One new species of *Thaxterogaster* subgenus *Riederorum* (Agaricales) from India

ABSTRACT

The Cortinariaceae family is one of the dominant groups of mushrooms in the Indian Himalayas. Currently, this family includes ten genera, with *Thaxterogaster* being one of them. This study introduces a new species, *T. thindii*, collected from the state of Meghalaya, and provides an overview of its morphology along with molecular phylogenetic analysis.

Keywords: Agaricales; Basidiomycota; macrofungi; morphology; phylogenetic inferences.

1. INTRODUCTION

The Cortinariaceae ~~family,~~ R. Heim ex Pouzar em. Niskanen & Liimat., remains largely understudied in India, with only 36 species of Cortinariaceae identified to date (Bose *et al.,* 2024a; Bose *et al.,* 2024b). In contrast, more than 3,157 species have been documented ~~globally~~, with many yet to be discovered (Soop *et al.,* 2019; Kalichman *et al.,* 2020; Liimatainen *et al.,* 2022). Recently, this family has been classified into ten genera: *Cortinarius* (Pers.) Gray, *Phlegmacium* (Fr.) Wünsche, *Thaxterogaster* Singer, *Calonarius* Niskanen & Liimat., *Aureonarius* Niskanen & Liimat., *Cystinarius* Niskanen & Liimat., *Volvanarius* Niskanen & Liimat., *Hygronarius* Niskanen & Liimat., *Mystinarius* Niskanen & Liimat., and *Austrocortinarius* Niskanen & Liimat. (Liimatainen *et al.,* 2022). Among these, *Thaxterogaster* includes over 170 species, with major research focused in Australasia, Europe, and North and South America (Xie *et al.,* 2024). For the past 50 years, *Thaxterogaster* was regarded as an independent genus (Xie *et al.,* 2024), until ITS- and LSU-based phylogenetic analyses led to its recognition as a synonym of *Cortinarius* (Peintner *et al.,* 2002). Recently, the genus *Thaxterogaster* ~~Singer, Niskanen & Liimatainen~~ has divided into six subgenera: *Thaxterogaster* Niskanen & Liimatainen, *Cretaces* Niskanen & Liimatainen, *Multiformes* Niskanen & Liimatainen, *Riederorum* Niskanen & Liimatainen, *Scauri* Niskanen & Liimatainen, and *Variegati* Niskanen & Liimatainen (Liimatainen *et al.,* 2023; Ghosh *et al.,* 2023). However, very little work has been done on Indian *T.~~haxterogaster~~* species, with only four species reported: *T.~~haxterogaster~~ carneus* ~~S.S. Ahmed, Z.A. Reshi & K.I. Andrabi~~, *T.~~haxterogaster~~ indopurpurascens* (Dima, Semwal, Brandrud, V. Papp, & V.K. Bhatt) A. Ghosh, D. Chakr., K. Das & Vizzini, *T.~~haxterogaster~~ purpurascens* (Fr.) Niskanen & Liimat., and *T.~~haxterogaster~~ shoreae* A. Ghosh, D. Chakr., K. Das & Vizzini (Bose *et al.,* 2024a).

Roland Thaxter (1905-1906) was the first to collect sequestrate taxa of this genus in Patagonia, South America, with subsequent descriptions by Dodge and Zeller (1934), Singer (1951, 1960), Singer and Smith (1963), Horak and Moser (1965), and Horak (1979). For example, *T. magellanicum* is a sequestrate species, confirming that the Cortinariaceae family, particularly the genus *Thaxterogaster*, includes sequestrate members (Nouhra *et al.,* 2021; Singer, 1951; Liimatainen *et al.,* 2022).

Cortinariaceae species are significant ectomycorrhizal fungi in India's forest ecosystems, ~~spanning~~ temperate to tropical regions. The primary host trees belong to families such as Caesalpiniaceae, Cistaceae, Dipterocarpaceae, Fagaceae, Myrtaceae, Nothofagaceae, Pinaceae, Rhamnaceae, Rosaceae, and Salicaceae, with some herbaceous plants ~~from~~ the Cyperaceae family (Ghosh *et al.,* 2023). These fungi are~~,~~ therefore~~,~~ essential components of tropical to subalpine terrestrial ecosystems (Bose *et al.,* 2024b).

In terms of economic value, *T. multiformis* (Fr.) Niskanen & Liimat. and *T. purpurascens* ~~(Fr.) Niskanen & Liimat.~~ are highly valued as edible species in China (Dai *et al.,* 2010), while *T. turmalis* (Fr.) Niskanen & Liimat. is ~~recognized~~ for its ~~antitumor~~ properties (Dai *et al.,* 2008).

