Studies in Mycology

New *Talaromyces* species from indoor environments in China

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Abstract: Talaromyces contains both asexual and sexually reproducing species. This genus is divided in seven sections and currently has 105 accepted species. In this study we investigated the Talaromyces isolates that were obtained during a study of indoor air collected in Beijing, China. These indoor Talaromyces strains are resolved in four sections, seven of them are identified as *T. islandicus*, *T. aurantiacus*, *T. siamensis* and *T. alboverticillius* according to BenA sequences, while 14 isolates have divergent sequences and are described here as nine new species. The new species are placed in four sections, namely sections *Helici*, *Islandici*, Talaromyces and *Trachyspermi*. They are described based on sequence data (ITS, BenA, CaM and RPB2) in combination with phenotypic and exo-lipid characters. Morphological descriptions and notes for distinguishing similar species are provided for each new species. The recently described *T. rubrifaciens* is synonymised with *T. alboverticillius* based on presented phylogenetic results.

Key words: Eurotiales, Indoor air, Polyphasic taxonomy, Talaromyces alboverticillius.


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INTRODUCTION

The genus *Talaromyces* was introduced by Benjamin (1955) to accommodate teleomorphic *Penicillium* species with soft ascomata, which are usually white or yellowish and surrounded by multiple layers of interwoven hyphae. Phylogenetic studies revealed that *Penicillium* was polyphyletic and Talaromyces species and members of *Penicillium* subgenus *Biverticillum* belonged in a clade distinct from *Penicillium sensu stricto* (LoBuglio et al. 1993, LoBuglio & Taylor 1993, Berbee et al. 1995, Ogawa et al. 1997, Ogawa & Sugiyama 2000, Wang & Zhuang 2007, Houbraken & Samson 2011). Following the concept of nomenclatural priority and single name nomenclature, Samson et al. (2011) subsequently transferred all accepted species of *Penicillium subgenus Biverticillum* to *Talaromyces*.


In the last decades the interest in indoor mycobiota has grown because of their adverse health effects in humans (Samson et al. 1994, Prezant et al. 2008, Flannigan et al. 2011, Adan & Samson 2011), Samson et al. (2010) listed 100 common indoor fungal species which belong to 47 genera. *Talaromyces funiculosus*, *T. rugulosus* and *T. wortmanni* are among the most frequently encountered species in indoor environments. Visagie et al. (2014) analysed Talaromyces species from dust samples collected from nine countries, and based on ITS and BenA sequences, 18 *Talaromyces* species were identified including three new species: *T. oumae-annae*, *T. sayulitensis* and *T. yelensis*.

Various studies investigated the mycobiota of indoor environments in China. However, most surveys focused on total fungal counts and identified fungi to genera or species level based on phenotypic characters (Wu et al. 1982, Wu et al. 2000, Fang et al. 2005, Li et al. 2006, Si et al. 2007, Liu et al. 2014). Molecular based identifications are occasionally being performed and Luo et al. (2016) reported *T. rubrifaciens* as a new taxon from heating, ventilation and air conditioning systems in China. During surveys of the mycobiota of indoor air in Beijing, China, numerous strains belonging to *Aspergillus*, *Cladosporium*, *Chaetomium*, *Penicillium* and other genera were isolated. Among them, 14 *Talaromyces* isolates could not be assigned to any described species. These strains are described here as nine new species based on multi-gene phylogenies based partial ITS, β-tubulin (BenA), calmodulin (CaM) and RNA polymerase II
second largest subunit (RPB2) gene sequences, phenotype and extrolite data.

**MATERIAL AND METHODS**

**Isolates**

Isolates used in this study were collected by the sedimentation plate method on various media in the vicinity of air-conditioning exhausts. These strains were subsequently deposited in the China General Microbiological Culture Collection Centre (CGMCC), Beijing, China. In addition, isolates from the culture collection of CBS-KNAW Fungal Biodiversity Centre (CBS), Utrecht, the Netherlands, and working collection of the Applied and Industrial Mycology department (DTO) housed at CBS-KNAW were used. An overview of strains is given in Table 1. For other strains used in the phylogenetic analyses, readers are referred to Yilmaz *et al.* (2014, 2016a, b), Visagie *et al.* (2014, 2015), Luo *et al.* (2016), Romero *et al.* (2016), and Wang *et al.* (2016).

**DNA extraction, PCR amplification and sequencing**

Strains were grown for 1 wk on malt extract agar (MEA, Oxoid malt) prior to DNA extraction. DNA was extracted using the Ultradean™ Microbial DNA isolation Kit (MoBio, Solana Beach, U.S.A.) and stored at −20 °C. The ITS, BenA, CaM, and RPB2 genes were amplified and sequenced using methods and primers previously described (Houbraken & Samson 2011, Yilmaz *et al.* 2014).

**Phylogenetic analysis**

A multi-gene phylogeny combining ITS, BenA, CaM and RPB2 sequences was used to accommodate the new species of *Talaromyces* in the different sections. Prior combining the datasets, single gene alignments were generated with MAFFT v. 7 (Katoh & Standley 2013), and then trimmed at both ends. Aligned datasets were subsequently concatenated using Mesquite v. 3.1 (Maddison & Maddison 2016). For each section, single gene phylogenies were generated to determine the phylogenetic relationship among species. The most suitable substitution model was determined using FindModel (Posada & Crandall 1998). Bayesian analyses were performed with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003). The sample frequency was set to 100 and the first 25 % of trees were removed as burn-in. Maximum likelihood analyses including 500 bootstrap replicates were run using RAxML BlackBox web-server (Gamma model of rate heterogeneity) (Stamatakis *et al.* 2008). *Trichocoma paradoxa* (CBS 788.83) was used as an outgroup in the *Talaromyces* phylogeny. Sequences of *T. ucranicus* (CBS 182.67), *T. subinflatus* (CBS 652.95), *T. dendriticus* (CBS 660.80) and *T. purpurogenus* (CBS 286.36) were used as outgroups in the *Talaromyces* sections *Helici, Islandici, Talaromyces* and *Trachyspermii* respectively. The resulting trees were visualised with FigTree v1.4.2 and edited in Adobe Illustrator CS5. Bayesian inference (BI) posterior probabilities (pp) values and bootstrap (bs) values are labelled on nodes. Values less than 0.95 pp and 70 % bs are not shown. Branches with posterior probability values of 1 and bootstrap values higher than 95 % are thickened. Newly obtained sequences were deposited in GenBank.

