ISSN 1179-3155 (print edition)
ISSN 1179-3163 (online edition)

# Phytotaxa

666

[illegible] September 2024

Magnolia Press, Auckland, New Zealand

Phytotaxa

Vol. 666 No. 1: 26 Sept. 2024

Published: 2024-09-26

DOI: https://doi.org/10.11646/phytotaxa.666.1

## Article

### Two new species and a new record of Entolomatoid fungi (Entolomataceae, Agaricales) from Pakistan

ABDUL NASIR KHALID, FAUZIA RAZZAQ, AROOJ NASEER, TAYYABA QASIM, SOBIA KANWAL

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.1

Page range: 1-16

Abstract views: 8

PDF downloaded: 0

PDF(26.49MB)

### Morphological characteristics and phylogenetic analyses revealed a new invertebrate-pathogenic fungus *Akanthomyces bannaensis* (Cordycipitaceae, Ascomycota), in China

XUNCHI ZHANG, ZHONGHONG FU, FEI LU, JIUSHAN SONG, CHANGLIN ZHAO

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.2

Page range: 17-30

Abstract views: 7

PDF downloaded: 0

PDF(12.96MB)

### *Dahlstedtia colombiana* (Millettieae, Papilionoideae, Fabaceae), a new species and first record of the genus from Colombia and its Seasonally Tropical Dry Forest

ANA MARÍA TRUJILLO-LÓPEZ, WILLIAM ARIZA-CORTÉS, YEISON LONDOÑO-ECHEVERRI

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.3

Page range: 31-41

Abstract views: 8

PDF downloaded: 1

PDF(14.09MB)

### *Aspidistra tripartita* (Asparagaceae, Convallarioideae), a new species from Vietnam

NIKOLAY A. VISLOBOKOV, NATALIA A. MOSHKINA, SVETLANA P. KUZNETSOVA, ANDREY N. KUZNETSOV, SON XUAN LE, MIKHAIL S. ROMANOV, VICTORIA G. DROKINA, DMITRY F. LYSKOV, YURY O. KOPYLOV-GUSKOV, MAXIM S. NURALIEV

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.4

Page range: 42-50

Abstract views: 5

PDF downloaded: 1

PDF(13.56MB)

## *Dicranum nepalense* (Dicranaceae, Dicranales), a new species with fragile leaves from Nepal Himalayas

WEN-ZHUAN HUANG, TIAN-XIONG ZHENG, YU-HUAN WU, MENG-JIE YU

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.5

Page range: 51-58

Abstract views: 7

PDF downloaded: 0

PDF(10.32MB)

## *Blakea cubarralensis* (Melastomataceae: Pyxidantheae): a new species from Colombia

JOHAN URREA, HUMBERTO MENDOZA-CIFUENTES, NÉSTOR GARCÍA, LYNDON CARVAJAL ROJAS

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.6

Page range: 59-66

Abstract views: 9

PDF downloaded: 2

PDF(7.04MB)

## EMENDED DESCRIPTION OF *NEPENTHES SURIGAOENSIS* (NEPENTHACEAE), A POORLY KNOWN SPECIES FROM MINDANAO (PHILIPPINES)

NOEL E. LAGUNDAY, VICTOR B. AMOROSO

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.7

Page range: 67-72

Abstract views: 6

PDF downloaded: 1

PDF(5.03MB)

## *Helichrysum emodi* (Gnaphalieae: Asteraceae), a new species from the Indian Himalaya

SUNIT SINGH, J.P. MEHTA, ANANT KUMAR

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.8

Page range: 75-78

Abstract views: 12

PDF downloaded: 1

PDF(9.50MB)

## A new species of *Hypericum* section *Olympia* (Hypericaceae) from Central Greece

ARIS ZOGRAFIDIS, ALEXIAN CHEMINAL, PANAYOTIS DIMOPOULOS

Published: 2024-09-26

DOI: 10.11646/phytotaxa.666.1.9

Page range: 79-87

Abstract views: 4

PDF downloaded: 1

PDF(11.67MB)

## Correspondence

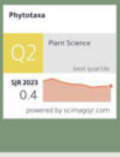
### Two new synonyms of *Lindenbergia philippensis* (Orobanchaceae)

S.K. SINGH, SAMEER PATEL, SUBHASMIT BHATTACHARYYA, POULAMI GHOSH

Published: 2024-09-26
DOI: 10.11646/phytotaxa.666.1.10
Page range: 88-92

PDF(4.50MB)

ISSN 1179-3155 (print); ISSN 1179-3163 (online)
Published by Magnolia Press, Auckland, New Zealand



*Phytotaxa* 666 (1): 017–030
https://www.mapress.com/pt/

**Article**

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.666.1.2

# Morphological characteristics and phylogenetic analyses revealed a new invertebrate-pathogenic fungus *Akanthomyces bannaensis* (Cordycipitaceae, Ascomycota), in China

XUNCHI ZHANG[1,3], ZHONGHONG FU[1,4], FEI LU[1,5], JIUSHAN SONG[2,6*] & CHANGLIN ZHAO[1,7*]
[1]*College of Forestry, Southwest Forestry University, Kunming 650224, P.R. China*
[2]*Pediatric department, The First Affiliated Hospital of Kunming Medical University, Kunming, 650032, Yunnan, P.R. China*
[3] *fungixunchizhang@163.com;* *https://orcid.org/0000-0003-3887-0979*
[4] *3152248052@qq.com;* *https://orcid.org/0009-0002-4019-6733*
[5] *2094307812@qq.com;* *https://orcid.org/0009-0007-8525-7727*
[6] *fungijssong@163.com;* *https://orcid.org/0000-0002-0461-8954*
[7] *fungichanglinz@163.com;* *https://orcid.org/0000-0002-8668-1075*
**Corresponding author: J.S. Song, e-mail: fungijssong@163.com, C.L. Zhao, e-mail: fungi@swfu.edu.cn; fungichanglinz@163.com*

## Abstract

The ubiquitous yet diverse associations between insects and fungi have long evolved. At the same time, the interactions between beetles, microbes, and hosts have not been well documented, especially for new fungi taxa. Two interesting specimens of *Akanthomyces* were found on adult moths of *Dudusa sphingiformis* in Yunnan Province, Southwest China. These specimens were identified as a new species based on morphology and phylogeny. *Akanthomyces bannaensis sp. nov.* is characterized by being determined to occur on an adult of *Dudusa sphingiformis* and synnemata arising from a moth body up to 5 cm long and 0.1–1.3 mm wide, unbranched, cylindrical to clavate with acute or blunt end. The morphological identification and phylogenetic analysis of combined ITS, nLSU, and *RPB2* sequence data support *A. bannaensis* as a new species, in which *A. bannaensis* is sister to *A. pyralidarum*. A full description, illustrations and phylogenetic analysis results of the new species are provided.

**Key words**: 1 new species, Entomopathogenic fungi, Fungal taxonomy, Phylogenetic analysis, Yunnan Province

## Introduction

The family Cordycipitaceae (Hypocreales) is known for its entomopathogenic nutritional habits, in which many species of this family have been originally isolated from dead insects and spiders that are either buried in the soil, leaf litter, or attached to the undersides or upper sides of leaves (Aini *et al.* 2020). Certain species, particularly those belonging to the genus *Beauveria* Vuill. (1912: 40), have been identified in soil habitats (Rehner & Buckley 2005, Wang *et al.* 2024) or as endophytes (Afandhi *et al.* 2019, Mantzoukas & Lagogiannis 2019). In addition, spider pathogens are closely associated with the fungal family Cordycipitaceae (Shrestha *et al.* 2019), and their anamorphs can be found in different genera: *Akanthomyces* Lebert (1858: 449), *Gibellula* Cavara (1894: 347), or *Hevansia* Luangsa-ard, Hywel-Jones & Spatafora (2017: 348) (Kepler *et al.* 2017). *Akanthomyces* is important in entomopathogenic fungi, and its diverse bioactive substances have attracted widespread attention (Madla *et al.* 2005, Kuephadungphan *et al.* 2014, Kinoshita *et al.* 2017).