During extensive macrofungal surveys in Sohra, Meghalaya, India, several intriguing specimens of *Thaxterogaster* were collected. In-depth morphological studies and molecular phylogenetic analyses, based on nrITS sequences of these recent specimens, revealed an undescribed species from the subgenus *Riederorum*, section *Riederorum*. Previously referred to as *Riederi*, this section was renamed to *Riederorum* following the application of Article 21.2 of the current version of the Code of Nomenclature ("Code Shenzhen" Turland~~, N.J~~. *et al.,* 2018). The present species is proposed herein as *Thaxterogaster thindii* sp. nov. This study presents detailed macro- and micromorphological descriptions, and illustrations of the new species, and comparisons with closely related taxa. Molecular phylogenetic estimation in support of the novel species is also given.

2. MATERIAL AND METHODS

2.1 Morphological Studies

Comment [1]: Family Cortinariaceae is one of the most represented within the Agaricales in the Indian Himalayas. At present, the family comprises ten genera, being *Thaxterogaster* one of them. This study presents the new species *T. thindii*, collected from the state of Meghalaya, and provides an overview of its morphology together with a molecular phylogenetic analysis with related species.

Comment [2]: Delete

Comment [3]: The family Cortinariaceae

Comment [4]: *emend.*

Comment [5]: worldwide

Comment [6]: Authors have already been cited

Comment [7]: The correct citation is *Thaxterogaster carneus* S.S. Ahmed & Z.A. Reshi

Comment [8]: The correct citation is *Thaxterogaster indopurpurascens* Dima, Semwal, Brandrud, V. Papp & V.K. Bhatt ex A. Ghosh, D. Chakr., K. Das & Vizzini (*nom. Inval.*) Art. 35.1 (Shen-zhen)

Comment [9]: The genus was dedicated to Roland Thaxter (1905-1906) who was the first to collect sequestrate taxa of this genus in Patagonia,

Comment [10]: Not in the References

Comment [11]: Not in the References

Comment [12]: Not in the References

Comment [13]: Not in the References

Comment [14]: important

Comment [15]: ranging from

Comment [16]: belonging to

Comment [17]: Authors have already been cited

Comment [18]: recognised

Comment [19]: antitumoral

A comprehensive macrofungal survey was carried out in Sohra, Meghalaya, India, during the rainy season of April, 2024. This led to the collection of several fresh basidiomata from the Cortinariaceae family. Macromorphological traits were examined directly in the field using fresh specimens, with photographs of the samples taken in both the field and at the basecamp using Samsung S23 and OnePlus Nord CE. The color codes followed the Methuen Handbook of Color (Kornerup & Wanscher, 1978). After recording all macromorphological details, the samples were dissected and dried using an electric dryer. Micromorphological analysis involved preparing freehand sections from the dried specimens, which were then mounted in a solution containing 5% KOH, 1% Phloxin, and 1% ammoniacal Congo red. These sections were observed under an Olympus CX 41 compound microscope. Anatomical features were illustrated with a drawing tube attached to the same microscope at 1000× magnification, and microphotographs were taken using a camera mounted on an Olympus BX 53 microscope. Basidiospores were examined in Melzer's reagent, and their measurements (excluding ornamentations) were taken in side view. Measurements for basidiospores and other micromorphological structures, including basidia, followed a standard protocol, with thirty (30) measurements for basidiospores and twenty (20) for other structures. The specimens were deposited in the Central National Herbarium (CAL), Howrah.

Comment [20]: resulted in

Comment [21]: belonging to

Comment [22]: features

Comment [23]: *in situ*

Comment [24]: Photographs

Comment [25]: were taken

Comment [26]: cameras

Comment [27]: Colour

2.2 DNA extraction, PCR amplification and sequencing

Genomic DNA was extracted from 100 mg of dried basidioma using the HiPurA Fungal DNA Purification Kit (HIMEDIA), in accordance with the manufacturer's instructions. The nrITS gene region was amplified with the primer pair ITS1-F and ITS4 (White *et al.,* 1990; Gardes & Bruns, 1993). The PCR conditions were as follows: initial denaturation at 94 °C for 3 minutes, followed by 35 cycles of denaturation at 94 °C for 1 minute, annealing at 50 °C for 30 seconds, and extension at 72 °C for 1 minute. The final extension step was at 72 °C for 7 minutes. The PCR products were purified using the QIAquick PCR Purification Kit. Both strands of the amplified fragments were sequenced using the same primers on a 3730xl DNA Analyzer. Sequence quality was assessed using Sequence Scanner Software version 1. Sequence alignment, editing, and contig assembly were performed with Geneious version 5.1 (Drummond *et al.,* 2010) as well as manually. Two sequences were obtained in this study, one for each species: *Thaxterogaster thindii* (DCM-1 and DCM-3). These sequences were subsequently submitted to GenBank (Table 1).

