

Disentangling cryptic species in the *Marasmius haematocephalus* and *M. siccus* species complexes
(Agaricales, Basidiomycota)

Démêler les espèces cryptiques dans les complexes d'espèces *Marasmius haematocephalus* et *M. siccus* (Agaricales, Basidiomycota)

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SUPPLEMENTARY MATERIAL

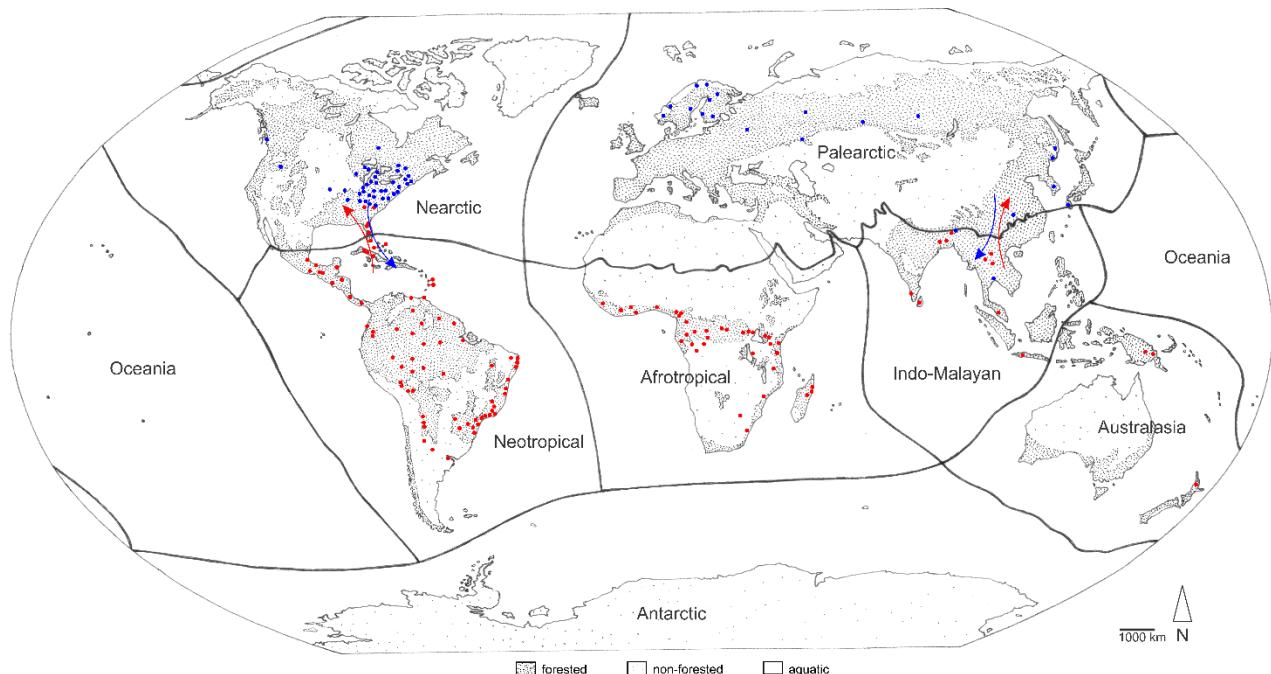


Fig. S1 Globe map of forested areas based on Olson *et al.* (2001) with geographic distribution of reports of *M. siccus* (blue circles) and *M. haematocephalus* (red circles) respectively based on: 1) Schweinitz (1822), Gilliam (1976), Tiffany *et al.* (1985), Noordeloos (1987), Desjardin (1989), Stephenson *et al.* (1994), Huffman *et al.* (2008), Antonín & Noordeloos (2010), Antonín *et al.* (2012), Kiyashko *et al.* (2014), Filippova *et al.* (2015), Sakolrak *et al.* (2019), Koch *et al.* (2020); 2) Montagne (1837, 1842), Berkeley (1856), Spegazzini (1926, as *M. rhodocephalus*), Baker & Dale (1951), Dennis (1951, 1961), Singer & Digilio (1952), Rick (1961), Singer (1959, 1964, 1965, 1976), Pegler (1966, 1983, 1986, 1987, 1997), Guzmán (1983), Desjardin (1989), Ovrebo (1996), Desjardin (1991), Desjardin & Horak (1997), Desjardin *et al.* (2000), Moreno-Arroyo *et al.* (2001), Antonín & Buyck (2006), Antonín (2007), Drechsler-Santos *et al.