The genus *Akanthomyces* was established by Lebert (1858), typfied with *A. aculeatus* Lebert (1858: 449), which was described on moths in Europe (Mains 1950). Morphologically, *Akanthomyces* species were characterized asexually by the white, cream or flesh-coloured cylindrical, attenuated synnematal growth covered by a hymenium-like layer of phialides producing one-celled catenulate conidia (Mains 1950, Samson & Evans 1974, Hsieh *et al.* 1997). The phialides exhibit an ellipsoidal, cylindrical, or narrowly cylindrical shape and taper gradually or abruptly, tapering to a more or less distinct neck (Hsieh *et al.* 1997). Owing to extensive overlap in their morphological characteristics, *Akanthomyces* was

*Accepted by Samantha C. Karunarathna: 19 Sept. 2024; published: 26 Sept. 2024*

once considered a synonym of *Lecanicillium* W. Gams & Zare (2001: 332), an anamorph within Cordycipitaceae with *verticillium*-like morphology (Gams & Zare 2001). Many species originally described in *Lecanicillium* did not form a single monophyletic clade and were distributed throughout the family Cordycipitaceae (Wang *et al.* 2020). Kepler *et al.* (2017) phylogenetically established the genetic boundaries within the family Cordycipitaceae and proposed that *Lecanicillium* should be rejected as a synonym of *Akanthomyces* (Kepler *et al.* 2017). The research showed that the type species of *Lecanicillium*, *L. lecanii* (Zimm.) Zare & W. Gams (2001: 333) (as *Cordyceps confragosa* (Mains) G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora (2007: 49), as well as several other *Lecanicillium* species, namely, *L. attenuatum* Zare & W.Gams (2001: 19), *L. muscarium* (Petch) Zare & W. Gams (2001: 13) and *L. sabanense* Chir.-Salom., S.Restrepo & T.I. Sanjuan (2015: 68), fell in the genus *Akanthomyces* (Kepler *et al.* 2017). The teleomorph of *Akanthomyces* species was originally described as *Torrubiella* Boud. (1885: 226), which was characterized by producing the superficial perithecia on a loose mat of hyphae (subiculum) or a highly reduced non-stipitate stroma (Boudier 1885). According to the taxonomic classification of the family Cordycipitaceae, the genus *Akanthomyces* is located in this family based on DNA sequencing and morphological characteristics (Kepler *et al.* 2017).

During the surveys of entomopathogenic fungi in the national parks and community forests in Yunnan Province, two collections of pathogens on adult moths were found on the underside of leaves of dicotyledonous forest plants. The phenotypic characteristics of the collections, having cylindrical to narrowly clavate synnemata and superficial perithecia scattered on the body and wings of the moth, identify them primarily as members of *Akanthomyces* in Cordycipitaceae.

The aim of this study is to describe *Akanthomyces bannaensis sp. nov.* from Yunnan, China.

## Materials and methods

### *Sample Collection and Herbarium Specimen Preparation*

Samples were collected from Dai Autonomous Prefecture of Xishuangbanna, Yunnan Province, China. The samples were photographed in the field, and fresh macroscopic details were recorded (Rathnayaka *et al.* 2024). Photographs were taken by a Nikon D7100 camera. Specimens were dried in an electric food dehydrator at 40 °C (Hu *et al*. 2022). After the specimens were dried, they were sealed, stored in an envelope bag, labeled, and deposited (Dong *et al.* 2024, Zhang *et al.* 2024). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

### *Morphological Studies*

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The color terminology followed Petersen (1996) and was confirmed in general terms according to the CMYK color code (Deep White Printing Team 2022). The micromorphological data were obtained from the dried specimens after observation under a light microscope with a magnification of 10 × 100 (Zhao *et al.* 2023). The following abbreviations are used: L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b (number of spores (a) measured from a given number (b) of specimens).

### *DNA extraction, Polymerase Chain Reaction, and Sequencing*

The EZNA HP Fungal DNA Kit (Omega Biotechnologies Co., Ltd., Kunming, China) was used to extract DNA with some modifications from the dried specimens. The internal transcribed spacer (ITS) region was amplified with ITS5 and ITS4 primers (White *et al.* 1990). The large subunit ribosomal RNA (nLSU) gene was amplified with the LR0R and LR7 primer pair (Vilgalys & Hester 1990). The RNA polymerase II second largest subunit (*RPB2*) gene was amplified with b*RPB2*-6F and b*RPB2*-7.1R primers (Matheny 2005). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR procedure for *RPB2* was as follows: (1) initial denaturation at 95 °C for 2.5 min, (2) denaturation at 95 °C for 30 s, (3) annealing at 52 °C for 1 min, (4) extension at 72 °C for 1 min (add 1 °C per cycle), (5) repeat for 40 cycles starting at step 2, (6) extension at 72 °C for 1.5 min, (7) repeat for 40 cycles starting at step 6, (8) leave at 72 °C for 5 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company, Yunnan Province, China. All the newly generated sequences were deposited in GenBank (Table 1), and the known species were obtained from a latest study (Wang *et al.* 2024).

**TABLE 1.** Names, specimen numbers, hosts, references, and corresponding GenBank accession numbers of the taxa used in this study. The new species are in bold.

| **Species name** | **Specimen number** | **Host/Substrate** | **GenBank accession number** | | | **Reference** |
|---|---|---|---|---|---|---|
| | | | **ITS** | **nLSU** | ***RPB2*** | |
| *Akanthomyces aculeatus* | HUA 186145 | – | – | MF416520 | – | Kepler *et al.* 2017 |
| *Akanthomyces aculeatus* | TS772 | Lepidoptera; Sphingidae | KC519371 | KC519370 | – | Sanjuan *et al.* 2014 |
| *Akanthomyces araneicola* | GY29011※ | Araneae; spider | MK942431 | – | MK955947 | Chen *et al.* 2019 |
| *Akanthomyces araneogenus* | YFCC 1811934 | Araneae; spider | OQ509518 | OQ509505 | OQ511544 | Wang *et al.* 2024 |
| *Akanthomyces araneogenus* | YFCC 2206935 | Araneae; spider | OQ509519 | OQ509506 | OQ511545 | Wang *et al.* 2024 |
| *Akanthomyces araneosus* | KY11341※ | Araneae; spider | ON502826 | ON502832 | ON525442 | Chen *et al.* 2022 |
| *Akanthomyces attenuatus* | CBS 170.76※ | Lepidoptera; *Carpocapsa pomonella* | MH860970 | OP752153 | OP762615 | Manfrino *et al.* 2022 |
| ***Akanthomyces bannaensis*** | **CLZhao 34016*** | **Lepidoptera; *Dudusa sphingiformis*** | **PP571895** | **PP571897** | **PP588774** | **This study** |
| ***Akanthomyces bannaensis*** | **CLZhao 34017** | **Lepidoptera; *Dudusa sphingiformis*** | **PP571896** | **PP571898** | **–** | **This study** |
| *Akanthomyces bashanensis* | CQ05621※ | Araneae; spider | OQ300412 | OQ300420 | OQ349684 | Chen *et al.* 2023 |
| *Akanthomyces beibeiensis* | CQ05921※ | Araneae; spider | OQ300415 | OQ300424 | OQ349688 | Chen *et al.* 2023 |
| *Akanthomyces coccidioperitheciatus* | NHJ 6709 | Araneae; spider | JN049865 | EU369042 | EU369086 | Kepler *et al.* 2012 |
| *Akanthomyces dipterigenus* | CBS 126.27 | Hemiptera; *Icerya purchasi* | AJ292385 | KM283797 | KM283862 | Kepler *et al.* 2017 |
| *Akanthomyces dipterigenus* | YFCC 2107933 | Soil | OQ509520 | OQ509507 | OQ511546 | Wang *et al.* 2024 |
| *Akanthomyces kanyawimiae* | TBRC 7242 | Araneae; spider | MF140751 | MF140718 | MF140808 | Mongkolsamrit *et al.* 2018 |
| *Akanthomyces kanyawimiae* | TBRC 7243 | Unidentified | MF140750 | MF140717 | MF140807 | Mongkolsamrit *et al.* 2018 |
| *Akanthomyces kunmingensis* | YFCC 1708939 | Araneae; spider | OQ509521 | OQ509508 | OQ511547 | Wang *et al.* 2024 |
| *Akanthomyces kunmingensis* | YFCC 1808940※ | Araneae; spider | OQ509522 | OQ509509 | OQ511548 | Wang *et al.* 2024 |
| *Akanthomyces laosensis* | YFCC 1910941※ | Lepidoptera; Noctuidae | OQ509523 | OQ509510 | OQ511549 | Wang *et al.* 2024 |
| *Akanthomyces laosensis* | YFCC 1910942 | Lepidoptera; Noctuidae | OQ509524 | OQ509511 | OQ511550 | Wang *et al.* 2024 |
| *Akanthomyces lecanii* | CBS 101247 | Hemiptera; *Coccus viridis* | JN049836 | AF339555 | DQ522466 | Kepler *et al.* 2012 |
| *Akanthomyces lepidopterorum* | GZAC SD05151※ | Lepidoptera (pupa) | MT705973 | – | MT727044 | Chen *et al.* 2020b |
| *Akanthomyces muscarius* | CBS 455.70B | – | – | MH871560 | – | Kepler *et al.* 2017 |
| *Akanthomyces neoaraneogenus* | GZU1031Lea※ | Araneae; spider | KX845703 | – | KX845701 | Chen *et al.* 2017 |

