

Amphibambusa hongheensis, a novel bambusicolous ascomycete from Yunnan, China

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Abstract

In the course of an ongoing survey of bambusicolous fungi from southwest China, we discover a novel species, *Amphibambusa hongheensis* on dead bamboo culms in Honghe County of Yunnan Province, China. The novel species is introduced based on the morpho-molecular approach. Morphologically, *A. hongheensis* fits well with *Amphibambusa* and is characterized by immersed, globose to subglobose ascomata, with protruding carbonaceous papilla, unitunicate, cylindrical to elongate fusiform, sessile to short pedicellate asci with a J+, subapical ring, and fusiform, hyaline to pale brown, 1-septate ascospores, with longitudinally striated, and surrounded by a thick mucilaginous sheath. Phylogenetic analyses of a concatenated ITS-LSU sequence dataset based on maximum-likelihood and Bayesian inference criteria revealed the phylogenetic affinity of *A. hongheensis* within Cainiaceae (Xylariales, Sordariomycetes). *Amphibambusa hongheensis* formed an independent subclade sister to *A. bambusicola* and clustered with the genus *Arecophila*. *Amphibambusa hongheensis* is the second species accommodated in *Amphibambusa* and is reported from Yunnan, China, for the first time. *Amphibambusa* is distributed from China and Thailand, and the host occurrence is only known on bamboos as saprobes.

Introduction

A monotypic genus *Amphibambusa* D.Q. Dai & K.D. Hyde was introduced by Liu et al. (2015), with *A. bambusicola* D.Q. Dai & K.D. Hyde as the type species. The genus was documented as a saprobe on bamboo in Thailand (Liu et al. 2015). *Amphibambusa* is a poorly known genus that accommodates only a single species, *A. bambusicola* (Hyde et al. 2020, Index Fungorum 2021). The genus is characterized by immersed, light brown, coriaceous, globose to subglobose, uni-loculate ascomata, with papillate ostiole, located by a white margin, unitunicate, cylindrical, asci with a J+, subapical ring, and fusiform, hyaline, 1-septate ascospores, longitudinally striated, surrounded by a gelatinous sheath. The asexual morph has not been determined yet for the genus (Liu et al. 2015, Hyde et al. 2020). Initially, *Amphibambusa* was placed in Amphisphaeriaceae (*sensu lato*) with limited phylogeny (Liu et al. 2015). However, Senanayake et al. (2015) investigated the phylogenetic relationship of taxa in Xylariomycetidae based on the combined LSU and ITS sequence matrix and reported that *Amphibambusa* should belong to Cainiaceae. In the course of an ongoing survey of bambusicolous fungi from southwest China, a novel species of *Amphibambusa* was discovered from southwest China (Yunnan Province) and is introduced here as *A. hongheensis*.

