Asian Journal of Mycology 6(1): 98–106 (2023) ISSN 2651-1339

www.asianjournalofmycology.org **Article**

Doi 10.5943/ajom/6/1/9

A new species of *Stephanonectria* (*Bionectriaceae*) from southwestern China

He SC[1,2,3], Wei DP[1,3,4*], Bhunjun CS[1,2], Zhao Q[3] and Jayawardena RS[1,2*]

[1] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[2] *School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[3] *Yunnan Key Laboratory of Fungal Diversity and Green Development, Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan 650201, China*
[4] *Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand*

He SC, Wei DP, Bhunjun CS, Zhao Q, Jayawardena RS 2023 – A new species of *Stephanonectria* (*Bionectriaceae*) from southwestern China. Asian Journal of Mycology 6(1), 98–106, Doi 10.5943/ajom/6/1/9

Abstract

A new species, *Stephanonectria ellipsoidea*, was isolated from decaying fruit in Kunming City, Yunnan Province, China. It is characterized by pale orange colonies, densely clustered, irregularly branched conidiophores, cylindrical phialides, and hyaline, ellipsoidal conidia. Its morphology fits well with the generic concept of *Stephanonectria*. This species is closely related to *S. keithii* based on phylogenetic analysis of concatenated LSU and ITS sequences. The combination of morphological observation and molecular data supports the erection of the new species.

Keywords – Asexual morph – Fruits – Hypocreales – New species

Introduction

Bionectriaceae (*Hypocreales*) was introduced by Rossman et al. (1999) and typified with *Bionectria*. The sexual-asexual connection between *Bionectria* and *Clonostachys* has been monographed by Schroers (2001). *Bionectriaceae* species were commonly encountered in soil or associated with bryophytes as symbionts (Döbbeler 2004), with plants as endophytes (White et al. 1993), epiphytes, saprotrophs (Torcato et al. 2020), and with lichen as parasites (Farkas & Flakus 2016). The sexual genus *Bionectria* subsequently was considered a synonym of the asexual genus *Clonostachys* (Rossman et al. 2013). Wijayawardene et al. (2022) listed 47 genera in *Bionectriaceae*, of which 14 genera (*Acremonium*, *Bryocentria*, *Clonostachys*, *Fusariella*, *Geosmithia*, *Gliomastix*, *Hydropisphaera*, *Ijuhya*, *Lasionectria*, *Nectriella*, *Nectriopsis*, *Pronectria*, *Protocreopsis*, *Trichonectria*) have more than ten species. Most genera in *Bionectriaceae* contain species with insufficient molecular data (Hyde et al. 2020a). Before the molecular era, the identification of nectriaceous fungi was based on the nature of stroma, perithecial surface characteristics and ascospore morphology (Forin et al. 2020). *Bionectriaceae* has typical features of nectriaceous fungi, but it can be separated from *Nectriaceae* by having white to orange or brown perithecia, which do not change colour in 3% potassium hydroxide (KOH) or 100% lactic acid (LA) (Rossman et al. 1999), while that of the latter family are orange to red and turning dark red or purple in KOH and yellow in LA (Hirooka et al. 2010). *Bionectriaceae* has been described as

Submitted 3 April 2023, Accepted 30 May 2023, Published 13 June 2023
Corresponding Author: Ruvishika S. Jayawardena – e-mail –ruvi.jaya@yahoo.com
De P Wei – e-mail – dp.wei.elina@qq.com

having ascomata that are perithecial or cleistothecial, superficial on the substrate or embedded in poorly or well-developed stroma, clavate to cylindrical asci, and ascospores ranging from aseptate to multi-septate, globose, fusiform to ellipsoidal (Hyde et al. 2020b). Several conidiophore structures, including acremonium-like, gliocladium-like or penicillium-like, have been recorded from *Bionectriaceae* (Hyde et al. 2020a). Generally, the establishment of the new genus and species in *Bionectriaceae* was based on molecular data: *act*-*rpb1*-LSU (Hirooka et al. 2010), ITS-*tub*-*rpb2*-*tef1α* (Grum-Grzhimaylo et al. 2013), LSU, *rpb1*, *rpb2*, *tef1α* (Voglmayr & Jaklitsch 2019), individual ITS (Forin et al. 2020), LSU-ITS (Trovão et al. 2022).