...continued on the next page

**TABLE 1.** (Continued)

| **Species name** | **Specimen number** | **Host/Substrate** | **GenBank accession number** | | | **Reference** |
|---|---|---|---|---|---|---|
| | | | **ITS** | **nLSU** | ***RPB2*** | |
| *Akanthomyces neocoleopterorum* | GY11241※ | Coleoptera | MN093296 | – | MN097812 | Chen *et al.* 2020a |
| *Akanthomyces neocoleopterorum* | GY11242 | Coleoptera | MN093298 | – | MN097814 | Chen *et al.* 2020a |
| *Akanthomyces noctuidarum* | BCC 36265※ | Lepidoptera; Noctuidae | MT356072 | MT356084 | MT477987 | Aini *et al.* 2020 |
| *Akanthomyces noctuidarum* | BCC 47498 | Lepidoptera; Noctuidae | MT356074 | MT356086 | MT477988 | Aini *et al.* 2020 |
| *Akanthomyces noctuidarum* | BCC 28571 | Lepidoptera; Noctuidae | MT356075 | MT356087 | MT478006 | Aini *et al.* 2020 |
| *Akanthomyces pissodis* | CBS 118231※ | Coleoptera; *Pissodes strobi* | – | KM283799 | KM283864 | Chen *et al.* 2020b |
| *Akanthomyces pseudonoctuidarum* | YFCC 1808943※ | Lepidoptera; Noctuidae | OQ509525 | OQ509512 | OQ511551 | Wang *et al.* 2024 |
| *Akanthomyces pseudonoctuidarum* | YFCC 1808944 | Lepidoptera; Noctuidae | OQ509526 | OQ509513 | OQ511552 | Wang *et al.* 2024 |
| *Akanthomyces pyralidarum* | BCC 28816※ | Lepidoptera; Pyralidae | MT356080 | MT356091 | MT478007 | Aini *et al.* 2020 |
| *Akanthomyces pyralidarum* | BCC 32191 | Lepidoptera; Pyralidae | MT356081 | MT356092 | MT477989 | Aini *et al.* 2020 |
| *Akanthomyces sabanensis* | ANDES-F 1023 | Hemiptera; *Pulvinaria caballeroramosae* | KC633237 | – | – | Kepler *et al.* 2017 |
| *Akanthomyces sabanensis* | ANDES-F 1024 | Hemiptera; *Pulvinaria caballeroramosae* | KC633232 | KC875225 | KC633249 | Kepler *et al.* 2017 |
| *Akanthomyces subaraneicola* | YFCC 2107937※ | Araneae; spider | OQ509527 | OQ509514 | OQ511553 | Wang *et al.* 2024 |
| *Akanthomyces subaraneicola* | YFCC 2107938 | Araneae; spider | OQ509528 | OQ509515 | OQ511554 | Wang *et al.* 2024 |
| *Akanthomyces sulphureus* | TBRC 7248※ | Araneae; spider | MF140758 | MF140722 | MF140812 | Mongkolsamrit *et al.* 2018 |
| *Akanthomyces sulphureus* | TBRC 7249 | Araneae; spider | MF140757 | MF140721 | MF140734 | Mongkolsamrit *et al.* 2018 |
| *Akanthomyces sulphureus* | YFCC 1710936 | Araneae; spider | OQ509529 | OQ509516 | OQ511555 | Wang *et al.* 2024 |
| *Akanthomyces thailandicus* | TBRC 7245※ | Araneae; spider | MF140754 | – | MF140809 | Mongkolsamrit *et al.* 2018 |
| *Akanthomyces tiankengensis* | KY11571※ | Araneae; spider | ON502848 | ON502825 | ON525446 | Chen *et al.* 2022 |
| *Akanthomyces tiankengensis* | KY11572 | Araneae; spider | ON502821 | ON502827 | ON525448 | Chen *et al.* 2022 |
| *Akanthomyces tortricidarum* | BCC 72638※ | Lepidoptera; Tortricidae | MT356076 | MT356088 | MT477992 | Aini *et al.* 2020 |
| *Akanthomyces tortricidarum* | BCC 41868 | Lepidoptera; Tortricidae | MT356077 | MT356089 | MT478008 | Aini *et al.* 2020 |
| *Akanthomyces tuberculatus* | OSC 111002 | Lepidoptera (adult moth) | – | DQ518767 | DQ522435 | Kepler *et al.* 2017 |

*...continued on the next page*

**TABLE 1.** (Continued)

| **Species name** | **Specimen number** | **Host/Substrate** | **GenBank accession number** | | | **Reference** |
|---|---|---|---|---|---|---|
| | | | **ITS** | **nLSU** | ***RPB2*** | |
| *Akanthomyces uredinophilus* | KACC 44066 | Rust | – | KM283784 | KM283850 | Park *et al.* 2016 |
| *Akanthomyces uredinophilus* | KACC 44082※ | Rust | – | KM283782 | KM283848 | Park *et al.* 2016 |
| *Akanthomyces uredinophilus* | KUN 101466 | Insect | MG948305 | MG948307 | MG948313 | Park *et al.* 2016 |
| *Akanthomyces uredinophilus* | KUN 101469 | Insect | MG948306 | MG948308 | MG948314 | Park *et al.* 2016 |
| *Akanthomyces waltergamsi* | TBRC 7251 | Araneae; spider | MF140747 | MF140713 | MF140805 | Mongkolsamrit *et al.* 2018 |
| *Akanthomyces waltergamsi* | TBRC 7252※ | Araneae; spider | MF140748 | MF140714 | MF140806 | Mongkolsamrit *et al.* 2018 |
| *Akanthomyces waltergamsii* | YFCC 883 | Araneae; spider | OQ509530 | OQ509517 | OQ511556 | Wang *et al.* 2024 |
| *Akanthomyces zaquensis* | HMAS 246915※ | Fungi; *Ophiocordyceps sinensis* | MT789699 | MT789697 | – | Wang *et al.* 2023 |
| *Akanthomyces zaquensis* | HMAS 246917 | Fungi; *Ophiocordyceps sinensis* | MT789698 | MT789696 | – | Wang *et al.* 2023 |
| *Samsoniella aurantia* | TBRC 7271※ | Lepidoptera | MF140764 | MF140728 | MF140818 | Mongkolsamrit *et al.* 2018 |
| *Samsoniella inthanonensis* | TBRC 7915※ | Lepidoptera (pupa) | MF140761 | MF140725 | MF140815 | Mongkolsamrit *et al.* 2018 |

* Indicates type material (holotype) in this study. Ex-type materials are marked with "※".

*Phylogenetic Analyses*

To determine the phylogeny, we compiled an ITS+nLSU+*RPB2* dataset. In the combined dataset, sequence of *Samsoniella aurantia* Mongkols., Noisrip., Thanakitp., Spatafora & Luangsa-ard (2018: 249) and *S. inthanonensis* Mongkols., Noisrip., Thanakitp., Spatafora & Luangsa-ard (2018: 251) from GenBank was used as an outgroup in ITS+nLSU+*RPB2* (Fig. 1) analysis following a previous study (Wang *et al.* 2024). The sequences were aligned initially by using MAFFT (https://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy and then manually optimized in AliView version 1.27 (Larsson 2014). Finally, the three gene fragments were concatenated with Mesquite v3.70 (Maddison & Maddison 2021; https://www.mesquiteproject.org/) for further phylogenetic analyses. ModelFinder v2.2.0 (Kalyaanamoorthy *et al.* 2017) was used to select the best-fit model using the BIC criterion. The best-fit model was selected according to BIC: GTR+F+I+G4. The alignment datasets were deposited in TreeBASE (Submission ID 31343; www.treebase.org).

Maximum likelihood (ML) analysis was performed with RAxML-HPC BlackBox in CIPRES Science Gateway (https://www.phylo.org/portal2/login!input.action, Miller *et al.* 2012) using a GTRCAT model of evolution with 1,000 bootstrap replicates. Bayesian Inference (BI) phylogenies were inferred using MrBayes v3.2.7a (Ronquist *et al.* 2012) under the GTR+I+G+F model with two independent runs, performing 3000000 replicates each for the dataset, sampling one tree every 1000 generations. The first 25% of the sampled trees were discarded as burn-in, and the remaining trees were used to reconstruct a majority rule consensus and calculate the BPP of the clades.

