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MARASMIUS TENUISSIMUS (AGARICALES, MARASMIACEAE): MARASMIOID THREAD BLIGHT DISEASE FROM SORONG, WEST PAPUA, INDONESIA

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Atik Retnowati & Anis S. Lestari 2025. *Marasmius tenuissimus* (Agaricales, Marasmiaceae): Jenis *Marasmius* penyebab penyakit hawar dari Sorong, Papua Barat, Indonesia. Floribunda 8(2) 54 – 66 — *Marasmius tenuissimus* merupakan salah satu jamur marasmioid penyebab penyakit hawar yang menginfeksi tanaman komersial dan non-komersial. Spesies ini dicirikan oleh tubuh buah berukuran sedang, tudung buah cembung tidak beraturan hingga *plano-convex*; spasi bilah jarang, *interwoven* dan anastomosis; batang absen; *cheilocystidia* dan *pileipellis* adalah *Siccus-type broom cell*. Penelitian ini merupakan bagian dari inventarisasi marga *Marasmius* di Indonesia yang bertujuan untuk mengetahui keanekaragaman jenisnya. Identifikasi morfologi dan analisis filogenetik berdasarkan DNA lokus ITS mengonfirmasi bahwa koleksi jamur marasmioid dari Sorong teridentifikasi sebagai *M. tenuissimus*. Koleksi dan sekuen nukleotida baru DNA *M. tenuissimus* dari Indonesia akan bermanfaat bagi penelitian keanekaragaman jamur Indonesia di masa datang.

Kata kunci: karakter makro-mikro, *Neosessile*, rizomorf, taksonomi

Atik Retnowati & Anis S. Lestari 2025. *Marasmius Tenuissimus* (Agaricales, Marasmiaceae): Marasmioid Thread Blight Disease from Sorong, West Papua, Indonesia. Floribunda 8(2) 54 – 66 — *Marasmius tenuissimus* is one of the marasmoid thread blight diseases that infects commercial, such as cacao and coffee, and non-commercial plants. The species is characterized by a medium fruiting body, an irregular convex to plano-convex pileus; remote, interwoven, and anastomosing lamellae; absence of stipe; *Siccus*-type broom cells of cheilocystidia and pileipellis. As part of an inventory of the genus *Marasmius* in Indonesia, this study aims to document the species diversity of the genus within the region. Field exploration was conducted in Sorong, followed by specimen drying, herbarium processing, and identification using both morphological and molecular analyses. Observation and phylogenetic analyses using nrDNA ITS highlighted the taxon placement of our new collected marasmioid species as *M. tenuissimus* and also provided the nucleotide sequence data which will be valuable for future study of fungal diversity in Indonesia.

Keywords: macro-micro characters, *Neosessile*, rhizomorph, taxonomy

Thread Blight Disease (TBD) is a fungal pathogen affecting several commercial and non-commercial plants, caused by various species of pathogenic fungi (Amoaka-Attah *et al*. 2016). The disease is widely distributed, particularly in humid tropical regions. The causal agent of TBD are *Corticium koleroga* (Cke) Hoehnel (Dechassa 2019), *Ceratobasidium niltonsouzanum* MP Melo, SI Moreira, PC. Ceresini and *Ceratobasidium chavesanum* MP. Melo, JA. Ventura, H. Costa, PC. Ceresini (de Melo *et al*. 2018).

Another causal agent of TBD was the marasmioid fungi, which often produce rhizomorphs as vegetative structures, appearing as a network of mycelial threads. These threads cover branches, leaves, twigs, flowers, or fruit of infected plants. *Marasmius infestans* Huamán, Ramos C., and Díaz Val. was found to be infecting cacao in Peru (Huaman-Pilco *et al*., 2024). Additionally, Amoaka-Attah *et al*. (2020) identified four species of marasmioid as the causal agents of TBD on Cacao in Ghana, and classified five types of rhizomorphs based on their morphotypes. Those four species were *Marasmius crinis-equi* F. Muell. ex Kalchbr., *Marasmius tenuissimus* (Jungh.) Singer, *Marasmiellus palmivorus* (Sharples) Desjardin, and *Marasmius scandens* Massee. The research concluded that marasmioid thread blight disease reveals distinct rhizomorph types depending on the species. Rhizomorph morphotype of *Marasmius crinis-equi* is black, *M. tenuissimus* is brown and whitish to brownish-white, *Marasmiellus palmivorus* is shiny or silky white, and *Marasmius scandens* is faint cream or dull white.