Stephanonectria was introduced by Schroers (1999) to accommodate *S. keithii* which was initially recognized as a member of *Nectria*, but this species was excluded from *Nectria* because of its crown-like structure around the ostiole (Schroers 1999). *Stephanonectria keithii* has been phylogenetically confirmed as a member of *Bionectriaceae* by several studies (Castlebury et al. 2004, Supaphon et al. 2017, Zeng & Zhuang 2018). *Stephanonectria* is characterised by forming brown, smooth, solitary to crown perithecia on flat superficial to erumpent stroma (Schroers et al. 1999). Perithecia are subglobose with slightly flat apex where the crowns are produced surrounding the ostioles. The colour of perithecia does not change in KOH. Asci are clavate and contain uniseriate to biseriate ascospores that are hyaline, ellipsoidal, 1–2-celled, and longitudinally oriented striae (Schroers et al. 1999).

In this study, dried fruits colonized by white to pale orange mycelia were collected from a forest in Yunnan Province, China. This isolate was identified as a new species of *Stephanonectria* on the basis of molecular and morphological evidence.

Materials & Methods

Collection, isolation and morphological study

Samples were surveyed from a deciduous forest near Songhuaba Reservoir in Kunming City, Yunnan Province, China. The specimens were collected into zip-lock bags and transported to the laboratory for further examination. The fungal colonies on dried fruit were observed using a Nikon SMZ 745T dissecting microscope. A small mass of mycelia was mounted in water on a slide using a sterile needle. A NIKON ECLIPSE Ni-U compound microscope was used to observe conidiophores and conidia. The micro-morphological images were photographed using a DS-Ri2 camera fitted onto the compound microscope. The images used for the figure were processed with Adobe Photoshop. Pure cultures were obtained via single spore isolation using potato dextrose agar (PDA) as described in Senanayake et al. (2020) and incubated at 25 °C for one week. The living cultures were deposited in the Kunming Institute of Botany Culture Collection (KUNCC). The dried specimens were deposited in the Herbarium of Cryptogamic Kunming Institute of Botany Academia Sinica (KUN) at the Chinese Academy of Sciences, Kunming, China. Facesoffungi and Index Fungorum numbers were registered following the protocol described in Jayasiri et al. (2015) and Index Fungorum (2023), respectively.

DNA extraction, PCR amplification and sequencing

DNA was extracted from mycelia growing on a PDA plate using Trilief™ Plant Genomic DNA Kit (Tsingke biological technology Co., LTD, Beijing, China), following the instructions of the manufacturer. Primers ITS5/ITS4 (White et al. 1990) and LROR/LR7 (Vilgalys & Hester 1990) were used for the amplification of the ITS and LSU sequences, respectively. Polymerase chain reaction (PCR) was performed in a 25 µl reaction volume containing 21 µl Taq PCR Master Mix (TSINGKE TSE101, Tsingke Biotechnology Co., Ltd., Beijing, China), 1 µl of each primer, and 2 µl of DNA template. PCR conditions of ITS and LSU were as follows: initialization for 5 min at 98 °C, followed by 40 cycles of denaturation for 30 s at 98 °C, annealing for 40 s at 53 °C and elongation for 30 s at 72 °C, and final extension for 10 min at 72 °C. The PCR products were visualized using agarose gel electrophoresis, and those with the targeted bands were sent to Tsingke

Biotech Co. Ltd., Kunming, China, for sequencing. The newly generated sequences were submitted to GenBank for assignment of accession numbers.

Sequence alignment and phylogenetic analyses

The raw sequences were assembled with Sequencing Project Management (SeqMan) (Clewley 1995). The assembled sequences were compared with the data in GenBank to determine their close relatives. The blast result shows that our specimens have a close affinity with species of *Bionectriaceae*. Reference sequences representing 11 genera of *Bionectriaceae* were sampled following Perera et al. (2023) and are presented in Table 1. Each gene matrix was independently aligned with MAFFT v 6.8 (Katoh et al. 2019). The aligned datasets were manually edited using BioEdit v. 7.0.9 (Hall 1999) and combined with SequenceMatrix v. 1.7.8 (Vaidya et al. 2011). The combined alignment was used for maximum likelihood (ML) and Bayesian inference (BI) analyses.