Branches of the consensus tree that received bootstrap support for Maximum Likelihood (ML) equal to or above 70%, Bayesian Inference (BI) equal to or above 0.95, respectively.

*Genealogical concordance phylogenetic species recognition (GCPSR) analysis*

We used the genealogical concordance phylogenetic species recognition analysis (GCPSR) to check for significant recombination events (Quaedvlieg *et al.* 2014). The data were analyzed using the pairwise homoplasy index (PHI) test in SplitsTree 4 to determine the recombination level with closely related species (Bruen *et al.* 2006, Huson & Bryant 2006, Quaedvlieg *et al.* 2014). Multilocus datasets (ITS+nLSU+*RPB2*) with closely related species were used for the analyses. The pairwise homoplasy index lower than 0.05 (Φw < 0.05) indicates significant recombination in the dataset. The relationships between closely related taxa were visualized by constructing split graphs from the concatenated datasets using the LogDet transformation and split decomposition options.

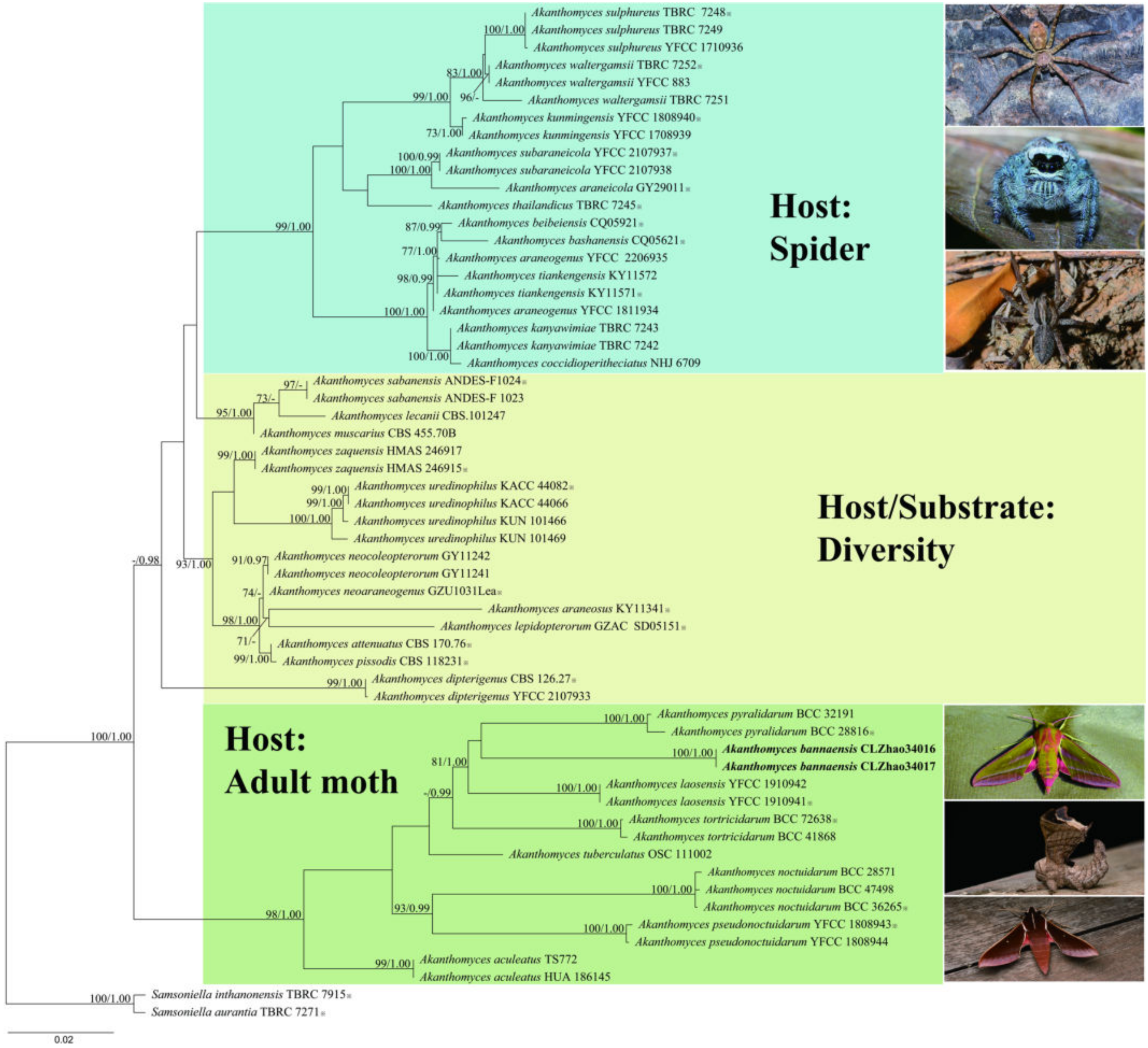


**FIGURE 1.** Phylogeny of *Akanthomyces* species by ML analysis of combined ITS+nLSU+*RPB2* sequences. Branches are labeled with maximum likelihood bootstrap equal to or higher than 70% and Bayesian posterior probabilities equal to or higher than 0.95, respectively (ML-BS/BI-PP). Ex-type materials are marked with “※”. Isolates in bold type are those analysed in this study.

## Results

### *Phylogenetic Analyses*

The combined ITS+nLSU+*RPB2* dataset (Fig. 1) included sequences from 58 fungal specimens representing 33 species. A total of 4 Markov chains were run for 2 runs from random starting trees for 3 million generations for the ITS+nLSU+*RPB2* dataset, with trees and parameters sampled every 1,000 generations. The best model for the combined ITS+nLSU+*RPB2* dataset estimated and applied in the Bayesian analysis was GTR+I+G+F. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis resulted in a similar topology with an average standard deviation of split frequencies = 0.008585 (BI), and the effective sample size (ESS) average ESS (avg ESS) = 1544.

In the phylogenetic tree (Fig. 1), the hosts of *Akanthomyces*, Araneae, and Lepidoptera form two distinct monophyletic groups, in which *Akanthomyces bannaensis* clustered with the close species *A. pyralidarum* Aini, Luangsa-ard, Mongkols. & Thanakitp. (2020: 11) and then grouped with *A. laosensis* Hong Yu bis & Y. Wang (2024: 123), *A. tortricidarum* Aini, Luangsa-ard, Mongkols. & Thanakitp. (2020: 13) and *A. tuberculatus* (Lebert) Spatafora, Kepler & B. Shrestha (2017: 343).

Application of pairwise homoplasy index (PHI) test to the combined partial ITS+nLSU+*RPB2* sequences data tree-locus sequences revealed no recombination level within phylogenetically related species. No significant recombination events were observed between *Akanthomyces bannaensis* and *A. pyralidarum* and phylogenetically closely related species *A. laosensis*, and *A. tortricidarum* (Fig. 2). The test results of the combined partial ITS+nLSU+*RPB2* sequences dataset show Φw = 0.7069 (Φw > 0.05) no recombination is present in the new species with *A. laosensis*, *A. pyralidarum*, and *A. tortricidarum* (Fig. 2).

