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New Species

中国海南异斑衣属 *Synarthonia* (斑衣菌科、斑衣菌目)一新种

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摘　要：本研究根据形态学、化学及系统发育分析发现异斑衣属 *Synarthonia* 一新种——海南异斑衣 *Synarthonia hainanensis*，该种分布于中国海南省。其主要特征为地衣体白绿色；子囊果短线状至长线状，红棕色至黑色，无粉霜；子实层遇碘变红紫色；子囊顶环 K/I 无反应；子囊孢子透明，具 4 横隔，呈长卵圆形，大小为 18–24.5 × 6.5–9.5 μm，顶端细胞增大。本文提供了该新种的分子数据、分类学描述、形态学和解剖学特征图片以及与相似物种区别的讨论。此外，本文提供了世界已知该属 25 种地衣的分种检索表。
关键词：地衣型真菌；形态学；系统发育学；分类学；新种

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A new species of *Synarthonia* (Arthoniaceae, Arthoniales) from Hainan Province, tropical China

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Abstract: Based on morphological, chemical, and phylogenetic analyses, a new species of the lichenized fungal genus *Synarthonia*, *Synarthonia hainanensis*, is described. This species is currently known only from Hainan Province. *Synarthonia hainanensis* is characterized by whitish-green thallus, short lirelliform

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to elongate, reddish-brown to black and epruinose ascomata, I+ reddish-purple hymenium, K/I- blue distinct ocular chamber in the asci, hyaline, 4-septate, and oblong-ovoid ascospores with the size of 18–24.5 × 6.5–9.5 μm. Molecular data, detailed taxonomic description, and images illustrating the morphological and anatomical characteristics of the new species are provided. A discussion on the differences between the new species and its similar species is also included. In addition, a key to 25 species of this genus is presented herein.

Keywords: lichenized fungi; morphology; phylogeny; taxonomy; new species

The genus *Synarthonia* Müll. Arg. was described by Johannes Müller Argoviensis, with *Synarthonia bicolor* Müll. Arg. from Costa Rica designated as the type species (Müller 1891). Joseph & Sinha (2015) noted that *Reichlingia* Diederich & Scheid (Frisch *et al.* 2014) and *Synarthonia* shared the morphological features of the individual ascomata, and they suggested the synonymy of *Reichlingia* and *Synarthonia*. Subsequently, van den Broeck *et al.* (2018) reaffirmed *Synarthonia* as a distinct genus within the Arthoniaceae and reinstated its taxonomic status, based on an integrated analysis of molecular and morphological data. They described six new species, established ten new combinations, and provided an identification key for the 20 known species of the genus, thereby clarifying the phylogenetic position of *Synarthonia* within the Arthoniaceae.

The genus *Synarthonia* is characterized by ascomata often aggregated in clusters, and *Arthonia*-type asci producing transversely septate ascospores with enlarged apical cell or muriform ascospores (Joseph & Sinha 2015; van den Broeck *et al*. 2018). Additional diagnostic features include: white, greyish or orange-pruinose, pale brown and almost translucent or blackish-brown disc with thallus remnants, 8-spored asci, and the presence or absence of K/I+ blue ring-like structures in the tholus. These characters are also used to distinguish species within the genus (Cannon *et al*. 2020).

Wei (2020) documented eight genera of Arthoniaceae from China. However, the only *Synarthonia* species, *S. lopingensis* (Zahlbr.) van den Broeck, Frisch & Ertz, was recorded under the name *Arthonia lopingensis* Zahlbr. In the present study, we provide a key to all known *Synarthonia* species and present a phylogenetic tree illustrating the position of the new species within the genus, based on chemical, morphological, and molecular data.

