

Original Research Article

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***Fomitiporia gaoligongensis* B. K. Cui and Hong Chen, sp. Nov: A New Addition to Indian Mycoflora from Manipur**

A. K. Chungreiliu^{ID}*, Mamtaj S. Dkhar^{ID}, Kuno Chuzho^{ID} and H. Kayang

Microbial Ecology Laboratory, Centre for Advanced Studies in Botany, North–Eastern Hill University, Shillong – 793022, Meghalaya, India

*Corresponding author

ABSTRACT

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Fomitiporia gaoligongensis was reported and described as a new species in 2017 by Chen & Cui from China through multi-locus phylogeny and morphological analysis. Molecular studies and sequencing output obtained from our present study showed that our fungal isolate with voucher number KAI2103 showed 100% similarity with *F. gaoligongensis* B.K. Cui & Hong Chen. sp. nov. The specimen also showed similarities in its ecological, morphological and microscopic characteristics with *F. gaoligongensis* and hence, it was confirmed as *F. gaoligongensis* B.K. Cui & Hong Chen. sp. nov and the species is a new addition to Indian mycoflora.

Introduction

The family, Hymenochaetaceae under the division Basidiomycota includes both saprophytic and pathogenic wood rotting macrofungi. Many pathogenic fungi are remarkably distributed under the genera *Fomitiporia*, *Phellinus* and *Phylloporia* and the species under these taxa are known pathogens on a variety of living angiospermic trees, bushes and grape vines (Nunez and Ryvarde, 2000; Fischer, 2002; Fischer *et al.*, 2005; Dai *et al.*, 2007; Cloete *et al.*, 2013; Ye *et al.*, 2021).

The genus *Fomitiporia* Murrill was introduced in 1907 by Murrill. The genus is characterized by

resupinate to pilatebasidiocarps, pseudodimetic to dimetichyphal system, presence of hymenial setae and thick walled, strongly dextrinoid, sub-globous to globousbasidiospores. Chen & Cui (2017) pointed that interests in studies on *Fomitiporia* has grown in recent years with a total of 24 species described in the last 20 years. The species shared similar morphological expressions but with several phylogenetic studies aided with geographical differences, many new species has been sorted and placed under this genus (Chen & Cui, 2017; Ye *et al.*, 2021). Most of the advanced researches on molecular studies and host-pathogen relationships including the enzymatic pathway regulations of *Fomitiporia* species and studies on bambusicolous

Fomitiporia species and have peaked in the past ten years and the last 3-4 years in particular (Terashima, 2013; Amalfi and Decock, 2014; Chen and Cui, 2017; Liu *et al.*, 2018; Chen *et al.*, 2021; Ye *et al.*, 2021; Pecetti *et al.*, 2022).

Studies on *Fomitiporia* species have been conducted from China, Japan, Brazil, USA, Mexico, South Africa and few other countries from Europe. From Asia, an impressive study on this genus has been well documented from China (Dai *et al.*, 2008; Dai & Cui, 2011; Zhou & Xue, 2012; Chen & Cui, 2017; Chen *et al.*, 2021). A new species of *Fomitiporia*, *F. tasmanica* was reported from Australia by Chen *et al.*, (2021).

One species, *F. apiahyna*, along with four other polypores was reported for the first time from India, by Kaur *et al.*, (2020) and to the best of our knowledge, this serves as the first species report of *F. gaoligongensis* from India. In the present study, *F. gaoligongensis* B.K. Cui & Hong Chen, sp. nov. is reported as a new addition to India mycoflora and the macro-, micro-morphological descriptions and cultural growth characters of the species are discussed.

Materials and Methods

Collection and morphological study

Basidiocarp was collected through opportunistic sampling during pre-monsoon season (April– May 2021) from Kaikao Community forest located within the geographical coordinates 24°52'02" N and 93°27'10" E of Tameng long district of Manipur, a north-east state of India. Initial identification of the basidiocarp was carried out in the laboratory based on the macroscopic and microscopic parameters using taxonomic keys provided by Nunez and Ryvarden (2000).