* (2007), Puccinelli & Capelari (2009), Rosa & Capelari (2009), Tan *et al.* (2009), Wannathes *et al.* (2009), Farook *et al.* (2012), Maekawa *et al.* (2013), Maziero *et al.* (2013), Gogoi & Parkash (2015), Lodge & Sourell (2015), Dutta (2017), Shay *et al.* (2017), Sourell *et al.* (2018), Goldman & Gryzenhout (2019), Grace *et al.* (2019), Rivas & Niveiro (2019), Fuente *et al.* (2020), Melgarejo-Estrada *et al.* (2020), speciesLink database (17 Jul. 2021);. This distribution map is consistent with GBIF maps of *M. siccus* (Fig. S2) and *M. haematocephalus* (Fig. S3) records below.



Fig. S2 Globe map provided by the Global Biodiversity Information Facility (GBIF) of georeferenced recorded of *Marasmius siccus* (Schwein.) Fr. © OpenStreetMap Contributors, © OpenMapTiles, GBIF. GBIF Secretariat (2021). GBIF Backbone Taxonomy. Checklist dataset <https://doi.org/10.15468/39omei> accessed via GBIF.org on 2021-12-277.



Fig. S3 Globe map provided by the Global Biodiversity Information Facility (GBIF) of georeferenced recorded of *Marasmius haematocephalus* (Mont.) Fr. © OpenStreetMap Contributors, © OpenMapTiles, GBIF. GBIF Secretariat (2021). GBIF Backbone Taxonomy. Checklist dataset <https://doi.org/10.15468/39omei> accessed via GBIF.org on 2021-12-27.

Phylogenetic analyses

Tab. S1 List of strains with nrITS and nrLSU sequences included in the phylogenetic analyses (DATASETS 1–4).