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**Table 1. Indoor *Talaromyces* strains used in this study.**

<table>
<thead>
<tr>
<th>Species name</th>
<th>Section</th>
<th>Strain no.</th>
<th>GenBank accession nr.</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Talaromyces diversiformis</em></td>
<td><em>Helici</em></td>
<td>CBS 141931T = CGMCC3.18204 = DTO 317-E3</td>
<td>KX961215</td>
</tr>
<tr>
<td>T. reverso-olivaceus</td>
<td><em>Helici</em></td>
<td>CBS 140672T = CGMCC3.18195 = DTO 317-C3</td>
<td>KX961216</td>
</tr>
<tr>
<td>T. reverso-olivaceus</td>
<td><em>Helici</em></td>
<td>CGMCC3.18216 = DTO 318-G2</td>
<td>KX961217</td>
</tr>
<tr>
<td>T. ceninus</td>
<td><em>Islandici</em></td>
<td>CBS 140622T = CGMCC3.18212 = DTO 318-A2</td>
<td>KX961218</td>
</tr>
<tr>
<td>T. chlamydosporus</td>
<td><em>Islandici</em></td>
<td>CBS 140635 = CGMCC3.18199 = DTO 317-D5</td>
<td>KX961219</td>
</tr>
<tr>
<td>T. islandicus</td>
<td><em>Islandici</em></td>
<td>CGMCC3.18196 = DTO 317-C5</td>
<td>KX961220</td>
</tr>
<tr>
<td>T. neorugulosus</td>
<td><em>Islandici</em></td>
<td>CBS 140623T = CGMCC3.18215 = DTO 318-A8</td>
<td>KX961221</td>
</tr>
<tr>
<td>T. adpressus</td>
<td><em>Talaromyces</em></td>
<td>CBS 140620T = CGMCC3.18211 = DTO 317-G4</td>
<td>KX961222</td>
</tr>
<tr>
<td>T. aurantiiacus</td>
<td><em>Talaromyces</em></td>
<td>CGMCC3.18198 = DTO 317-C9</td>
<td>KX961223</td>
</tr>
<tr>
<td>T. beijingensis</td>
<td><em>Talaromyces</em></td>
<td>CBS 140617T = CGMCC3.18202 = DTO 317-D6</td>
<td>KX961224</td>
</tr>
<tr>
<td>T. beijingersis</td>
<td><em>Talaromyces</em></td>
<td>CGMCC3.18201 = DTO 317-D9</td>
<td>KX961225</td>
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<tr>
<td>T. beijengensis</td>
<td><em>Talaromyces</em></td>
<td>CGMCC3.18202 = DTO 317-E1</td>
<td>KX961226</td>
</tr>
<tr>
<td>T. beijengensis</td>
<td><em>Talaromyces</em></td>
<td>CBS 140619 = CGMCC3.18208 = DTO 317-E9</td>
<td>KX961227</td>
</tr>
<tr>
<td>T. fusiformis</td>
<td><em>Talaromyces</em></td>
<td>CBS 140637 = CGMCC3.18210 = DTO 317-F4</td>
<td>KX961228</td>
</tr>
<tr>
<td>T. fusiformis</td>
<td><em>Talaromyces</em></td>
<td>CBS 140636 = CGMCC3.18209 = DTO 317-F3</td>
<td>KX961229</td>
</tr>
<tr>
<td>T. siamensis</td>
<td><em>Talaromyces</em></td>
<td>CGMCC3.18214 = DTO 318-B6</td>
<td>KX961230</td>
</tr>
<tr>
<td>T. aerius</td>
<td><em>Trachyspermii</em></td>
<td>CBS 140611T = CGMCC3.18197 = DTO 317-C7</td>
<td>KX961231</td>
</tr>
<tr>
<td>T. albobiverticillus</td>
<td><em>Trachyspermii</em></td>
<td>CGMCC3.18203 = DTO 317-E2</td>
<td>KX961232</td>
</tr>
<tr>
<td>T. albobiverticillus</td>
<td><em>Trachyspermii</em></td>
<td>CGMCC3.18205 = DTO 317-E4</td>
<td>KX961233</td>
</tr>
<tr>
<td>T. albobiverticillus</td>
<td><em>Trachyspermii</em></td>
<td>CGMCC3.18206 = DTO 317-E5</td>
<td>KX961234</td>
</tr>
<tr>
<td>T. albobiverticillus</td>
<td><em>Trachyspermii</em></td>
<td>CGMCC3.18207 = DTO 317-E6</td>
<td>KX961235</td>
</tr>
</tbody>
</table>
Morphological analysis

Macroscopic characters were studied on Czapek yeast autolysate agar (CYA), CYA supplemented with 5 % NaCl (CYAS), yeast extract sucrose agar (YES), creatine sucrose agar (CREA), dichloran 18 % glycerol agar (DG18), oatmeal agar (OA) and malt extract agar (MEA; Oxoid malt) (Samson et al. 2010). Isolates were inoculated at three points on 90 mm Petri dishes and incubated for 7 d at 25 °C in darkness. Additional CYA plates were incubated at 30 and 37 °C, while additional MEA plates were incubated at 30 °C. After 7 d of incubation, colony diameters were recorded. The colony texture, degree of sporulation, obverse and reverse colony colours, the production of soluble pigments and exudates were noted. Acid production on CREA is indicated by a change in the pH sensitive bromocresol purple dye, from a purple to yellow colour in media surrounding colonies. For ascoma production, OA, MEA and CYA plates were incubated for up to four weeks.

Microscope preparations were made from 1 wk old colonies grown on MEA and ascomata, ascii and ascospores were observed on OA. Lactic acid (60 %) was used as mounting fluid and 96 % ethanol was applied to remove the excess of condida. A Zeiss Stereo Discovery V20 dissecting microscope and Zeiss AX10 Imager A2 light microscope equipped with Nikon DS-R2 cameras and software NIS-Elements D v4.50 were used to capture digital images.