Comment [28]: according to

Comment [29]: using the ITS1-F and ITS4 primer pair

Comment [30]: voucher

2.3 Phylogenetic analysis

The nrITS sequences for the newly identified *Thaxterogaster thindii* and its close relatives were retrieved from GenBank (https://www.ncbi.nlm.nih.gov/genbank) as well as from relevant published phylogenies (Xie *et al.,* 2023; Xie *et al.,* 2024). The raw nrITS dataset was compiled independently. Sequence alignment was carried out using the online version of the MAFFT v. 7 program (https://mafft.cbrc.jp/alignment/software/), applying the L-INS-i algorithm, a 200PAM/k = 2 scoring matrix, a gap open penalty of 1.53, and an offset value of 0.123. The alignment was manually inspected and trimmed in MEGA v. 7 (Kumar *et al.,* 2016) to ensure the preservation of conserved motifs. Both forward and reverse reads were manually corrected when necessary. Phylogenetic analysis was performed using the maximum likelihood (ML) method with RAxMLGUI version 2.0, employing the GTRGAMMA model. To evaluate nodal support, an ultrafast bootstrap with 1,000 replicates was conducted. Maximum likelihood bootstrap (MLbs) values ≥70% are displayed in the phylogenetic trees (Fig. 1).

Comment [31]: The selection of nucleotide substitution model is one of the main steps in phylogenetic analysis. Please indicate with which program it has been calculated. The other side, it would be desirable to carry out a second Bayesian analysis to verify the robustness of the topology in the phylogenetic tree.

3. RESULTS AND DISCUSSION

3.1 Phylogenetic inferences

In our maximum likelihood (ML) phylogenetic analysis, the nrITS data matrix included 35 taxa and 685 nucleotide positions (gaps included), with *Phlegmacium boreicyanites* (Kytöv., Liimat., Niskanen & A.F.S. Taylor) Niskanen & Liimat. and *Phlegmacium cyanites* (Fr.) M.M. Moser serving as the outgroup (Xie *et al.,* 2023). The nrITS dataset comprised 1464/1726 conserved sites, of which 177/1726 were parsimony-informative, 51/1726 were singleton sites. The rate parameters were as follows: A-C: 0.46484, A-G: 2.79781, A-T: 1.00000, C-G: 0.46484, C-T: 2.79781, and G-T: 1.00000. The base frequencies were A: 0.245, C: 0.199, G: 0.205, and T: 0.350.

Comment [32]: There is an inconsistency in the alignment values. Experimental procedures must be reproducible. It would be desirable to deposit the alignment into some repository of phylogenetic information, specifically user-submitted phylogenetic trees and the data used to generate them (Figshare or Treebase) and reflect it in the text

In our nrITS-based phylogenetic tree (Fig. 1), the two collections of *Thaxterogaster thindii* (voucher nos. DCM-1 and DCM-3) grouped into a distinct lineage with strong statistical support (MLbs = 100%) and were found to be closely related to *T. pallidoriederi*, *T. glaucocyanopus*, and *T. riederi*. However our present species is recovered as a distinct taxon with strong statistical support (MLbs = 96%) being sister with the clade comprising four species: *T. glaucocyanopus, T. pallidoriederi* and *T. riederi*.

Comment [33]: In our nrITS-based phylogenetic tree (Fig. 1), the two collections of the new species (vouchers DCM-1 and DCM-3) clustered with maximum statistical support (MLbs = 100%) and were found to be closely related to *T. pallidoriederi* (Brandrud, Dima & Bellù) Niskanen & Liimat., *T. glaucocyanopus (Rob. Henry) Niskanen & Liimat.* and *T. riederi* (Weinm.) Niskanen & Liimat., clustering in a clade with strong statistical support (MLbs = 96%), but in a distinct lineage that we recognise as a separate taxon.

3.2 Taxonomy

Thaxterogaster thindii A. Bose & D. Chakr., *sp. nov.* (Fig. 2–3)

MycoBank: MB857312

GenBank: PQ686617 (ITS, Holotype), PQ686634 (ITS, Paratype).

Holotype: Sohra, Meghalaya, India, 25°16′16″N, 91°43′55″E, 1321 m a.s.l., 24 April 2024, on the soil under *Castanopsis* sp., *Dyutiparna Chakraborty*, DCM-1 (CAL 2129).

Etymology: Commemorating Dr K.S. Thind for his significant contributions to Indian mycobiota.

Diagnosis: *Thaxterogaster thindii* is distinct from its closely allied species i.e. *T. pallidoriederi*, *T. glaucocyanopus* and *T. riederi* in terms of its host preference, deep violet to greyish violet lamellae, subamygdaloid-ellipsoid basidiospores along with nrITS- based sequence data.

Description: Pileus 30–100 mm in diam., convex to planoconvex when young, then applanate at maturity; margin enrolled; surface viscid when moist, brown (7E6–5) at the center, gradually orange (5A7) to greyish orange (5B6) towards the margin. Lamellae decurrent to sinuate, crowded (12/cm at pileus margin), brownish orange (5C6); lamellulae present in 5 series, margin wavy. Stipe 55–80 × 7–18 mm, central, curved, bulbous base with white (1A1) basal mycelium; surface dry, light orange to pale orange (5A3–4) with longitudinally striated on the surface. Pileus context solid, greyish yellow (2B3–4); unchanging when bruised. Stipe context solid, fibrous, yellowish grey to dull yellow (3B2–3). Smell and taste not recorded. Spore print rusty-brown.

