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RESEARCH ARTICLE

First report of *Fulvifomes siamensis* (*Hymenochaetaceae*) from India, with notes on morphology and nrITS–nrLSU-based phylogeny

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Abstract. *Fulvifomes siamensis* was initially described from Thailand and has been reported from several parts of Southeast Asia. In the present study, basidiomata of *F. siamensis* were collected during macrofungal surveys conducted in Thiruvananthapuram District of Kerala, India. The specimens were found growing on *Peltophorum pterocarpum*. Identification was based on detailed macro- and micromorphological characters, as well as molecular phylogenetic analyses using the nrITS and nrLSU gene regions. The Indian collections were confirmed to be conspecific with *F. siamensis*. This study presents the first report of *F. siamensis* from India, supported by comprehensive morphological descriptions, illustrations, nrITS–nrLSU-based phylogenetic analysis, and comparisons with closely related taxa.

Keywords: *Basidiomycota*, *Hymenochaetaceae*, India, morphology, nrITS, nrLSU, phylogeny, taxonomy

Introduction

The family *Hymenochaetaceae* Donk (*Basidiomycota*) comprises wood-decaying fungi, predominantly known for their perennial, resupinate to pileate basidiomata, dimitic hyphal system, presence of setae, brown, thick-walled basidiospores, and contains both poroid and non-poroid genera (Liu et al., 2025). Globally, 32 poroid genera with 672 species are recognized in this family, and the actual diversity is believed to be significantly higher (Wu et al., 2022). Integrative approaches combining morphological data with multilocus phylogenetic analyses have led to major taxonomic revisions within the family, resulting in the identification of new genera and clarification of species complexes (Wu et al., 2022; Liu et al., 2025).

The genus *Fulvifomes* Murrill (Murrill, 1914) is distinguished by its perennial basidiomata, which may or may not possess a crust on the pileal surface. It exhibits a monomitic to dimitic hyphal system and may show the presence or absence of dark

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lines in the context. The basidiospores are yellowish, subglobose to ellipsoid in shape, sometimes flattened on one side, and typically darken in potassium hydroxide (KOH) solution (Zhou, 2014; Salvador-Montoya et al., 2018, 2022). Historically, *Fulvifomes* was long regarded as a synonym of *Phellinus* sensu lato or a subgenus within *Phellinus* (Dai, 1999). However, molecular phylogenetic analyses later confirmed its status as a separate and well distinguished genus (Wagner, Fisher, 2001, 2002).

Fulvifomes siamensis T. Hatt., Sakay. & E.B.G. Jones was described initially from Thailand on the root or butt of *Xylocarpus granatum* J. Koenig (*Meliaceae*) (Sakayaroj et al., 2012). Subsequent reports from Southeast Asia documented this species on other hardwood hosts (Hong et al., 2023), indicating a broader host range in tropical forest ecosystems.

During macrofungal surveys conducted in the tropical evergreen forests of Thiruvananthapuram District, Kerala, basidiomata of *Fulvifomes* were collected from *Peltophorum pterocarpum* (DC.) Backer ex K. Heyne (*Fabaceae*). Morphological examination, combined with phylogenetic analyses based on nuclear ribosomal ITS and LSU gene sequences, confirmed the identity of the specimens as *F. siamensis*. This constitutes the first report of *F. siamensis* from India. The present study provides detailed morphological description, photographic documentation, and molecular phylogenetic evidence to support this new record.

Materials and Methods

Study area and specimen collection

Basidiomata of *Fulvifomes siamensis* were collected during a macrofungal survey conducted in the Thiruvananthapuram District, Kerala, India (2023–2025). The specimens grew on the trunks of a living *Peltophorum pterocarpum* tree. Collected specimens were documented *in situ*, photographed, and deposited at the Mycological Herbarium of Jawaharlal Nehru Tropical Botanic Garden and Research Institute, Thiruvananthapuram [TBGT(M)].

Morphological analysis

Each basidioma was individually tagged with pertinent information, including locality, habitat, host, collection number, date of collection, and the type of rot observed. Detailed macromorphological characteristics — such as the basidiomata size, shape, and color, including features of the pileal surface, context, tubes, pores, and dissepiments — were documented. Pore density was determined by counting the number of pores per millimeter. Color notations were standardized using the color chart of Kornerup and Wanscher (1978). Microscopic analysis was conducted using freehand sections mounted in a range of diagnostic reagents: 1% Congo Red (to highlight cell wall structures), 5% KOH (to test for xanthochroic reactions), Melzer's reagent (to identify dextrinoid or amyloid reactions), and Cotton Blue (to detect cyanophilic structures), following the methodology of Ryvarden (1991). For spore measurements, 20 basidiospores were measured for length and width to determine size range, and the spore quotient (Q = L/W) was calculated. All measurements (n = 20) were performed in 5% aqueous KOH. Observations were made using an Olympus CX43 optical microscope (Olympus, Japan), and microphotographs were captured using a Magcam DC10 digital camera mounted on the same microscope.