We reported specifically here the occurrence of *M. tenuissimus* from Sorong, Indonesia. The species belongs to the genus *Marasmius*, section *Neosessile*. The section is characterised by the pleurotoid habit, absent or eccentric stipe, medium or large basidiospores, and *Siccus*-type broom cells of pileipellis. *Marasmius tenuissimus* was initially described from Indonesia, based on the type collection of Junghuhn (Singer 1976), collected from Kebokuning (Central Java), as well as other materials from Brazil and Bolivia. Previously, the species had been reported from Peru (Huaman-Pilco *et al*. 2022), Korea (Lee *et al*. 2023), the Philippines (Dulay *et al*. 2020), Malaysia (Tan *et al*. 2009), Thailand (Wannathes *et al*. 2009), and Taiwan (Wei *et al*. 2021). The Global Biodiversity Information Facility (GBIF) mapped 123 occurrences of *M. tenuissimus* in the world, which are distributed into 10 countries: Ghana, Thailand, Australia, Indonesia, Japan, Brazil, Malaysia, the Cook Islands, Peru and China. The highest number of occurrences is in Ghana (79 records) (accessed on 17 September 2025). This report enriches the previous distribution record of *M. tenuissimus* in the world.

MATERIALS AND METHODS

Study area and sampling method

The Klamono Nature Tourism Park (TWA Klamono) is situated in Klamono Village, Klamono District, Sorong Regency, Southwest Papua Province. The TWA Klamono spans an area of 1,909.37 hectares, established as a conservation area (Maruapey *et al*. 2024). This nature reserve is geographically characterized as a lowland tropical rainforest ecosystem. It is a vital water catchment area and a significant "green lung" near Sorong City in Southwest Papua, Indonesia. The average maximum temperature can reach up to 32°C, with a mean annual temperature of around 27°C. The region receives substantial rainfall, with an annual precipitation of up to 3,066 mm. The area has high humidity and experiences frequent rainfall throughout the year.

A specimen of *M. tenuissimus* was obtained during the ectomycorrhizal expedition in Klamono Nature Reserve, Sorong, West Papua, Indonesia, in July 2022. While collecting ectomycorrhizal fungi, we also collected some marasmioid fungi, including *M. tenuissimus*. The basidiocarp of the species was stored in a collecting box. In-situ photo documentation was conducted, with a focus on the overall fruiting body and its habitat. The fresh specimens were photographed with a focus on the detail features of the pileus, lamellae, and stipe.

Morphological study

The macroscopic characters of the pileus, lamellae, and stipe were documented from the fresh material in the field before drying process. The colour of fresh basidiomes was related to the codes of Kornerup & Wanscher (1967). Then, the specimens were placed in an electric dryer for drying. The dried collection was then placed individually in sealed plastic bags and buried under silica gel. Microscopic characters were examined in the Biosystematics Laboratory, BRIN, using a light microscope of OLYMPUS CX 22LED. The 3% KOH, Congo Red, and Melzer's reagent were applied for basidiospores, basidia, sterile cells, pileipellis, and hyphae. The arithmetic mean-standard deviation (x_m), and the quotient of the length by the width, expressed as range (Q) and arithmetic mean (Q_m), of basidiopsores were calculated. The dimensions of basidia and basidiospores were measured with at least 25 spores. The examined specimen is kept in Herbarium Bogoriense (BO).

Molecular study

DNA extraction, PCR amplification, and sequencing

The total DNA was extracted from dried material using the Plant Genomic DNA Mini Kit (Geneaid Biotech, Taiwan, ROC) following the protocol provided by the manufacturer. We amplified the ITS region using Primer ITS4 (5`–TCC TCC GCT TAT TGA TAT GC –3`) and primer ITS5 (5`– GGA AGT AAA AGT CGT AAC AAG G –3`) (White *et al*. 1990). The PCR amplification for ITS was conducted in three steps for 35 cycles. The process began with a heat shock at 95°C for 3 minutes, then denaturing the DNA at 95°C for 30 seconds and annealing at 55°C for 30 seconds. DNA extension was then performed at 72°C for 60-90 seconds. A final extension at 72°C for 7 minutes was carried out. The PCR products were purified and sequenced at the manufacturing of 1st BASE (Selangor, Malaysia, https://base-asia.com/).

