

A new thermotolerant species of *Taifanglania*

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Abstract: *Taifanglania parvispora* sp. nov. was isolated from the river mud of Sanya, Hainan Province, China. This new species was distinguished from other related taxa by its inflated hyphal bodies, short phialides, small, and pyriform to obovate conidia. The phylogenetic tree was constructed based on the ITS1-5.8S-ITS2 rDNA sequences of some species of *Taifanglania*, *Humicola*, *Phialemonium* and *Phialophora* and the results showed that the new species was clustered with *Taifanglania* spp. in a clade, and became a separated subclade in the *Taifanglania* clade. Morphological and molecular analysis indicated that it was reasonable that *T. parvispora* was proposed as a new taxon in the genus *Taifanglania*.

Key words: anamorphic fungi, taxonomy, molecular phylogeny, morphology

一个耐热的戴氏霉新种

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摘要: 从海南三亚的河泥中分离获得戴氏霉属一新种, 即小孢戴氏霉 *Taifanglania parvispora*。它与相近种的主要区别是菌丝段有时稍膨大, 瓶梗短和分生孢子小且呈梨形至倒卵形。基于戴氏霉属、腐质霉属、单瓶霉属和瓶霉属中一些种的 ITS1-5.8S-ITS2 rDNA 序列构建了系统发育树, 结果表明新种与戴氏霉属亲缘关系较近, 聚在一个分支中, 并在该分支中独立为一亚分支。形态和分子特征分析表明小孢戴氏霉可以作为戴氏霉属中的一个新分类单元。

关键词: 无性型真菌, 分类, 分子系统发育, 形态学

INTRODUCTION

The genus *Taifanglania* Z.Q. Liang, Y.F. Han, H.L. Chu & R.T.V. Fox was established in 2009 and *T.*

hechuanensis was the type species (Liang *et al.* 2009). Its main characters were as follows: Phialides directly grew from the aerial hyphae, mostly solitary; conidia formed long chains; saprophytic, thermotolerant and

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laccase-producing (Han *et al.* 2010a). So far, eleven species had been reported in the genus. *T. inflata* (Burnside) Z.Q. Liang, Y.F. Han & H.L. Chu was the only one mesophilic species. Recently, it was transferred to the genus *Phialemonium* according to the molecular phylogenetic analysis (Haybrig *et al.* 2013). So, there were ten species which were all thermotolerant in the genus *Taifanglania*.

Recently, species producing laccase and cellulase more and more attract people's attention. Chu (2005) screened a strain of *T. furcata* (Z.Q. Liang, H.L. Chu & Y.F. Han) Z.Q. Liang, Y.F. Han & H.L. Chu producing laccase with higher activity. Zhao (2006) further studied the conditions of producing laccase and degradation to 4-chlorinated phenols of this fungus. Zhang (2013) studied the cellulase production of *Taifanglania* spp. and found *T. hechuanensis* Z.Q. Liang, Y.F. Han, H.L. Chu & R.T.V. Fox having higher cellulase activity, then optimized the culture condition through using orthogonal design (Han *et al.* 2012).

During 2009–2013 a survey of thermotolerant *Taifanglania* in Southwest China was conducted and some new species were further reported (Han *et al.* 2010b). In this paper, the strain E21402H isolated from the river mud of Sanya, Hainan Province was proposed as a new taxon and named as *T. parvispora*.

1 MATERIALS AND METHODS

1.1 Sample collection and strain isolation

Strain E21402H was isolated from Sanya, Hainan Province. Two grams of soil were added to a flask containing 20mL sterilized water and glass beads. The soil suspension was shaken for about 10min, and then diluted to concentrations of 10^{-2} . 1mL suspension was mixed with Martin's medium in a sterilized 9cm diam.

Petri dish and incubated at 40°C for 7 days (Zhang *et al.* 2013).

1.2 Strain identification

The strain studied was transplanted onto Czapek agar and potato dextrose agar (PDA). After incubation at 40°C for 14 days, the strain was identified based on colony character and conidiogenous structures according to Liang *et al.* (2009). In addition, the strain was cultured at different temperature for observation of the growth.