Extrolites analysis

For extrolite extractions, three agar plugs (6 mm diam) were taken from colonies grown on CYA and YES (incubated for 1 wk at 25 °C), and combined in one Eppendorf vial. In addition, three plugs were taken from colonies grown on OA and Blakeslee’s MEA (Blakeslee 1915), and combined in another Eppendorf vial. The plugs were ultrasonicated in ethylacetate/isopropanol (3:1) with 1 % formic acid for 50 min. After extraction, the liquid was transferred to another Eppendorf vial and thereafter evaporated. The remaining dry fraction was redissolved in 300 μl methanol and ultrasonicated for 10 min. The extract was centrifuged at 13 400 rpm in an Eppendorf centrifuge (Minispin), transferred to a V-formed vial with a 300 μl capacity, and subsequently injected into an Ultra high performance liquid chromatograph (UHPLC) via an autosampler. The Liquid chromatograph was a Dionex Ultimate 3000 UHPLC connected to a Dionex 3000 RS Diode array detector and an Agilent 1321A fluorescence detector. The column used was a Poroshell Phenylix 120 (100 mm x 2.1 mm) column with 2.7 μm particles (Agilent). The UHPLC gradient, injection volume and other conditions are given in Klitgaard et al. (2014). Standards of rugulosin, skyrin, rugulovasine, duclauxin and other Talaromyces derived extrolites were used as standards in the comparison of retention times and UV spectra.

RESULTS

Phylogeny

The phylogenetic relationships among the species in Talaromyces were studied using concatenated sequence data of four loci, ITS, BenA, CaM and RPB2. The total length of the aligned dataset was 2420 characters, and the single gene datasets consisted of 500, 493, 624 and 803 characters for ITS, BenA, CaM and RPB2 respectively. The most optimal models for the concatenated and the single gene phylogenies are shown in Table 2. The multi-gene analysis reveals the presence of seven well-supported lineages in Talaromyces (Fig. 1), and these lineages correspond with sections Bacillispori, Helici, Islandici, Purpurei, Subinflati, Talaromyces, and Trachyspermi. Our indoor Talaromyces strains are resolved in four sections, seven of them are identified as T. islandicus, T. aurantiacus, T. siamensis and T. alboverticillatus based on BenA sequences, while 14 of them are described as nine new species: T. diversiformis and T. reverso-olivaceus in section Helici, T. chlamydosporus, T. cerinus and T. neorugulosus in section Islandici, T. beijingensis, T. fusiformis and T. adpressus in section Talaromyces, and T. aerius in section Trachyspermi.

Talaromyces diversiformis and T. reverso-olivaceus, both belonging to section Helici are in the combined analysis related with T. aerugineus and T. boninensis, respectively (Fig. 1). Talaromyces reverso-olivaceus is in the BenA, CaM and RPB2 analysis is a sister species of T. boninensis (>0.98 pp; >98 % bs). The phylogenetic relationship of T. diversiformis is more difficult to determine based on the single gene phylogenies and this species appears to be related to T. aerugineus and T. bohemicus in the BenA, CaM and RPB2 phylogenies (>0.98 pp; >70 % bs). The ITS phylogram is poorly resolved. The T. reverso-olivaceus isolates cluster together (1 pp; 98 % bs) and these isolates are on a well-supported branch together with T. helicus and T. boninensis. The relationship of T. diversiformis is unresolved in the ITS phylogram (Fig. 2, Suppl. 1–3). Talaromyces chlamydosporus and T. cerinus are both members of section Islandici and are, with exception in the CaM analysis, related with high statistical support to T. subaurantiacus (Figs 1, 3, Suppl. 4–6). The multi-gene phylogeny and the ITS and RPB2 phylogenies show that T. neorugulosus is most closely related to T. rugulosus. This species is unresolved in the CaM analysis, and related to T. rugulosus, T. infraolivaceus, T. atricola and T. acaricola in the

Table 2. Sequence data sets and models used in phylogeny.

<table>
<thead>
<tr>
<th>Section</th>
<th>ITS (bp)</th>
<th>Substitution model</th>
<th>BenA (bp)</th>
<th>Substitution model</th>
<th>CaM (bp)</th>
<th>Substitution model</th>
<th>RPB2 (bp)</th>
<th>Substitution model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview Talaromyces</td>
<td>500</td>
<td>GTR+G</td>
<td>493</td>
<td>GTR+G</td>
<td>624</td>
<td>K2P+G</td>
<td>803</td>
<td>GTR+G</td>
</tr>
<tr>
<td>Section Helici</td>
<td>464</td>
<td>HKY+G</td>
<td>427</td>
<td>HKY+G</td>
<td>550</td>
<td>GTR+G</td>
<td>852</td>
<td>GTR+G</td>
</tr>
<tr>
<td>Section Islandici</td>
<td>502</td>
<td>GTR+G</td>
<td>474</td>
<td>GTR+G</td>
<td>458</td>
<td>K2P+G</td>
<td>803</td>
<td>GTR+G</td>
</tr>
<tr>
<td>Section Talaromyces</td>
<td>469</td>
<td>GTR+G</td>
<td>402</td>
<td>HKY+G</td>
<td>523</td>
<td>GTR+G</td>
<td>779</td>
<td>HKY+G</td>
</tr>
<tr>
<td>Section Trachyspermi</td>
<td>478</td>
<td>GTR+G</td>
<td>388</td>
<td>HKY+G</td>
<td>491</td>
<td>K2P+G</td>
<td>680</td>
<td>GTR+G</td>
</tr>
</tbody>
</table>
Strains of *T. beijingensis* cluster together in a single clade, separate from other sect. *Talaromyces* species. The relationship of this species with other species is in all analysis (including the combined analysis) unresolved. Both strains of *T. fusiformis* form a single, separate clade in the four gene phylogenies, and they are a sister clade of *T. aurantiacus*. *Talaromyces adpressus* is in BenA phylogeny with statistical support related to *T. sayulitensis* (0.99 pp; 98 % bs), while it clusters with *T. pinophilus* in the CaM (1.00 pp; 98 % bs). The RPB2 sequence of *T. sayulitensis* is unavailable thus cannot be compared here (Fig. 4, Suppl. 7–9). In section *Trachyspermi*, *T. aeuris* clusters with statistical support with *T. solicola* in the three (CaM, ITS and RPB2) of the four single gene phylogenies (Fig. 5, Suppl. 10–12).
Identification