Sequence alignment and phylogenetic analysis

The newly derived ITS sequences of *M. tenuissimus* fungi were checked, edited, and assembled with SeqMan V. 7.0.0 (DNASTAR, Madison, WI), then browsed in the NCBI BLASTn for the homologous sequences. The reference sequences of *Marasmius* from previous studies for alignment were downloaded from GenBank (Amoako-Attah *et al*. 2020, Oliveira *et al*. 2022, Dutta *et al*. 2015, Guard *et al*. 2023, Huamán-Pilco *et al*. 2024, Lee *et al*. 2023, Tan *et al*. 2009, Wannathes *et al*. 2009, Wei *et al*. 2021). The ITS dataset was aligned and trimmed manually using BioEdit v. 7.2 software (Hall 1999). The list of the *Marasmius* sequences used in the analysis is provided (Table 1).

The ITS dataset of marasmoid fungi in this study was aligned in MAFFT v. 7 (Katoh *et al*. 2019) with default parameters, trimmed, and adjusted manually, if necessary, in BioEdit v 7.0.9.0 (Hall 1999). The IQ-tree web server was used to perform Maximum Likelihood analysis (ML) with 1000 ultrafast bootstrap replication TPM2u+F+G4 as the model of evolution (Hoang *et al*. 2018, Kalyaanamoorthy *et al*. 2017, Nguyen *et al*. 2015). Maximum Parsimony (MP) analysis was conducted in MEGA 12 (Kumar *et al*. 2024). The MP tree was obtained using the Subtree-Pruning-Regrafting (SPF) algorithm (Nei & Kumar 2000) with search level 1, in which the initial trees were obtained by the random addition of sequences (10 replicates) with the overall 1000 replication Bootstrap value for the analysis were added in the tree (Figure 1).

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Table 1. Accession numbers and origin of *Marasmius tenuissimus* and other *Marasmius* species used in the phylogenetic analysis.

No.	Species	Accession number (ITS)	Specimen codes[a]	Location	References
1	*Marasmius auranticapitatus* (T)	NR184982	SP 445584	Brazil	Oliveira *et al*. 2022
2	*Marasmius bambusiniformis*	MW504974	NW1504	Thai-land	Wannathes *et al*. 2009
3	*Marasmius haematocephalus*	MW426456	NW1431	Thailand	Wannathes *et al*. 2009
4	*Marasmius haematocephalus*	MW426466	NW1466	Thailand	Wannathes *et al*. 2009
5	*Marasmius leveilleanus*	OR636656	KUM60142	Malaysia	Oliveira *et al*. 2024
6	*Marasmius leveilleanus*	MW426416	NW1337	Thailand	Wannathes *et al*. 2009
7	*Marasmius roseus* (T)	NR184983	SP 445510	Brazil	Oliveira *et al*. 2022
8	*Marasmius rhabarbarinoides* (T)	NR177126	JO 66	Brazil	Oliveira *et al*. 2022
9	*Marasmius rubicundus*	ON502664	JO 246	Brazil	Oliveira *et al*. 2022
10	*Marasmius rubicundus* (T)	NR184981	JO 464	Brazil	Oliveira *et al*. 2022
11	*Marasmius tenuissimus*	OM720123	INDES-AFHP31	Peru	Huaman-Pilco *et al*. 2022
12	*Marasmius tenuissimus*	PQ584399	S3R37	China	Ren 2024 (unpublished)
13	*Marasmius tenuissimus*	MW504967	W1486	Thailand	Kumla & Wannathes 2021
14	*Marasmius tenuissimus*	EU935569	NW199	Thailand	Wannathes *et al*. 2009
15	*Marasmius tenuissimus*	MF189066	AKD 304/2015	India	Dutta *et al*. 2015
16	*Marasmius tenuissimus*	MF061773	SCAU111	China	Zhang *et al*. 2019
17	*Marasmius tenuissimus*	EU935568	NW192	Thailand	Wannathes *et al*. 2009
18	*Marasmius tenuissimus*	OQ186707	SMF3295	Australia	Guard *et al*. 2023
19	*Marasmius tenuissimus*	OQ186706	FBT2163	Australia	Guard *et al*. 2023
20	*Marasmius tenuissimus*	OQ186703	FBT2527	Australia	Guard *et al*. 2023
21	*Marasmius tenuissimus*	OQ186702	FG019	Australia	Guard *et al*. 2023
22	*Marasmius tenuissimus*	OQ186705	FBT2738	Australia	Guard *et al*. 2023
23	*Marasmius tenuissimus*	OQ186704	FG020	Australia	Guard *et al*. 2023
24	*Marasmius tenuissimus*	OR177790	JBRI-M20-022	Korea	Guard *et al*. 2023
25	*Marasmius tenuissimus*	MW527104	WEI 17-238	Taiwan	Wei *et al*. 2021
26	*Marasmius tenuissimus*	MN794170	GH-69	Ghana	Amoako-Attah *et al*. 2020
27	*Marasmius tenuissimus*	MN794163	GH-61	Ghana	Amoako-Attah *et al*. 2020
28	*Marasmius tenuissimus*	MN794158	GH-56	Ghana	Amoako-Attah *et al*. 2020
29	*Marasmius tenuissimus*	MN794168	GH-66	Ghana	Amoako-Attah *et al*. 2020
30	*Marasmius tenuissimus*	MN794164	GH-62	Ghana	Amoako-Attah *et al*. 2020
31	*Marasmius tenuissimus*	MN794156	GH-51	Ghana	Amoako-Attah *et al*. 2020
32	*Marasmius tenuissimus*	MN794165	GH-63	Ghana	Amoako-Attah *et al*. 2020
33	*Marasmius tenuissimus*	MN794171	GH-7	Ghana	Amoako-Attah *et al*. 2020
34	*Marasmius tenuissimus*	MN794134	GH-14	Ghana	Amoako-Attah *et al*. 2020
35	*Marasmius tenuissimus*	MN794176	GH-78	Ghana	Amoako-Attah *et al*. 2020