Basidiospores 7.08–*9.26*–10.65 × 4.16–*5.54*–6.47 µm, Q=1.46–1.67–2.11, n=30, oval to elliptical, weakly to moderately verrucose, dextrinoid. Basidia 38.8–44.4 × 8.3–9.4 µm, clavate, 4-spored; sterigmata triangular. Sterile marginal elements 16–26 × 5–9 µm, cylindrical to clavate, thin-walled, colourless. Cheilocystidia 24–27 × 4.4–6.0 µm, emergent up to 1.5 µm beyond the basidiole tips, cylindrical to subcylindrical, occasional. Pleurocystidia 26.0–36.6 × 3.3–10.0 µm, emergent up to 0.8 µm beyond the basidiole tips, cylindrical to subcylindrical. Pileipellis duplex up to 144.4 µm; suprapellis up to 47.2 µm thick, composed of compactly arranged repent parallel hyphae, 70–80 × 3–5 µm wide; subpellis up to 97.2 µm thick consisting of inflated elements 45–50 × 16–18 µm wide, no contents. Clamp connections present.

Additional specimen examined: Sohra, Meghalaya, India, 29°18′16″N, 95°46′55″E, 1325 m a.s.l., 27 April 2024, on the soil under Castanopsis sp., *Dyutiparna Chakraborty*, DCM-3 (Paratype: CAL 2130).

Remarks: ~~Our Indian collection~~ is classified ~~under the~~ subgenus *Riederorum*, section *Riederorum*. Morphologically, it aligns under the above section based on the combination of following characteristics: pileus 25 to 120 mm wide, viscid; lamellae crowded; stipe base distinctly bulbous; basidiospores elliptical; pileipellis duplex with a notable ~~gluten~~ layer on ~~top~~ (Liimatainen *et al.,* 2022).

Phylogenetically, *T. thindii* is most closely related to *T. pallidoriederi* ~~(Brandrud, Dima & Bellù) Niskanen & Liimat.~~, *T. glaucocyanopus* ~~(Rob. Henry) Niskanen & Liimat.~~, and *T. riederi* ~~(Weinm.) Niskanen & Liimat.~~, all of which have been reported from Europe. However, these European ~~specimens~~ can easily be distinguished from our Indian specimens by possessing lamellae that range from deep violet to greyish violet, subamygdaloid basidiospores, and occurrence under *Fagus* or *Pinus* to *Picea* (Brandrud *et al.,* 2018).

Table 1. ~~A list of species~~, specimen voucher and GenBank accession no. ~~of species used in this study~~.

Species name (as reported in GenBank)	Voucher/strain no.	Country	GenBank accession no. (nrITS)
Phlegmacium boreicyanites Type	S:CFP931	Sweden	KF732296
Phlegmacium cyanites Type	UPS:A. Taylor 2005069	Sweden	KF732355
Thaxterogaster argyrionus Type	MEL:2331642	Australia	NR_152999
Thaxterogaster borealicremeolinus	HMAS:287398	China	NR_198606

Comment [34]: leg.

Comment [35]: italic

Comment [36]: leg.

Comment [37]: The new species

Comment [38]: in *Thaxterogaster*

Comment [39]: glutinous

Comment [40]: the surface

Comment [41]: taxa

Comment [42]: List of species used in this study

Comment [43]: , origin

Type			
Thaxterogaster borealicremeolinus	LY418	China	OR395363
Thaxterogaster cremeolina *Type*	PDD:70506	New Zealand	NR_157889
Thaxterogaster cremeorufus *Type*	PDD:94056	New Zealand	NR_153064
Thaxterogaster cremeorufus	PDD:72649	New Zealand	KT833622
Thaxterogaster dulciorum *Type*	PDD:78797	New Zealand	NR_157898
Thaxterogaster dulciorum	PDD:107708	New Zealand	KT875195
Thaxterogaster dovrensis *Type*	NR_160640	Norway	NR_160640
Thaxterogaster glaucocyanopus *Type*	G:5034	France	MH846274
Thaxterogaster iringa *Type*	PDD:73135	New Zealand	NR_120131
Thaxterogaster kaimanawa *Type*	PDD:73133	New Zealand	NR_157891
Thaxterogaster mendax *Type*	PC:A. Bidaud 07-10-162	France	NR_153019
Thaxterogaster melleicarneus *Type*	H:I. Kytovuori 01-053	Estonia	KF732577
Thaxterogaster natarajanii Type	AP23-63	India	PP892258
Thaxterogaster natarajanii	AP23-64	India	PP892259
Thaxterogaster nebulobrunneus *Type*	MEL:2331648	Australia	NR_152995
Thaxterogaster occidentalis Type	MICH:10382	USA	NR_130234
Thaxterogaster porphyropus *Type*	S:F47381	Sweden	NR_130246
Thaxterogaster pallidoriederi *Type*	BOZ:Bellu 30-09-2011	Italy	NR_160639
Thaxterogaster pallidirimosus *Type*	H:6035694	Finland	KF732578

