



Arthrobotrys xiangyunensis, a novel nematode-trapping taxon from a hot-spring in Yunnan Province, China

SHUORAN LIU^{a†}, HONGYAN SU^{a†}, XIJUN SU^a, FA ZHANG^a, GUANGHUI LIAO^a & XIAOYAN YANG^{a*}

^aCollege of Agriculture and Biology, Dali University, Dali, 671003, P.R. China.

[†]These authors have equally contributed to this paper.

*Corresponding author: Xiaoyan YANG

Email: yangxy.dlu@gmail.com

Abstract

An *Arthrobotrys* species with adhesive nets (trapping device) was isolated from hot-spring waterlogged soil during research on evolutionary patterns of nematode-trapping fungi in Yunnan Province, China. Morphological and phylogenetic analyses indicate this is a novel predatory species of *Arthrobotrys*, which we herein introduce as *A. xiangyunensis*. The new species is characterized by occasionally branched conidiophores, colorless, fusiform to oval or clavate conidia which mostly have 1–5 septa and measure 27–72(55.8) × 14.5–28.5(21.9) μm. The new species is introduced with illustrations in this paper. Its morphology is rather similar to *Monacrosporium guizhouense*, *M. longiphorum*, *M. sphaeroides*, *M. eudermatum* and *Arthrobotrys mangrovispora*, but the phylogenetic analysis shows that *A. xiangyunensis* and its morphological relatives are distinct.

Key words: Predatory fungi, *Arthrobotrys*, new species, phylogeny

Introduction

Predatory fungi have been studied for over 120 years since the detailed report by Zopf (1888). The taxonomy of nematode-trapping fungi has been controversial, although a new classification system based on the types of trapping device and genetic analysis was proposed by Scholler *et al.* (1999) and Hagedorn & Scholler (1999), and subsequently improved by Li *et al.* (2005) and Yang & Liu (2006). The system based on trapping device has now been widely accepted (Zhang *et al.* 2014). The main problem with identifying new collections of nematode-trapping fungi using molecular data is that many taxa have not yet been sequenced and thus not available in public sequence databases. We must therefore revert to using morphology to identify species which cannot distinguish between species complexes. Qiao *et al.* (2012) suggested that high genetic and also morphological diversity (conidial shapes) occur in a single asexual species complex and thus considerable research is needed.

Studies on the origin and evolution on nematode-trapping fungi (especially the trapping devices) have partially resolved taxonomic issues (Yang *et al.*, 2012; Yang *et al.*, 2007; Li *et al.*, 2005). Research to date has mostly been conducted in terrestrial, freshwater and marine habitats, and rarely in extreme environments (Swe *et al.*, 2011). Hot-springs are extreme environments and the organisms in these habitats may be morphologically and genetically primitive. Hot-springs are also geographically isolated habitats, making them as ideal sites to study the evolutionary patterns (Papke *et al.*, 2003, Rothschild & Mancinelli, 2001, Barns *et al.*, 1994).

There are presently no known hot-spring nematode-trapping fungi. In the present study on the evolution of predatory fungi, hot-spring waterlogged soil samples were collected from Yunnan Province, China. A previously undescribed nematode-trapping taxon was isolated in *Arthrobotrys*. Morphological and phylogenetic comparison with *Arthrobotrys* species showed this to be a novel taxa; therefore it is reported here as a novel nematode-trapping species, *A. xiangyunensis* sp. nov.

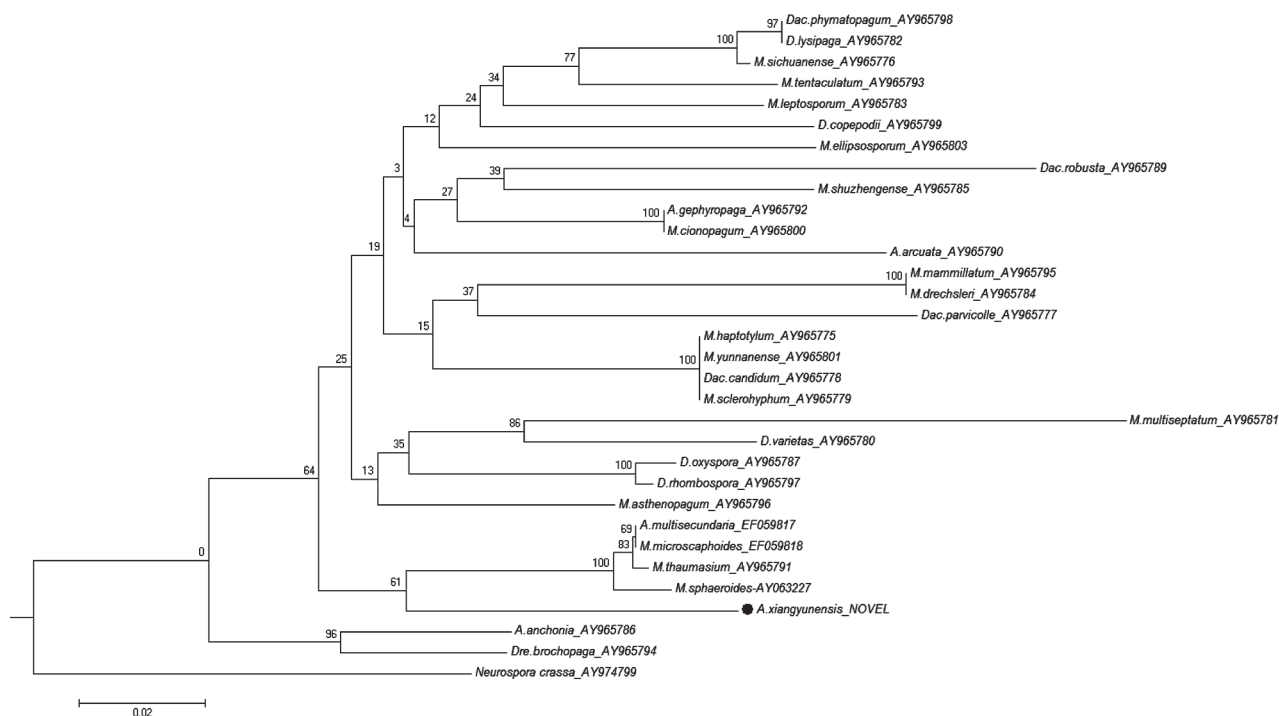


FIGURE 3. Neighbor-joining tree generated based on beta-tubulin complete sequences of nematode-trapping fungi species. Bootstrap values were indicated on the branches. *Neurospora crassa* was set as outgroup. Scale bar at the bottom showed the tree length. *M.* = *Monacrosporium*, *A.* = *Arthrotrys*, *D.* = *Dactylella*, *Dac.* = *Dactylellina*, *Dre.* = *Drechslerella*.

Acknowledgements

This research was supported by the National Natural Science Foundation Program of P.R. China [31100093, 31360013, 31060019]. We sincerely thank Dr. Kevin D. Hyde and Prof. Hans-Otto Baral for all their help and suggestions on this paper.

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