Materials and Methods

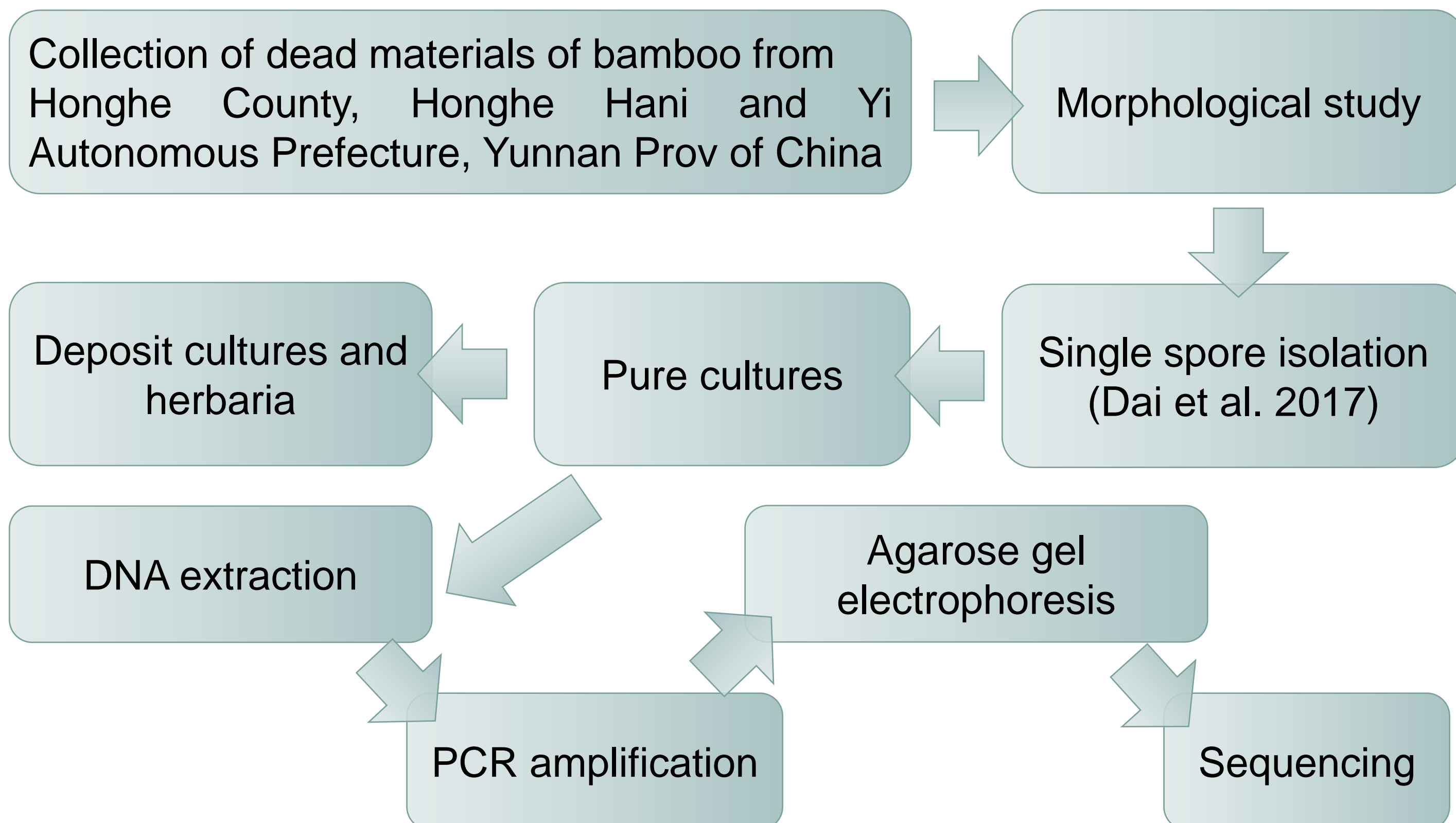


Table 1 Primers to amplify fungal nuclear DNA genes will be used in this study.

| Target gene | Primers | Nucleotide sequence (5' – 3') | References |
|----------------|---------|-------------------------------|------------------------|
| ITS1-5.8S-ITS2 | ITS1 | F: TCCGTAGGTGAACCTGCGG | White et al. 1990 |
| | ITS5 | F: GGAAGTAAAAGTCGTAACAAGG | |
| | ITS4 | R: TCCTCCGCTTATTGATATGC | |
| 28S rDNA | LROR | F: ACCCGCTGAACCTAAGC | Vilgalys & Hester 1990 |
| | LR5 | R: TCCTGAGGGAACTTCG | |