Maximum likelihood analysis was performed using RAxML-HPC2 on XSEDE (8.2.10) in CIPRES Science Gateway V. 3.3 (Miller et al. 2010), employing default parameters but with the following adjustments: bootstrap iterations were set to 1000, and the substitution model was set to GTR+GAMMA+I. Mrmodeltest v. 2.3 was used to select the best model for each gene. Bayesian Inference analysis was carried out in MrBayes v3.2.6 (Ronquist et al. 2012). Six simultaneous Markov Chain Monte Carlo (MCMC) chains were run for 500,000 generations, and trees were sampled at every 1000th generation until the standard deviation of the split frequencies fell below 0.01. The phylogenetic trees were summarized, and posterior probabilities (PP) were calculated by discarding the first 25% of generations as the burn-in phase (Huelsenbeck & Ronquist 2001). The phylogenetic tree was visualized using FigTree v.1.4.0 and edited with Adobe Illustrator 2020 (Adobe Systems Incorporated, America).

Results

Phylogenetic analyses

The combined ITS and LSU dataset comprised 43 taxa, with *Calcarisporium arbuscula* (CBS:900.68), *C. arbuscula* (CBS:552.66) and *C. xylariicola* (IT 1264) as the outgroup taxa. The dataset consisted of 1307 total characters, including gaps (LSU: 1–805 bp and ITS: 806–1307). The matrix had 438 distinct alignment patterns, with 22.21% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0. 239146, C = 0. 244522, G = 0. 291527, T = 0. 224805; substitution rates: AC = 2.292484, AG = 3.067293, AT = 2.505902, CG = 1.061138, CT = 8.264153, GT = 1.000000; gamma distribution shape parameter α = 0.621905. The best-scoring RAxML tree with a final likelihood value of -7395.876990 is presented in Fig. 1. The tree topology obtained from ML analysis is similar to the one inferred from BI analysis. Our isolates formed a distinct clade sister to *Stephanonectria keithii* with 99% ML bootstrap support and 1.00 posterior probability support (Fig. 1).

Table 1. GenBank accession numbers of the taxa used in the phylogenetic analyses in this study.

Taxon name	Culture collection number	GenBank accession numbers	
		LSU	ITS
Calcarisporium arbuscula	**CBS:900.68**	**MH870978**	**MH859249**
C. arbuscula	CBS:552.66	MH870538	MH858880
C. xylariicola	**IT 1264**	**KX442601**	**KX442603**
Clonostachys agarwalii	CBS:533.81	N/A	MH861375
C. agarwalii	MFLU:19-0976	OM276821	OM276726
C. aureofulvella	CBS 195.93	N/A	AF358226
C. aranearum	**GZAC-QLS0625**	**N/A**	**KT895417**
C. buxi	CBS 696.93	KM231721	KM231840

Table 1. Continued.

Taxon name	Culture collection number	GenBank accession numbers	
		LSU	ITS
C. candelabrum	P6634	MN308617	MN310304
C. candelabrum	P6636	MN308618	MN310305
Heleococcum aurantiacum	CBS:201.35	MH867154	MH855645
H. japonense	CBS 397.67	JX158442	JX158420
Lasionectria antillana	**CBS 122797**	**KY607552**	**KY607537**
L. krabiense	**MFLUCC 15-0673**	**MH376725**	**MH388352**
L. lecanodes	NE322	N/A	MH393445
L. lecanodes	NE321	N/A	MH393446
L. oenanthicola	**CBS 129747**	**KY607557**	**KY607542**
Lasionectriella herbicola	**CBS 140156**	**KU593582**	**N/A**
L. rubioi	**CBS 140157**	**KU593581**	**N/A**
Nectriopsis exigua	CBS:126110	MH875481	MH864022
N. exigua	CBS:400.66	MH870474	MH858837
N. fuliginicola	**CBS 400.82**	**N/A**	**KU382175**
Ochronectria calami	CBS125.87	AY489717	N/A
O. thailandica	**MFLUCC 15-0140**	**KU564069**	**KU564071**
Paracylindrocarpon aloicola	**CPC 27362**	**KX228328**	**KX228277**
P. nabanheensis	**KUMCC 16-0147**	**MH376730**	**MH388356**
P. pandanicola	**KUMCC 17-0272**	**MH376731**	**MH388357**
Protocreopsis caricicola	**CLL15081**	**KU198184**	**N/A**
P. euphorbiae	**CPC 38896**	**OK663739**	**OK664700**
P. korfii	**CBS 138733**	**KT852955**	**N/A**
P. pertusa	C.T.R. 72-184	GQ506002	N/A
P. phormiicola	CBS:567.76	MH872774	MH861001
Roumegueriella rufula	GJS 91-164	EF469082	N/A
R. rufula	CBS 346.85	DQ518776	N/A
Stephanonectria chromolaenae	**MFLUCC 18-0589**	**ON230059**	**ON230051**
S. ellipsoidea	**HKAS 124022**	**OP205363**	**OP205375**
S. ellipsoidea	HKAS 124024	OP205362	OP205374
S. keithii	CBS:943.72	MH878469	N/A
S. keithii	CBS:434.70	MH871546	MH859783
S. keithii	GJS92-133	AY489727	N/A
Synnemellisia acaciae	**BRIP 71652**	**N/A**	**OK342123**
S. aurantia	**COAD:2070**	**KX866396**	**KX866395**
S. urenae	**BRIP 71675**	**OK342135**	**N/A**

Notes: The newly generated sequences are shown in red, while the type strains are in bold font. N/A means the data are not available in GenBank.