Establishment of culture

Tissue culture technique described by Rajaratnam and Thiagarajan (2012) with slight modification was

used for raising a pure culture of the specimen using Malt extract agar (malt extract 15 g l⁻¹, agar 20 g l⁻¹, HiMedia) and incubated under dark condition for about two weeks at 28±2°C. For DNA extraction, mycelia cultures were raised in liquid culture medium (malt extract 10 g l⁻¹, glucose 5 g l⁻¹) for 10– 15 days at 27±2°C.

Molecular identification

Using the HiPurA® Fungal DNA Purification Kit (HiMedia Cat#MB543– 50PR), genomic DNA was isolated from the fresh mycelia of fungal cultures that were 10 to 15 days old. The ITS (Internal Transcribed Spacer) region of the rDNA was amplified by PCR using the universal primers ITS1 (5'– TCC GTA GGT GAA CCT GCG G– 3') and ITS4 (5'– TCC TCC GCT TAT TGA TAT GC– 3') as described by White *et al.*, (1990) and Vasava *et al.*, (2018) with minor modifications. Gel results were visualized in Gel Doc EZ Imager (Bio–Rad USA) to confirm the expected size of the product. The amplified products were sent to Eurofins Genomics India Pvt. Ltd., Bangalore for purification and sequencing.

Following sequencing, the data was analyzed for sequence matches using NCBI's Basic Local Alignment Search Tool (BLAST) for molecular identification. By comparing the sequence acquired to the nearest accessible reference sequences with a 100% base– pair match, the sequence was identified.

Following the preliminary analysis, the sequence was submitted to Genbank, NCBI using the BankIt tool in accordance with the instructions given on the NCBI website (<http://www.ncbi.nlm.nih.gov/>). Following molecular identification, the distinguishing traits of the identified species were also compared to existing literature (Cui & Chen, 2021).

Results and Discussion

Fomitiporia gaoligongensis B. K. Cui & Hong Chen Fig. 1 (a – c) Mycobank number: MB 819445

Ecology

F. gaoligongensis was found growing on the bark of a living angiospermic tree belonging to the genus *Choerospondias*. *F. gaoligongensis* was sampled during pre-monsoon season from the state of Manipur, Northeast India.

Basidiocarp

Perennial, pileate, consistently woody hard and light weight when dry, appanate and slightly umbo, semicircular, up to 18 cm long, 20.2 cm wide and 7 cm thick at base.

Pilear surface with a fairly thick dark brown to black hard cuticle, concentrically sulcate with wide zones which are darker towards the base, smooth, margin distinct, brown and obtuse; pore surface grayish to dark brown, slightly bruised when handled, pores circular, 7 – 8 per mm, dissepiments thick, entire; context brown, woody hard up to 4 cm thick; tubes yellow or lighter than the context up to 3 cm thick sometimes separated by a layer of context tissue, concolorous with pore, distinctly stratified.

Hyphal system (Fig. 1, d – e) dimitic; generative hyphae hyaline, thick-walled, simple-septate, branching is frequent in context; skeletal hyphae dominant, hyaline, yellowish brown to reddish-brown, thick-walled with distinct lumen, more or less straight, regularly arranged or run subparallel along the tubes, rarely branched. Setal hyphae and hymenial setae absent. Cystidia absent. Cystidiole present, fusoid to subulate, colourless, thin-walled. Basidia barrel-shaped basidia, with four sterigmata and simple septate at the base. Basidiole similar to basidia in shape but smaller in size. Basidiospores (Fig. 1, f) globose to subglobose, reddish-brown in Melzer's reagent, smooth and thick-walled.

Cultural characteristics (Fig. 1, g – i)

Growth very slow, first mycelial growth appeared after 6 days and plates fully covered only after 30 to 32 days. Mat downy to cottony wooly in

appearance, initially light brown but turned brown with time. Advancing zones even, raised with distinct circular zones.

Molecular identification (Fig. 1, j)

The species could be accurately identified after DNA sequencing. Sequence of our collection deposited in the GenBank with accession number ON557743 corresponds perfectly (100% similarity) to the other existing *F. gaoligongensis* sequences deposited as confirmed by BLAST comparison.

Prior to the publication of this report, the literature provided by Chen & Cui (2017) remained the only source for consultation and description of this particular species. According to Chen & Cui (2017), *F. gaoligongensis* is distinct from other species of the same generic taxa in having a semicircular pileus and globose to subglobose basidiospores, which was also observed from the present study.