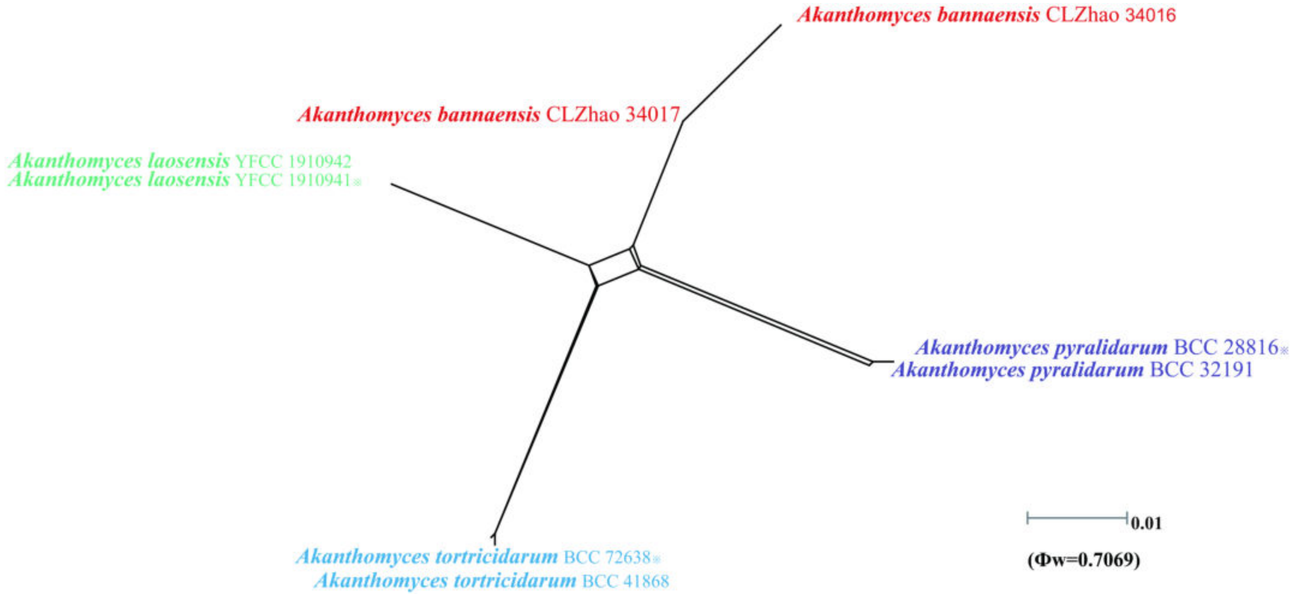


**FIGURE 2.** The results of the pairwise homoplasy index (PHI) test for the combined partial ITS+nLSU+*RPB2* sequences data of *Akanthomyces bannaensis* closely related taxa using LogDet transformation and splits decomposition. PHI test results Φw ≤ 0.05 indicate a significant recombination within the dataset. New taxa are in red, while closely related species to new species are in other colors. Ex-type materials are marked with "※".

## Taxonomy

***Akanthomyces bannaensis*** X.C. Zhang & C.L. Zhao, *sp. nov.* Figs. 3, 4
MycoBank no.: MB 853954

***Diagnosis*:**—The species is distinguished from other *Akanthomyces* species by it occurring on an adult of *Dudusa sphingiformis* and synnemata arising from a moth body up to 5 cm long and 0.1–1.3 mm wide, unbranched, cylindrical to clavate with acute or blunt end.

***Etymology*:**—*bannaensis* (Lat.) refers to the locality (Dai Autonomous Prefecture of Xishuangbanna) of the type specimen.

***Type*:**—CHINA. Yunnan Province, Dai Autonomous Prefecture of Xishuangbanna, Jinghong, Menglun Town, 21°55′N, 101°13′E, elev. 544 m, on the underside of the leaves of angiosperms, 9 October 2023, leg. C.L. Zhao, CLZhao 34016 (**holotype**, SWFC F0034016), GenBank No. (ITS PP571895; nLSU PP571897; *RPB2* PP588774).

***Description*:—*Sexual morph*:** Undetermined. ***Asexual morph*:** Specimens examined in this study can be found on the underside of the leaves of angiosperms. The hosts were adult moths, ca. 4 × 2.5 cm. Synnemata arising from moth body and wings, white (C0 M0 Y5 K0) to cream (C0 M10 Y40 K0), up to 5 cm long and 0.1–1.3 mm wide, unbranched, cylindrical to clavate with acute or blunt end. Hyphae smooth-walled, branched, septate, hyaline, 2.65–2.90 μm wide. Conidiogenous cells produced along synnemata, monophialidic or polyphialidic. Phialides smooth-walled, hyaline, cylindrical with papillate end, (7–) 8–10 × (2.2–) 2.5–3.8 μm (n = 20/1). Conidia smooth-walled, colorless, single-celled, ellipsoidal or obovoid, (3.8–) 4–5.8 × 2–3 μm, L = 4.80 μm, W = 2.52 μm, Q = 1.74–2.08 (n = 60/2).

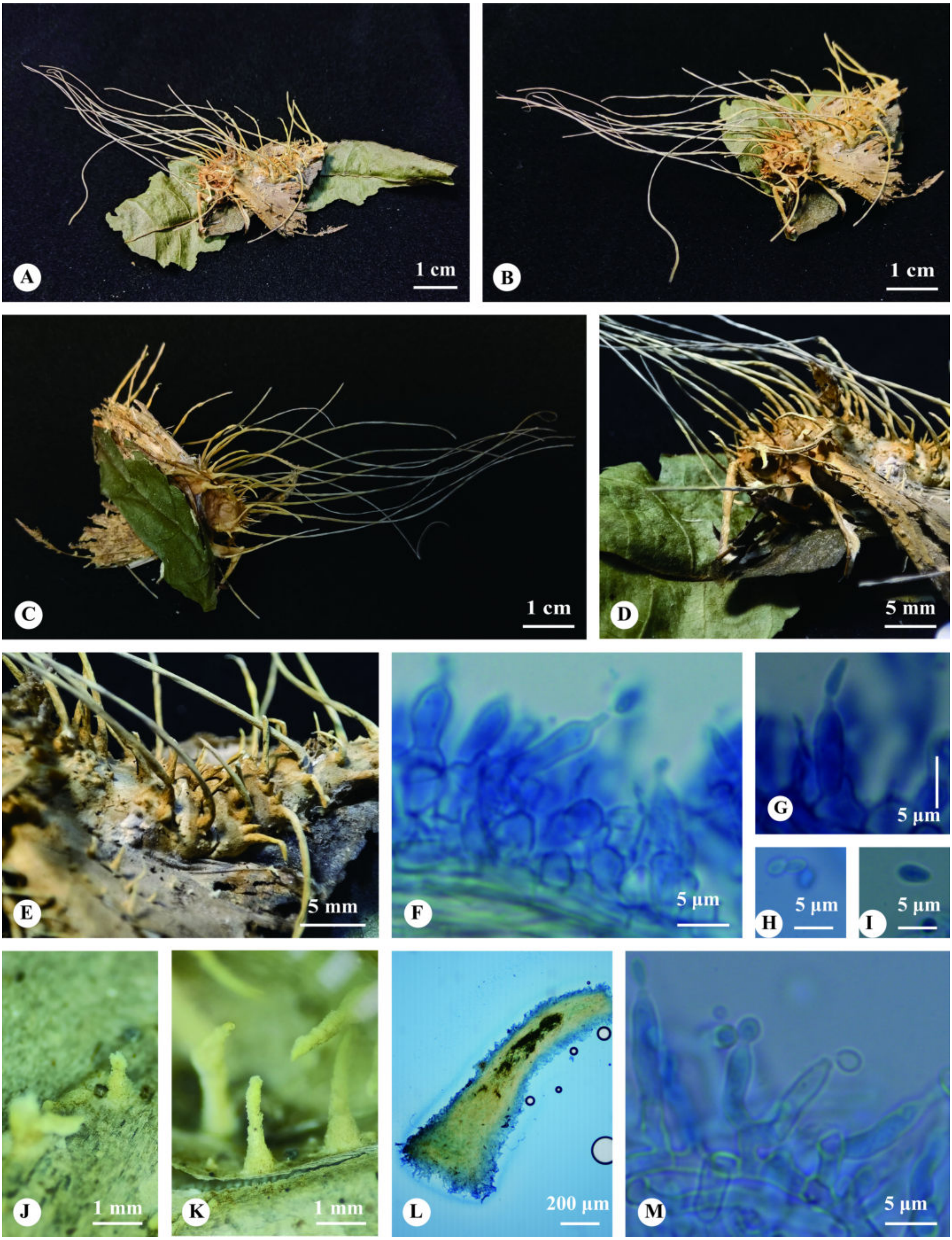


**FIGURE 3.** *Akanthomyces bannaensis* (Photos from the Holotype CLZhao 34016). A–C. fungus on adult moth; D, E. synnema from host body; F, G. Phialides arising from tramal hypha; H. Ellipsoidal conidia; I. Obovoid conidia; J–L. synnema from moth wings. M. Phialides at the tip of synnema.