Thaxterogaster rhipiduranus	PDD:72617	New Zealand	MH101624
Thaxterogaster rhipiduranus Type	PDD:88269	New Zealand	NR_157902
Thaxterogaster riederi	TEB141-10	Sweden	MH923056
Thaxterogaster riederi	Bellu 12-08-2012	Italy	MH923057
Thaxterogaster rufoallutus *Type*	PC:P. Moenne-Loccoz 635	France	KF732413
Thaxterogaster rufopurpureus *Type*	HMAS287399	China	OR395229
Thaterogaster shoreae Type	AGDC 21-04	New Zealand	OP473976
Thaxterogaster sinopurpurascens Type	HMAS287400	China	OR395230
Thaxterogaster thindii ***Type***	**~~DCM-1~~ CAL 2129**	**India**	**PQ686617**
Thaxterogaster thindii	**~~DCM-3~~ CAL 2130**	**India**	**PQ686634**

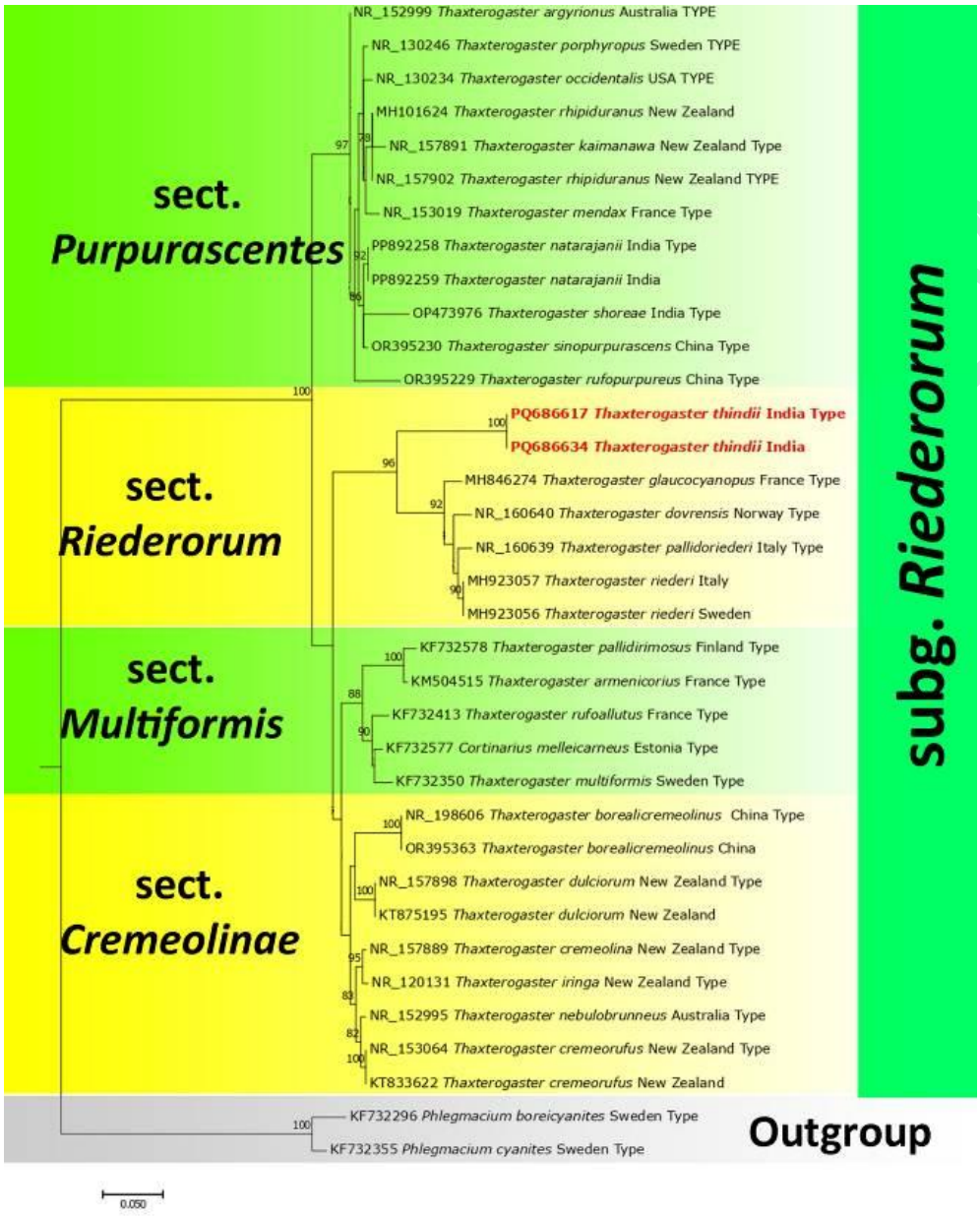

Fig. 1. Phylogram generated by maximum likelihood (ML) analysis based on ITS sequence data for *Thaxterogaster thindii* and allied species. Maximum likelihood bootstrap support values (MLbs) ≥ 70% are shown. The new species is highlighted in red to mark their phylogenetic positions in the tree.