All nine new species described here can be identified via BenA, CaM and RPB2 sequences. Seven of them have unique ITS sequences. Talaromyces neorugulosus cannot be separated from T. rugulosus (strain CBS 285.37 and CBS 378.48) by its ITS sequence. Talaromyces diversiformis is similar to T. aerugineus (99.8 % similarity, 447/448 bp) and T. ryukyuensis (99.1 % similarity, 445/449 bp) by ITS sequences.
**TAXONOMY**

*Talaromyces aerius* A.J. Chen, Frisvad & Samson, *sp. nov.* MycoBank MB817398. Fig. 6.

**Etymology**: Latin, *aerius* refers to its origin, isolated from indoor air.

**Diagnosis**: This species produces smooth, ellipsoidal conidia; does not produce red pigments or red exudates on any of the used media.

**In**: *Talaromyces* section *Trachyspermi*

**Typus**: China, Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22506, culture ex-type CBS 140611 = CGMCC3.18197 = DTO 317-C7).

**ITS barcode**: KU866647. (Alternative markers: BenA = KU866835; CaM = KU866731; RPB2 = KU866991).

**Colony diam, 7 d (mm)**: CYA 17–18; CYA 30 °C 20–22; CYA 37 °C No growth; MEA 32–33; MEA 30 °C 34–36; DG18 11–12; CYAS 2–3; OA 28–30; CREA 2–4; YES 21–22.

**Colony characters**: CYA, 25 °C, 7 d: Colonies moderately deep, crateriform; margins entire; mycelium white; texture floccose; sporulation sparse, conidia *en masse* greyish green to olive green; soluble pigments absent; exudates absent; reverse saffron. MEA, 25 °C, 7 d: Colonies low, plane; margins entire; mycelium white; texture velvety; sporulation dense, conidia *en masse* greyish green; soluble pigments absent; exudates absent; reverse saffron. OA, 25 °C, 7 d: Colonies low, plane; mycelium white and light yellow; texture velvety; sporulation dense, conidia *en masse* greyish green to yellow green; soluble pigments absent; exudates absent; reverse purplish red at centre, yellowish brown at edge. CREA, 25 °C, 7 d: Acid production absent.

**Micromorphology**: Conidiophores biverticillate, sometimes with extra subterminal branches; stipes smooth, 70–130 × 3–4 μm, extra branches 22–34 μm; metulae 3–5, divergent, 8–14 × 3–4 μm; phialides 4–6, acerose, 9–12 × 2–4 μm; conidia smooth, ellipsoidal, 2–3.5(–4.5) × 2–3 μm. Ascomata not observed.

**Extrolites**: Mitrorubrinic acid.

**Distinguishing characters**: *Talaromyces aerius* is phylogenetically related to *T. solicola*, *T. albobiverticillius* and *T. erythromellis*. *Talaromyces solicola* produces rough conidia, *T. albobiverticillius* produces intense red soluble pigment on CYA and *T. erythromellis* grows restrictedly on CYA, MEA, YES and OA, and produces red exudates on MEA.

*Talaromyces adpressus* A.J. Chen, Frisvad & Samson, *sp. nov.* MycoBank MB817397. Fig. 7.
**Etymology**: Latin, *adpressus* refers to its appressed metulae.

**Diagnosis**: This species produces white mycelium on MEA and OA; does not produce acid compounds on CREA and produces smooth, subglobose to ellipsoidal conidia measuring 2.5–4.5(–5) × 2–3.5 μm.

In: *Talaromyces* section *Talaromyces*

**Typus**: China, Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22508, culture ex-type CBS 140617 = CGMCC3. 18200 = D30 317-G4).

**ITS barcode**: KU866657. (*Alternative markers: BenA = KU866844; CaM = KU866741; RPB2 = KU867001*).

**Colony diam, 7 d (mm)**:
- CYA 32–33; CYA 30 °C 45–46; CYA 37 °C 35–38; MEA 42–43; MEA 30 °C 57–58; DG18 11–12; CYAS 1–2; OA 41–42; CREA 21–22; YES 42–43.

**Colony characters**:
- CYA, 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium white; texture velvety; sporulation dense, conidia smooth, ellipsoidal to fusiform, 3–4 × 2–3.5 μm; Ascomata not observed.

**Extroiltes**: Duclauxin, rugulosavine A.

**Distinguishing characters**: *Talaromyces adpressus* is closely related to *T. sayulitensis* and *T. pinophilus*; however, the latter two species produce large amounts of acid compounds on CREA. The micromorphology of these three species is identical, but they can be phylogenetically distinguished.

**Talaromyces beijingensis** A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB817395. Fig. 8.

**Etymology**: Latin, *beijingensis* refers to its origin, isolated from Beijing, China.

**Diagnosis**: This species grows moderately on CYA and MEA, the colony reverse on CYA and MEA is peach coloured, and it produces smooth, subglobose to fusiform conidia.

In: *Talaromyces* section *Talaromyces*

**Typus**: China, Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22508, culture ex-type CBS 140617 = CGMCC3. 18200 = D30 317-G4).

**ITS barcode**: KU866649. (*Alternative markers: BenA = KU866837; CaM = KU866733; RPB2 = KU866993*).

**Colony diam, 7 d (mm)**:

**Colony characters**:
- CYA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture velvety; sporulation dense, conidia en masse yellow green to greyish green; soluble pigments absent; exudates clear droplets; reverse peach fading into rosy buff.
- MEA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture velvety; sporulation dense, conidia en masse dark green; soluble pigments absent; exudates clear droplets; reverse peach fading into yellowish brown.
- YES, 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium white; texture velvety; sporulation dense, conidia en masse greyish green to dark green; soluble pigments absent; exudates clear droplets; reverse orange brown.
- OA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture velvety; sporulation dense, conidia en masse greyish green; soluble pigments absent; exudates clear droplets; reverse light yellow at centre, cream white at edge.