Species/Section	Coll. N°	Herbarium	Origin	nrITS	nrLSU
Fungal endophyte	D2-6B6-2		China	FJ025271 [◊]	
<i>Marasmius</i> sp.	NW503	CMU	Thailand	KJ588402 ^ω	
<i>Marasmius</i> sp.	Z. W. Ge 1624	HKAS 53710	China	HQ832734 ^ξ	
<i>Marasmius</i> sp. (uncultured clone)	HATFD14-61		India	KU752322 ^σ	
<i>Marasmius anomalus</i> SH	JO346	SP445506	Brazil	KP635205 ^ū	
<i>M. asiaticus</i> SH	TYS478		Malaysia	FJ431239 ^α	
<i>M. auranticapitatus</i> sp. nov. SH	JO42	SP445408	Brazil	ON502676 ^δ	ON502738 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	JO224	SP445445	Brazil	ON502668 ^δ	ON502735 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	JO226	SP445446	Brazil	ON502671 ^δ	ON502743 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	JO276	SP445460	Brazil	ON502667 ^δ	ON502739 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	JO277	SP445461	Brazil	ON502672 ^δ	ON502741 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	JO279	SP445463	Brazil	ON502669 ^δ	ON502742 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	JO282	SP445465	Brazil	ON502674 ^δ	ON502744 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	JO300	SP445479	Brazil	ON502677 ^δ	ON502740 ^δ
<i>M. auranticapitatus</i> sp. nov. SH	MC4554	SP445584	Brazil	ON502670 ^δ	ON502734 ^δ
<i>M. castanocephalus</i> sp. nov. SH	JO523	SP445573	Brazil	ON502679 ^δ	ON502746 ^δ
<i>M. coasiaticus</i> sp. nov. SH	JO323	SP445491	Brazil	ON502680 ^δ	ON502747 ^δ
<i>M. coasiaticus</i> sp. nov. SH	JO339	SP445502	Brazil	ON502681 ^δ	ON502748 ^δ
<i>M. curreyi</i> MS	DED5142	SFSU:	USA	FJ431237 ^α	
<i>M. ferrugineus</i> SH	KG226	BRNM	South Korea	HQ616662 ^λ	HQ616663 ^λ
		724480			
<i>M. ferrugineus</i> SH	ZMU99		China	MW724227 ^β	
<i>M. cf. ferrugineus</i> SH	HBAU15684	HQ616662	China	MW871617 ^ε	
<i>M. fulvoferrugineus</i> ?	JNH010	TENN:070783	USA	MF686511 ^ο	
<i>M. gardneri</i> SH	JO387	SP445521	Brazil	ON502685 ^δ	ON502752 ^δ
<i>M. gardneri</i> SH	JO438	SP445532	Brazil	ON502682 ^δ	ON502749 ^δ
<i>M. gardneri</i> SH	JO454	SP445542	Brazil	ON502684 ^δ	ON502751 ^δ
<i>M. gardneri</i> SH	JO491	SP445564	Brazil	ON502683 ^δ	ON502750 ^δ
<i>M. graminum</i> MS	NN005953		Denmark	JN943595 ^ε	
<i>M. grandisetulosus</i> SH	DED8225	SFSU	São Tomé	KX953743 ^δ	
<i>M. grandisetulosus</i> SH	DED8257	SFSU	São Tomé	KX953744 ^δ	
<i>M. haematocephalus</i> SH	JO533	SP445580	Brazil	ON502673 ^δ	ON502729 ^δ
<i>M. haematocephalus</i> SH	AKD 200/2014		India	MF189048 ^v	
<i>M. haematocephalus</i> SH	AKD 201/2014		India	MF189050 ^k	
<i>M. haematocephalus</i> SH	CAL 1518		India	MF189047 ^k	
<i>M. haematocephalus</i> SH	CAL 1519		India	MF189046 ^k	
<i>M. haematocephalus</i> SH	CUH AM121		India	KX154214 ^v	
<i>M. haematocephalus</i> SH	Buyck 00.1820	PC	Madagascar	KX148977 ^τ	
<i>M. haematocephalus</i> SH	JES202	SFSU	Madagascar	KX148986 ^τ	
<i>M. haematocephalus</i> SH	JES193	SFSU	Madagascar	KX148985 ^τ	
<i>M. haematocephalus</i> SH	JES110	SFSU	Madagascar	KX148984 ^τ	
<i>M. haematocephalus</i> SH	JES142	SFSU	Madagascar	KX148987 ^τ	
<i>M. haematocephalus</i> SH	TYS523	KLU, SFSU	Malaysia	FJ431248 ^α	
<i>M. haematocephalus</i> SH	G1164		French Guiana	MF061333 ^λ	
<i>M. haematocephalus</i> SH	G3554		French Guiana	MN994663 ^λ	
<i>M. haematocephalus</i> SH	G3599		French Guiana	MN994665 ^λ	
<i>M. haematocephalus</i> SH	G3628		French Guiana	MN994666 ^λ	
<i>M. haematocephalus</i> SH	G7550		French Guiana	MN994810 ^λ	