1 MATERIALS AND METHODS

1.1 Morphological and chemical analyses

The specimen examined was collected from Hainan Province of China and deposited in the Fungarium of Liaocheng University (LCUF). An Olympus dissecting microscope (SZX16) and an Olympus light microscope (BX53) were used for morphological and anatomical studies. Spot tests with K (10% aqueous solution of potassium hydroxide), C (saturated solution of aqueous sodium hypochlorite), P (saturated solution of p-phenylenediamine in 95% ethylalcohol), and UV (fluorescence at 365 nm) were performed on the surface of thallus. The lichen substances were detected and identified using a UV light source and thin-layer chromatography (TLC) in solvent C (Orange *et al*. 2001).

1.2 DNA extraction, PCR sequencing and phylogenetic analysis

Genomic DNA was extracted from the ascomata and thallus of the specimen using DNA secure Plant Kit (Tsingke) according to the manufacturer's instructions. The mtSSU region was amplified using the primer pair mtSSU1/3R (Zoller *et al.* 1999). Polymerase chain reaction cycling conditions were set to an initial denaturation at 95 ℃ for 5 min; followed by 35 cycles of denaturation at 95 ℃ for 45 s, annealing at 50 ℃ for 1 min, extension at 72 ℃ for 1.5 min; and a final extension at 72 ℃ for 10 min (He & Jia 2023). The PCR products were checked on 1% electrophoresis gels stained with ethidium bromide, and sequenced by Tsingke Biotech Co., Ltd.

The new sequence was assembled *via* Geneious v.9.0.2 (Biomatters Ltd.), and compared with available sequences in the GenBank database (http://www.ncbi.nlm.nih.gov/BLAST/). All available sequences of *Synarthonia* were selected for further analysis (Table 1), with *Herpothallon inopinatum* Frisch & G. Thor (belonging to Arthoniaceae, Arthoniales) as the outgroup. The assembled sequences were aligned with the online version of

MAFFT v.7 (https://mafft.cbrc.jp/alignment/server/, accessed on 6 October 2025). Ambiguously aligned regions were delimited using Gblocks v.0.91b with the least stringent selection (Castresana 2000). Geneious v.2025.0.2 was used to concatenate the mtSSU and RPB2 genes and produce a two-locus dataset. Maximum likelihood (ML) analysis and Bayesian inference (BI) were used to infer phylogenetic trees based on the concatenated mtSSU and RPB2 datasets. The maximum likelihood analysis was conducted with the RAxML-HPC 2 on ACCESS v.8.2.12 employing a GTRGAMMA approximation with a rapid bootstrap analysis of 1 000 replicates on the CIPRES scientific gateway portal (http://www.phylo.org/portal2/, accessed on 6 October 2025) for verification (Miller *et al*. 2010; Stamatakis 2014). For BI analysis, PartitionFinder 2 (Lanfear *et al*. 2017) was used to determine the best-fit model for each partition. Based on the results, the GTR+F+I+G4 model was used for mtSSU and the GTR+F+I+G4 model for RPB2. Bayesian Inference phylogenies were inferred using MrBayes v.3.2 under partition model (Ronquist *et al*. 2012). A run with 2 million generations, in which the initial 25% of sampled data were discarded as burn-in. Bayesian inference posterior probability (BIPP) equal to and above 95% was considered significant support and shown at the nodes. Generated phylogenetic trees were visualized under Figtree v.1.4.4 and edited in Adobe Illustrator CC2019 software.