1.3 DNA extraction and PCR amplification

2×Taq PCR MasterMix were from Shanghai TianGen. Strain E21402H used for the molecular identification were incubated on potato dextrose agar. Subsequently, the fresh sporulating cultures were used for DNA extraction and PCR amplification according to Han *et al.* (2013). PCR products were sequenced by Beijing Sinogenomax Co. Ltd. The sequence of ITS1-5.8S-ITS2 rDNA region of strain E21402H was submitted to GenBank (accession number: KF719170).

1.4 Sequence alignment and phylogenetic analysis

Some ITS1-5.8S-ITS2 region nucleotide sequences of *Taifanglania* spp. and other related genera were obtained from GenBank database. The sequence of the new species was aligned with related fungi using the Clustal ×1.83 computer program for multiple sequence alignment and manually corrected. The phylogenetic tree was constructed by neighbor-joining method (NJ) of MEGA version 5.0. Confidence values for individual branches were determined by bootstrap analysis (1 000 replications).

2 RESULTS AND DISCUSSIONS

2.1 Taxonomy

Taifanglania parvispora Y. Wang, Y.R. Wang, Y.F. Han

& Z.Q. Liang, sp. nov. Fig. 1

MycoBank MB 805936

Etymology: The specific epithet refers to the small conidia of this fungus.

Colonies on Czapek agar at 40°C, 7d, reaching 63mm diam., sparse, thin, white, regular in the margin; reverse creamy.

Colonies on PDA at 40°C, 7d, reaching 42mm diam., felty, flat, with irregular fold on the surface, yellow to brown, wavy in the margin; reverse brown, clear creasy.

Hyphae smooth, hyaline, mostly slender, 0.9–1.6µm in the width; some hyphal bodies short, somewhat inflate, 2.5–4.4µm (few up to 8.0µm) in the width; Phialides mostly solitary, produced directly from the aerial hyphae, sometimes proliferation, ellipsoidal to cylindrical at the base, 3.2–8.6×1.1–4.3µm, with a long and thin (2.2–6.5×1.1µm) neck; Conidia hyaline, smooth, forming long chains, pyriform to obovate, occasionally subglobose to ellipsoidal, 1.1–4.3×1.1–3.2µm. Chlamydospores absent.

Teleomorph not observed.

Temperature: It is able to grow at 15–50°C, the optimal temperature is 40°C.

Strain studied: E21402H was isolated from the river mud of Sanya, Hainan Province, China. Dried specimen (GZUIFR-E21402H, holotype) is deposited in the Institute of Fungus Resources, Guizhou University (GZUIFR).

Distribution: Hainan Province, China.

Comments: This species with conidia less than 5µm in the size is close to *T. ampullaris* (Matsush.) Z.Q. Liang, Y.F. Han & H.L. Chu (2.2–3.4×2–2.6µm). However, the conidia of *T. ampullaris* were subglobose, and the phialides were 6–20×2.5–3.5µm (Matushima 1975).

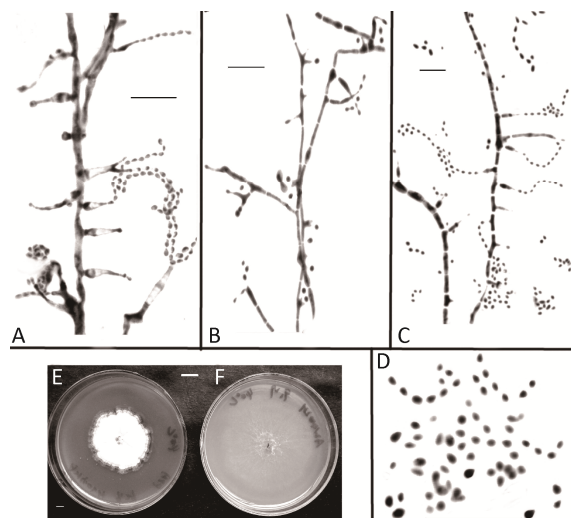


Fig. 1 *Taifanglania parvispora* Y. Wang, Y.R. Wang, Y.F. Han & Z.Q. Liang. A–C: Conidiogenous structures; D: Conidia; E–F: Colony in PDA and in CZA. Bars: A–D=10µm, E–F=1cm.