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from fresh basidiome tissue following the protocol of Izumitsu et al. (2012). The nuclear ribosomal large subunit (nrLSU) and internal transcribed spacer (nrITS) regions were amplified and sequenced for the studied species. PCR amplification of the nrITS region was carried out using the primer pair ITS1 and ITS4 (White et al., 1990), while LR0R and LR7 primers (Vilgalys, Hester, 1990) were used for the nrLSU region. PCR amplification and sequencing procedures followed the methodology described by Kumar et al. (2018). The newly generated sequences have been deposited in GenBank (nrITS — PV030183, nrLSU — PV034407).

Sequence alignment and phylogenetic analysis

The molecular phylogenetic analysis was conducted using both the nrITS and nrLSU sequences. A combined data matrix was constructed, comprising the newly generated nrITS and nrLSU sequences of *F. siamensis* from India, along with 70 nrITS and 64 nrLSU sequences representing 33 taxa (including the outgroup; Table 1) retrieved from GenBank. The sequences were selected based on their similarity indices and the sequences of *Fulvifomes* used in the previous phylogenetic

analyses (Sakayaroj et al., 2012; Hattori et al., 2014; Hong et al., 2023). *Phellinus populicola* Niemelä and *Phellinotus neoaridus* Drechsler-Santos & Robledo (current name *Fomitiporella neoarida* (Drechsler-Santos & Robledo) Y.C. Dai & F. Wu) were chosen as the outgroup for rooting purposes following Crous et al. (2023). The sequence data matrix with default settings was aligned using the online web tool MAFFT (www.ebi.ac.uk/Tools/msa/mafft/). The aligned data matrix was then imported into BioEdit v7.2.6.1 (Hall, 1999) for manual modification. Maximum likelihood (ML) analysis was performed in the web platform http://iqtree.cibiv.univie.ac.at (Trifinopoulos et al., 2016) with 1000 ultrafast bootstrap replicates. The transition model with equal frequency (TNe+G4) was automatically selected as the best-fit substitution model per the BIC score in the same web platform. Bootstrap values ≥ 60% (Jeewon, Hyde, 2016) were considered significant. The phylogram inferred from ML analysis is displayed with MEGA XI (Tamura et al., 2021).

Table 1. **List of species, sources, GenBank accession numbers of nrITS and nLSU sequences used in the molecular analysis**

No.	Species	Voucher / Strain no.	GenBank no. nrITS	GenBank no. nrLSU	Geographical location
1	*Fulvifomes azonatus*	Dai 17203	MH390419	MH390397	China
2	*F. azonatus*	Dai 17470	MH390418	MH390395	China
3	*F. azonatus*	Cui 8452	MH390417	MH390396	China
4	*F. caligoporus*	Dai 17668	MH390420	MH390390	China
5	*F. caligoporus*	Dai 17660	MH390421	MH390391	China
6	*F. centroamericanus*	JV 0611_III	KX960763	KX960764	Guatemala
7	*F. coffeatoporus* (as *F. krugiodendri*)	JV0904_1	KX960762	KX960765	USA/Florida
8	*F. coffeatoporus* (as *F. krugiodendri*)	JV0312_24.10J	KX960760	KX960766	USA/Florida
9	*F. coffeatoporus* (as *F. krugiodendri*)	JV1008_21	KX960761	KX960767	USA/Florida
10	*F. costaricense*	JV 1607/103	MH390414	MH390386	Costa Rica
11	*F. costaricense*	JV 1407/87	MH390412	MH390387	Costa Rica
12	*F. dracaenicola*	Dai 22093	MW559799	MW559804	China
13	*F. dracaenicola*	Dai 22097	MW559800	MW559805	China
14	*F. elaeodendri*	CMW 47808	MH599093	MH599131	South Africa
15	*F. elaeodendri*	CMW 47825	MH599094	MH599134	South Africa
16	*F. elaeodendri*	CMW 47909	MH599096	MH599132	South Africa
17	*F. elaeodendri*	CMW 48154	MH599097	MH599135	South Africa
18	*F. elaeodendri*	CMW 48610	MH599095	MH599133	South Africa
19	*F. fastuosus*	Dai 18292	MH390411	MH390381	Vietnam
20	*F. fastuosus*	LWZ 20140731-13	KR905674	KR905668	Thailand
21	*F. fastuosus*	LWZ 20140728-29	KR905673	–	Thailand
22	*F. floridanus*	JV 0904/65	MH390422	–	USA
23	*F. floridanus*	JV 0312/23.1	MH390423	–	USA
24	*F. floridanus*	JV 0904/76	MH390424	MH390388	USA
25	*F. halophilus*	JV 1502/4	MH390427	MH390392	USA
26	*F. imbricatus*	LWZ 20140728-16	KR905677	KR905670	Thailand
27	*F. imbricatus*	LWZ 20140729-26	KR905679	KR905671	Thailand
28	*F. jawadhuvensis*	MUBL4011	MW040079	MW048886	India
29	*F. karaiensis*	MUBL4016	ON333609	ON326580	India
30	*F. karaiensis*	CRKK2/2A	OP028976	OP028972	India