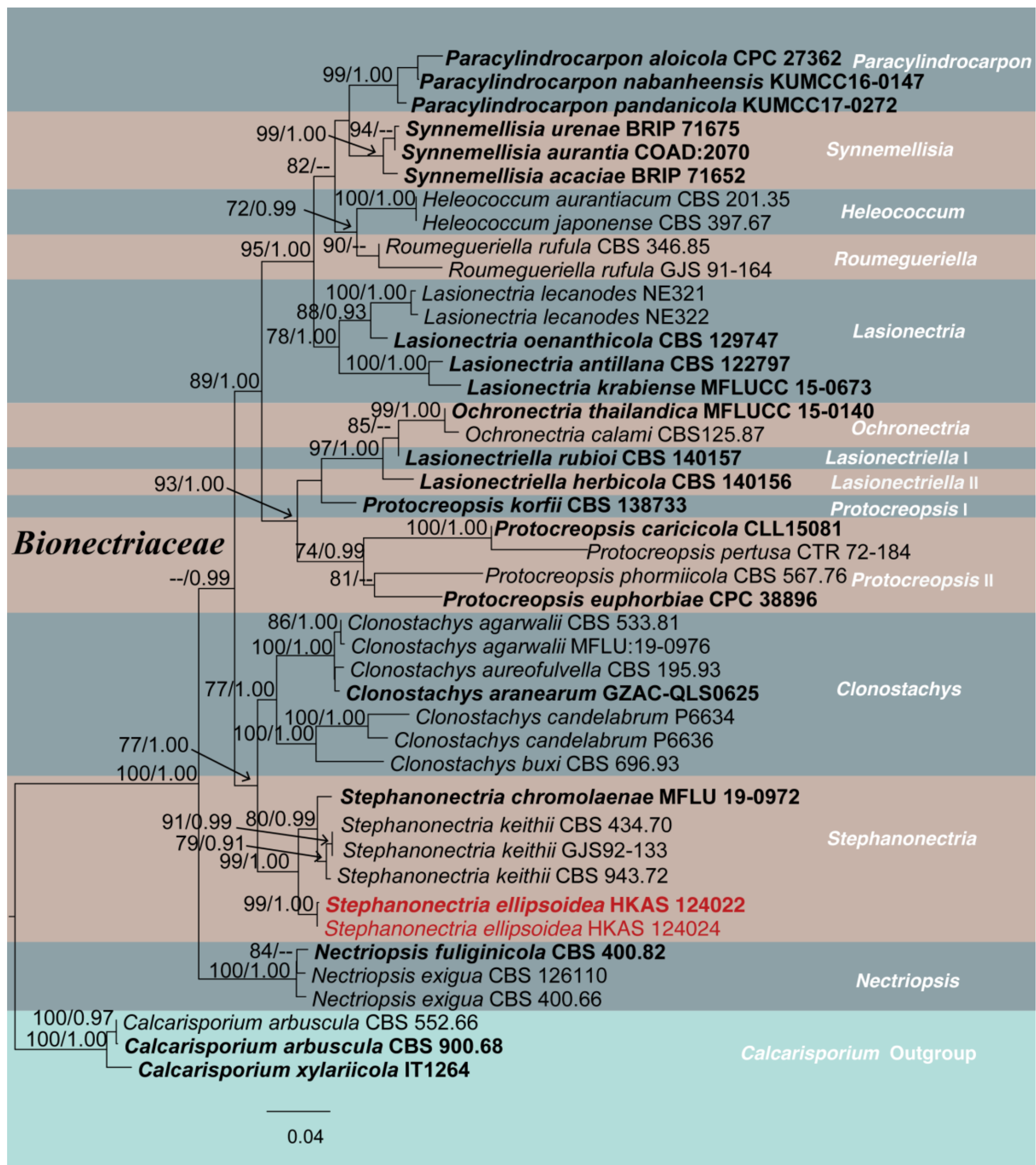

Fig. 1 – Phylogram generated from maximum likelihood analysis based on concatenated LSU and ITS sequence data. Maximum likelihood bootstrap support values (MLBS) equal to or greater than 70% and Bayesian posterior probabilities (BYPP) equal to or higher than 0.90 are placed on the nodes. The type strains are in bold, and the newly generated sequences are indicated in red bold.