<i>M. haematocephalus</i> SH	G7760	French Guiana	MN994821 ^κ		
<i>M. haematocephalus</i> SH	PC0713081	French Guiana	MN994737 ^κ		
<i>M. haematocephalus</i> SH	PC0713668	French Guiana	MK546998 ^κ		
<i>M. haematocephalus</i> SH	PC0713897	French Guiana	MF038985 ^κ		
<i>M. haematocephalus</i> SH	MR-SAU-13-157	French Guiana	MK546926 ^κ		
<i>M. haematocephalus</i> SH	TFB12243	TENN60257	USA	HQ665550 ^η	
<i>M. haematocephalus</i> “f. <i>atrobrunneus</i> ” SH	NW117	CMU, SFSU	Thailand	EU935525 ^β	
<i>M. haematocephalus</i> “f. <i>atrovilaceus</i> ” SH	NW193	CMU, SFSU	Thailand	EU935531 ^β	
<i>M. haematocephalus</i> “f. <i>atrovilaceus</i> ” SH	NW339	CMU, SFSU	Thailand	EU935532 ^β	
<i>M. haematocephalus</i> “f. <i>atrovilaceus</i> ” SH	NW413	CMU, SFSU	Thailand	EU935533 ^β	
<i>M. haematocephalus</i> var. <i>atrovilaceus</i> SH	AKD 06/2011		India	MF189049 ^κ	
<i>M. haematocephalus</i> var. <i>atrovilaceus</i> SH	AF 81		India	MW281776 ^β	
<i>M. haematocephalus</i> “f. <i>haematocephalus</i> ” SH	NW296	CMU, SFSU	Thailand	EU935526 ^β	
<i>M. haematocephalus</i> “f. <i>haematocephalus</i> ” SH	NW409	CMU, SFSU	Thailand	EU935527 ^β	
<i>M. haematocephalus</i> “f. <i>haematocephalus</i> ” SH	NW428	CMU, SFSU	Thailand	EU935528 ^β	
<i>M. haematocephalus</i> “f. <i>haematocephalus</i> ” SH	NW434	CMU, SFSU	Thailand	EU935529 ^β	
<i>M. haematocephalus</i> “f. <i>haematocephalus</i> ” SH	TYS277	CMU, SFSU	Thailand	EU935530 ^β	
<i>M. haematocephalus</i> “f. <i>luteocephalus</i> ” SH	NW310	CMU, SFSU	Thailand	EU935534 ^β	
<i>M. haematocephalus</i> SH	NW1395		Thailand	MW426442 ^ε	
<i>M. haematocephalus</i> SH	NW1403		Thailand	MW426447 ^ε	
<i>M. haematocephalus</i> SH	NW1431		Thailand	MW426456 ^ε	
<i>M. haematocephalus</i> SH	NW1436		Thailand	MW426462 ^ε	
<i>M. haematocephalus</i> SH	NW1441		Thailand	MW426460 ^ε	
<i>M. haematocephalus</i> SH	NW1465		Thailand	MW426465 ^ε	
<i>M. haematocephalus</i> SH	NW1466		Thailand	MW426466 ^ε	
<i>M. haematocephalus</i> “f. <i>luteocephalus</i> ” SH	NW330	CMU, SFSU	Thailand	EU935537 ^β	
<i>M. haematocephalus</i> “f. <i>robustus</i> ” SH	NW433	CMU, SFSU	Thailand	EU935536 ^β	
<i>M. haematocephalus</i> “f. <i>variabilis</i> ” SH	NW430	CMU, SFSU	Thailand	EU935535 ^β	
<i>M. aff. haematocephalus</i> SH	MC4555	SP445586	Brazil	ON502675 ^δ	ON502736 ^δ
<i>M. hinnuleus</i> SH	JES217	TAN	Madagascar	KX148988 ^τ	
<i>M. hypophaeus</i> SH	NW285	CMU, SFSU	Thailand	EU935484 ^β	
<i>M. nigrobrunneus</i> MS	NW416	CMU, SFSU	Thailand	EU935571 ^β	
<i>M. aff. pallescens</i> SH	NW424	CMU, SFSU	Thailand	EU935500 ^β	
<i>M. pulcherripes</i> SH	KG190	BRNM 714692	South Korea	FJ917615 ^λ	FJ917600 ^λ
<i>M. pulcherripes</i> SH	KG122	BRNM 714693	South Korea	FJ917616 ^λ	FJ917601 ^λ
<i>M. pulcherripes</i> SH	RA705-12b		USA	MK217466 ^κ	
<i>M. pulcherripes</i> SH	iNAT:30809942		USA	MZ267775 ^κ	
<i>M. pulcherripes</i> SH	RAK 435		USA	MN930539 ^ο	
<i>M. pulcherripes</i> SH			USA	MT032485 [†]	
<i>M. pulcherripes</i> SH	BHI-F448a	FH	USA	MF161270 ^η	
<i>M. rhodopurpureus</i> SH		BRNM 724483	South Korea	HQ607382 ^λ	HQ607383 ^λ
<i>M. roseus</i> sp. nov. SH	JO352	SP445510	Brazil	ON502678 ^δ	ON502745 ^δ