Table 1 The specimens and sequences used in the phylogenetic analysis

Species	Specimen voucher	GenBank accession number	
		mtSSU	RPB2
Arthonia apotheciorum	Sweden; Frisch 11/Se23 (UPS)	KJ850970	KJ851148
Arthonia calcarea	France; Ertz 7539 (BR)	EU704064	EU704028
Arthonia radiata	Sweden; Frisch 11/Se25 (UPS)	KJ850969	KJ851109
Arthonia subfuscicola	Sweden; Frisch 11/Se15 (UPS)	KJ850972	KJ851111
Coniocarpon cinnabarinum	Norway; Johnsen 111003 (UPS)	KJ850976	KJ851103
Coniocarpon cinnabarinum 1	Uganda; Frisch 11/Ug297 (UPS)	KJ850977	KJ851104
Coniocarpon cinnabarinum 2	Uganda; Frisch 11/Ug296 (UPS)	KP870158	KP870170
Coniocarpon cinnabarinum 3	Rwanda; Ertz 8730 (BR)	EU704046	EU704009
Coniocarpon fallax	Great Britain (L10175)	KJ850979	KJ851101
Herpothallon inopinatum	Mexico; Rudolphi 12 (UPS)	KJ850964	KJ851099
Reichlingia leopoldii	Belgium; Ertz 13294 (BR)	JF830774	HQ454723
Reichlingia syncesioides	Uganda; Frisch 11/Ug14 (UPS)	KF707651	KF707656
Reichlingia zwackhii	Sweden; Thor 26800 (UPS)	KF707652	HQ454655
Synarthonia aurantiacopruinosa	DR Congo; van den Broeck 5764 (BR)	MH251874	MH271697
Synarthonia albopruinosa	DR Congo; van den Broeck 6086 (BR)	MH251873	MH271696
Synarthonia fuscata	DR Congo; van den Broeck 6101 (BR)	MH251875	MH271706
Synarthonia hainanensis	**China; HN250146 (LCUF)**	**PX404716**	**NA**
Synarthonia inconspicua 1	Florida; Common 10048 (hb Common)	MH251878	NA
Synarthonia inconspicua 2	Madagascar; Ertz 19739A (BR)	MH251879	MH271700
Synarthonia inconspicua 3	Uganda; van den Broeck 6325 (BR)	MH251880	MH271701
Synarthonia inconspicua 4	Tanzania; van den Broeck 7013B (BR)	MH251881	MH271702
Synarthonia inconspicua 5	Tanzania; van den Broeck 7034 (BR)	MH251882	MH271703
Synarthonia josephiana	Madagascar; Ertz 19739B (BR)	MH251876	MH271698
Synarthonia muriformis 1	Uganda; Frisch 11/Ug41 (UPS)	KJ851025	KJ851100
Synarthonia muriformis 2	Madagascar; Ertz 19344 (BR)	MH251877	MH271699
Synarthonia ochracea	France; van den Broeck 6653 (BR)	MH251884	MH271705
Synarthonia pilosella	Rwanda; Ertz 7808 (BR)	MH251883	MH271704

Notes: Newly generated sequence is shown in bold.

2 RESULTS AND DISCUSSION

2.1 Phylogenetic analyses

Twenty-seven specimens comprising 52 DNA sequences (27 mtSSU sequences and 25 RPB2 sequences), including 1 mtSSU sequences newly generated in this study were used (Table 1). Phylogenetic trees obtained from ML and BI showed the same topology; therefore, only the Bayesian tree is presented here, with BS ≥ 70% for ML analysis and PP ≥ 0.95 for Bayesian analysis.

In the phylogenetic tree (Fig. 1), the main well-supported lineages of *Synarthonia* are following the results obtained by van den Broeck *et al*. (2018). The specimen of *Synarthonia hainanensis* sp. nov. forms a well-supported monophyletic clade (72/0.95, BS/PP) (Fig. 1). Based on the differences in phylogeny and morphology compared to other species, *Synarthonia hainanensis* is described here as new to science.

2.2 Taxonomy

Synarthonia hainanensis C.Y. Hao, S.H. Jiang & Z.F. Jia, **sp. nov.** Fig. 2

Fungal Names: FN 573014

Chinese name: 海南异斑衣

Etymology: The specific epithet *hainanensis* refers to the type locality, Hainan Province.

Diagnosis: The new species externally resembles *Synarthonia fuscata* van den Broeck & Ertz., but differs by the longer asci with the presence of a K/I- blue ring-like structure, and the longer, broader ascospores.

Type: China. Hainan Province: Baisha County, Yinggeling Nature Reserve, alt. 605 m, on bark, 1 January 2025, Shuhao Jiang HN250146 (Holotype, LCUF; GenBank PX404716 for mtSSU).

