaromyces ginkgonis* (10725). (A) Colony phenotypes (25 °C, 7 days; top row left to right, obverse CYA, MEA, YES, and PDA; bottom row left to right, reverse CYA, MEA, YES, and PDA); (B–F) Conidiophores; (G) Conidia. Bars: B = 15 μm, applies to C; D = 12.5 μm; E = 10 μm, applies to F and G.
Note: This species is phylogenetically related to *T. aspriconidius*, *T. calidicanius*, *T. duclauxii*, *T. flavus*, *T. haitouensis*, and *T. marneffei*, with strong support in the combined three-gene tree (Figure 1). Morphologically, it differs from *T. aspriconidius* and *T. calidicanius* in the smooth conidia; from *T. marneffei* in the ellipsoidal conidia; and from *T. duclauxii*, *T. flavus*, and *T. haitouensis* in the slower growth rate on MEA and YES at 25 °C (Table 3).

Table 3. Morphological comparisons of new *Talaromyces* species and their closely related species.

| Species          | CYA 25 °C (mm) | CYA 37 °C (mm) | MEA (mm) | YES (mm) | Conidiophore | Conidia Shape | Conidia Wall          | Conidia Size (µm) | Reference       |
|------------------|----------------|----------------|----------|----------|---------------|---------------|-----------------------|--------------------|-----------------|
| *T. aspriconidius* | 22–23          | 22–23          | 36–37    | 28–29    | biverticillate | globose        | strikingly roughened   | 3–4                | [4]             |
| *T. calidicanius* | 27–30          | no growth      | 47–48    | 40–41    | biverticillate | ellipsoidal to fusiform | finely rough with spiral striations | 2.5–4.5 × 2–3     | [2]             |
| *T. duclauxii*    | 25–27          | 3–4            | 48–50    | 43–44    | biverticillate | ellipsoidal    | smooth to finely rough | 3–4 × 1.5–3.5     | [2]             |
| *T. flavus*       | 9–10           | 19–20          | 31–32    | 24–26    | monoverticillate | ellipsoidal    | smooth                | 2–3 × 1.5–2.5     | [2]             |
| *T. haitouensis*  | 22–25          | 18–20          | 48–51    | 25–28    | biverticillate | pyriform to ellipsoidal | smooth                | 2.5–3 × 2–2.5     | [10]            |
| *T. marneffei*    | 13–25          | 5–10           | 15–27    | 17–25    | mono- to biverticillate | subglobose | smooth                | 2.4 × 2–3         | [2]             |
| *T. ginkgonis*    | 9–13           | no growth      | 19–21    | 12–13    | biverticillate | ellipsoidal to fusiform | smooth                | 3.5–4 × 2–3       | This study       |
| *T. kahodenensis* | 15–25          | no growth      | 37–44    | 28–35    | biverticillate | ovoidal to fusiform | finely rough with spiral striations | 2.5–3.5 × 1.5–2.5 | [24]            |
| *T. primulinus*   | 5–6            | no growth      | 20–25    | 8–10     | biverticillate | ellipsoidal to fusiform | smooth to finely rough | 2–4 × 1.5–3       | [2]             |
| *T. shilinensis*  | 10–11          | no growth      | 36–38    | 18–19    | biverticillate | ellipsoidal to broad fusiform | smooth                | 2.5–3.5 × 2–2.5   | This study       |

*Talaromyces shilinensis* X.C. Wang & W.Y. Zhuang, sp. nov. Figure 3

Fungal Names: FN570955

Etymology: The specific epithet refers to the type locality in *Talaromyces* sect. *Talaromyces*

Typification: CHINA. Yunnan Province, Kunming City, Shilin Yi Autonomous County, Gui Mountain National Forest Park, 24°38′15″ N 103°35′49″ E, isolated from a rotten twig associated with ascomata of *Pseudocosmospora* sp., 26 September 2017, Yi Zhang, Yu-Bo Zhang and Huan-Di Zheng 11,825, cultured by Yu-Bo Zhang, XCW_SN259 (holotype HMAS 247854, ex-type strain CGMCC 3.20699)

DNA barcodes: ITS OL638159, BenA OL689845, CaM OL689847, RPB2 OL689849

Colony diam., 7 days, 25 °C (unless stated otherwise): CYA 10–11 mm; CYA 37 °C no growth; MEA 36–38 mm; YES 18–19 mm; PDA 35–37 mm

Colony characteristics: On CYA 25 °C, 7 days: Colonies nearly circular, plain; margins wide, entire; mycelia colorless; texture velutinous; sporulation sparse; conidia *en masse* light yellowish green; soluble pigments absent; exudates absent; reverse almost colorless but light brown at centers

On MEA 25 °C, 7 days: Colonies nearly circular, plain, slightly protuberant at centers; margins very wide, entire; mycelia colorless and white; texture velutinous, funiculose at central areas; sporulation dense; conidia *en masse* dull green; soluble pigments absent; exudates absent; reverse buff but pink to reddish brown at centers.