**Micromorphology**: Conidiophores biverticillate, with symmetrical subterminal branches; stipes smooth, 91–175 × 3–4 μm, extra branches 16–20 μm; metulae 3–4, acerose, 11–14 × 2–4 μm; phialides 2–4, acerose, 9–12 × 2–3 μm; conidia smooth, ellipsoidal to fusiform, 3–4 × 2–3 μm. Ascomata not observed.

**Extroiltes**: Duclauxin.

**Distinguishing characters**: Phylogenetically *T. beijingensis* belongs to section *Talaromyces*, but it cannot be assigned to any section members. Morphologically this species resembles *T. flavovirens* in having moderately growing, velvety, yellow green to greyish green colonies on CYA and MEA, biverticillate conidiophores and ellipsoidal to fusiform conidia. *Talaromyces flavovirens* can be differentiated by the production of synnemata (up to 750 μm) and yellow mycelium.

**Talaromyces cerinus** A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB817393. Fig. 9.
Section Islandici BenA
Section Talaromyces BenA

Fig. 3. Phylogeny of BenA for species classified in Talaromyces section Islandici. Branches with 1 pp and bootstrap support values of more than 95 % are thickened. Talaromyces subinflatus was chosen as outgroup. Indoor isolates were marked with yellow star.

Fig. 4. Phylogeny of BenA for species classified in Talaromyces section Talaromyces. Branches with 1 pp and bootstrap support values of more than 95 % are thickened. Talaromyces dendriticus was chosen as outgroup. Indoor isolates were marked with yellow star.
Fig. 4. (Continued).
Fig. 5. Phylogeny of BenA for species classified in Talaromyces section Trachyspermi. Branches with 1 pp and bootstrap support values of more than 95 % are thickened. Talaromyces purpurogenus was chosen as outgroup. Indoor isolates were marked with yellow star. * indicates isolates previously identified as T. rubrifaciens.
Fig. 6. Morphological characters of *Talaromyces aerius*. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. conidiophores; G. Conidia. Scale bars = 10 μm.
Fig. 7. Morphological characters of Talaromyces adpressus. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.
Fig. 8. Morphological characters of Talaromyces beijingensis. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.

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Fig. 9. Morphological characters of Talaromyces cerinus. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.
Fig. 10. Morphological characters of Talaromyces chlamydosporus. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.
Fig. 11. Morphological characters of Talaromyces diversiformis. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.
Etyymology. Latin, *cerinus* refers to its yellow mycelium on MEA.

Diagnosis: This species produces yellow mycelium on MEA and orange centred reverse on CYA, does not grow on CYA at 37 °C.

In: *Talaromyces* section *Islandici*

**Typus: China.** Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22513, culture ex-type CBS 140622 = CGMCC3.18212 = DTO 318-A2).

**ITS barcode:** KU866658. (Alternative markers: *BenA = KU866845; CaM = KU866742; RPB2 = KU867002*).

**Colony diam, 7 d (mm):** CYA 17–18; CYA 30 °C 20–21; CYA 37 °C No growth; MEA 19–20; MEA 30 °C 25–26; DG18 12–13; CYAS 10–11; OA 17–19; CREA 2–3; YES 19–21.

**Colony characters:** CYA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white to buff; texture floccose; sporulation dense, conidia *en masse* on CYA; reverse yellowish brown. DG18, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture velvety; sporulation moderately dense, conidia *en masse* on CYA; reverse yellowish brown. YES, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture velvety; sporulation moderately dense, conidia *en masse* on CYA; reverse yellowish brown.

**Extritolites:** Emodin, mitorubrin, mitorubrinol, rugulosin, rugulovasin A, skyrin.

**Distinguishing characters:** *Talaromyces cerinus* resembles *T. subaurantiacus* and *T. chlamydosporus*, but *T. subaurantiacus* produces orange mycelium on CYA and MEA, and *T. chlamydosporus* produces globose to subglobose swollen cells resembling chlamydospores. In addition, *T. cerinus* does not grow on CYA at 37 °C.

*Talaromyces chlamydosporus* A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB817392. Fig. 10.

**Etymology:** Latin, *chlamydosporus* refers to the globose to subglobose swollen cells resembling chlamydospores.

**Diagnosis:** This species grows restrictedly on CYA and MEA, reaches 3–4 mm on CYA at 37 °C after 7 days, and produces globose to subglobose swollen cells resembling chlamydospores. In: *Talaromyces* section *Islandici*

**Typus: China.** Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22509, culture ex-type CBS 140635 = CGMCC 3.18199 = DTO 317-D5).

**ITS barcode:** KU866648. (Alternative markers: *BenA = KU866836; CaM = KU866732; RPB2 = KU866992*).

**Colony diam, 7 d (mm):** CYA 12–13; CYA 30 °C 12–13; CYA 37 °C 3–4; MEA 18–19; MEA 30 °C 17–18; DG18 9–11; CYAS 9–10; OA 15–16; CREA 3–4; YES 16–17.

**Colony characters:** CYA, 25 °C, 7 d: Colonies moderately deep, raised at centre, plane; margins entire; mycelium buff; texture velvety; sporulation moderately dense, conidia *en masse* olive green to greyish green; soluble pigments absent; exudates absent; reverse orange at centre, yellowish brown at edge. MEA, 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins slightly irregular; mycelium white; texture floccose; sporulation moderately dense, conidia *en masse* blue green; soluble pigments absent; exudates clear droplets; reverse yellowish brown. YES, 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium white; texture velvety; sporulation moderately dense, conidia *en masse* greyish green; soluble pigments absent; exudates absent; reverse yellowish brown.

**Extritolites:** Mitorubrin, mitorubrinol, mitorubrinol acetate, rugulovasin A & B, skyrin.

**Distinguishing characters:** *Talaromyces cerinus* grows restrictedly and produce compact colonies on CYA and MEA, and can produce globose to subglobose swollen cells. These characters distinguish it from the closely related *T. subaurantiacus* and *T. cerinus*.