Table 1 (continued)

No.	Species	Voucher / Strain no.	GenBank no. nrITS	GenBank no. nrLSU	Geographical location
31	*F. kawakamii*	CBS 428.86	–	AY059028	USA
32	*F. kawakamii*	PPT152	MH048095	–	Brazil
33	*F. lloydii*	Dai 11978	MH390430	MH390380	China
34	*F. lloydii*	Dai 10809	MH390428	MH390378	China
35	*F. lloydii*	Dai 9642	MH390429	MH390379	China
36	*F. malaiyanurensis*	CAL 1681	MF155651	MW048883	India
37	*F. mangroviensis*	MUBL4012	MW040083	MW048909	India
38	*F. mangroviensis*	KSM-MP12a	OM897221	OM897222	India
39	*F. maritimus*	MUBL1095	OR520888	OR512084	India
40	*F. merrillii*	6Kout	MH390416	MH390383	Thailand
41	*F. merrillii*	Dai 12094	MH390415	MH390382	China
42	*F. natarajanii*	MUBL1047	–	OQ608722	India
43	*F. natarajanii*	MUBL1048	–	OQ608723	India
44	*F. nilgheriensis*	URM 3028	MH390431	MH390384	Brazil
45	*F. nilgheriensis*	CBS 209.36	AY558633	AY059023	USA
46	*F. pannaensis*	MUBL4017	MW040080	OP028971	India
47	*F. pannaensis*	PRF32/2	OP028975	MW048890	India
48	*F. rigidus*	Dai 17507	MH390433	MH390399	China
49	*F. rigidus*	Dai 17496	MH390432	MH390398	China
50	***F. siamensis***	**TBGT(M)GWC-05**	**PV030183**	**PV034407**	**India**
51	*F. siamensis*	S2T26M1	JX104707	JX104754	Thailand
52	*F. siamensis*	Dai 18309	MH390434	MH390389	Vietnam
53	*F. siamensis*	KBXG3	JX104706	JX104753	Thailand
54	*F. siamensis*	XG3	JX104710	JX104757	Thailand
55	*F. siamensis*	YF166FB1	OQ558847	–	Singapore
56	*F. siamensis*	YF166FB2	OQ558849	–	Singapore
57	*F. siamensis*	SM135DT	OQ558846	–	Singapore
58	*F. siamensis*	YF157FB	OQ558848	–	Singapore
59	*F. siamensis*	YF156FB	OQ558850	–	Singapore
60	*F. subazonatus*	MUBL1046	OR502858	OR502859	India
61	*F. subazonatus*	AT03	OR502858	OR502859	India
62	*F. subindicus*	Dai 17743	MH390435	MH390393	China
63	*F. subindicus*	Cui 13908	MH390436	MH390394	China
64	*F. submerrillii*	Dai 17917	MH390406	MH390372	China
65	*F. submerrillii*	Dai 17911	MH390405	MH390371	China
66	*F. subramanianii*	MUBL 4019	OM912447	OM909042	India
67	*F. subthailandicus*	MUBL4025	OQ064102	OQ062657	India
68	*F. subthailandicus*	MEII2_2	PP827158	PP816284	India
69	*F. thiruvannamalaiensis*	MUBL4013	MZ221598	MZ221600	India
70	*F. tubogeneratus*	GXU2468	MT580805	MT580800	China
71	*F. tubogeneratus*	GXU2478	MT580806	MT580801	China
72	*Phellinotus neoaridus* (Outgroup)	URM 80362	KM211294	KM211286	Brazil
73	*Phellinotus populicola* (Outgroup)	CBS 638.75	MH860960	MH872729	Finland

Results

Molecular phylogeny

The phylogeny inferred from the combined nrITS and nrLSU dataset, shown in Fig. 1, places *F. siamensis* [TBGT(M)GWC-05] from the present study within a strongly supported clade (100% bootstrap) comprising isolates of *F. siamensis* from Thailand and Singapore. The Indian isolate forms a well-resolved lineage within this clade, indicating high genetic similarity and confirming its conspecificity with *F. siamensis*. The close phylogenetic proximity of TBGT(M)GWC-05 to other Southeast Asian isolates, without any significant divergence, suggests a genetically stable and geographically widespread species.