Stephanonectria ellipsoidea S.C. He, D.P. Wei & R.S. Jayawardena sp. nov. Fig. 2

Index Fungorum number: IF900157; Facesoffungi number: FoF 13351

Etymology – The specific epithet refers to the ellipsoidal conidia of this fungus

Saprobic on decaying fruit of an unidentified plant. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate surface pale orange, irregularly shaped, effuse, dense, smooth. *Conidiophores* micronematous, penicillate, sporodochial, straight or flexuous, irregularly branched, aseptate, hyaline, smooth-walled, terminal branches developing into phialides, 67–101 × 2.4–3.3 µm ($\bar{x}$ = 84 × 3 µm, n = 10). *Phialides* monophialidic, flask-shaped, discrete, hyaline, smooth-walled, 11.3–14.3 × 2.1–2.9 µm ($\bar{x}$ = 12.8 × 2.5 µm, n = 20). *Conidia* solitary, acrogenous, oblong with obtuse ends, amerospores, minutely guttulate, hyaline, smooth-walled,

6.2–6.8 × 3.3–3.7 µm ($\bar{x}$ = 6.5 × 3.5 µm, n = 30), germinating on the substrate. On PDA, *Conidiophores* monomorphic, penicillate, sporodochial, straight or flexuous, irregularly branched, smooth-walled, hyaline. *Phialides* monophialidic, flask-shaped, discrete, hyaline, 11.2–14.2 × 2.2–2.8 µm ($\bar{x}$ = 12.7 × 2.5 µm, n = 20). *Conidia* amerospores, acrogenous, ellipsoidal, smooth-walled, guttulate, hyaline, 6.2–6.6 × 3.3–3.5 µm ($\bar{x}$ = 6.4 × 3.4 µm, n = 30).