Table 1. Accession numbers and origin of *Marasmius tenuissimus* and other *Marasmius* species used in the phylogenetic analysis. (*continue*)

No.	Species	Accession number (ITS)	Specimen codes[a]	Location	References
36	*Marasmius tenuissimus*	MN794166	GH-64	Ghana	Amoako-Attah *et al*. 2020
37	*Marasmius tenuissimus*	MN794162	GH-60	Ghana	Amoako-Attah *et al*. 2020
38	*Marasmius tenuissimus*	MN794155	GH-50	Ghana	Amoako-Attah *et al*. 2020
39	*Marasmius tenuissimus*	MN794153	GH-47	Ghana	Amoako-Attah *et al*. 2020
40	*Marasmius tenuissimus*	MN794151	GH-42	Ghana	Amoako-Attah *et al*. 2020
41	*Marasmius tenuissimus*	MN794150	GH-41	Ghana	Amoako-Attah *et al*. 2020
42	*Marasmius tenuissimus*	MN794148	GH-38	Ghana	Amoako-Attah *et al*. 2020
43	*Marasmius tenuissimus*	MN794147	GH-37	Ghana	Amoako-Attah *et al*. 2020
44	*Marasmius tenuissimus*	MN794144	GH-34	Ghana	Amoako-Attah *et al*. 2020
45	*Marasmius tenuissimus*	MN794145	GH-35	Ghana	Amoako-Attah *et al*. 2020
46	*Marasmius tenuissimus*	MN794142	GH-32	Ghana	Amoako-Attah *et al*. 2020
47	*Marasmius tenuissimus*	MN794177	GH-79	Ghana	Amoako-Attah *et al*. 2020
48	*Marasmius tenuissimus*	MN794173	GH-74	Ghana	Amoako-Attah *et al*. 2020
49	*Marasmius tenuissimus*	MN794143	GH-33	Ghana	Amoako-Attah *et al*. 2020
50	*Marasmius tenuissimus*	MN794154	GH-49	Ghana	Amoako-Attah *et al*. 2020
51	*Marasmius tenuissimus*	MN794149	GH-40	Ghana	Amoako-Attah *et al*. 2020
52	*Marasmius tenuissimus*	MN794157	GH-54	Ghana	Amoako-Attah *et al*. 2020
53	*Marasmius tenuissimus*	MN794159	GH-57	Ghana	Amoako-Attah *et al*. 2020
54	*Marasmius tenuissimus*	MN794167	GH-65	Ghana	Amoako-Attah *et al*. 2020
55	*Marasmius tenuissimus*	MN794169	GH-67	Ghana	Amoako-Attah *et al*. 2020
56	*Marasmius tenuissimus*	MN794172	GH-70	Ghana	Amoako-Attah *et al*. 2020
57	*Marasmius tenuissimus*	MN794140	GH-26	Ghana	Amoako-Attah *et al*. 2020
58	*Marasmius tenuissimus*	MN794133	GH-13	Ghana	Amoako-Attah *et al*. 2020
59	*Marasmius tenuissimus*	MN794181	GH-9	Ghana	Amoako-Attah *et al*. 2020
60	*Marasmius tenuissimus*	MN794178	GH-8	Ghana	Amoako-Attah *et al*. 2020
61	*Marasmius tenuissimus*	MN794161	GH-6	Ghana	Amoako-Attah *et al*. 2020
62	*Marasmius tenuissimus*	MN794185	MS-4	Ghana	Amoako-Attah *et al*. 2020
63	*Marasmius tenuissimus*	MN794184	MS-3	Ghana	Amoako-Attah *et al*. 2020
64	*Marasmius tenuissimus*	MN794183	MS-2	Ghana	Amoako-Attah *et al*. 2020
65	*Marasmius tenuissimus*	MN794182	MS-1	Ghana	Amoako-Attah *et al*. 2020
66	*Marasmius tenuissimus*	MN794160	GH-59	Ghana	Amoako-Attah *et al*. 2020
67	*Marasmius tenuissimus*	PP789877	P7	Thailand	Surawut *et al*. 2025
68	*Marasmius tenuissimus*	KM246277	C2/33	Brazil	Leite *et al*. 2014
69	*Marasmius tenuissimus*	KM246261	C20/6	Brazil	Leite *et al*. 2014
70	***Marasmius tenuissimus***	**PX443589**	**AR-1561**	**Indonesia**	**this study**
71	*Marasmius venatifollius* (T)	NR177127	SP 445485	Brazil	Oliveira *et al*. 2022