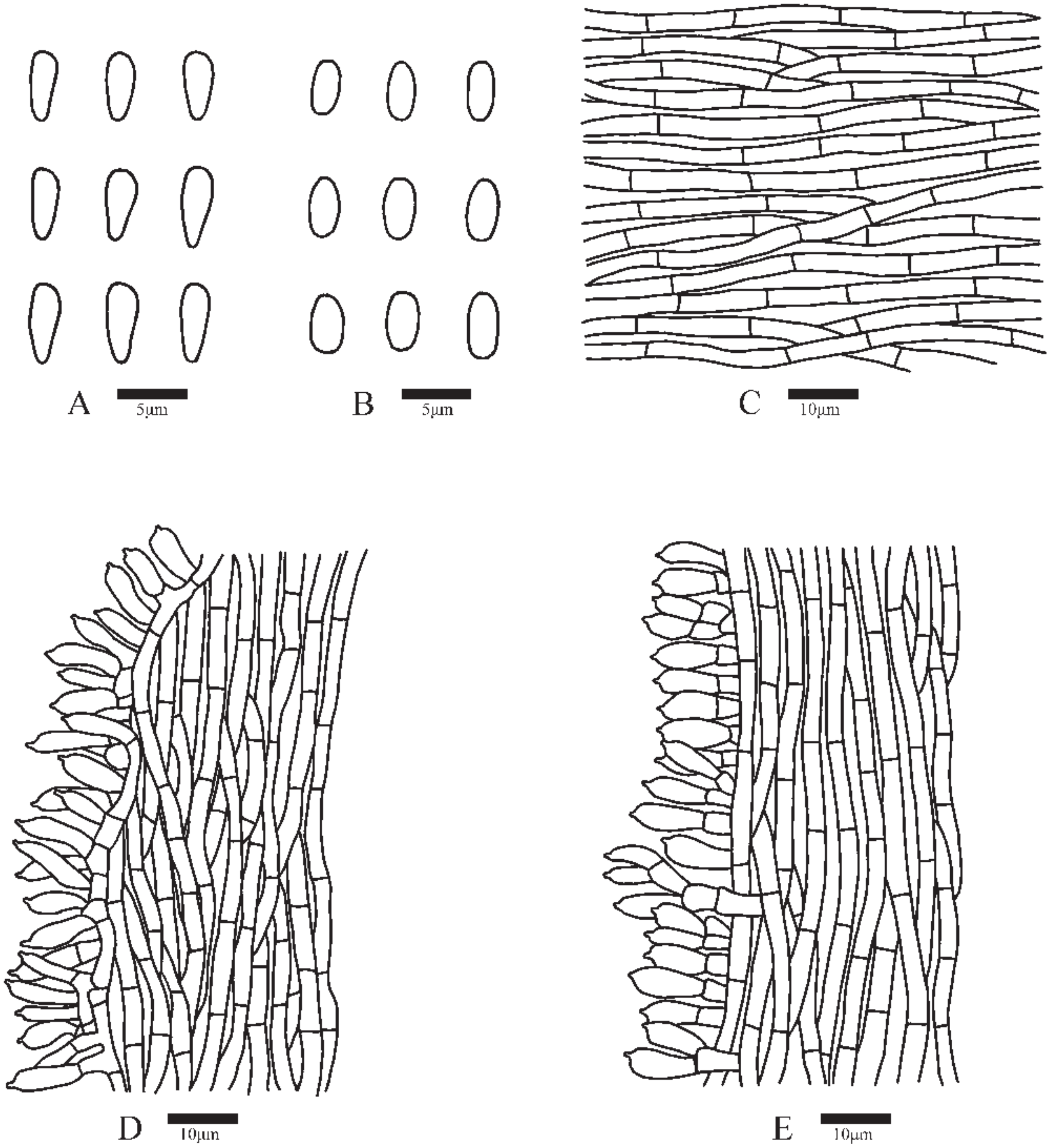


**FIGURE 4.** Microscopic structures of *Akanthomyces bannaensis* (Drawn from the Holotype CLZhao 34016). A. Obovoid conidia; B. Ellipsoidal conidia; C. Tramal hypha; D. Phialides at the tip of synnema; E. Phialides arising from tramal hypha.

***Host*:**—Adult moth (*Dudusa sphingiformis*, Notodontidae, Lepidoptera).

***Habit*:**—On the adults of *Dudusa sphingiformis* attached to the underside of the leaves of an angiosperm.

***Distribution*:**—CHINA. Yunnan Province, Dai Autonomous Prefecture of Xishuangbanna, Jinghong, Menglun Town.

***Additional specimen examined (paratype)*:**—CHINA. Yunnan Province, Dai Autonomous Prefecture of Xishuangbanna, Jinghong, Menglun Town, 21°55′N, 101°13′E, elev. 544 m, on the underside of leaves of an angiosperm, 9 October 2023, leg. C.L. Zhao, CLZhao 34017 (SWFC F0034017), GenBank No. (ITS PP571896; nLSU PP571898).

***Notes*:**—*Akanthomyces bannaensis* was found only in its anamorph state on an adult *Dudusa sphingiformis*, while *A. pyralidarum* was reported on an adult of the family Pyralidae sp. In fact, this new species is easily distinguished from other known species of *Akanthomyces* by occurring on an adult of *Dudusa sphingiformis* and synnemata arising from a moth body up to 5 cm long and 0.1–1.3 mm wide, unbranched, cylindrical to clavate with acute or blunt end (Table 2).

**TABLE 2.** Morphological comparisons of *Akanthomyces bannaensis* and its closely related *Akanthomyces* species used in this study.

| Species name | Host | Synnemata | Phialides | Conidia | References |
|---|---|---|---|---|---|
| *Akanthomyces aculeatus* | Adult moth (Sphingidae; Noctuidae) | Yellowish, cylindrical, narrowing upward, 1–8 mm long and 0.1–0.5 mm wide | Subcylindric to narrowly ellipsoidal, 6–16 × 2.5–4 µm | Ellipsoidal or obovoid, 3–6 × 2–3 µm | Mains 1950, Sanjuan *et al.* 2014 |
| *Akanthomyces bannaensis* | Adult moth (*Dudusa sphingiformis*) | White to cream, unbranched, cylindrical to clavate with acute or blunt end, up to 5 cm long and 0.1–1.3 mm wide | Cylindrical with papillate end, (7–)8–10 × (2.2–)2.5–3.8 µm | Ellipsoidal or obovoid, (3.8–)4–5.8 × 2–3 µm | This study |
| *Akanthomyces laosensis* | Adult moth (Noctuidae) | White, rarely branched, feathery to clavate with acute or blunt ends, up to 15.6 mm long and 0.6–1.3 mm wide | Cylindrical, 11.5–30.0 × 2.0–4.2 µm | Cylindrical or long oval, 4.1–9.8 × 2.3–4.2 µm | Wang *et al.* 2024 |
| *Akanthomyces noctuidarum* | Adult moth (Noctuidae) | White to cream, simple, cylindrical to clavate, (650–)668–1191(–1500) × (50–)53–102(–120) µm | Cylindrical with papillate end, (5–)6.8–9(–10) × (1.8–)2–2.4(–3) µm | Cylindrical with round end, (3–)3.5– 4.7(–6) × 1 µm | Aini *et al.* 2020 |
| *Akanthomyces pseudonoctuidarum* | Adult moth (Noctuidae) | Cream to light yellow, erect, simple, cylindrical to clavate, 800–2000 × 120–350 µm | Phialides verticillate, usually in whorls of 2–3 or solitary on hyphae, cylindrical with papillate end, hyaline, 6.8–26.0 × 2.1–3.6 µm | Cylindrical, 6.5–13.8 × 1.8–3.6 µm | Wang *et al.* 2024 |
| *Akanthomyces tortricidarum* | Adult moth (Tortricidae) | Long synnemata white to cream, rarely branched, cylindrical to clavate with acute or blunt end, up to 5 mm long and ca. 120–150 µm wide | Cylindrical to ellipsoidal with papillate end, (5–)6–8(–10) × (1.8–)2–2.7(–3) µm | Fusoid, (2–)2.5–3(–3.2) × 1–2 µm | Aini *et al.* 2020 |
| | | Short synnemata white to cream, cylindrical with subglobose or oblong at the end, (197–)200–267(–300) × (15–)17.7–31.6(–40) µm, with diameter of the tip (43–)51.5–73(–75) µm | Cylindrical to ellipsoidal with papillate end, (5–)6.2–8.3(–10) × (1.8–)2–2.5(–3) µm | Fusoid, (1–)1.8–2.7(–3) × 1–2 µm | |
| *Akanthomyces tuberculatus* | Adult moth (Lepidoptera) | White to creamish, simple, occasionally branched, cylindrical to clavate and stipitate, 1–6 mm long and 50–300 µm wide | Cylindrical, 7–10.5 × 2.7–3.5 µm | Cylindrical to narrowly fusiform, 4.5–6 × 1.2–1.5 µm | Aini *et al.* 2020 |

## Discussion

The phenotypic characteristics of the collections such as having the cylindrical to narrowly clavate synnemata and superficial perithecia scattered on the body and wings of the moth, identify them primarily to be members of *Akanthomyces* in the family Cordycipitaceae, and are mostly similar to *Akanthomyces tuberculatus* (Lebert) Spatafora, Kepler & B. Shrestha (2017: 343), with subtle differences in morphology and growth patterns. *Akanthomyces* comprises at least 33 species with major host/substrate associations (Table 1). Based on the phylogenetic analyses and morphological characteristics, *A. bannaensis* is identified as a new species. However, the isolate did not yield conidia or reproductive structures when cultured on potato dextrose agar medium (PDA).