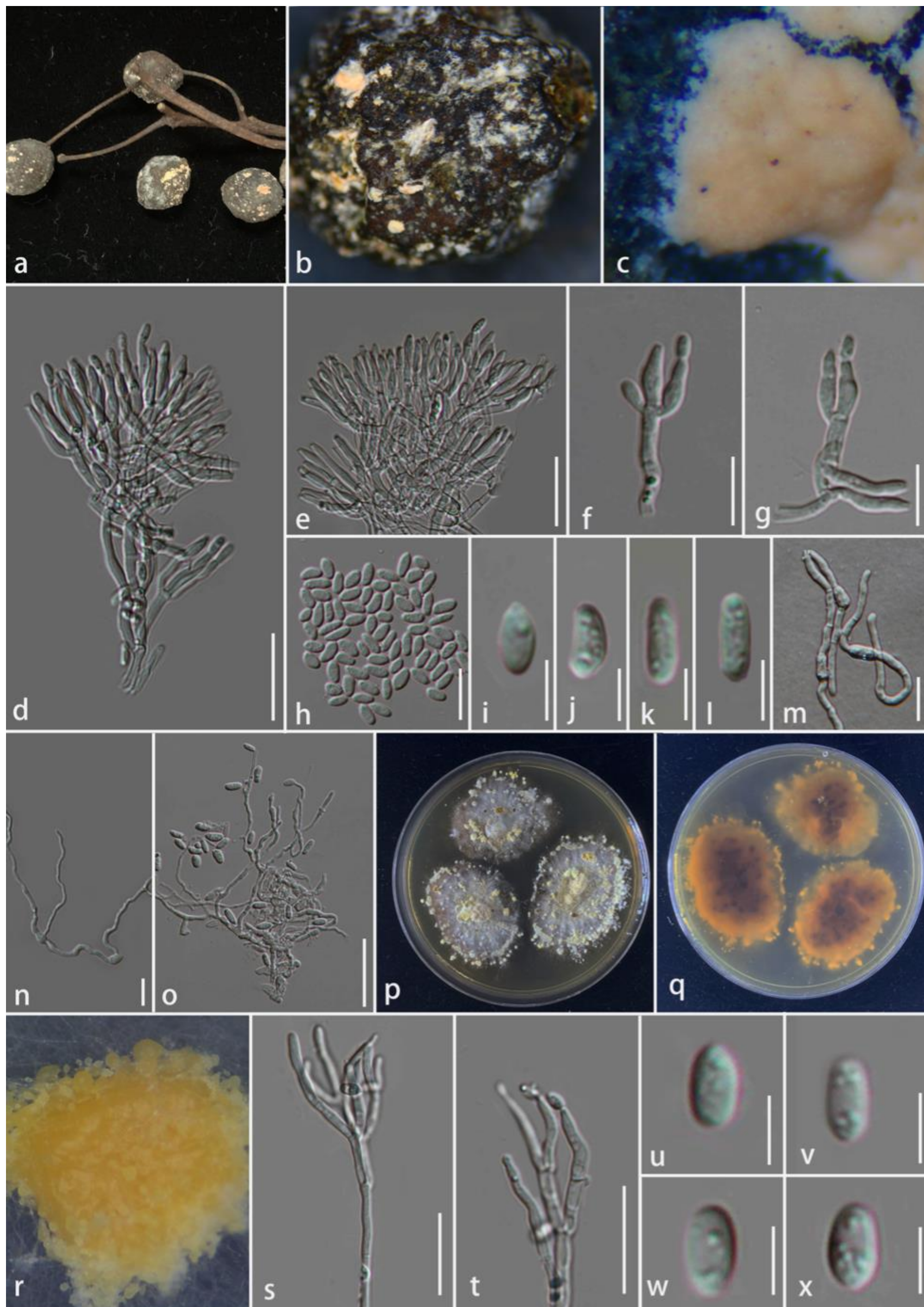

Fig. 2 – *Stephanonectria ellipsoidea* (HKAS124022, holotype). (a–o from the substrate, p–x from culture). a–c Colonies on natural substrate. d, e, s Conidiophores. f, g, t Phialides. h–l, u–x Conidia. m–o Germinating conidia. p, q Upper and lower view of culture on PDA. r Sporodochia formed on the PDA surface. Scale bars: m, o, s, t = 25 µm, d, e, h = 20 µm, f, g, n = 10 µm, i–l, u–x = 5 µm.

Culture characteristics – Conidia germinating within 12 h on the PDA media at 25 °C, reaching 2.3–2.5 cm after 20 days of incubation, colony white, nearly circular, flat, surface rough, fimbriate, mycelia medium sparse, sporodochia formed on PDA in concentric rings.

Material examined – China, Yunnan province, Kunming City, Panglong District, forest near to Songhuaba reservoir, on dried fruit of a woody plant, 1 December 2021, Shu-Cheng He, HSC203 (HKAS 124022, holotype), ex-type living culture, KUNCC 22-12394; *ibid.* HSC323 (HKAS 124024, paratype); living culture, KUNCC22-12395.

Notes – Phylogenetically, our isolates (HKAS124022) formed a monophyletic clade with *Stephanonectria keithii* and *S. chromolaenae* with 99% ML bootstrap support and 1.00 posterior probability support (Fig. 1). *Stephanonectria ellipsoidea* morphologically resembles *S. keithii* and *S. chromolaenae* in having penicillate conidiophore, flask-shaped phialides and ellipsoidal conidia (Schroers et al. 1999). It is hard to distinguish *S. ellipsoidea* from *S. keithii* and *S. chromolaenae* solely based on morphological observation. However, the comparison of nucleotide sequences between our new species and *S. keithii* (CBS 434.70) shows 35 bp differences and 6 bp differences across 521 bp ITS and 795 bp LSU sequences, respectively. Our new species and *S. chromolaenae* (MFLUCC 18-0589) are different in 28 bp and 14 bp across 516 bp ITS and 795 bp LSU sequences, respectively.

Discussion

In this study, the phylogenetic analysis was conducted based on concatenated LSU and ITS sequence data of 41 ingroup taxa representing 11 genera of *Bionectriaceae*. The other 36 genera of this family have not been included in this phylogenetic analysis due to the lack of molecular sequence data. Even though the generic relationship in this tree was well supported, *Lasionectriella* and *Protocreopsis* were polyphyletic groups. The asexual morph has been observed from 11 genera of *Bionectriaceae*. They are *Bullanockia* (Crous et al. 2016), *Clonostachys* (Hyde et al. 2020a, Torcato et al. 2020), *Heleococcum* (Bilanenko et al. 2005), *Lasionectriella* (Lechat & Fournier, 2016), *Nectriella* (Crous et al. 2022), *Paracylindrocarpon* (Tibpromma et al. 2018), *Protocreopsis* (Crous et al. 2021), *Stephanonectria* (Schroers et al. 1999), *Stromatonectria* (Jaklitsch & Voglmayr 2011), and *Xanthonectria* (Lechat et al. 2016). Morphologically, *Stephanonectria* is similar to *Gliocladium* and *Clonostachys* (Schroers et al. 1999). This indicates that molecular data and morphological features of fresh collections are needed to determine the natural classification of taxa in *Bionectriaceae*.