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RESULTS

PHYLOGENETIC ANALYSIS

The ITS sequence dataset of marasmoid fungi contains 79 fungal taxa, including the new graphical record. The best final likelihood value for ML is -2498.967 and was assembled from 568 bp of ITS. The matrix comprises 196 distinct alignment patterns with 31.87 % of gaps and undetermined characters. Base frequencies were estimated as follows; A = 0.234, C = 0.208, G = 0.223, T = 0.335 with substitution rates AC = 2.31606, AG = 5.21602, AT = 2.390752, CG = 1.00, CT = 5.21602, GT = 1.00; gamma distribution shape parameter α = 0.264. For the MP analysis, the consistency index is 0.699405, the retention index is 0.848348, and the composite index is 0.593339 for all sites and parsimony-informative sites (in parentheses).

The ITS sequence of our collection matches with *M. tenuissimus* sequences deposited in GenBank following the BLAST search. The phylogenetic analysis based on the ITS gene region of *Marasmius* taxa resulted in well-supported clades as depicted in the phylogram (Figure 1). The newly collected *Marasmius tenuissimus* (AR-1561) was placed in the *Marasmius tenuissimus*-clade statistical support (95% ML and 98% MP).

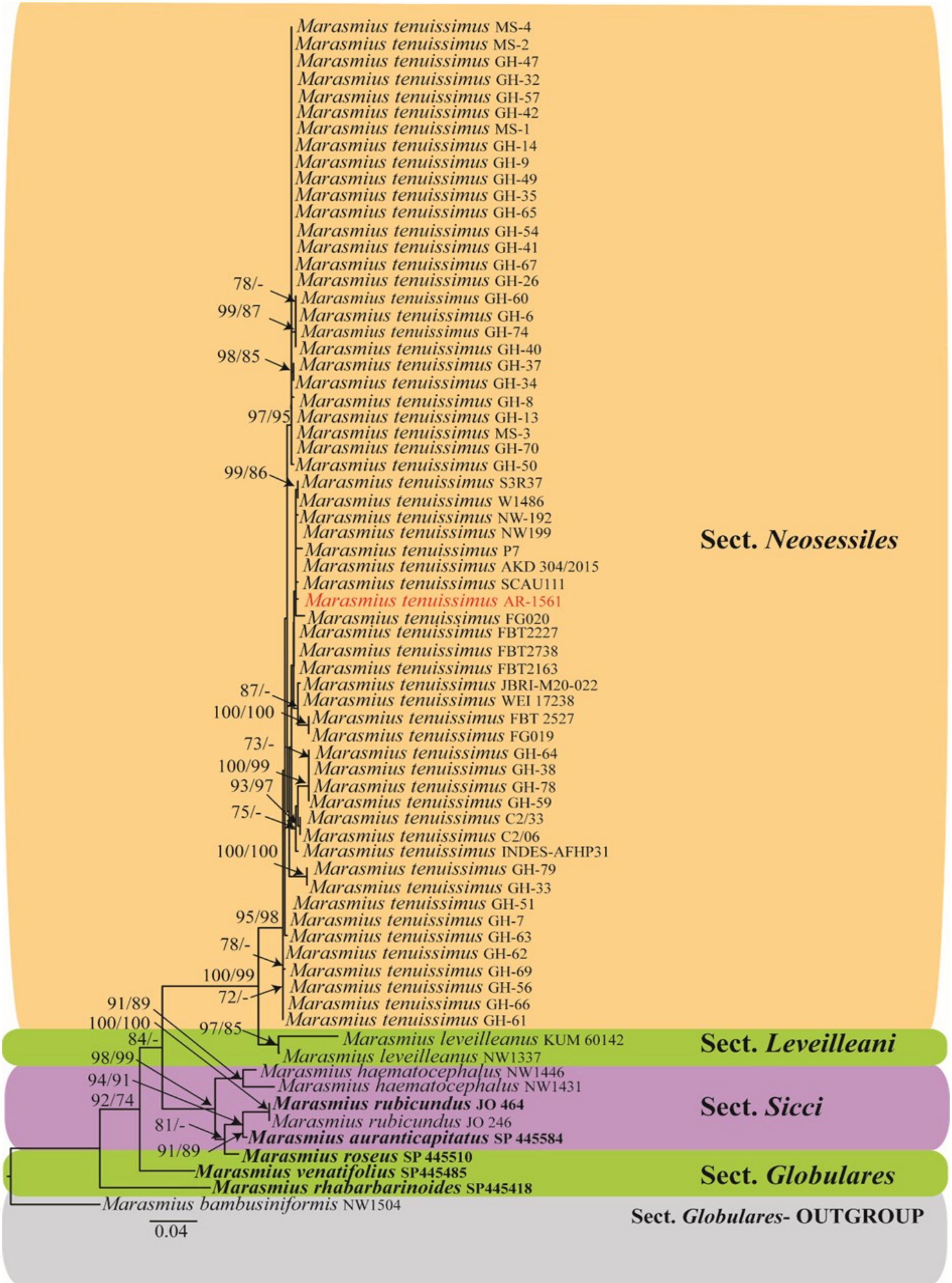

Figure 1. The Maximum likelihood phylogram of ITS data for *Marasmius tenuissimus* and some other *Marasmius* species. The bootstrap values of ML and MP greater than 70% are given near the nodes. The new collected *Marasmius* is highlighted in red, and type strains are in bold. The tree is rooted to *Marasmius bambusiniformis* (NW1504). *Sect.: Section

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TAXONOMY TREATMENT

***Marasmius tenuissimus* (Jungh.) Singer.** Figs. 2 and 3.
Section *Neosessiles* Singer, Mycologia 50: 104. 1958.
Type: Indonesia, Java, near Kebokoening, May (L).

Synonymy:
Agaricus tenuissimus Jungh., Verh. Batav. Genootsch. Kunst. Wet. 17(2): 84 (1838)