Taxonomy

***Fulvifomes siamensis* T. Hatt., Sakayaroj & E.B.G. Jones**, Mycoscience 55(5): 346 (2014) — Figs. 2, 3.

Basidiocarps perennial, sessile, broadly attached, resupinate to effused-reflexed or pileate in form, solitary or in coalesced imbricate clusters. *Pileus* dimidate, flabelliform to irregular, applanate to convex, projecting up to 10 cm, up to 13.5 cm wide and 4 cm thick. *Pileus surface* slightly velutinous in young specimens, broadly zonate, becoming irregular, indistinctly sulcate, nodulose, glabrous on maturity, without a distinct crust, rust brown (6E8) to dark brown (7F8). *Pileus margin* entire, acute to obtuse, off-white to yellowish white (4A2). *Context* woody to corky, tough, yellowish brown (5E8) to brown (6E7), up to 6 mm thick. *Tubes* stratified, woody, dark brown (8F6). *Pores* round, 6–7 mm. *Dissepiments* thin and entire. *Pore surface* yellowish brown to brown (6E7–7F5), with yellowish to amber colored non-sticky, odorless exudates in the early morning. *Hyphal system* dimitic. *Generative hyphae* thin- to slightly thick-walled, occasionally branched, septate without clamp-connections, hyaline to light brown, up to 3.5 µm wide. Skeletal hyphae thick-walled, unbranched, aseptate, light brown to brown, up to 4 µm wide. Setae absent. *Basidia* clavate, four-sterigmate, thin-walled, hyaline, 8.5–17.5 × 5–6.5 µm. Basidioles clavate, thin-walled, hyaline, 9.0–15.5 × 5–6 µm. *Basidiospores* subglobose, thick-walled, smooth, yellow in water, turning rust-brown in KOH, (3.8–)4.2–5.0 (–5.5) × (3.4–)4.0–4.8(–5.2) µm (Lm = 4.5 ± 0.32, Wm = 4.3 ± 0.13); Q = 1.05–1.15; Qm = 1.10, CB^-, IKI^-.

Specimens examined: India, Kerala, Thiruvananthapuram, Government College for Women, 12.64°54'19.1" N, 79°18'33" E, 24 November 2023, Manoj TBGT(M)GCW-05; *ibid*., 6 June 2024, Manoj TBGT(M)GCW-13; *ibid*., 28 June 2024, Manoj TBGT(M)GCW-17; *ibid*., 7 October 2024, Gireeshma TBGT(M)GCW-20; *ibid*., 26 November 2024, Aparna TBGT(M)GCW-24; *ibid*., 30 April 2025, Gireeshma TBGT(M)GCW-30; *ibid*., 2 May 2025, Greeshma TBGT(M)GCW-31; *ibid*., 8 May 2025, Lakshmi TBGT(M)GCW-39; *ibid*., 7 June 2025, Aparna TBGT(M)GCW-43; *ibid*., 8 July 2025, Gireeshma TBGT(M)GCW-88; *ibid*., 8 July 2025, Aparna TBGT(M)GCW-89; *ibid*., 10 July 2025, Manoj TBGT(M)GCW-91.

Habitat: on the stem of a living angiosperm tree *Peltophorum pterocarpum* (DC.) Backer ex K. Heyne (*Fabaceae*).

Remarks: *Fulvifomes siamensis* was originally described from Thailand on the roots and butt of a mangrove tree, *Xylocarpus granatum* (Hattori et al., 2014), based on both morphological and molecular evidence. This study was based on the original materials collected by Sakayaroj et al. (2012). In a metagenomic survey of wood decay fungi in the urban trees of Singapore by Hong et al. (2023), the presence of *F. siamensis* OTUs were detected in soil, fruiting bodies, and diseased tissues of several host plants, including *Peltophorum pterocarpum*. Based on the morphology and molecular phylogenetic analysis (combined nrITS and nrLSU dataset), the Indian specimen of *F. siamensis* is clearly affiliated with the *F. siamensis* clade originally described from Thailand (Sakayaroj et al., 2012; Hattori et al., 2014). The Indian and Thai specimens of *F. siamensis* share many core morphological and microscopic characteristics but exhibit subtle differences that reflect geographic and possibly ecological variation within the species. Both exhibit perennial, sessile basidiocarps that are broadly attached and occur solitary or in imbricate clusters. The pileus in Indian collections is dimidiate, flabelliform to irregular, and zonate with a rust to dark brown color. In contrast, the Thai specimens have a semicircular to irregular, applanate to convex pileus that becomes rimose and almost black with age. The Indian specimens are slightly larger in pileus dimensions (up to 13.5 cm wide) and more prominently zonate and nodulose, while the Thai material is up to 12 cm wide and lacks distinct zoning. Microscopic comparisons show that both are dimitic in trama, but the Thai context is monomitic, whereas the Indian material remains dimitic throughout. Generative