F. gaoligongensis was sampled from a living tree belonging to the genus *Choerospondias*. This also supported the finding of Chen & Cui (2017) who reported the fungus growing on living tree. It can thus be stated that *F. gaoligongensis* preferably grows on living angiospermic hosts. Future studies on host-specificity and its potential pathogenicity is expected to provide a better understanding on the ecological aspects of this fungus. In addition, another species, *F. apiahyna* has been recently reported for the first time from India by Kaur *et al.*, (2020). This report is the first species report of *F. gaoligongensis* from India, which is an addition to the rich, Indian mycofloral diversity.

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Conflict of interest

All contributing authors have no conflicting of interest to declare.

Fig.1 **a** Basidiocarp on substratum. **b** dorsal view. **c** ventral view. **d** Section through the tube. **e** Skeletal hyphae. **f** Basidiospore. **g-h** Sub cultures on petriplates. **i** Hyphae from culture. **j** Gel photograph showing isolated DNA bands



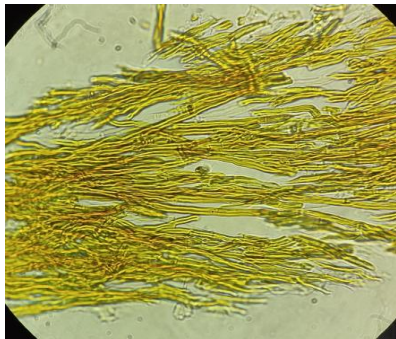
a



b



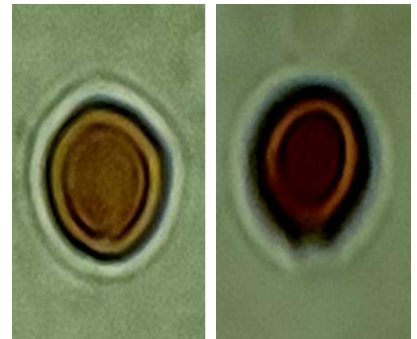
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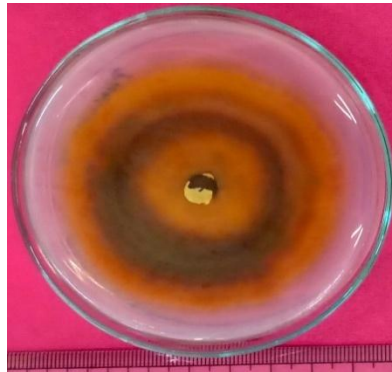
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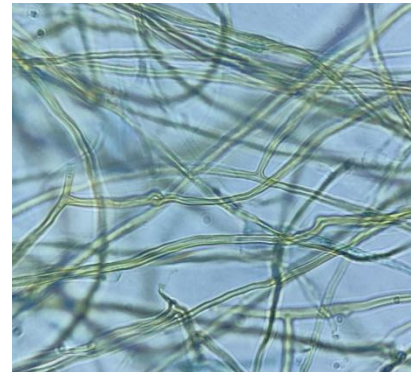
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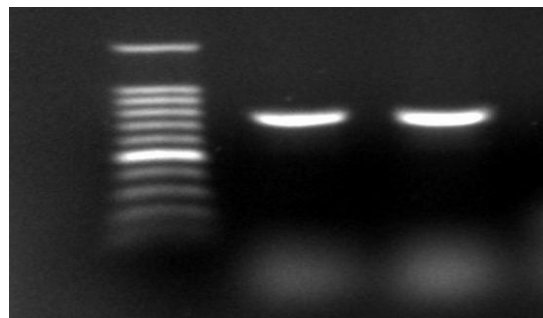
g