Comment [44]: It would be desirable to re-edit the tree so that bootstrap values do not overlap with lines and to use arrows

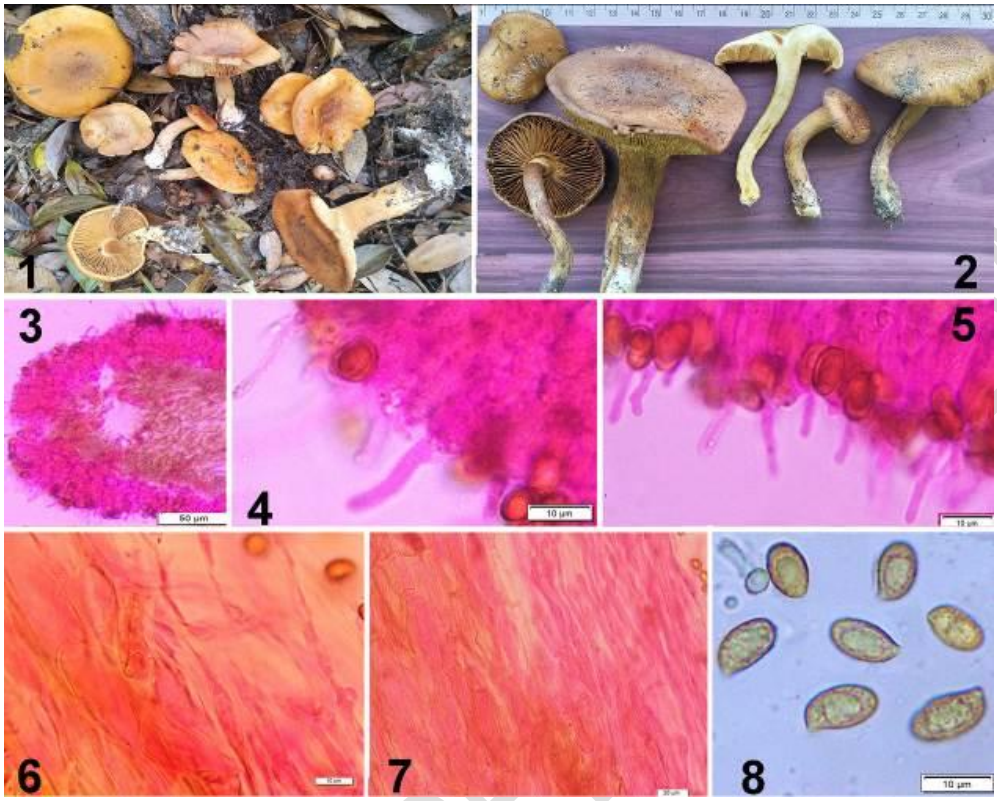

Fig. 2. ***Thaxterogaster thindii*** **sp. nov. (~~DCM-1~~, holotype). (1–2) Fresh basidiomata, (3–4) cheilocystidia, (5) pleurocystidia, (6–7) transverse section through pileipellis ~~of pileus~~, (8) basidiospores. Scale bars: 3 = 50 µm, 4 = 10 µm, 5 = 10 µm, 6 = 10 µm, 7 = 20 µm and 8 = 10 µm.**