2.2 Molecular identification

ITS-5.8S sequences of *Taifanglania* spp. and their related species were constructed for phylogenetic analysis with the NJ methods in Mega 5.0 and *Cookeina venezuelae* (Berk. & M.A. Curtis) Le Gal was used as the outgroup (Fig. 2). There were five clades in the tree. Clade I consisted of *Taifanglania* spp. with 100% bs. Clade II consisted of *Humicola* spp. with 100% bs. Clade III included *Phialemonium curvatum* and *P. dimorphosporum* with 100% bs. Clade IV consisted of three other *Phialemonium* species with 93% bs. Clade V consisted of *Phialophora* spp. with 100% bs; obviously, the strain E21402H was closely clustered together with all other *Taifanglania* spp. supported by 100% bs, but it was a separated subclade in the *Taifanglania* clade in the phylogenetic tree.

Comments: Recent reports indicated that *Humicola* Traaen, *Phialophora* Medlar and *Taifanglania* are the anamorphic genera of

Chaetomiaceae (Hyde *et al.* 2011). When the phylogenetic tree was constructed, their molecular sequences were selected. *Phialemonium inflatum* (Burnside) D. Garcia, H. Perdomo, Gene, Cano & Guarro once belonged to the genus *Taifanglania* (Liang *et al.* 2009), and *Phialemonium* spp. were

also used for comparison. The results showed that these sequences could be divided into obviously different clades with high bs value in the different genera. The molecular phylogenetic analysis supported strain E21402H as a new taxon in the genus *Taifanglania*.

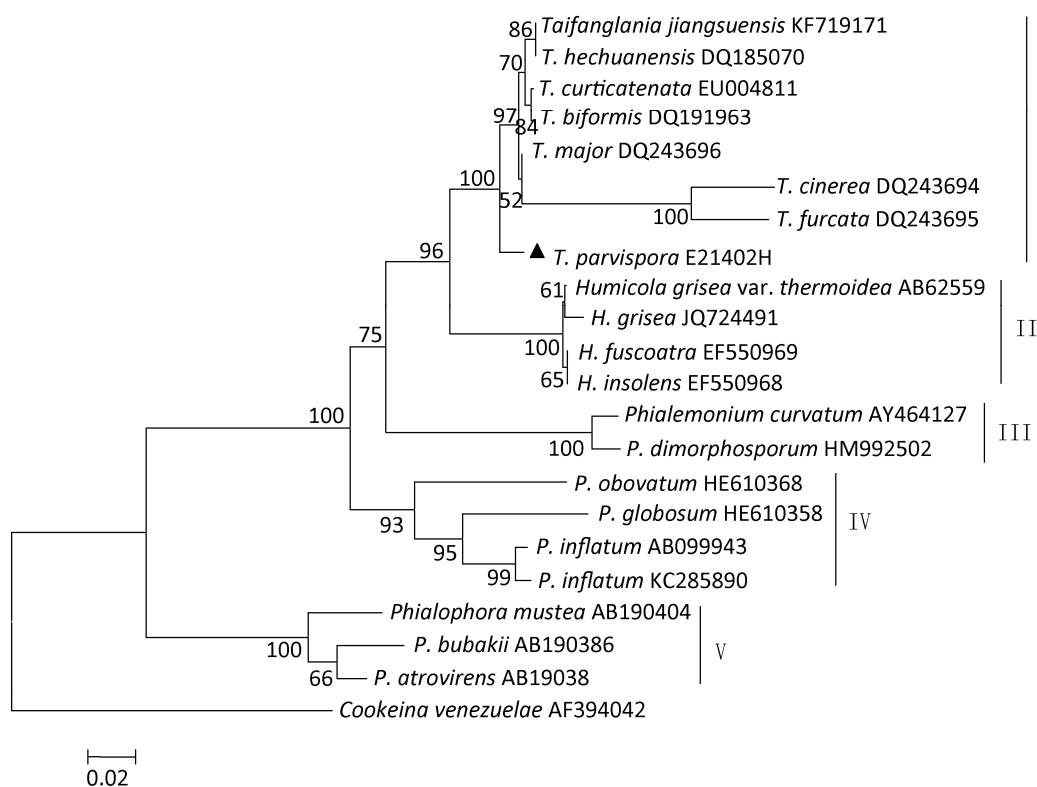


Fig. 2 Phylogenetic tree based on the ITS-5.8S rDNA sequences of *Taifanglania* and related *Humicola* spp., *Phialemonium* spp. and *Phialophora* spp. with the outgroup *Cookeina venezuelae* by the NJ method in Mega 5.0.

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