Data Analysis

SEQUENCE QUALITY, CONSENSUS SEQUENCE AND BLASTN



TRIM ALIGNMENT, FORMAT CONVERSION, MODELTEST AND PHYLOGENETIC ANALYSES



Results

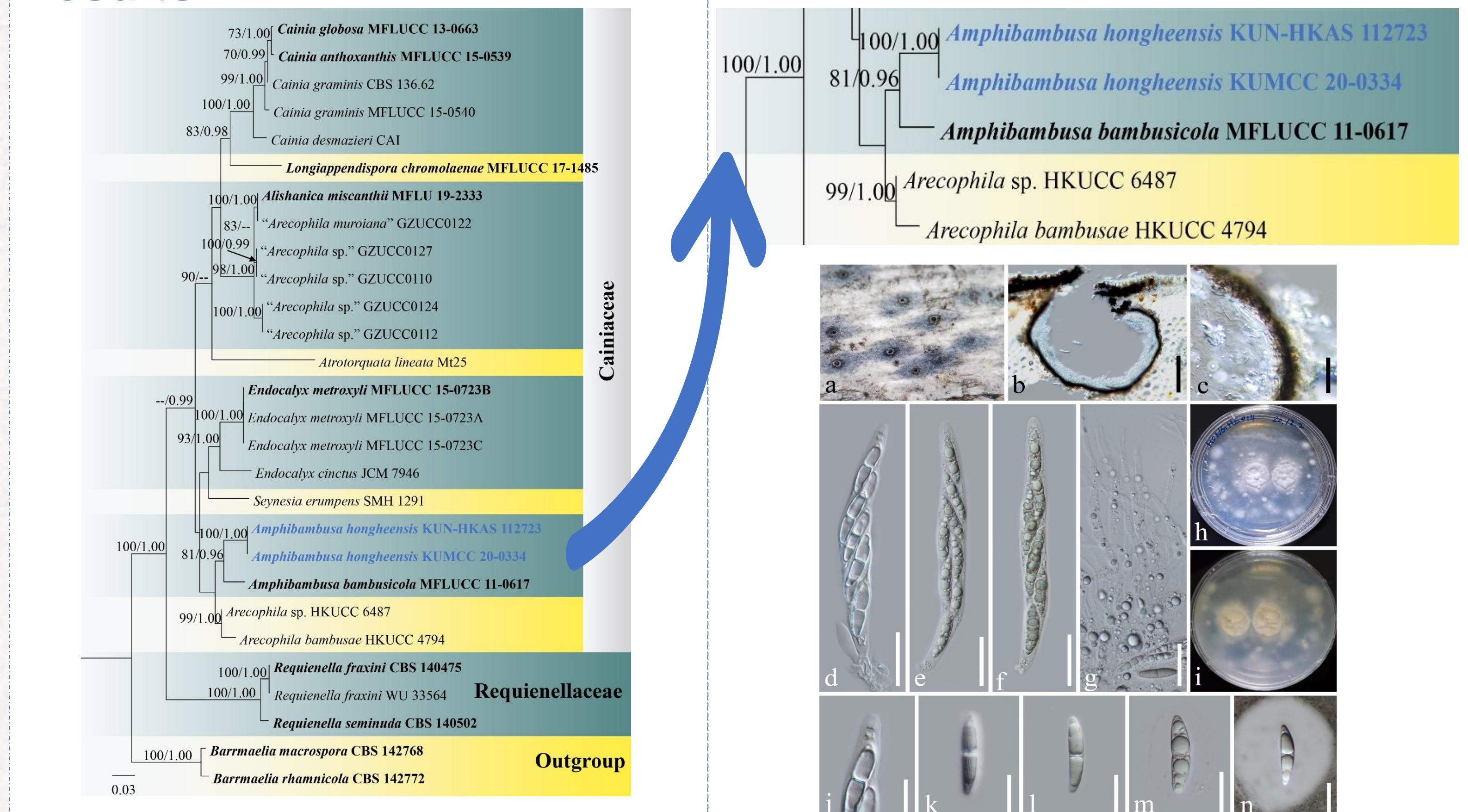


Fig. 1 Maximum likelihood tree based on RAXML analysis of a concatenated ITS-LSU sequence dataset to represent the phylogenetic relationships of taxa in Cainiaceae and Requiellaceae. Bootstrap support values for ML equal to or greater than 70% and the Bayesian posterior probabilities equal to or higher than 0.95 PP are indicated above the nodes as ML/PP. Ex-type strains are in bold and the new species are indicated in blue bold.

Conclusion

- Amphibambusa* is distributed from China and Thailand, and the host occurrence is only known on bamboos as saprobes (Liu et al. 2015, this study).
- Amphibambusa* can be easily distinguished from other genera in Cainiaceae in having hyaline to pale brown ascospores while the other genera have brown to dark brown ascospores (Hyde et al. 2020, Konta et al. 2021).
- In the preliminary ITS nucleotide BLAST result, *Arecophila muroiana* (strain GZUCC0122) and *Arecophila* sp. (strains GZUCC0110, GZUCC0112, GZUCC0124, GZUCC0127) also showed the similarities with *Amphibambusa hongheensis*, but with low percentage queries cover (73%). This may be because of the gaps and variable characters between our new strains and these strains, indicating that these strains are not relatives to our new strains.
- We report *Amphibambusa* species in Yunnan, China for the first time and enrich the distribution of *Amphibambusa*.

Acknowledgements

This study was supported by the Key Research Project Agroforestry Systems for Restoration and Bio-industry Technology Development (grant no. 2017YFC0505101), Ministry of Sciences and Technology of China (grant no. 2017YFC0505100) and Key Research Program of Frontier Sciences of the Chinese Academy of Sciences (grant no. QYZDY-SSW-SMC014). The authors gracefully thank the Biology Experimental Center, Germplasm Bank of Wild Species, Kunming Institute of Botany, Chinese Academy of Sciences for providing the facilities of molecular laboratory. We also thank Shaun Pennycok from Manaaki Whenua - Landcare Research for his assistance in naming the new species in the genus *Amphibambusa*. Rungtiwa Phookamsak sincerely acknowledges the CAS President's International Fellowship Initiative (PIFI) for young staff (grant no. Y9215811Q1), the National Science Foundation of China (NSFC) project code 31850410489 (grant no. Y811982211) and Chiang Mai University for financial support. Hong-Bo Jiang would like to thank Mae Fah Luang University for a Ph.D scholarship.

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