Stephanonectria has been reported in hosts, including *Brassica* sp, soil and dead stem of *Chromolaena odorata* (*Asteraceae*), mainly distributed in Europe (England, France), Japan, New Zealand, Netherlands and Thailand (Perera et al. 2023, Schroers et al. 1999). In this study, we collected a saprobic *S. ellipsoidea* that occurs on dried fruit from a deciduous forest plant in Yunnan Province, China. Morphologically, our isolate is characterized by forming penicillate conidiophores that aggregate in clusters forming superficial sporodochia with pale orange mucoid spore masses. The phialides are monophialidic with minute collarette, cylindrical, smooth-walled, and tapering toward the apex. These features have been reported in *Clonostachys, Protocreopsis* and *Stephanonectria*. However, the phylogenetic analysis supports our isolates having a close relationship with *Stephanonectria*. Thus, we determine our isolate as a new species of *Stephanonectria*.

Acknowledgements

This study is supported by the Second Tibetan Plateau Scientific Expedition and Research (STEP) Program (Grant No. 2019QZKK0503), the Flexible introduction of high-level expert program, Kunming Institute of Botany, Chinese Academy of Sciences (Grant No. E1644111K1). Chitrabhanu S. Bhunjun would like to thank the National Research Council of Thailand (NRCT) grant “Total fungal diversity in a given forest area with implications towards species numbers, chemical diversity and biotechnology” (grant no. N42A650547).

References

Bilanenko E, Sorokin D, Ivanova M, Kozlova M. 2005 – *Heleococcum alkalinum*, a new alkali-tolerant *ascomycete* from saline soda soils. Mycotaxon 91, 497–507.

Castlebury LA, Rossman AY, Sung GH, Hyten AS, et al. 2004 – Multigene phylogeny reveals new lineage for *Stachybotrys chartarum*, the indoor air fungus. Mycological Research 108, 864–872.

Clewley JP. 1995 – Macintosh sequence analysis software - DNAStar's LaserGene. Molecular Biotechnology 3, 221–224.

Crous PW, Wingfield MJ, Burgess TI, Crane C, et al. 2016 – Fungal Planet description sheets 469–557, 218–403.

Crous PW, Osieck ER, Jurjević Ž, Boers J, et al. 2021 – Fungal Planet description sheets 1284–1382, 178–374.

Crous PW, Boers J, Holdom D, Osieck ER, et al. 2022 – Fungal Planet description sheets 1383–1435, 261–371.

Döbbeler P. 2004 – *Bryocentria* (*Hypocreales*), a new genus of bryophilous ascomycetes. Mycological Progress 3, 247–56.

Farkas E, FlAKuS A. 2016 – *Trichonectria calopadiicola* sp. nov. *Hypocreales*, *Ascomycota*: the second species of the family *Bionectriaceae* parasitic on foliicolous lichens discovered in Tanzania. Phytotaxa 278, 281–286.

Forin N, Vizzini A, Nigris S, Ercole E, et al. 2020 – Illuminating type collections of nectriaceous fungi in Saccardo's fungarium. Persoonia 45, 221–249.

Grum-Grzhimaylo AA, Georgieva ML, Debets AJ, Bilanenko EN. 2013 – Are alkalitolerant fungi of the *Emericellopsis lineage* (*Bionectriaceae*) of marine origin. IMA fungus 4, 213–28.

Hall T. 1999 – BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41, 95–98.

Hirooka Y, Kobayashi T, Ono T, Rossman AY, et al. 2010 – *Verrucostoma*, a new genus in the *Bionectriaceae* from the Bonin Islands, Japan. Mycologia 102, 418–429.

Huelsenbeck JP, Ronquist F. 2001 – MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17, 754–755.

Hyde KD, Dong Y, Phookamsak R, Jeewon R, et al. 2020a – Fungal diversity notes: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 1151–1276.

Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ, et al. 2020b – Refined families of *Sordariomycetes*. Mycosphere 11, 305–1059.