The new species' phylogenetic position was evaluated based on combined ITS, nLSU, and *RPB2* (Fig. 1). The pairwise homoplasy index (PHI) test (Fig. 2) confirmed no recombination in the new species compared to the closely related taxa. Based on phylogenetic and morphological evidence, the taxon *A. bannaensis* is proposed as a new species.

Amongst the hosts of the fungal genus *Akanthomyces*, Araneae and Lepidoptera are the two major animal orders. The genus *Akanthomyces* species hosting the adult moths are a monophyletic group in our phylogenetic analysis, with similar statistical support as Wang *et al.* (2024). Eight species with adult moth entomopathogens formed the monophyletic group as *A. aculeatus*, *A. bannaensis*, *A. laosensis*, *A. noctuidarum* Aini, Luangsa-ard, Mongkols. & Thanakitp. (2020: 9), *A. pseudonoctuidarum* Hong Yu bis & Y. Wang (2024: 124), *A. pyralidarum*, *A. tortricidarum*, and *A. tuberculatus*. Phylogenetically, *A. bannaensis* is closely related to *A. pyralidarum* in the combined partial ITS+nLSU+*RPB2* sequences dataset (Fig. 1). However, *A. pyralidarum* differs from *A. bannaensis* by its presence on an adult of Pyralidae sp. (Aini *et al.* 2020) and ITS sequence differences of more than 3%.

*Akanthomyces* parasitizes adult moths consisting of eight species with subtle variations in morphology and growth patterns. Morphologically, *Akanthomyces bannaensis* resembles six similar species *viz. A. aculeatus*, *A. laosensis*, *A. noctuidarum*, *A. pseudonoctuidarum*, *A. tortricidarum*, and *A. tuberculatus*. A morphological comparison of *A. bannaensis* and six species is presented in Table 2.

Many invertebrate-pathogenic fungi were recently reported from China (Chen *et al.* 2017, 2018, 2019, 2020a, 2020b, 2022, 2023, Wang *et al.* 2023, 2024), and *A. bannaensis* is described in the present study from southwestern China, which represents the eighteenth species of *Akanthomyces* reported in China.

## Acknowledgements

The research was supported by the National Natural Science Foundation of China (Project nos. 32170004), the High-level Talents Program of Yunnan Province (Project no. YNQR-QNRC-2018-111), and the Yunnan Province College Students Innovation and Entrepreneurship Training Program (Project no. s202310677028, s202310677041).

## References

Afandhi, A., Widjayanti, T., Emi, A.A.L., Tarno, H., Afiyanti, M. & Handoko, R.N.S. (2019) Endophytic fungi *Beauveria bassiana* balsam accelerates growth of common bean (*Phaeseolus vulgaris* L.). *Chemical and Biological Technologies in Agriculture* 11 (6): 2–6. https://doi.org/10.1186/s40538-019-0148-1

Aini, A.N., Mongkolsamrit, S., Wijanarka, W., Thanakitpipattana, D., Luangsaard, J.J. & Budiharjo, A. (2020) Diversity of *Akanthomyces* on moths (Lepidoptera) in Thailand. *MycoKeys* 71: 1–22. https://doi.org/10.3897/mycokeys.71.55126

Boudier, E. (1885) Note sur un nouveau genre et quelques nouvelles especes des Pyrenomycetes. *Revue Mycologique Toulouse* 7: 224–227.

Bruen, T.C., Philippe, H. & Bryant, D. (2006) A simple and robust statistical test for detecting the presence of recombination. *Genetics* 172: 2665–2681. https://doi.org/10.1534/genetics.105.048975

Chen, W.H., Han, Y.F., Liang, Z.Q. & Jin, D.C. (2017) *Lecanicillium araneogenum* sp. nov., a new araneogenous fungus. *Phytotaxa* 305 (1): 29–34. https://doi.org/10.11646/phytotaxa.305.1.4

Chen, W.H., Liu, C., Han, Y.F., Liang, J.D. & Liang, Z.Q. (2018) *Akanthomyces araneogenum*, a new Isaria-like araneogenous species. *Phytotaxa* 379 (1): 66–72. https://doi.org/10.11646/phytotaxa.379.1.6

Chen, W.H., Liu, C., Han, Y.F., Liang, J.D., Tian, W.Y. & Liang, Z.Q. (2019) *Akanthomyces araneicola*, new araneogenous species from Southwest China. *Phytotaxa* 409 (4): 227–232. https://doi.org/10.11646/phytotaxa.409.4.5

Chen, W.H., Han, Y.F., Liang, J.D. & Liang, Z.Q. (2020a) *Akanthomyces neocoleopterorum*, a new *verticillium*-like species. *Phytotaxa*

432 (2): 119–124.
https://doi.org/10.11646/phytotaxa.432.2.2

Chen, W.H., Han, Y.F., Liang, J.D. & Liang, Z.Q. (2020b) *Akanthomyces lepidopterorum*, a new lecanicillium-like species. *Phytotaxa* 459 (2): 117–123.
https://doi.org/10.11646/phytotaxa.459.2.3

Chen, W.H., Liang JD, Ren, X.X., Zhao, J.H., Han, Y.F. & Liang, Z.Q. (2022) Species diversity of *Cordyceps*-like fungi in the Tiankeng karst region of China. *Microbiology Spectrum* 10 (5): e01975–e22.
https://doi.org/10.1128/spectrum.01975-22

Chen, W.H., Liang, J.D., Ren, X.X., Zhao, J.H. & Han, Y.F. (2023) Study on species diversity of *Akanthomyces* (Cordycipitaceae, Hypocreales) in the Jinyun Mountains, Chongqing, China. *MycoKeys* 98: 299–315.
https://doi.org/10.3897/mycokeys.98.106415

Deep White Printing Team (2022) *COMPLETE PROCESS COLOR CHART & Four-color superimposition gold and silver*. High Color International Publishing House, Hong Kong. pp. 1–135.

Dong, J.H., Li, Q., Yuan, Q., Luo, Y.X., Zhang, X.C., Dai, Y.F., Zhou, Q., Liu, X.F., Deng, Y.L., Zhou, H.M., Muhammad, A. & Zhao, C.L. (2024) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. *Mycosphere* 15 (1): 1110–1293.
https://doi.org/10.5943/mycosphere/15/1/10

Gams, W. & Zare, R. (2001) A revision of *Verticillium* sect. *Prostrata*. III. Generic classification. *Nova Hedwigia* 72 (3–4): 329–337.
https://doi.org/10.1127/nova.hedwigia/72/2001/329

Hsieh, L.S., Tzean, S.S. & Wu, W.J. (1997) The genus *Akanthomyces* on spiders from Taiwan. *Mycologia* 89 (2): 319–324.
https://doi.org/10.1080/00275514.1997.12026788

Hu, Y., Karunarathna, S.C., Li, H., Galappaththi, M.C., Zhao, C.L., Kakumyan, P. & Mortimer, P.E. (2022) The impact of drying temperature on basidiospore size. *Diversity* 14 (4): 239.
https://doi.org/10.3390/d14040239

Huson, D.H. & Bryant, D. (2006) Application of phylogenetic networks in evolutionary studies. *Molecular Biology and Evolution* 23: 254–267.
https://doi.org/10.1093/molbev/msj030

Kalyaanamoorthy, S., Minh, B.Q., Wong, T.K.F., von Haeseler, A. & Jermiin, L.S. (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* 14: 587–589.
https://doi.org/10.1038/nmeth.4285

Kepler, R.M., Sung, G.H., Ban, S., Nakagiri, A., Chen, M.J., Huang, B., Li, Z. & Spatafora, J.W. (2012) New teleomorph combinations in the entomopathogenic genus *Metacordyceps*. *Mycologia* 104 (1): 182–197.
https://doi.org/10.3852/11-070

Kepler, R.M., Luangsa-ard, J.J., Hywel-Jones, N.L., Quandt, C.A., Sung, G.H., Rehner, S.A., Aime, M.C., Henkel, T.W., Sanjuan, T., Zare, R., Chen, M.J., Li, Z.Z., Rossman, A.Y., Spatafora, J.W. & Shrestha, B. (2017) A phylogenetically-based nomenclature for Cordycipitaceae (Hypocreales). *IMA Fungus* 8 (2): 335–353.
https://doi.org/10.5598/imafungus.2017.08.02.08