*Talaromyces diversiformis* A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB818696. Fig. 11.

**Etymology:** Latin, *diversiformis* refers to its diverse conidiophore branches.

**Diagnosis:** This species produces solitary phialides, biverticillate conidiophores, which have in some cases extra subterminal...
Fig. 12. Morphological characters of Talaromyces fusiformis. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.
Fig. 13. Morphological characters of Talaromyces neorugulosus. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.
branches. This species furthermore produces large, ellipsoidal to fusiform conidia measuring 4–6(–8) × 2–4 μm.

In: Talaromyces section Helici

*Typus:* **China,** Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22941, culture ex-type CBS 141931 = CGMCC 3.18204 = DTO 317-E3).

**ITS barcode:** KX961215. (Alternative markers: *BenA* = KX961216; *CaM* = KX961259; *RPB2* = KX961274).

**Colony diam, 7 d (mm):** CYA 13–14; CYA 30 °C 14–16; CYA 37 °C 17–19; MEA 45–48; MEA 30 °C 56–57; DG18 5–6; CYAS No growth; OA 52–53; CREA No growth; YES 22–24.

**Colonies:** CYA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation moderate, dense, conidia ellipsoidal to fusiform, smooth, 4–6 μm; stipes smooth, 42–70 × 2.5–4 μm; soluble pigments absent; exudates absent; reverse yellowish brown fading into greyish green. MEA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture velvety; sporulation dense, conidia en masse greyish green; soluble pigments absent; exudates absent; reverse dark olive green fading into yellow brown. YES, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture funiculose; moderately dense, conidia en masse brown; soluble pigments absent; exudates absent; reverse dark greenish glaucous. CREA, 25 °C, 7 d: No growth.

**Micromorphology:** Conidiophores with solitary phialides, or biverticillate, or with extra subterminal branches; stipes smooth, 13–70 × 2.5–4 μm; metulae 2–3, 16–18 × 3–4 μm; phialides 1–3, flask shaped to acerate, (8–)16–18(–23) × 3–4.5 μm; conidia ellipsoidal to fusiform, smooth, 4–6(–8) × 2–4 μm.

Ascomata not observed.

**Extrólites:** no extrólites detected.

**Distinguishing characters:** *Talaromyces diversiformis* is phylogenetically closely related to *T. aurigenous* and *T. bohemicus.* This species has, compared with *T. aurigenous,* more complex branched conidiophores. *T. bohemicus* produces light brown mycelium which turns to cinnamon brown (*Fassatiouva & Peckova 1990*).

**Talaromyces fusiformis** A.J. Chen, Frisvad & Samson, sp. nov. MycoBank MB817396. Fig. 12.

**Etymology:** Latin, *fusiformis* refers to its fusiform conidia.

**Diagnosis:** This species produces funiculose colonies on OA, does not grow on CREA, produces smooth, ellipsoidal to fusiform conidia measuring 3–4(–6) × 2–3 μm.

In: Talaromyces section Talaromyces

**Typus:** **China,** Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22510, culture ex-type CBS 140637 = CGMCC 3.18210 = DTO 317-F4).

**ITS barcode:** KU866656. (Alternative markers: *BenA* = KU866843; *CaM* = KU866740; *RPB2* = KU867000).

**Colony diam, 7 d (mm):** CYA 28–29; CYA 30 °C 26–28; CYA 37 °C 24–25; MEA 37–38; MEA 30 °C 49–51; DG18 8–9; CYAS No growth; OA 39–40; CREA No growth; YES 30–31.

**Colonies:** CYA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium light yellow at centre; texture floccose; sporulation sparse, conidia en masse yellow green; soluble pigments absent; exudates light yellow droplets; reverse orange at centre, yellowish brown at edge. MEA, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture loosely funiculose; sporulation dense, conidia en masse greyish green; soluble pigments absent; exudates clear droplets; reverse orange at centre, yellowish brown at edge. YES, 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium light yellow at centre, white at edge; texture floccose; sporulation absent to sparse, conidia en masse pale green; soluble pigments absent; exudates light yellow droplets; reverse yellowish brown. DG18, 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation sparse, conidia en masse greyish green; soluble pigments absent; exudates absent; reverse white. OA, 25 °C, 7 d: Colonies deep, plane; margins entire; mycelium white, texture funiculose, sporulation dense, conidia en masse greyish green; soluble pigments absent; exudates clear droplets; reverse yellowish green. CREA, 25 °C, 7 d: No growth.

**Micromorphology:** Conidiophores biverticillate, with symmetrical subterminal branches; stipes smooth, 42–70 × 2.5–4 μm, extra branches 28–37 μm; metulae 3–4, appressed, 12–15 × 2.5–4 μm; phialides 3–4, acerose, 11–15 × 2–3 μm; conidia smooth, ellipsoidal to fusiform, 3–4(–6) × 2–3 μm. Ascomata not observed.

**Extrólites:** A purpactin, secalonic acid D, a chrodrimanin = thailandolide.

**Distinguishing characters:** *Talaromyces fusiformis* is close to *T. aurantium* and *T. funiculosus,* but *T. aurantium* does not sporulate on CYA, MEA and YES and produces cylindrical to ellipsoidoid conidia. *T. funiculosus* produces strong acid on CREA.

**Talaromyces neorugulosus** A.J. Chen, Frisvad & Samson, sp. nov. MycoBank MB817394. Fig. 13.

**Etymology:** latin, *neorugulosus* refers to its resemblance with *T. rugulosus.*

**Diagnosis:** This species produces compact, velvety, olive green to dark green colony, produces globose, subglobose to ellipsoidoid conidia measuring 3–4(–6) × 2–3(–4) μm, phylogenetically distinct from *T. rugulosus.*
Fig. 14. Morphological characters of Talaromyces reverso-olivaceus. A. Colonies from left to right (top row) CYA, MEA, YES and OA; (bottom row) CYA reverse, MEA reverse, DG 18 and CREA; B–F. Conidiophores; G. Conidia. Scale bars = 10 μm.
In: *Talaromyces* section *Islandici*

**Typus:** China, Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22511, culture ex-type CBS 140623 = CGMCC3.18215 = DTO 316-A6).