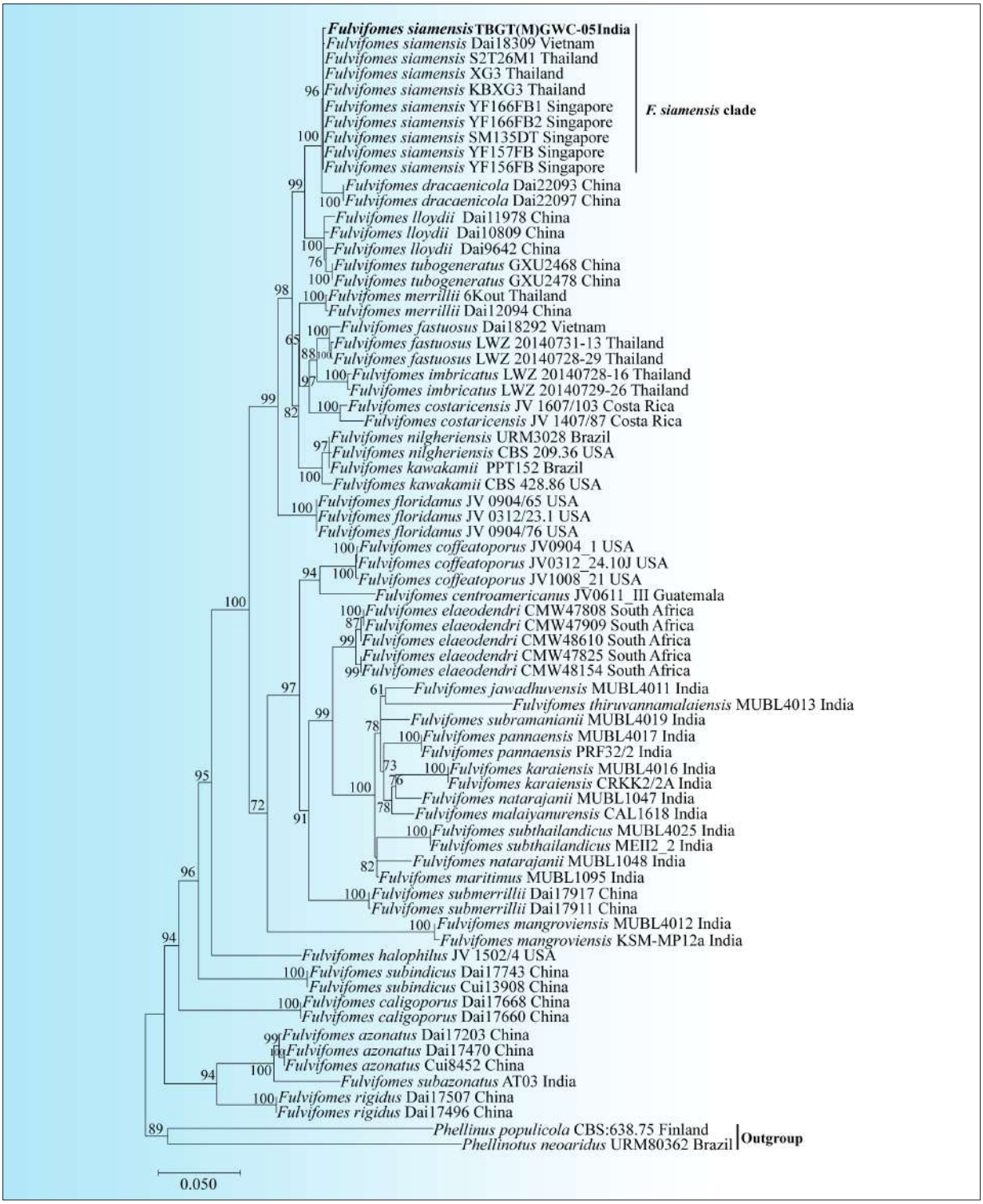

Fig. 1. Phylogenetic analysis of *Fulvifomes* species based on combined nrITS and nrLSU sequences. Bootstrap values (ML > 50%) are shown above or below the branches. Voucher / Strain numbers and geographic locations of the taxa are listed following the species names. The newly recorded *Fulvifomes siamensis* accession from India is in bold font

Fig. 2. *Fulvifomes siamensis*. A–C, E, H: habit *in situ*; D, F: habit — lower surface showing pore surface; G: pore surface enlarged; H: basidioma showing exudates. Scale bars: A–F, H — 10 mm; G — 5 mm. Photos by K.A. Manoj