Kinoshita, H., Wongsuntornpoj, S., Ihara, F. & Nihira, T. (2017) Anti-Rhodotorula activity of mycophenolic acid enhanced in the presence of polyene antibiotic nystatin. *Letters in Applied Microbiology* 64 (2): 144–149.
https://doi.org/10.1111/lam.12692

Kuephadungphan, W., Phongpaichit, S., Luangsa-ard, J.J. & Rukachaisirikul, V. (2014) Antimicrobial activity of invertebrate-pathogenic fungi in the genera *Akanthomyces* and *Gibellula*. *Mycoscience* 55 (2): 127–133.
https://doi.org/10.1016/j.myc.2013.06.007

Larsson, A. (2014) AliView: a fast and lightweight alignment viewer and editor for large datasets. *Bioinformatics* 30 (22): 3276–3278.
https://doi.org/10.1093/bioinformatics/btu531

Maddison, W.P. & Maddison, D.R. (2021) Mesquite: a modular system for evolutionary analysis, version 3.70. [http://www.mesquiteproject.org]

Madla, S., Methacanon, P., Prasitsil, M. & Kirtikara, K., (2005) Characterization of biocompatible fungi-derived polymers that induce IL-8 production. *Carbohydrate Polymers* 59 (3): 275–280.
https://doi.org/10.1016/j.carbpol.2004.07.002

Mains, E.B. (1950) Entomogenous species of *Akanthomyces*, *Hymenostilbe* and *Insecticola* in North America. *Mycologia* 42 (4): 566–589.
https://doi.org/10.1080/00275514.1950.12017861

Manfrino, R., Gutierrez, A., Diez del Valle, F., Schuster, C., Ben Gharsa, H., López Lastra, C. & Leclerque, A. (2022) First description of

*Akanthomyces uredinophilus* comb. nov. from Hemipteran insects in America. *Diversity* 14 (12): e1118.
https://doi.org/10.3390/d14121118

Mantzoukas, S. & Lagogiannis, I. (2019) Endophytic colonization of pepper (*Capsicum annum*) controls aphids (*Myzus persicae* Sulzer). *Applied Science* 9 (11): 2–12.
https://doi.org/10.3390/app9112239

Matheny, P.B. (2005) Improving phylogenetic inference of mushrooms with *RPB1* and *RPB2* nucleotide sequences (*Inocybe*; Agaricales). *Molecular Phylogenetics and Evolution* 35 (1): 1–20.
https://doi.org/10.1016/j.ympev.2004.11.014

Miller, M.A., Pfeiffer, W. & Schwartz, T. (2012) The CIPRES science gateway: enabling high-impact science for phylogenetics researchers with limited Resources. *Extreme Science and Engineering Discovery Environment* 39: 1–8.
https://doi.org/10.1145/2335755.2335836

Mongkolsamrit, S., Noisripoom, W., Thanakitpipattana, D., Wutikhun, T., Spatafora, J.W. & Luangsa-Ard, J. (2018) Disentangling cryptic species with *Isaria*-like morphs in Cordycipitaceae. *Mycologia* 110 (1): 230–257.

Park, M.J., Hong, S.B. & Shin, H.D. (2016) *Lecanicillium uredinophilum* sp. nov. associated with rust fungi from Korea. *Mycotaxon* 130 (4): 997–1005.
https://doi.org/10.5248/130.997

Petersen, J.H. (1996) *Farvekort*. *The Danish Mycological Society's colour-chart*. Foreningen til Svampekundskabens Fremme, Greve. pp. 1–6.

Quaedvlieg, W., Binder, M., Groenewald, J.Z., Summerell, B.A., Carnegie, A.J., Burgess, T.I. & Crous, P.W. (2014) Introducing the consolidated species concept to resolve species in the Teratosphaeriaceae. *Persoonia* 33: 1–40.
https://doi.org/10.3767/003158514X681981

Rathnayaka, A.R., Tennakoon, D.S., Jones, G.E., Wanasinghe, D.N., Bhat, D.J., Priyashantha, A.H., Stephenson, S.L., Tibpromma, S. & Karunarathna, S.C. (2024) Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. *New Zealand Journal of Botany*.
https://doi.org/10.1080/0028825X.2024.2381734

Rehner, B. & Buckley, E. (2005) A *Beauveria* phylogeny inferred from ITS and EF1-α sequences: evidence for cryptic diversification and links to *Cordyceps teleomorphs*. *Mycologia* 97 (1): 84–98.
https://doi.org/10.3852/mycologia.97.1.84

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A. & Huelsenbeck, J.P. (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61 (3): 539–542.
https://doi.org/10.1093/sysbio/sys029

Samson, R.A. & Evans, H.C. (1974) Notes on entomogenous fungi from Ghana II. The genus *Akanthomyces Acta Botanica Neerlandica* 23 (1): 28–35.
https://doi.org/10.1111/j.1438-8677.1974.tb00913.x

Sanjuan, T. Tabima, J., Restrepo, S., Læssøe, T., Spatafora, J.W. & Franco-Molano, A.E. (2014) Entomopathogens of Amazonian stick insects and locusts are members of the *Beauveria* species complex (*Cordyceps sensu* stricto). *Mycologia* 106 (2): 260–275.
https://doi.org/10.3852/13-020

Shrestha, B., Kubátová, A., Tanaka, E., Oh, J., Yoon, D.H., Sung, J.M. & Sung, G.H. (2019) Spider-pathogenic fungi within Hypocreales (Ascomycota): their current nomenclature, diversity, and distribution. *Mycological Progress* 18 (8): 983–1003.
https://doi.org/10.1007/s11557-019-01512-3

Vega, F.E., Meyling, N.V., Luangsa-ard, J.J. & Blackwell, M. (2012) Fungal entomopathogens. *In:* Vega, F.E. & Kaya, H.K. (Eds.) *Insect Pathology.* pp. 171–220.
https://doi.org/10.1016/B978-0-12-384984-7.00006-3

Vilgalys, R. & Hester, M. (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172 (8): 4238–4246.
https://doi.org/10.1128/jb.172.8.4238-4246

Wang, Y.B., Wang, Y., Fan, Q., Duan, D.E., Zhang, G.D., Dai, R.Q., Dai, Y.D., Zeng, W.B., Chen, Z.H., Li, D.D., Tang, D.X., Xu, Z.H., Sun, T., Nguyen, T.T., Tran, N.L., Dao, V.M., Zhang, C.M., Huang, L.D., Liu, Y.J., Zhang, X.M., Yang, D.R., Sanjuan, T., Liu, X.Z., Yang, Z.L. & Yu, H. (2020) Multigene phylogeny of the family Cordycipitaceae (Hypocreales): New taxa and the new systematic position of the Chinese cordycipitoid fungus *Paecilomyces hepiali*. *Fungal Diversity* 103 (1): 1–46.
https://doi.org/10.1007/s13225-020-00457-3

Wang, Y., Wang., Z.Q., Luo, R., Souvanhnachit, S., Thanarut, C., Dao, V.M. & Yu, H. (2024) Species diversity and major host/substrate associations of the genus *Akanthomyces* (Hypocreales, Cordycipitaceae). *MycoKeys* 101: 113–141.

https://doi.org/10.3897/mycokeys.101.109751

Wang, Y.H., Wang, W.J., Wang, K., Dong, C.H., Hao, J.R., Kirk, P.M. & Yao, Y.J. (2023) *Akanthomyces zaquensis* (Cordycipitaceae, Hypocreales), a new species isolated from both the stroma and the sclerotium of *Ophiocordyceps sinensis* in Qinghai, China. *Phytotaxa* 579 (3): 198–208.
https://doi.org/10.11646/phytotaxa.579.3.5

White, T.J., Bruns, T., Lee, S. & Taylor, J. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *In:* Innis, M.A., Gelfand, D.H., Sninsky, J.J. & White, T.J. (eds.) *PCR protocols: A guide to methods and applications.* Academic Press, San Diego, pp. 315–322.
https://doi.org/10.1016/B978-0-12-372180-8.50042-1.

Zhang, X.C., Li, Y.C., Wang, Y.Y., Xu, Z., Zhao, C.L. & Zhou, H.M. (2024) *Xylodon asiaticus* (Hymenochaetales, Basidiomycota), a new species of corticioid fungus from southern China. *Phytotaxa* 634 (1): 1–15.
https://doi.org/10.11646/phytotaxa.634.1.1

Zhao, C.L., Qu, M.H., Huang, R.X. & Karunarathna, S.C. (2023) Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). *Journal of Fungi* 9: 320.
https://doi.org/10.3390/jof9030320