Comment [45]: CAL 2129,

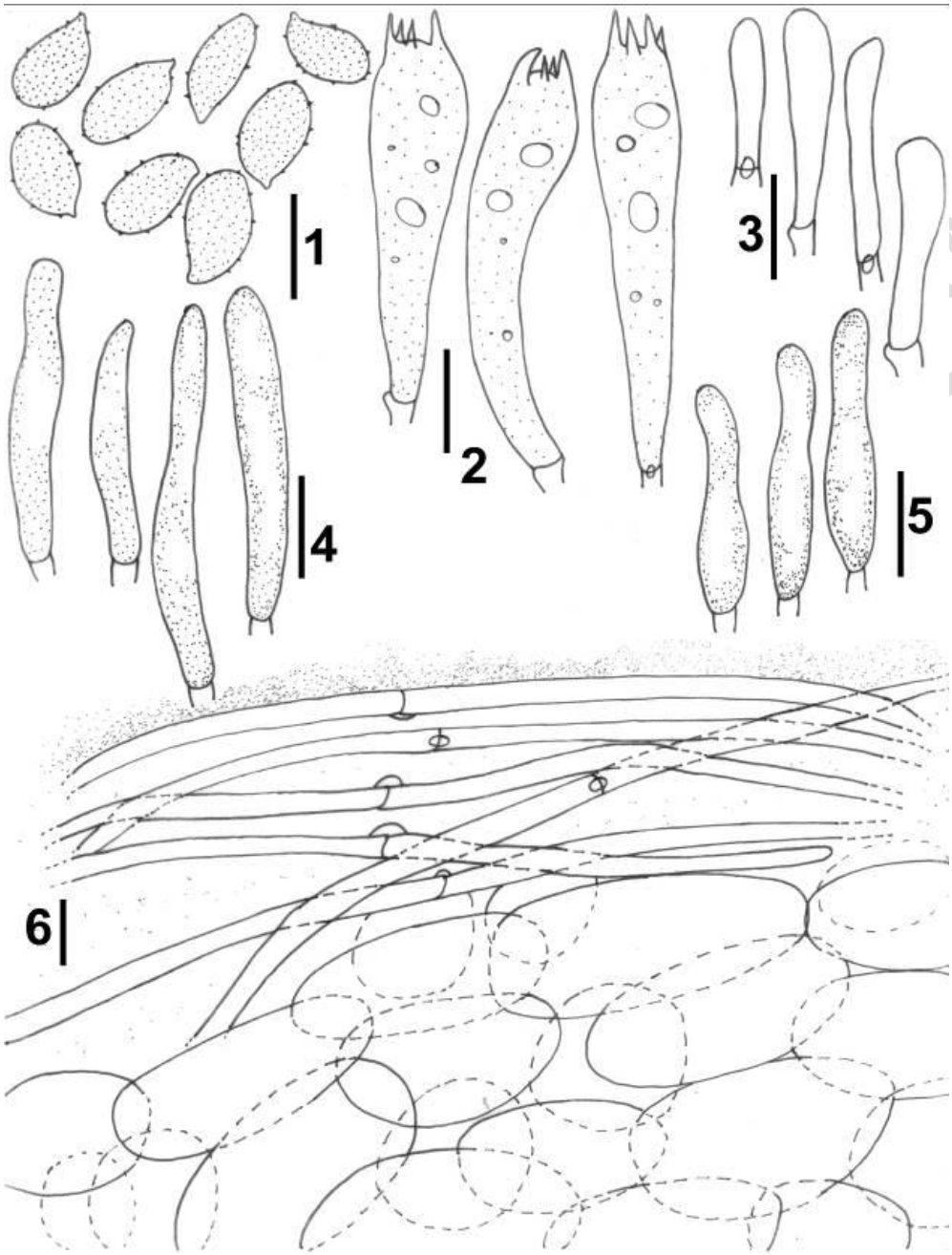

Fig. 3. ***Thaxterogaster thindii*** **sp. nov. (~~DCM-1~~, holotype). (1) Basidiospores, (2) basidia, (3) sterile marginal elements, (4) pleurocystidia, (5) cheilocystidia, (6) transverse section of pileipellis ~~through pileu~~s. Scale bars: 1–6 = 10 µm.**

Comment [46]: CAL 2129

4. CONCLUSION

The Cortinariaceae family remains largely unexplored in India. This family includes significant ectomycorrhizal fungi that play a crucial role in maintaining ~~terrestrial~~ ecosystems. Our ongoing and extensive macrofungal surveys across various Indian states, including Uttarakhand, Himachal Pradesh, West Bengal, and Sikkim, have uncovered numerous previously overlooked species from several genera. Through a combination of morphological and molecular phylogenetic studies, our research confirms that India harbors many undiscovered or potentially new species of Cortinariaceae. We anticipate that, as we continue our macrofungal explorations across all climatic regions of India, the diversity of mushrooms in general and the Cortinariaceae in particular will be unfolded in the near future.

REFERENCES

Bose, A., Niskanen, T., Datta, S., Ghosh, A., Vizzini, A. & Das, K. (2024b). Two new species and a new record of *Cortinarius* subgenus *Telamonia* (Agaricales) from India, 970: 38–60. Doi.org/10.5852/ejt.2024.970.2747

Bose, A., Uniyal, P., Vizzini, A. & Das, K. (2024a). Morphotaxonomy and molecular phylogeny unveil one new species and two new records of *Phlegmacium* (Cortinariaceae) from India, 2024: e04552. Doi: 10.1111/njb.04552

Brandrud, T.E., Schmidt-Stohn, G., Liimatainen, K., Niskanen, T., Frøslev, T.G., Soop, K. *et al.* (2018). *Cortinarius* sect. *Riederi*: taxonomy and phylogeny of the new section with European and North American distribution, 17: 1323–1354. https://doi.org/10.1007/s11557-018-1443-0

Dai, Y.C., & Yang. (2008). A revised checklist of medicinal fungi in China, 27: 801–824.