Description: Thallus whitish-green, smooth, continuous to cracked. Prothallus a black to brown

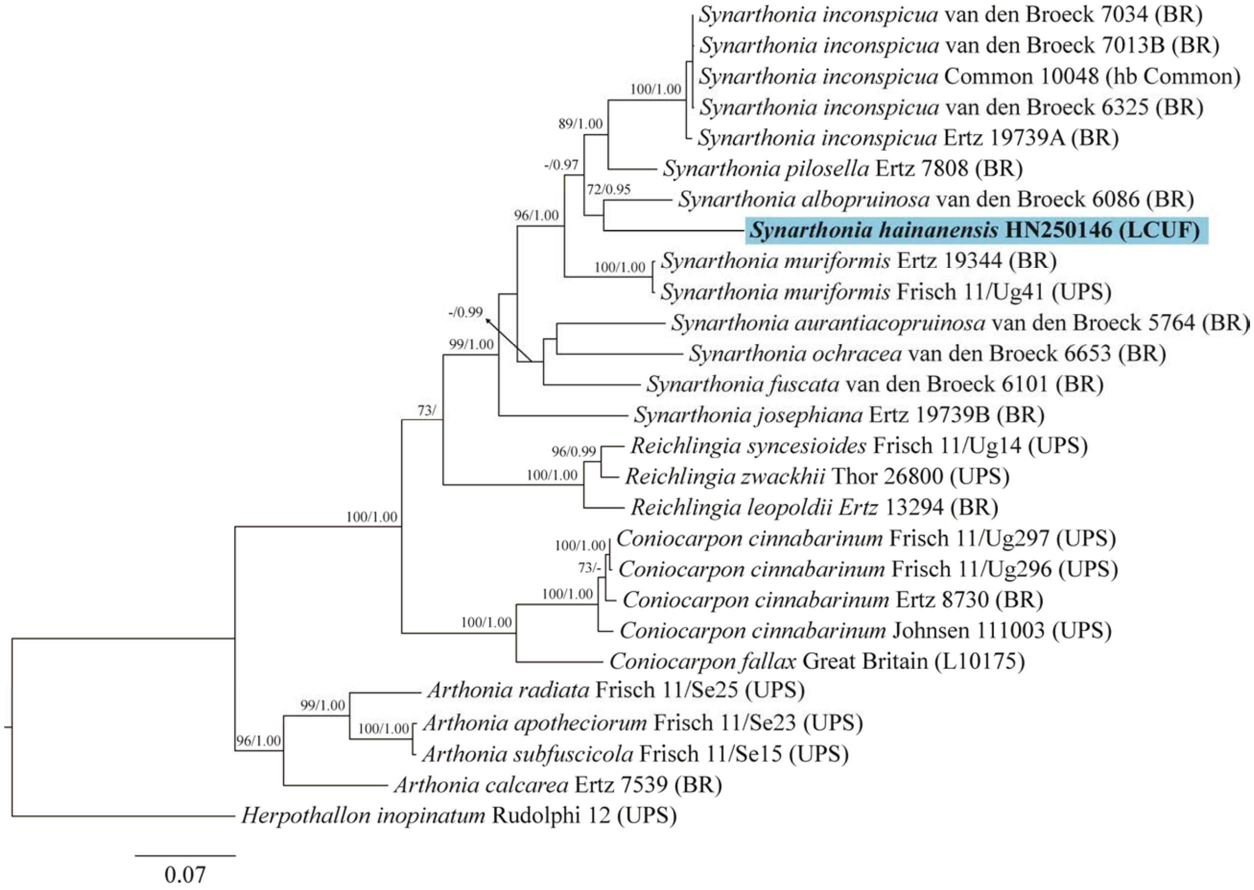

Fig. 1 Phylogenetic tree of the family Arthoniaceae constructed from ML analyses based on a two-gene dataset (mtSSU and RPB2). Bayesian inference posterior probabilities above 0.95 (left) and maximum likelihood bootstrap support above 70% (right) are shown at nodes [left: bootstrap value (BS)/right: posterior probability (PP)]. The new sequence generated in this study is in bold font.