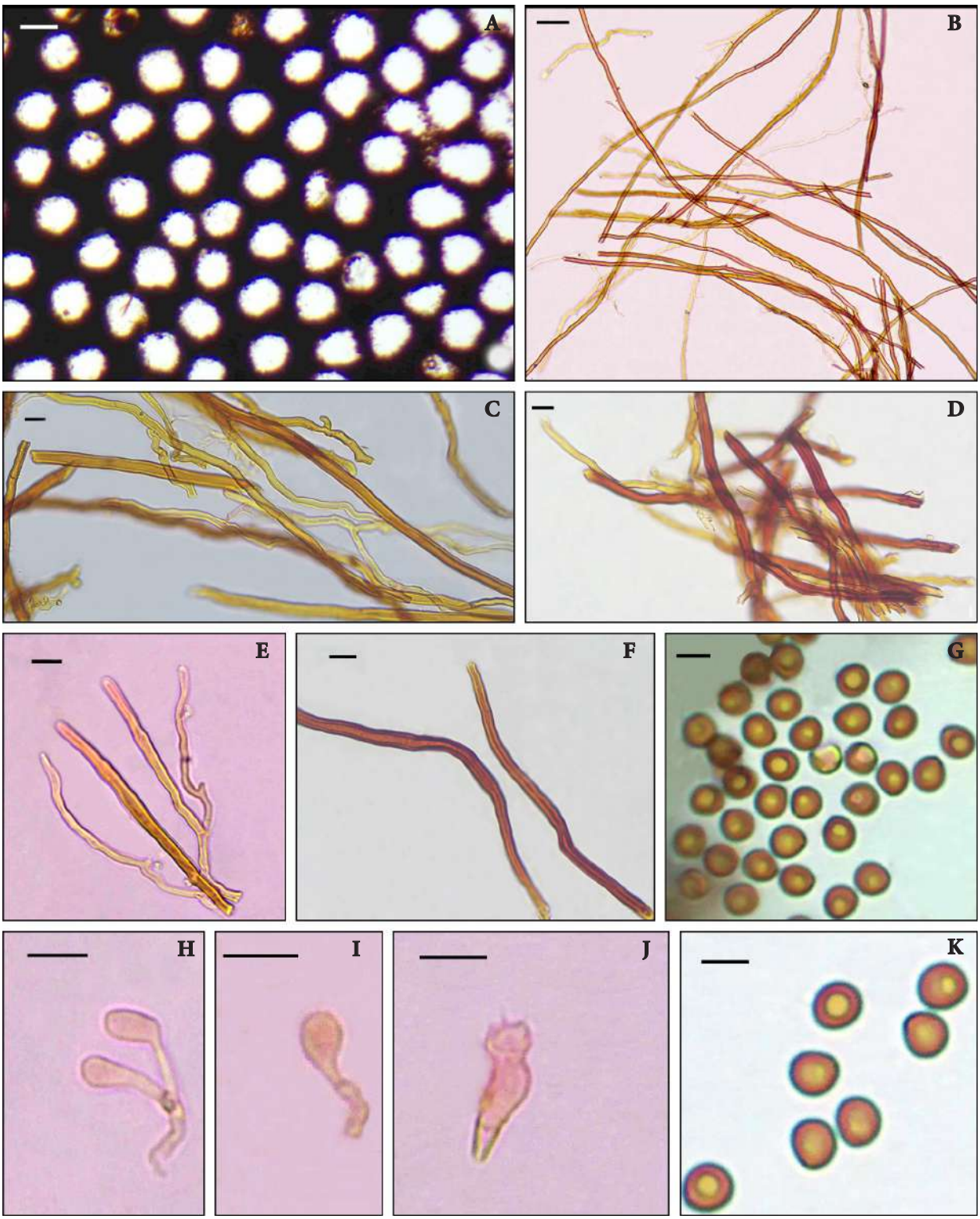

Fig. 3. *Fulvifomes siamensis*. A: pores on lower surface; B, C, E: generative hyphae of context; D, F: skeletal hyphae of trama; G, K: basidiospores; H, I: basidioles; J: basidium. Scale bars: A — 100 µm, B — 50 µm, C–K — 10 µm. Photos by K.A. Manoj

and skeletal hyphae are similar in wall thickness and color, though the hyphae in the Thai collections are slightly broader. Basidia and basidioles were observed in the Indian specimen but not in the Thai type. Basidiospores in both are subglobose, thick-walled, and yellowish, but those in the Indian collection are slightly smaller [(3.8–)4.2–5.0(–5.5) × (3.4–)4.0–4.8(–5.2) μm] compared to those from Thailand (4.5–6.0 × 4–5 μm). Despite these differences, both specimens share diagnostic features such as the absence of setae, stratified tubes, and thick-walled spores that react similarly in chemical reagents (CB–, IKI–). These results confirm that the Indian specimen is conspecific with *F. siamensis* from Thailand, but the observed slight variations, including spore size, likely reflect environmental influences or natural infraspecific variability. Hence, the Indian collection represents a new regional record of *F. siamensis* and broadens the known morphological and geographic distribution of the species.

Conclusion

The present study reports *F. siamensis* from India for the first time, based on morphological and molecular evidence (nrITS and nrLSU sequences). The discovery expands the known geographic and host range of *F. siamensis*, underlining the rich but underexplored fungal diversity of the Western Ghats. Notably, *F. siamensis* has been associated with stem and butt rot of *Xylocarpus granatum* in Thai mangrove ecosystems, where it was frequently isolated from decayed trunks and roots. The fungus exhibits traits consistent with wood-decaying pathogens in the family *Hymenochaetaceae*, causing internal decay that weakens structural integrity. Its occurrence on living trees and capacity to cause extensive heartwood degradation suggest its potential pathogenicity in natural forest systems. The detection of *F. siamensis* in India raises concerns about its possible impact on tree species, emphasizing the need for further pathological studies to assess its host range, virulence, and ecological role in Indian forests.