**ITS barcode:** KU866659. (Alternative markers: BenA = KU866846; CaM = KU866743; RPB2 = KU867003).

**Colony diam, 7 d (mm):** CYA: 17–18; CYA 30 °C 20–21; CYA 37 °C No growth; MEA 19–20; MEA 30 °C 25–26; DG18 12–13; CYAS 10–11; OA 17–19; CREA 2–3; YES 19–21.

**Colony characters:** CYA, 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium light yellow; texture velvety; sporulation moderately dense, conidia *en masse* olive green; soluble pigments absent; exudates absent; reverse buff.

**Micromorphology:** Conidiophores biverticillate, sometimes with additional branches; stipes smooth, 15–100 × 2–4 μm, extra branches 14–30 μm; metulae 3–5, divergent, 8–14 × 3–4 μm; phialides 2–5, flask shaped, 7–12 × 2–4 μm; conidia smooth, globose, subglobose to ellipsoidal, 3–4(–5) × 2–3(–4) μm. Ascomata not observed.

**Extróites:** Ukulactones = pruginosins.

**Distinguishing characters:** *Talaromyces neorugulosus* is close to *T. rugulosus*, *T. atrocula* and *T. sorceus*. However, *T. sorceus* grows more restrictedly on CYA, MEA, YES and OA, *T. atrocula* is characterised by floccose colonies and poor sporulation. Morphologically, *T. neorugulosus* resembles *T. rugulosus* and only small differences were found of the colony colour: *T. rugulosus* produces dull to dark green colonies on CYA, YES and DG18 and *T. neorugulosus* in shades of olive green. Phylogenetically, these two species can be distinguished by *BenA*, *CaM* and *RPB2* sequences.

**Talaromyces reverso-olivaceus** A.J. Chen, Frisvad & Samson, sp. nov. MycoBank MB817391. Fig. 14.

**Etymology:** Latin, *reverso-olivaceus* refers to the olive centred reverse.

**Diagnosis:** This species produces olive green centred reverse on CYA and saffron reverse on MEA, produces ellipsoidal to fusiform, finely roughed conidia measuring 2.5–4.5 × 2.5–3 μm.

In: *Talaromyces* section *Helici*

**Typus:** China, Beijing, indoor air, May 2014, isolated by B.D. Sun (holotype CBS H-22512, culture ex-type CBS 140672 = CGMCC3.18195 = DTO 317-C3).

**ITS barcode:** KU866646. (Alternative markers: BenA = KU866834; CaM = KU866730; RPB2 = KU866990).

**Colony diam, 7 d (mm):** CYA 19–23; CYA 30 °C 23–27; CYA 37 °C 18–20; MEA 34–37; MEA 30 °C 46–49; DG18 9–12; CYAS 4–6; OA 33–36; CREA No growth; YES 25–26.

**Colony characters:** CYA, 25 °C, 7 d: Colonies moderately deep, sulcate, raised at centre; margins entire; mycelium white; texture floccose; sporulation moderately dense, conidia *en masse* greyish green; soluble pigments absent; exudates absent; reverse olive green at centre fading into white. MEA, 25 °C, 7 d: Colonies moderately deep, plane to light sulcate; margins entire; mycelium white; texture velvety to floccose; sporulation dense, conidia *en masse* blue green; soluble pigments absent; exudates absent; reverse saffron. YES, 25 °C, 7 d: Colonies moderately deep, sulcate; margins entire; mycelium white; texture floccose; sporulation sparse to moderately dense, conidia *en masse* blue green to greyish green; soluble pigments absent; exudates absent; reverse olive green at centre fading into white. OA, 25 °C, 7 d: Colonies low, plane; margins entire; mycelium white; texture velvety; sporulation dense, conidia *en masse* dark green; soluble pigments absent; exudates absent; reverse light buff. CREA, 25 °C, 7 d: No growth.

**Micromorphology:** Conidiophores biverticillate, sometimes with extra subterminal branches; stipes smooth, 50–100 × 2.5–4 μm; branches 12–15 × 2–3 μm; metulae 3–5, 10–13 × 3–4 μm; phialides 3–5, aceros, 10–12(–14) × 2.5–3 μm; conidia ellipsoidal to fusiform, finely roughed, 2.5–4.5 × 2.5–3 μm. Ascomata not observed.

**Extróites:** rugulovasine A.

**Distinguishing characters:** Phylogenetically, *Talaromyces* reverso-olivaceus clusters in section *Helici*, related to *T. boninensis* and *T. helicus*. *Talaromyces boninensis* sporulates poorly on CYA and MEA, has a light orange reverse on CYA and white to orange reverse on MEA, and produces globose to subglobose ascospores. *Talaromyces helicus* produces greyish red to yellowish brown reverse on CYA, brownish orange reverse on MEA, and produces ellipsoidal ascospores. In addition, *T. reverso-olivaceus* produces finely roughed conidia, while *T. boninensis* and *T. helicus* produce smooth-walled conidia.

**DISCUSSION**

The genus *Talaromyces* was recently monographed (Yilmaz *et al.* 2014), accepting seven sections and 88 species. This study promoted the taxonomy of this genus, and since more than 17 new species were described (Visagie *et al.*, 2015, Yilmaz *et al.*).
In this study, Talaromyces isolates obtained from indoor air in China were studied. These isolates can be classified in four sections, and nine species are described here as new based on a polyphasic approach.

Talaromyces section Helici includes two clades (Yilmaz et al. 2014), and two of our new species fall into these two distinct clades. Talaromyces reverso-olivaceus clusters in the main clade containing T. helicus, T. boninensis and T. varians, and these species share the production of pigmented conidiophores. The other new species, T. diversiformis, clusters with the monoverticilicate species T. aeruginosus and T. bohemicus. This branching complexity of T. diversiformis is variable and both monoverticilicate and biverticilicate (occasionally with subterminal branches) conidiophores are observed.