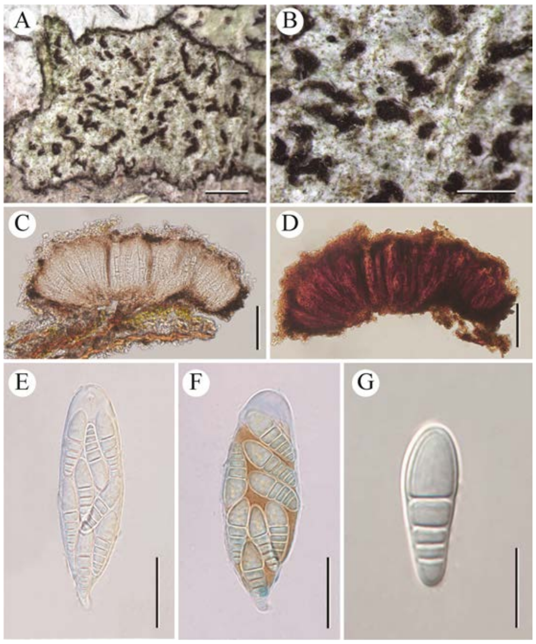

Fig. 2 *Synarthonia hainanensis* (LCUF HN250146). A, B: Thallus with ascomata; C: Apothecium section; D: Apothecium section, I+ redish-purple; E: Ascus, with 8 ascospores; F: Ascus in 10% KOH stained with Lugol's solution; G: Ascospores in water. Bars: A=2 mm; B=0.2 mm; C, D=50 μm; E, F=20 μm; G=10 μm.

compact line in contact with other lichens. Photobiont trentepohlioid, forming a distinct algal layer, irregular, angular. Ascomata usually solitary, reddish-brown to black, 0.2–0.9 × 0.15–0.25 mm, lirellate, slightly elevated above thallus level, scattered more or less evenly over the thallus; disc flat and epruinose. Excipulum 15–17.5 μm wide, with loosely intricate hyphae, I+ orange-yellow, inspersed with orange-brown granules which are K+ uncompletely dissolving. Epihymenium 6–12 μm tall, and inspersed with orange-brown granules which are K+ uncompletely dissolving. Hymenium 57–68.5 μm tall, hyaline to pale brown, not inspersed, I+ redish-purple, K/I+ greenish-blue. Paraphysoids loosely intricate around the asci, *ca*. 2 μm, hyaline to light brown. Hypothecium 10–21 μm thick, pale brown, composed of loosely intricate hyphae, inspersed with orange granules, K+ uncompletely dissolving and darken. Asci 8-spored, 45–70.5 × 18–26.5 μm (N=7), clavate, obovoid to ellipsoid, stipitate, occasionally with a distinct ocular chamber, K/I-. Ascospores 18–24.5 × 6.5–9.5 μm (N=20), hyaline, with enlarged apical cell, oblong-ovoid, 4-septate, becoming brown at late maturity sometimes already in the asci. Pycnidia black, more or less immersed or slightly elevated above thallus level. Conidia not observed.

Chemistry: Thallus K-, C-, KC-, UV-. No substances were detected by TLC.

Ecology and distribution: The new species is distributed in tropical forest in Hainan Province of China, growing on bark.

Notes: *Synarthonia fuscata* van den Broeck & Ertz resembles the new species in having epruinose ascomata, but differs by the smaller ascospores and the presence of a K/I+ blue ring-like structure in the ascus. *S. josephiana* resembles the new species in similar ascospores size, but can be distinguished by its rounded, black ascomata, and the presence of a K/I+ blue ring-like structure in the ascus. *Synarthonia sikkimensis* S. Joseph & G.P. Sinha can be distinguished from *S. hainanensis* by its sorediate thallus. The similar species *S. muriformis* and *S. sarcographoides* differ by their muriform ascospores. *Synarthonia albopruinosa*, *S. astroidestera*, *S. aurantiacopruinosa*, *S. borbonica*, *S. ferruginea*, *S. hodgesii*, *S. inconspicua*, *S. karunaratnei*, *S. ochracea*, *S. pilosella*, *S. psoromica*, *S. rimeliicola*, and *S. stigmatidialis* are distinguished from the new species by the presence of pruina on their ascomata.