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ETHICS DECLARATION

The authors declare no conflict of interest.

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REFERENCES

Crous P.W., Costa M.M., Kandemir H., Vermaas M., Vu D., Zhao L., Arumugam E., Flakus A., Jurjević Ž., Kaliyaperumal M., Mahadevakumar S., Murugadoss R., Shivas R.G., Tan Y.P., Wingfield M.J., Abell S.E., Marney T.S., Danteswari C., Darmostuk V., Denchev C.M., Denchev T.T., Etayo J., Gené J., Gunaseelan S., Hubka V., Illescas T., Jansen G.M., Kezo K., Kumar S., Larsson E., Mufeeda K.T., Piątek M., Rodriguez-Flakus P., Sarma P.V.S.R.N., Stryjak-Bogacka M., Torres-Garcia D., Vauras J., Acal D.A., Akulov A., Alhudaib K., Asif M., Balashov S., Baral H.O., Baturo-Cieśniewska A., Begerow D., Beja-Pereira A., Bianchinotti M.V., Bilański P., Chandranayaka S., Chellappan N., Cowan D.A., Custódio F.A., Czachura P., Delgado G., De Silva N.I., Dijksterhuis J., Dueñas M., Eisvand P., Fachada V., Fournier J., Fritsche Y., Fuljer F., Ganga K.G.G., Guerra M.P., Hansen K., Hywel-Jones N., Ismail A.M., Jacobs C.R., Jankowiak R., Karich A., Kemler M., Kisło K., Klofac W., Krisai-Greilhuber I., Latha K.P.D., Lebeuf R., Lopes M.E., Lumyong S., Maciá-Vicente J.G., Maggs-Kölling G., Magistà D., Manimohan P., Martín M.P., Mazur E., Mehrabi-Koushki M., Miller A.N., Mombert A., Ossowska E.A., Patejuk K., Pereira O.L., Piskorski S., Plaza M., Podile A.R., Polhorský A., Pusz W., Raza M., Ruszkiewicz-Michalska M., Saba M., Sánchez R.M., Singh R., Śliwa L., Smith M.E., Stefenon V.M., Strasiftáková D., Suwannarach N., Szczepańska K., Telleria M.T., Tennakoon D.S., Thines M., Thorn R.G., Urbaniak J., van der Vegte M., Vasan V., Vila-Viçosa C., Voglmayr H., Wrzosek M., Zappelini J., Groenewald J.Z. 2023. Fungal Planet description sheets: 1550–1613. *Persoonia*, 51: 280–417. https://doi.org/10.3767/persoonia.2023.51.08

Dai Y.C. 1999. *Phellinus* sensu lato (*Aphyllophorales, Hymenochaetaceae*) in East Asia. *Acta Botanica Fennica*, 166: 43–103.

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

Hattori T., Sakayaroj J., Jones E.B.G., Suetrong S., Preedanon S., Klaysuban A. 2014. Three species of *Fulvifomes* (*Basidiomycota*, *Hymenochaetales*) associated with rots on mangrove tree *Xylocarpus granatum* in Thailand. *Mycoscience*, 55(5): 344–354. https://doi.org/10.1016/j.myc.2014.01.001

Hong Y., Tan J.Y., Xue H., Chow M.L., Ali M., Ng A., Leong A., Yeo J., Koh S.M., Tang M. S.Y., Lee Y.Y., Choong A.M.F., Lee S.M.L., Delli Ponti R., Chan P.M., Lee D., Wong J.Y., Mutwil M., Fong Y.K. 2023. A metagenomic survey of wood decay fungi in the urban trees of Singapore. *Journal of Fungi*, 9(4): 460. https://doi.org/10.3390/jof9040460

Izumitsu K., Hatoh K., Sumita T., Kitade Y., Morita A., Gafur A., Ohta A., Kawai M., Yamanaka T., Neda H., Ota Y., Tanaka C. 2012. Rapid and simple preparation of mushroom DNA directly from colonies and fruiting bodies for PCR. *Mycoscience*, 53(5): 396–401. https://doi.org/10.1007/s10267-012-0182-3

Jeewon R., Hyde K.D. 2016. Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. *Mycosphere*, 7(11): 1669–1677. https://doi.org/10.5943/mycosphere/7/11/4

Kornerup A., Wanscher J.H. 1978. *Methuen Handbook of colour.* 3rd ed. London: Methuen & Co. Ltd., 252 pp.