Jaklitsch WM, Voglmayr H. 2011 – *Stromatonectria* gen. nov. and notes on *Myrmaeciella*. Mycologia 103, 431–440.

Katoh K, Rozewicki J, Yamada KD. 2019 – MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20, 1160–1166.

Lechat C, Fournier J. 2016 – *Lasionectriella*, a new genus in the *Bionectriaceae*, with two new species from France and Spain, *L. herbicola* and *L. rubioi*. Ascomycete.Org 8, 59–65.

Lechat C, Fournier J, Moreau PA. 2016 – *Xanthonectria*, a new genus for the nectrioid fungus *Nectria pseudopeziza*. Ascomycete.Org 8, 172–178.

Miller MA, Pfeiffer W, Schwartz T. 2010 – Gateway Computing Environments Workshop. 2010 Gateway Computing Environments Workshop.

Perera RH, Hyde KD, Jones EBG, Maharachchikumbura SSN, et al. 2023 – Profile of *Bionectriaceae*, *Calcarisporiaceae*, *Hypocreaceae*, *Nectriaceae*, *Tilachlidiaceae*, *Ijuhyaceae* fam. nov., *Stromatonectriaceae* fam. nov. and *Xanthonectriaceae* fam. nov. Fungal Diversity 118, 95–271.

Ronquist F, Teslenko M, Mark P, Ayres DL, et al. 2012 – Mrbayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61, 539–542.

Rossman AY, Samuels GJ, Rogerson CT, Lowen R. 1999 – Genera of *Bionectriaceae*, *Hypocreaceae* and *Nectriaceae* (*Hypocreales*, *Ascomycetes*). Studies in Mycology 42, 0166–0616.

Rossman AY, Seifert KA, Samuels GJ, Minnis AM. et al. 2013 – Genera in *Bionectriaceae*, *Hypocreaceae*, and *Nectriaceae* (*Hypocreales*) proposed for acceptance or rejection. IMA Fungus 4, 41–51.

Schroers HJ. 2001 – A monograph of *Bionectria* (*Ascomycota*, *Hypocreales*, *Bionectriaceae*) and its *Clonostachys* anamorphs. Studies in Mycology 46, 1–214

Schroers HJ, Samuels GJ, Gams W. 1999 – *Stephanonectria*, a new genus of the *Hypocreales* (*Bionectriaceae*), and its sporodochial anamorph. Sydowia 51, 114–126.

Supaphon P, Phongpaichit S, Sakayaroj J, Rukachaisirikul V, et al. 2017 – Phylogenetic community structure of fungal endophytes in seagrass species. Botanica Marina 60, 489–501.

Tibpromma S, Hyde KD, McKenzie EHC, Bhat DJ, et al. 2018 – Fungal diversity notes: micro-fungi associated with *Pandanaceae*. Fungal Diversity 93, 840–928.

Torcato C, Goncalves MFM, Rodríguez-Gálvez E, Alves A. 2020 – *Clonostachys viticola* sp. nov., a novel species isolated from *Vitis vinifera*. International Journal of Systematic and Evolutionary Microbiology 70, 4321–4328.

Trovão J, Soares F, Paiva DS, Tiago I, et al. 2022 – *Circumfusicillium cavernae* gen. et sp. nov. (*Bionectriaceae*, *Hypocreales*) Isolated from a Hypogean Roman Cryptoporticus. Journal of Fungi 8, 837.

Vaidya G, Lohman DJ, Meier R. 2011 – SequenceMatrix: Concatenation software for the fast assembly of multi-gene datasets with character set and codon information. Cladistics 27, 171–180.

Vilgalys R, Hester M. 1990 – Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172, 4238–4246.

Voglmayr H, Jaklitsch WM. 2019 – *Stilbocrea walteri* sp. nov., an unusual species of *Bionectriaceae*. Mycological progress 18, 91–105.

White TJ, Bruns T, Lee S, Taylor J. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications 18, 315–322.

White JF, Morgan-Jones G, Morrow AC. 1993 – Taxonomy, life cycle, reproduction and detection of *Acremonium endophytes*. Agriculture, Ecosystems & Environment 44, 13–37.

Wijayawardene N, Hyde KD, Dai D, Sánchez-García M, et al. 2022 – Outline of Fungi and fungus-like taxa. Mycosphere 13, 53–453.

Zeng Z-Q, Zhuang W-Y. 2018 – Discovery of a second species of *Hyalocylindrophora* and the phylogenetic position of the genus in *Bionectriaceae*. Mycologia 110, 941–947.