<i>M. rubicundus</i> stat. nov. SH	DED8675	SP445665	Brazil	ON502661 ^δ	
<i>M. rubicundus</i> stat. nov. SH	JO228	SP445448	Brazil	ON502659 ^δ	ON502730 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO246	SP445454	Brazil	ON502664 ^δ	ON502725 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO281	SP445464	Brazil	ON502662 ^δ	ON502732 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO283	SP446061	Brazil	ON502656 ^δ	ON502726 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO295	SP446063	Brazil	ON502660 ^δ	ON502733 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO296	SP445476	Brazil	ON502657 ^δ	ON502724 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO316	SP445488	Brazil	ON502665 ^δ	ON502737 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO445	SP445537	Brazil	ON502663 ^δ	ON502723 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO464	SP445549	Brazil	ON502658 ^δ	ON502728 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO483	SP445560	Brazil	ON502655 ^δ	ON502727 ^δ
<i>M. rubicundus</i> stat. nov. SH	JO529	SP445577	Brazil	ON502666 ^δ	ON502731 ^δ
<i>M. ruforotula</i> MS	KG107	BRNM 714676	South Korea	FJ936152 ^μ	FJ917614 ^μ
<i>M. ruforotula</i> MS	V. Antonín 07.158	BRNM 714674	South Korea	FJ936150 ^μ	FJ917612 ^μ
<i>M. siccus</i> SH	KG028	BRNM 714680	South Korea	FJ904985 ^λ	FJ904980 ^λ
<i>M. siccus</i> SH	KG099	BRNM 714687	South Korea	FJ904987 ^λ	FJ904982 ^λ
<i>M. siccus</i> SH	KG119	BRNM 714688	South Korea	FJ904988 ^λ	FJ904983 ^λ
<i>M. siccus</i> SH	KG144	BRNM 714689	South Korea	FJ904989 ^λ	
<i>M. siccus</i> SH	KG148	BRNM 714690	South Korea	FJ904990 ^λ	
<i>M. siccus</i> SH	KG156	BRNM 724486	South Korea	FJ904991 ^λ	
<i>M. siccus</i> SH	V. Antonín 07.50	BRNM 714682	South Korea	FJ917625 ^λ	FJ936145 ^λ
<i>M. siccus</i> SH	V. Antonín 07.97	BRNM 714681	South Korea	FJ904986 ^λ	FJ904981 ^λ
<i>M. siccus</i> SH	V. Antonín 07.156	BRNM 714683	South Korea	FJ917626 ^λ	FJ936146 ^λ
<i>M. siccus</i> SH	V. Antonín 08.69	BRNM	South Korea	FJ904992 ^λ	FJ904984 ^λ
<i>M. siccus</i> SH	KA12-1250		South Korea	KR673501 ^ι	
<i>M. siccus</i> SH	DED5255	SFSU	USA	FJ431272 ^α	
<i>M. siccus</i> SH		BRNM 552709	USA	HQ607384 ^λ	HQ607385 ^λ
<i>M. siccus</i> SH	RAK 436		USA	MN930540 ^ο	
<i>M. siccus</i> SH		LE 253535	Russia	KF774134 ^π	
<i>M. siccus</i> SH		LE 295980	Russia	KF774130 ^π	
<i>M. siccus</i> SH		LE 295983	Russia	KF774133 ^π	
<i>M. siccus</i> SH		LE 295984	Russia	KF774131 ^π	
<i>M. siccus</i> SH		LE 295985	Russia	KF774132 ^π	
<i>M. siccus</i> SH	NN050245		Russia	JN943596 ^ε	JN941142 ^ε
<i>M. siccus</i> SH	AKD 300/2015		India	MF189051 ^κ	
<i>M. siccus</i> SH	AKD 301/2015		India	MF189052 ^κ	
<i>M. siccus</i> SH	ANT202- QFB28665		Canada	MN992470 ^{^K}	
<i>M. siccus</i> SH	HMAS 290057		China	MK966524 [‡]	
<i>M. siccus</i> SH	HMAS 290077		China	MK966523 [‡]	
<i>M. siccus</i> SH	HFJAU-TD377		China	MN622731 [∞]	
<i>M. siccus</i> SH	HBAU15117	MN992470	China	OL441621 ^ε	
<i>M. siccus</i> SH	HBAU15293	MN992470	China	OL441623 ^ε	
<i>M. siccus</i> SH	HBAU15371	MN992470	China	OL441624 ^ε	
<i>M. siccus</i> SH	HBAU15429	MN992470	China	OL441625 ^ε	
<i>M. siccus</i> SH	HBAU15670	MN992470	China	OL441626 ^ε	
<i>M. siccus</i> SH	HBAU15738	MN992470	China	OL441622 ^ε	
<i>M. siccus</i> SH	HBAU15047		China	MW848822 ^ε	
<i>M. subtangerinus</i> SH		BRNM 718756	South Korea	HQ607380 ^λ	HQ607381 ^λ
Uncultured Basidiomycota	man22 litter H12		USA	GU328526 ^χ	