Pleurotus tenuissimus Sacc., Syll. fung. (Abellini) 5: 374 (1887)

Basidiomata medium. Pileus 0.4–2.7 cm diam, irregularly convex to convex or plano convex, non-striate, reticulate; surface dull, dry, glabrous, pale orange (5A3) when young, greyish orange (6B5) in age. Context thin, white. Lamellae adnate, remote (5–10), interwoven and anastomosing to subreticulate, non-marginate. Stipe absent at first, then present in mature fruiting bodies; 1–53 × 0.5–51 mm, cylindrical, hollow, velutinous, insititious, grey. Odor and taste not distinctive. Rhizomorph absent.

Basidiospores 8–10.4 × 4.22–5.8 µm (x_m = 9.47 ± 0.55 × 4.97 ± 0.51 µm; Q = 1.54–2.31; Q_m = 1.54–2.31); n = 25 spores per 1 specimen, ellipsoid, smooth, hyaline, inamyloid, thin-walled. Basidia 20.6–23.5 × 5.9–6.9 µm, 4-spored, clavate. Basidioles 20.4–21.4 × 5.3–6.3µm, clavate and fusoid. Cheilocystidia composed of *Siccus*-type broom cells; main body 7.9–16.7 × 5.3–8.9 µm, cylindrical to clavate or vesiculose, often irregularly forked or branched, brown, thick-walled in apical region; apical setulae 1–3 × 1 µm, conical to cylindrical, obtuse. Pleurocystidia absent. Pileipellis composed of *Siccus*-type broom cells; main body 12–20 × 8–16 µm, clavate to broadly clavate or turbinate, hyaline to pale brown, apically thick-walled; apical setulae 1–3 × 0.5–1 µm, cylindrical to conical, obtuse to subacute, usually wavy in outline, brown, thick-walled. Pileus trama intervowen, incrusted, hyaline to yellowish brown. Stipe tissue monomitic; cortical hyphae 4–5 µm diam, parallel, cylindrical, yellowish brown, smooth, dextrinoid, thin to thick-walled up to 4.8 µm; medullary hyphae 3.5-6.5 µm diam, parallel, hyaline, thin-walled. Caulocystidia composed of two types of cells: 1) *Siccus*-type broom cells, uncommon; 19 × 8 µm, clavate, hyaline to yellowish brown; b) cylindrical elements, 15–23 × 5–9 µm, hyaline to yellowish brown, thin to thick-walled. Clamp connections present.