Key to the species of *Synarthonia*

1. Thallus sorediate	*S. sikkimensis*
1. Thallus esorediate or absent	2
2. Ascospores muriform	3
2. Ascospores transversely septate	5
3. Ascospores 22.0–36.5 × 10.0–14.5 μm	*S. muriformis*
3. Ascospores <22 μm long	4
4. Ascospores 20.0–22.0 × 11.0–12.5 μm	*S. sarcographoides*
4. Ascospores 20–22 × 8–9 μm	*S. xanthosarcographoides*
5. Ascomata epruinose or with remnants of thallus, appearing black or dull brown	6
5. Ascomata distinctly orange or white pruinose, or appearing bright orange	8
6. Ascospores usually 3-septate	*S. fuscata*
6. Ascospores usually 4-septate	7
7. A K/I- blue ring-like structure in the ascus	*S. hainanensis*

7. A K/I+ blue ring-like structure in the ascus ······ *S. josephiana*
8. Ascomata with orange pruina or pigmentation ······ 9
8. Ascomata white or greyish pruinose ······ 16
9. Ascospores consistently 2-septate; 9.0–10.5 × 3.5–4.5 µm ······ *S. karunaratnei*
9. Ascospores with more septa; exceeding 10.5 µm in length ······ 10
10. Ascospores consistently 5-septate; 19.5–27.0 µm ······ *S. ferruginea*
10. Ascospores (2–)3(–4)-septate; not exceeding 20 µm in length ······ 11
11. Hymenium I+ blue, rapidly turning into red ······ 12
11. Hymenium persistently I+ blue [*S. ochracea* complex] ······ 13
12. Ascospores 7.0–8.0 µm broad; asci with a K/I+ blue ring like structure in the tholus ······ *S. borbonica*
12. Ascospores 5.5–6.5 µm broad; asci without a K/I+ blue ring like structure in the tholus ······ *S. aurantiacopruinosa*
13. Ascomata evenly orange, with a non-granulose pigmentation; lichenicolous on *Graphis lineola* in southeastern North America ······ *S. hodgesii*
13. Ascomata brown to brownish black, with orange pruina; lichenized or lichenicolous on *Graphis* species in Cuba, E Asia or Europe ······ 14
14. Ascomata not aggregated in clusters; lichenicolous on unknown *Graphis* species in Cuba ······ *S. ochrodes*
14. Ascomata aggregated in irregular clusters; lichenized or lichenicolous on *Graphis* species in E Asia or Europe ······ 15
15. Ascomata in irregular star-shaped clusters; lichenized or lichenicolous on different species of *Graphis* (including *G. handelii*, *G. intricata* and *G. mikuraensis*) in E Asia (China, Japan) ······ *S. lopingensis*
15. Ascomata in irregular lobed clusters; lichenized or lichenicolous on *Graphis scripta s. lat.* in Europe ······ *S. ochracea*
16. Lichenicolous, independent thallus absent, on thallus of Parmeliaceae ······ *S. rimeliicola*
16. Not lichenicolous, independent thallus present ······ 17
17. Psoromic acid present ······ 18
17. Psoromic acid absent ······ 19
18. Corticolous ······ *S. psoromica*
18. Saxicolous ······ *S. leproidica*
19. Ascospores 9–14 µm wide ······ *S. robertiana*
19. Ascospores <9 µm wide ······ 20
20. Hymenium I+ blue ······ 21
20. Hymenium I+ red or I+ blue turning red ······ 22
21. Ascospores 2-septate ······ *S. xanthonica*
21. Ascospores (3–)4(–5)-septate ······ *S. stigmatidialis*
22. Clusters of ascomata not elongated with individual ascomata arranged in lines and usually not star-shaped ······ *S. inconspicua*
22. Clusters of ascomata mainly elongated with individual ascomata arranged in lines or ascomata star-shaped ······ 23
23. Thallus and ascomata UV- or UV+ pale yellowish (xanthone absent) ······ *S. albopruinosa*
23. Thallus and/or ascomata UV+ brightly orange-yellow (xanthone present, at least patchily) ······ 24
24. Ascomata without hyaline hair like extensions; ascospores 18–24 µm long, (3–)4-septate; hypothecium I+ blue; hymenial disc often thinly pruinose appearing then greyish to dark brown-almost blackish; Europe ······ *S. astroidestera*
24. Ascomata with hyaline hair like extensions; ascospores 14.5–19.0 µm long, (2–)3(–4)-septate; hypothecium I+ red; hymenial disc heavily white pruinose and pale brown-orange when pruina removed; tropical Africa ······ *S. pilosella*