Authors of the data: Adnaan Farook (GenBank – 2020^β), Alanbagi *et al.* (GenBank – 2018^γ), Alshammari & Stepheson (GenBank –

2020 ^j), Antonín *et al.* (2012 ^k, 2014 ^l), Deng *et al.* (GenBank – 2010 ⁵), Dutta (2017 ⁿ), Dutta & Acharya (GenBank – 2016 ^v, 2017 ^v), Edwards & Zak (2010 ^x), Grace *et al.* (2019 ^b), Haelewaters *et al.* (2018 ^u), Hema *et al.* (GenBank – 2016 ^o), Hughes & Petersen (GenBank – 2010 ^u), Jaouen *et al.* (2019 ^b), Landry & Berube (GenBank – 2020 ^A), Kim *et al.* (2015 ⁱ), Kiyashko *et al.* (2014 ⁿ), Koch *et al.* (2020 ^o), Kumla & Wannathes (GenBank – 2021 ^x), Liu (GenBank – 2021 ^b), Matheny & Sanchez-Garcia (GenBank – 2017 ^o), Oliveira *et al.* (2020 ^u), Schoch *et al.* (2012 ^e), Schimann *et al.* (GenBank – 2017 ^u), Shay *et al.* (2017 ^r), Shi (GenBank – 2021 ^o), Sun & Guo (GenBank – 2008 ^o), Taylor (GenBank – 2021 ^x), Tan *et al.* (2009 ^a), Wang (GenBank – 2019 ^x), Wannathes & Lumyong (GenBank – 2014 ^o), Wannathes *et al.* (2009 ^b), Wei (GenBank – 2019 ^z), and this study ^d.

Tab. S2 List of strains with *rpb2* and *efl- α* sequences (all produced in this study) included in the multilocus analyses of DATASET 5.

Species/Section	Coll. N°	Herbarium	<i>rpb2</i>	<i>efl-α</i>
<i>M. auranticapitatus</i> sp. nov. SH	JO276	SP445460	ON553941	ON553952
<i>M. auranticapitatus</i> sp. nov. SH	JO282	SP445465	ON553942	ON553953
<i>M. castanocephalus</i> sp. nov. SH	JO523	SP445573	ON553943	ON553955
<i>M. roseus</i> sp. nov. SH	JO352	SP445510	ON553944	ON553954
<i>M. rubicundus</i> stat. nov. SH	JO228	SP445448	ON553938	ON553949
<i>M. rubicundus</i> stat. nov. SH	JO246	SP445454	ON553935	ON553946
<i>M. rubicundus</i> stat. nov. SH	JO295	SP446063	ON553939	ON553950
<i>M. rubicundus</i> stat. nov. SH	JO296	SP445476		ON553945
<i>M. rubicundus</i> stat. nov. SH	JO316	SP445488	ON553940	ON553951
<i>M. rubicundus</i> stat. nov. SH	JO464	SP445549	ON553937	ON553948
<i>M. rubicundus</i> stat. nov. SH	JO483	SP445560	ON553936	ON553947