Drummond, A. J., Ashton, B., Buxton, S., Cheung, M., Cooper, A., Heled, J., A. *et al.* (2010). Geneious v. 5.1. Available from http://www.geneious.com

Gardes, M. & Bruns, T.D. (1993). ITS primers with enhanced specificity for basidiomycetes-application to the identification of mycorrhizae and rusts, 2: 113–118. https://doi.org/10.1111/j.1365-294X.1993.tb00005.x

Ghosh, A., Chakraborty, D., Hembrom, M.E., Vizzini, A., & Ddas, K. (2023). *Thaxterogaster shoreae*, a new species of *Thaxterogaster* subg. *Scauri* sect. *Purpurascentes* from Sal Forest of India based on morphology and molecular phylogeny, 68: 23–30. Doi: 10.6165/tai.2023.68.23

Kalichman, J., Kirk, P. M., & Matheny, P. B. (2020). A compendium of generic names of agarics and Agaricales, 69: 425–447. doi.org/10.1002/tax.12240

Kornerup, A., & Wanscher, J. H. (1978). Methuen handbook of colour (3rd ed.). Eyre Methuen.

Kumar, S., Stecher, G. & Tamura, K. (2016). MEGA7: Molecular Evolutionary Genetics analysis version 7.0 for bigger datasets, 33(7): 1870–1874. https://doi.org/10.1093/molbev/msw054

Liimatainen, K., Niskanen, T., Dima, B., Ammirati, J. F., Kirk, P. M., & Kytövuori, I. (2020). Mission impossible completed: unlocking the nomenclature of the largest and most complicated subgenus of Cortinarius, Telamonia, 104: 291–331. doi.org/10.1007/s13225-020-00459-1

Liimatainen, K., Kim, J. T., Pokorny, L., Kirk, P. M., Dentinger, B., & Niskanen, T. (2022). Taming the beast: a revised classification of Cortinariaceae based on genomic data, 112: 89–170. doi.org/10.1007/s13225-022-00499-9

Nouhra, E., Kuhar, F., Truong, C., Pastor, N., Crespo, E., Mujic, A., Caiafa, M.V., & Smith, M.E. (2021). *Thaxterogaster* revisited: a phylogenetic and taxonomic overview of sequestrate *Cortinarius* from Patagonia, 113(5): 1022–1055. DOI: 10.1080/00275514.2021.1894535

Peintner, U., Moser, M., & Vilgalys, R. (2002). *Thaxterogaster* is a taxonomic synonym of *Cortinarius*: New combinations and new names. Mycotaxon, 81: 177–184.

Singer, R. (1951). *Thaxterogaster*—A new link between Gastromycetes and Agaricales, 43: 215–228.

Comment [47]: forest

Comment [48]: European Journal of Taxonomy

Comment [49]: Nordic Journal of Botany

Comment [50]: Mycological Progress 17(6)

Comment [51]: Molecular Ecology

Comment [52]: Taiwania 68(1)

Comment [53]: Taxon 69(3)

Comment [54]: Molecular Biology and Evolution

Comment [55]: italic

Comment [56]: Not cited Liimatainen *et al*., (2020) in the text

Comment [57]: Fungal Diversity

Comment [58]: Mycologia

Comment [59]: Mycologia

Soop, K., Dima, B., Cooper, J.A., Park, D., & Oertel, B. (2019). A phylogenetic approach to a global supraspecific taxonomy of *Cortinarius* (Agaricales) with an emphasis on the southern mycota, ~~2019~~: 261–290. doi.org/10.3767/persoonia.2019.42.10

Turland, N.J., Wiersema, J.H., Barrie, F.R., Greuter, W., Hawksworth, D.L., Herendeen, P.S., et al. (Eds.). (2018). International Code of Nomenclature for Algae, Fungi, and Plants (Shenzhen Code) Adopted by the Nineteenth International Botanical Congress Shenzhen, China, July 2017. Regnum Vegetabile 159; Koeltz Botanical Books. Glashütten: Germany.

~~White, T.J., Bruns, T., Lee, S. & Taylor, J.W. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR Protocols: a guide to method and applications, 315–322.~~

Xie, M.L., Feng, N., Lin, W.F., Su, W.Y., Li, Y. & Yang, Z.Q. (2023). Morphological and Phylogenetic Characterization of Three Novel *Thaxterogaster* (Cortinariaceae) Species from China with an Emphasis on Their Subtropical Distribution, 9(11):1058, https://doi.org/10.3390/jof9111058

XIE, M.L., LI, Y., WEI, T.Z., LI, Y., & LI, C.T. (2024). A new species and five new combinations of Thaxterogaster (Cortinariaceae, Agaricales) from China, 677 (2): 155–165. doi.org/10.11646/phytotaxa.677.2.4

Comment [60]: Persoonia - Molecular Phylogeny and Evolution of Fungi (42)

Comment [61]: White, T.J., Bruns, T.D., Lee, S.B. & Taylor, J.W. (1990). Amplification and Direct Sequencing of Fungal Ribosomal RNA Genes for Phylogenetics. In: Innis, M.A., Gelfand, D.H., Sninsky, J.J. and White, T.J., Eds., PCR Protocols: A Guide to Methods and Applications, Academic Press, New York, 315-322. http://dx.doi.org/10.1016/B978-0-12-372180-8.50042-1

Comment [62]: J. Fungi 2023, 9(11), 1058

Comment [63]: lowercase

Comment [64]: italic

Comment [65]: Phytotaxa