Habit, habitat, and known distribution. Gregarious on twigs of dicot, Africa, Mexico, Peru, Ghana, Brazil, Malaysia, Indonesia, Northern Thailand, Taiwan.

Material examined. Indonesia: West Papua, Sorong, Klamono Nature Reserve (-1° 066' 751" S, 131° 431' 862" E), 17 July 2022, collected by Ectomycorrhizal Team, *A. Retnowati 1561*, identified by A. Retnowati.

GenBank accession number. AR-1561 – ITS = PX443589

Notes. *Marasmius tenuissimus* is characterized by a medium fruiting body, an irregular convex to plano-convex pileus; remote, interwoven, and anastomosing lamellae; absence to presence of stipe; *Siccus*-type broom cells of cheilocystidia and pileipellis (Figures 2 and 3).

The phylogram's topology in this study is roughly similar to Tan *et al*. (2009), with the reverse position of Sect. *Neosessiles* and *Leveilleani* at the top phylogram (Figure 1). In addition, based on the phylogram, our newly collected data confirmed its taxonomic placement as *M. tenuissimus*. Hence, this paper amends the morphology, sequence data, and reference specimen of *M. tenuissimus* in Indonesia. Additionally, *M. tenuissimus* has been previously recorded in various countries, including Australia, Brazil, China, Ghana, India, Peru, and Thailand (Table 1).

This study documents a new collection of marasmoid species found in West Papua, Indonesia, based on morphology and single-gene phylogeny. Our newly collected sample was identified as *M. tenuissimus*, which was previously recorded and described by Singer (1976) in Java; however, no reference specimen was deposited. Consequently, the herbarium specimen of the species will be a new collection in Herbarium Bogoriense (BO). The comparison character of *M. tenussimus* collected in Java (Holotype) and Papua (this study) is listed in Table 2.

In Table 2, varied characters between *M. tenuissimus* from Java and Papua on pileus size, surface, lamellae space, the presence of stipe, and basidioles are shown.

Figure 2. Fruiting bodies of *Marasmius tenuissimus* collected from Klamono Nature Reserve, Sorong, West Papua. Scale bars: A = 1 cm; B = 1.5 cm; C = 2.25 cm; D = 0.75 cm, E = 1 cm.