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Author contributions

HAO Chengyue: Methodology, formal analysis, investigation, writing original draft, writing review & editing; CUI Can: Investigation, writing original draft, funding acquisition, supervision; JIANG Shuhua: Investigation, writing review & editing, supervision; JIA Zefeng: Conceptualization, investigation, funding acquisition, supervision.

Declaration of competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

[REFERENCES]

Cannon P, Ertz D, Frisch A, Aptroot A, Chambers S, Coppins B, Sanderson N, Simkin J, Wolseley P, 2020. Arthoniales: Arthoniaceae, including the genera *Arthonia*, *Arthothelium*, *Briancoppinsia*, *Bryostigma*, *Coniocarpon*, *Diarthonis*, *Inoderma*, *Naevia*, *Pachnolepia*, *Reichlingia*, *Snippocia*, *Sporodophoron*, *Synarthonia* and *Tylophoron*. Revisions of British and Irish Lichens, 1: 3-48

Castresana J, 2000. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. Molecular Biology and Evolution, 17: 540-552

Frisch A, Thor G, Sheil D, 2014. Four new Arthoniomycetes from Bwindi Impenetrable National Park, Uganda – supported by molecular data. Nova Hedwigia, 98: 295-312

He XX, Jia ZF, 2023. *Ocellularia arecae*, a new record of the lichen genus *Ocellularia* in China. Journal of Liaocheng University (Natural Science Edition), 36(5): 86-90 (in Chinese)

Joseph S, Sinha GP, 2015. Contributions to the genus *Synarthonia* (lichenized Ascomycota, Arthoniaceae). Lichenologist, 47(2): 123-130

Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B, 2017. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. Molecular Biology and Evolution, 34(3): 772-773

Miller MA, Pfeiffer W, Schwartz T, 2010. Creating the CIPRES science gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Work Shop (GCE), New Orleans, Louisiana. 1-8

Müller J, 1891. Lichenes. In: Durand TH, Pittier H (eds.) Primitiae Florae Costaricensis. Bulletin de la Société Royale de Botanique de Belgique, 30: 49-97

Orange A, James PW, White FJ, 2001. Microchemical methods for the identification of lichens. British Lichen Society, London. 1-101

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP, 2012. MrBayes 3.2: efficient bayesian phylogenetic inference and model choice across a large model space. Systematic Biology, 61(3): 539-542

Stamatakis A, 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics, 30(9): 1312-1313

van den Broeck D, Frisch A, Razafindrahaja T, van de Vijver B, Ertz D, 2018. Phylogenetic position of *Synarthonia* (lichenized Ascomycota, Arthoniaceae), with the description of six new species. Plant Ecology and Evolution, 151(3): 327-351

Wei JC, 2020. An enumeration of lichens in China. China Forestry Publishing House, Beijing. 1-606

Zoller S, Scheidegger C, Sperisen C, 1999. PCR primers for the amplification of mitochondrial small subunit ribosomal DNA of lichen-forming ascomycetes. Lichenologist, 31(5): 511-516

[附中文参考文献]

何宣宣，贾泽峰，2023. 槟榔点衣，中国点衣属地衣一新记录种. 聊城大学学报(自然科学版)，36(5): 86-90