Kumar A.M., Vrinda K.B., Pradeep C.K. 2018. Two new species of *Crepidotus* (*Basidiomycota*, *Agaricales*) from peninsular India. *Phytotaxa*, 372: 67–78. https://doi.org/10.11646/phytotaxa.372.1.5

Liu Z.B., Yuan Y., Dai Y., Liu H.G., Vlasák J., Zeng G.Y., He S.H., Wu F. 2025. Global diversity and systematics of *Hymenochaetaceae* with non-poroid hymenophore. *Fungal Diversity*, 131(1): 1–97. https://doi.org/10.1007/s13225-025-00552-3

Murrill W.A. 1914. *North American Polypores*. New York: The New Era Printing Company, 64 pp.

Ryvarden L. 1991. Genera of polypores. Nomenclature and taxonomy. *Synopsis Fungorum*, 5: 1–363.

Sakayaroj J., Preedanon S., Suetrong S., Klaysuban A., Jones E.G., Hattori T. 2012. Molecular characterization of basidiomycetes associated with the decayed mangrove tree *Xylocarpus granatum* in Thailand. *Fungal Diversity*, 56: 145–156. https://doi.org/10.1007/s13225-012-0195-4

Salvador-Montoya C.A., Martínez M., Drechsler-Santos E.R. 2022. Taxonomic update of species closely related to *Fulvifomes robiniae* in America. *Mycological Progress*, 21, 95. https://doi.org/10.1007/s11557-022-01843-8

Salvador-Montoya C.A., Popoff O.F., Reck M., Drechsler-Santos E.R. 2018. Taxonomic delimitation of *Fulvifomes robiniae* (*Hymenochaetales*, *Basidiomycota*) and related species in America: *F. squamosus* sp. nov. *Plant Systematics and Evolution*, 304(3): 445–459. https://doi.org/10.1007/s00606-017-1487-7

Tamura K., Stecher G., Kumar S. 2021. MEGA11: Molecular Evolutionary Genetics Analysis Version 11. *Molecular Biology and Evolution*, 38(7): 3022–3027. https://doi.org/10.1093/molbev/msab120

Trifinopoulos J., Nguyen L.T., von Haeseler A., Minh B.Q. 2016. W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research*, 44(W1): W232–W235. https://doi.org/10.1093/nar/gkw256

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. https://doi.org/10. 1128/jb.172.8.4238-4246.1990

Wagner T., Fischer M. 2001. Natural groups and a revised system for the European poroid *Hymenochaetales* (*Basidiomycota*) supported by nLSU rDNA sequence data. *Mycological Research*, 105(7): 773–782. https://doi.org/10.1017/s0953756201004257

Wagner T., Fischer M. 2002. Proceedings towards a natural classification of the worldwide taxa *Phellinus* s. l. and *Inonotus* s. l., and phylogenetic relationships of allied genera. *Mycologia*, 94(6): 998–1016. https://doi.org/10.1080/15572536.2003.11833156

White T.J., Bruns T., Lee S., Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: *PCR protocols: a guide to methods and applications*. Eds M.A. Innis., D.H. Gelfand, J.J. Sninsky, T.J. White. New York: Academic Press, pp. 315–322. https://doi.org/10.1016/b978-0-12- 372180-8.50042-1

Wu F., Zhou L.W., Vlasák J., Dai Y.C. 2022. Global diversity and systematics of *Hymenochaetaceae* with poroid hymenophore. *Fungal Diversity*, 113(1): 1–192. https://doi.org/10.1007/s13225-021-00496-4

Zhou L.W. 2014. *Fulvifomes hainanensis* sp. nov. and *F. indicus* comb. nov. (*Hymenochaetales*, *Basidiomycota*) evidenced by a combination of morphology and phylogeny. *Mycoscience*, 55(1): 70–77. https://doi.org/10.1016/j.myc.2013.05.006

Перша знахідка *Fulvifomes siamensis* (*Hymenochaetaceae*) в Індії з нотатками про морфологію та філогенію на основі nrITS–nrLSU

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Реферат. Гриб *Fulvifomes siamensis*, уперше описаний з Таїланду, відомий також із кількох місцезнаходжень у Південно-Східній Азії. Базидіоми *F. siamensis* було зібрано на *Peltophorum pterocarpum* під час досліджень макроміцетів у районі Тіруванантапурам штату Керала, Індія. Гриб було ідентифіковано на основі детальних макро- і мікроморфологічних ознак та молекулярно-генетичного аналізу з використанням nrITS і nrLSU. Було встановлено, що індійські зразки є конспецифічними з *F. siamensis*. Це перше повідомлення про знахідку *F. siamensis* в Індії, підтверджене детальними морфологічними описами, ілюстраціями, філогенетичним аналізом на основі nrITS–nrLSU та наведеним порівнянням із близькоспорідненими таксонами.

Ключові слова: *Basidiomycota*, *Hymenochaetaceae*, nrITS, nrLSU, Індія, морфологія, таксономія, філогенія