On YES 25 °C, 7 days: Colonies nearly circular, plain, slightly protuberant at centers; margins moderately wide, entire; mycelia colorless; texture velutinous; sporulation dense; conidia *en masse* greyish green; soluble pigments absent; exudates absent; reverse buff but light brown at centers.
Figure 3. Colonial and microscopic morphology of *Talaromyces shilinensis* (XCW_SN259). (A) Colony phenotypes (25 °C, 7 days; top row left to right, obverse CYA, MEA, YES, and PDA; bottom row left to right, reverse CYA, MEA, YES, and PDA); (B–F) Conidiophores; (G) Conidia. Bars: B = 15 μm; C = 12.5 μm; D = 10 μm, applies to E and G; F = 7.5 μm.
On PDA 25 °C, 7 days: Colonies nearly circular, plain, slightly protuberant at centers; margins very wide, entire; mycelia colorless; texture velutinous; sporulation dense; conidia en masse dull green; soluble pigments absent; exudates absent; reverse white, pink to reddish brown at centers.

Micromorphology: Conidiophores biverticillate, rarely quaterverticillate; stipes smooth-walled, 50–110 × 2.0–3.0 µm; metulae 4–6, 8.5–12.5 × 2.5–3.0 µm; phialides acerose, tapering into very thin neck, 4–5 per metula, 9.0–13.0 × 1.8–2.5 µm; conidia ellipsoidal to broad-fusiform, smooth, 2.5–3.5 × 2.0–2.5 µm

Note: This species is a sister of *T. primulinus* with strong support in the phylogenies inferred from all datasets (Figure 1 and Figures S1–S3), and it also related to *T. kabodanensis* in the BenA and combined trees (Figure 1 and Figure S1). It has 27 pairwise nucleotide differences from *T. primulinus* and 23 bp from *T. kabodanensis* in the BenA dataset; 29 nucleotide differences from *T. primulinus* in CaM; and 45 nucleotide differences from *T. primulinus* in RPB2. Morphologically, it differs from *T. kabodanensis* in the smooth conidia and from *T. primulinus* in the faster growth rate on CYA, MEA, and YES at 25 °C (Table 3).

4. Discussion

Forty-three species of the *Talaromyces* have been reported as new to science based on materials collected from China. They are distributed all over the country, especially in southwestern regions, for example, *T. chongqingensis* and *T. wushanicus* are from Chongqing, *T. albisclerotius*, *T. guizhouensis*, *T. penicillioides*, *T. resinae*, *T. rosarhiza*, and *T. tenuis* are from Guizhou, *T. ginkgonis* is from Sichuan, *T. neofusisporas* and *T. qi* are from Tibet, and *T. aspriconidius*, *T. aureolinus*, *T. bannicus*, *T. rufus*, *T. shiliensis*, and *T. yunnanensis* are from Yunnan [1,4,6,9–11]. This proves that southwestern China is one of the global biodiversity hotspots. In northern China, 13 species were recorded from Beijing; in eastern parts of the country, 9 were from Jiangsu, Shandong, Shanghai, Taiwan, and Zhejiang; and a few species were occasionally found in the south, central, and northeast. This might be due to the frequency of investigations, climates, richness of plants, as well as human activities. We certainly expect to discover more species of the group in unexplored regions and even in surveyed areas in different seasons.

Along with the joining of the two new species, *Talaromyces* sect. *Talaromyces* currently possesses up to 86 species around the world. Forty species were originally described as being from Asia, of which 29 are from China, four are from Japan, two are from South Korea and Thailand, respectively, and only one was reported in India, Iran, and Vietnam; 18 taxa are from North America, including 14 from the USA and a single one from Canada, Cuba, Mexico, and Panama; 12 species are distributed in Europe (France, Italy, Netherlands, Spain, UK); six are reported in South America (Brazil, Colombia, and Ecuador); five are from Africa (Ghana and South Africa); and four are from Oceania (Australia and New Zealand). Concerning the known distribution of the genus, one may easily imagine that the biodiversity of *Talaromyces* may have been underrated, although it is well recognized in areas of East Asia and North America, intensive excursions covering a broad range of areas in the world should be suggested to have a better understanding of the biodiversity of this group.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/jof8070647/s1, Figure S1: ML phylogeny of *Talaromyces* sect. *Talaromyces* inferred from BenA dataset. Bootstrap values ≥70% (left) or posterior probability values ≥0.95 (right) are indicated at nodes. Asterisk denotes 100% bootstrap or 1.00 posterior probability; Figure S2: ML phylogeny of *Talaromyces* sect. *Talaromyces* inferred from CaM dataset. Bootstrap values ≥70% (left) or posterior probability values ≥0.95 (right) are indicated at nodes. Asterisk denotes 100% bootstrap or 1.00 posterior probability; Figure S3: ML phylogeny of *Talaromyces* sect. *Talaromyces* inferred from RPB2 dataset. Bootstrap values ≥70% (left) or posterior probability values ≥0.95 (right) are indicated at nodes. Asterisk denotes 100% bootstrap or 1.00 posterior probability.
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Conflicts of Interest: The authors declare no conflict of interest.

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