h



i



j

References

- Amalfi M, Decock C. 2014. *Fomitiporia expansa*, an undescribed species from French Guiana. *Cryptogamie Mycologie* 35(1):73–85 <https://doi.org/10.7872/crym.v35.iss1.2014.73>
- Chen H, Cui B K. 2017. Multi-locus phylogeny and morphology reveal five new species of *Fomitiporia* (Hymenochaetales) from China. *Mycological Progress* 16:687–701
- Chen J J, Wu Y D, Ji X H, Gates G, Xu X. 2021. A new species of *Fomitiporia* (Hymenochaetales) from Australia. *Phytotaxa* 489(2) 489.2.8 <https://doi.org/10.11646/phytotaxa.489.2.8>
- Cloete M, Fischer M, Mostert L, Halleen F. 2013 A novel *Fomitiporia* species associated with the esca on grapevine in South Africa. *Mycological Progress* 13(2):303–311 <https://doi.org/10.1007/s11557-013-0915-5>
- Dai Y C, Cui B K, Decock C. 2008. A new species of *Fomitiporia* (Hymenochaetales, Basidiomycota) from China based on morphological and molecular characters. *Mycological Research* 112(3):375–380 <https://doi.org/10.1016/j.mycres.2007.11.020>
- Dai Y C, Cui B K, Yuan H S, Li B D. 2007. Pathogenic wood-decaying fungi in China. *Forest Pathology* 37(2):105–120 <https://doi.org/10.1111/j.1439-0329.2007.00485.x>
- Dai Y C, Cui B K. 2011 *Fomitiporia ellipsoidea* has the largest fruiting body among the fungi. *Fungal Biology* 115:813–814 <https://doi.org/10.1016/j.funbio.2011.06.008>
- Fischer M, Edwards J, Cunningham J. 2005. Basidiomycetous pathogen on grapevine: A new species from Australia – *Fomitiporia australiensis*. *Mycotaxon* 91:85–96
- Fischer M. (2002). A new wood-decaying basidiomycete species associated with esca of grapevine: *Fomitiporia mediterranea* (Hymenochaetales). *Mycological Progress* 1:315–324. <https://doi.org/10.1007/s11557-006-0029-4>
- Kaur R, Kaur G, Singh A P, Dhingra G S. 2020. Five polypore species new to India. *Czech Mycology* 72(2):151–161 <https://doi.org/10.33585/cmy.72202>
- Liu T Z, Chen Q, Han M L, Wu F. 2018. *Fomitiporia rhamnoides* sp. nov. (Hymenochaetales, Basidiomycota), a new polypore, growing on *Hippophae* from China. *Mycokeys* 36(4): 35–43 <https://doi.org/10.3897/mycokeys.36.25986>
- Murrill W A. 1907. Polyporaceae, Part 1. North American Flora 9(1): pp. 7. New York Botanical Gardens
- Nunez M, Ryvarden, L. 2000. East Asian polypores – Volume 1 – Ganodermataceae and Hymenochaetales. *Fungiflora*, Oslo, Norway, pp. 1–168
- Pecetti A, Moretti S, Perrin C, Gelhaye E, Bieler E, Kassemeyer H, Mugnai L, Farine S, Bertsch C. 2022. Grapevine wood-degradation activity of *Fomitiporia mediterranea* M. Fisch.: A focus on the enzymatic regulation. *Frontiers in Microbiology* 13:1–17 <https://doi.org/10.3389/fmicb.2022.844264>
- Rajaratnam S., Thiagarajan T. 2012. Molecular characterization of wild mushroom. *European Journal of Experimental Biology* 2(2):369–373
- Terashima Y. 2013. Physiological characteristics of the trunk sap rot pathogen *Fomitiporia* species on the “Sanbu-sugi” cultivar of *Cryptomeria japonica*. *Mycoscience* 54(3):171–177 <https://doi.org/10.1016/j.myc.2012.09.010>
- Vasava A M, Patel R S, Koyani R D, Rajput K S. 2018. Distribution and diversity of Polyporaceae in Western India: An overview and addition to mycoflora of the Gujarat state. *Plant Science Today* 5(1):32–38 <https://doi.org/10.14719/pst.2018.5.1.353>
- White T, 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, New York, USA; 1990. pp. 315–322

Ye Q, Jia J, Manawasinghe I S, Li X, Zhang W, Mugnai L, Wu X, Hyde K D, Yan J. 2021. *Fomitiporia punicata* and *Phaeoacremonium minimum* associated with esca complex of grapevine in China. *Phytopathological Research* 3(11):1–17.

<https://doi.org/10.1186/s42483-021-00087-w>

Zhou L W, Xue H J. 2012 *Fomitiporia pentaphylacis* and *Fomitiporia tenuitubus* sp. nov. (Hymenochaetales, Basidiomycota) from Guanxi, Southern China. *Mycological Progress* 11(4):907–913

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