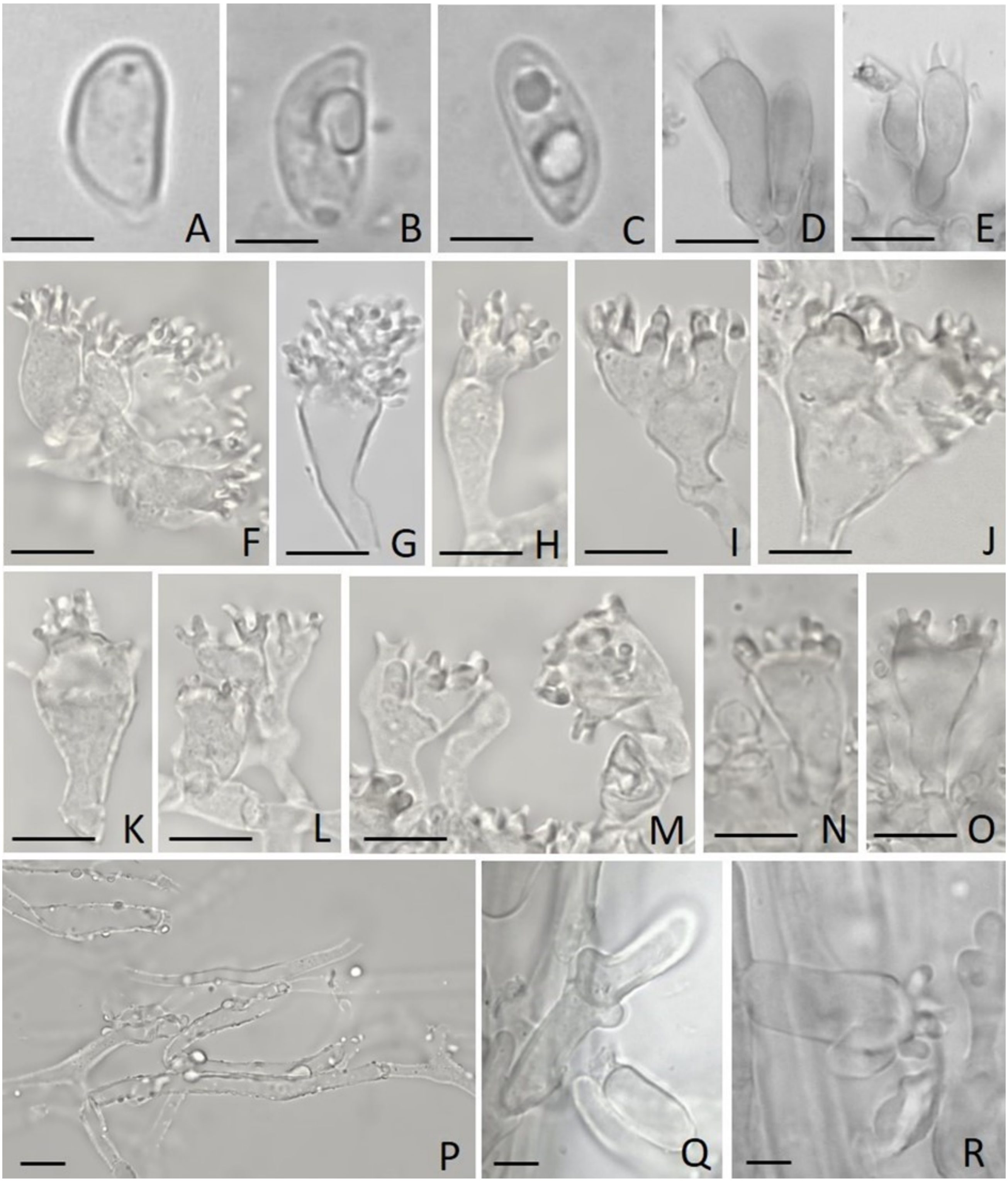

Figure 3. Microscopic characters of *Marasmius tenuissimus*: A–C. Basidiospores; D–E. Basidia-basidioles; F–J. Cheilocystidia; K–O. Pileipellis; P. incrusted wall hyphae of pileal trama; Q–R. Caulocystidia. Scale bars: A–C = 4 µm; D–E = 9 µm; F–J = 5.5 µm; K–O = 7 µm; P = 5 µm; Q–R = 4 µm.

Table 2. The morphological description of *M. tenuissimus* was found in Indonesia.

		Java (Singer, 1976)	Papua (This study)
Pileus	Colour	dirty ochraceous to cinnamon brownish, fresh rusty brown	pale orange when young, greyish orange in age
	Shape	convex	irregularly convex to convex or plano convex
	Surface	smooth	dull, dry, glabrous
	Size	0.7–1.4 cm diam	0.4–2.7 cm diam
Lamellae	Colour	white to cream pallid	off white
	Space	distant (3–6)	remote (5–10)
		some forked, not or only distantly intervenose	interwoven and anastomosing to subreticulate
	Lamellulae	intermixed	0 series
	attachment	attenuate-subadnate	adnate
Stipe	Colour	white to deep brown	grey
	Surface	glabrous or subglabrous, or very whitish flocculose	velutinous
	Size	1–2 × 0.1–0.5 mm	1–53 × 0.5–51 mm
Basidiospores	Size	(7–)8–10.5 × 3.8–4.8 µm, ellipsoid-oblong, smooth, hyaline, inamyloid	8–10.4 × 4.22–5.8 µm, ellipsoid, smooth, hyaline, inamyloid, thin-walled
Basidioles	Shape	fusoid	clavate and fusoid
Cheilocystidia	Shape	*Siccus*-type broom cells	*Siccus*-type broom cells
Pleurocystidia		absent	absent
Caulocystidia	size and shape	NA	*Siccus*-type broom cells, 19 × 8 µm, clavate, hyaline to yellowish brown Cylindrical elements, 15–23 × 5–9 µm, hyaline to yellowish brown
Habitat		on dead living twigs, leaves, and bark of dicotyledonous trees	on twigs of dicotyledonous trees
Rhizomorph		absent	absent

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