The majority of species belonging to Talaromyces section Islandici grow restrictedly on most media, produce yellow mycelium and characteristic mycotoxins (Yilmaz et al. 2014, 2016b). The three new Islandici species grow restrictedly and produce yellow mycelium on DG18, confirming their relationship with other members of this section. Furthermore, T. neorugulosus produces pruginosins, and T. chlamydosporus and T. cerinus produce emodin, mitorubrin, mitorubrinol, rugulosin, skyrin and rugulosavasine A. These extrolites are commonly shared by members of section Islandici. Besides shared characteristics, these species can also be distinguished based on morphological and physiological characters. Talaromyces chlamydosporus produces globose to subglobose swollen cells resembling chlamydospores and T. cerinus does not grow on CYA incubated at 37 °C, in contrast to the closely related species T. chlamydosporus and T. subaurantianus. Talaromyces neo-rugulosus is morphologically similar to T. rugulosus. These species can be distinguished on their conidial colour on CYA and DG18; however, BenA, CaM or RPB2 sequencing is recommended for accurate identification.

Talaromyces section Talaromyces was initially introduced for species producing yellow, white, creamish, pinkish or reddish ascomata and yellow ascospores (Stolk & Samson 1972), and this section currently contains both asexual and sexual species (Samson et al. 2011, Yilmaz et al. 2012, Manoch et al. 2013, Sang et al. 2013, Yilmaz et al. 2014, Visagie et al. 2014, Wang et al. 2016). Morphologically, the two new Talaromyces species proposed in this section (T. beijingensis and T. fusiformis) can be distinguished from related species by mycelial colour, conidial shape and ornamentation (see notes in Taxonomy section).

Talaromyces aerius resembles other species of section Trachyspermia by restricted growth on CYA, YES and DG18, a slightly faster growth rate on MEA, and poor growth on CREA. Talaromyces aerius differs from the phylogenetically related species T. solicina by its conidial ornamentation (smooth-walled in T. aerius vs. rough-walled in T. solicina). The two recently described Trachyspermia members, T. sylustus and T. rubrificans, were included in the phylogenetic analyses. Talaromyces sylustus is well-separated from its sister species T. trachyspermus and T. assimilens, while all of T. rubrificans strains cluster together with T. albobicverticillus. The BenA gene, which is recommended as the identification marker in Talaromyces (Yilmaz et al. 2014), is identical for these two species. Talaromyces albobicverticillus has a large intraspecies sequence variation (Frisvad et al. 2013). For the description of T. rubrificans, Luo et al. (2016) included a limited number of T. albobicverticillus sequences in their phylogenetic analyses. This selection did not fully represent the sequence diversity within this species. The noticeable features like the formation of restricted colonies on MEA and CYA, soluble red pigment production on YES and MEA and green coloured conidia are common in T. albobicverticillus (Frisvad et al. 2013, Yilmaz et al. 2014). Other reported characters to distinguish T. rubrificans from T. albobicverticillus are the number of metulae (9–15) and phialides (6–10). These characters were, however, not depicted in the original figures (Luo et al. 2016). Based on molecular and morphological characters, we consider T. rubrificans a synonym of T. albobicverticillus. Interestingly, four of our indoor isolates were also identified as T. albobicverticillus. Visagie et al. (2014) reported this species in house dust from Thailand and South Africa, and all of these results indicate a widespread occurrence of this species in indoor environments.

The research on airborne fungi started in China in 1957, when Wu et al. (1982) compared the outdoor fungal concentration from 1957 to 1982 in Beijing, China. The predominant genera found were Cladosporium, Aspergillus, Alternaria and Penicillium. Later, several investigations were conducted on airborne fungi in different cities and seasons. In most studies only the fungal propagules were quantified and if identification was performed, then it was based on morphology (Wu et al. 2000, Li et al. 2006, Si et al. 2007, Liu et al. 2014). Fang et al. (2005) analysed the culturable airborne fungi in outdoor environments in Beijing, China. Talaromyces funiculosus (= Penicillium funiculosum), T. pinophilus (= P. pinophilum), T. ruber (= P. rubrum), T. wortmannii (= P. variabile), and T. flavus were identified using the Biolog Microstation System (Biolog, Hayward, CA). Li et al. (2006) analysed the indoor and outdoor Penicillium population in Nanchang city, Jiangxi province, and using morphological identification, T. islandicus (= P. islandicum) was found to be one of the predominant species. During a study on indoor fungi in Beijing, Fang et al. (2013) identified their isolates on genus level using ITS sequences, and three of them belong to Talaromyces. In Flora Fungorum Sinicum v35 Penicillium et teleomorphi cognati, Kong (2007) described the most complete records of Penicillium and its teleomorphs in China. Talaromyces funiculosus (= Penicillium funiculosum), T. verruculosus (= Penicillium verruculosum) and T. flavus were recorded from air. Talaromyces contains several important etiologic agents. Talaromyces marneffei, the only known dimorphic species in Talaromyces, has been considered to be exclusively associated with acquired immunodeficiency syndrome (AIDS) caused by human immunodeficiency virus (HIV) infections (Supparatpinyo et al. 1994). Nowadays the epidemiology of T. marneffei infection has changed significantly with the improved treatment of HIV, and an increasing number and proportion of cases have been reported in non-HIV-infected patients, who had other immunocompromising conditions (Tang et al. 2010, Lee et al. 2012, Lee et al. 2014, Chan et al. 2016). In our survey of indoor fungi in China we did not detect T. marneffei.

T. diversiformis, T. fusiformis and T. reverso-olivaceus grow well at 37 °C, thus are more risky for human health.

In our study, 13 species were identified including T. islandicus, T. aurantiacus, T. siamensis, T. albobiverticillus and nine new species. The main focus of our study was to describe the indoor Talaromyces diversity in houses in Beijing, China, and further research is needed to study the ecology of these species. The ‘old’ Penicillium and Talaromyces concepts and morphological identification are still used in China nowadays, and it is expected that with the broad application of molecular diagnostics, the number of indoor Talaromyces species in China will increase.

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APPENDIX A. SUPPLEMENTARY MATERIAL

Supplementary material related to this article can be found at http://dx.doi.org/10.1016/j.simyco.2016.11.003.

REFERENCES