GTR+ Γ +I was selected for both partitions nrITS and nrLSU of DATASETS 1–4. In DATASET 5 (with and without MC4554), models were HKY+I for nrITS, GTR+I for *rpb2* and SYM+I for *efl- α* . For the BA analyses, the estimated marginal likelihood arithmetic means of the two runs were -6692.96 (DATASET 1), -3111.58 (DATASET 2), -3656.52 (DATASET 3), -2471.98 (DATASET 4), -3807.32 (DATASET 5 with MC4554) and -3794.87 (DATASET 5 without MC4554). For the ML analyses, final optimization likelihoods were -6496.963232 (DATASET 1), -3052.191019 (DATASET 2), -3551.318709 (DATASET 3), -2427.821819 (DATASET 4), -3789.190558 (DATASET 5 with MC4554) and -3779.879356 (DATASET 5 without MC4554). The model parameters of the analyses were summarized in the Tab. S3–S8.

Tab. S3 Data from the ML and BA analyses on DATASET 1.

Alignment data		
Taxa	138	
Characters	1,570 (nrITS 695; nrLSU 875)	
Maximum Likelihood		
	nrITS (means)	nrLSU (means)
alpha	0.352577	0.020000
kappa	-	-
pinvar	-	-
Substitution rates		
(A<=>C)	1.355904	0.397611
(A<=>G)	4.310971	0.406733
(A<=>T)	1.414113	0.314391
(C<=>G)	0.895867	0.201055
(C<=>T)	4.977414	2.048758
(G<=>T)	1.000000	1.000000
Bases freq.		
pi(A)	0.247141	0.262228
pi(C)	0.198425	0.194233

pi(G)	0.215291	0.304273
pi(T)	0.339144	0.239266
Bayesian		
	nrITS (means)	nrLSU (means)
m	0.052287	1.752755
alpha	0.587734	0.061014
pinvar	0.202867	0.806476
Substitution rates		
(A<=>C)	0.095936	0.123912
(A<=>G)	0.298073	0.138387
(A<=>T)	0.092399	0.090692
(C<=>G)	0.067746	0.071074
(C<=>T)	0.341968	0.490885
(G<=>T)	0.103878	0.085050
Bases freq.		
pi(A)	0.254775	0.255258
pi(C)	0.183805	0.197953
pi(G)	0.210901	0.299158
pi(T)	0.350519	0.247632

Tab. S4 Data from the ML and BA analyses on DATASET 2.

	Alignment data	
Taxa	43	
Characters	1,543 (nrITS 668; nrLSU 875)	
Maximum Likelihood		
	nrITS (means)	nrLSU (means)
alpha	0.020000	0.020000
kappa	-	-
pinvar	0.035832	0.000100
Substitution rates		
(A<=>C)	0.791976	0.710071
(A<=>G)	6.854948	0.000000
(A<=>T)	0.974168	0.742617
(C<=>G)	1.868683	0.194622
(C<=>T)	5.761739	1.908362
(G<=>T)	1.000000	1.000000
Bases freq.		
pi(A)	0.242452	0.259124
pi(C)	0.201385	0.197500
pi(G)	0.218850	0.305844
pi(T)	0.337313	0.237532
Bayesian		
	nrITS (means)	nrLSU (means)
m	0.032722	1.738448
alpha	79.188379	0.055558
pinvar	0.730148	0.947151
Substitution rates		
(A<=>C)	0.058604	0.219940
(A<=>G)	0.359492	0.032264
(A<=>T)	0.053957	0.149602
(C<=>G)	0.106368	0.085287

(C<=>T)	0.320137	0.441381
(G<=>T)	0.101443	0.071526
Bases freq.		
pi(A)	0.253365	0.256892
pi(C)	0.197006	0.198321
pi(G)	0.214876	0.306522
pi(T)	0.334752	0.238265

Tab. S5 Data from the ML and BA analyses on DATASET 3.

Alignment data		
Taxa	67	
Characters	1,535 (nrITS 668; nrLSU 867)	
Maximum Likelihood		
	nrITS (means)	nrLSU (means)
alpha	0.207344	0.274362
kappa	-	-
pinvar	0.107675	0.764951
Substitution rates		
(A<=>C)	0.746554	2.268441
(A<=>G)	2.308005	1.364969
(A<=>T)	0.752681	0.705998
(C<=>G)	0.182499	0.979650
(C<=>T)	2.735664	8.754182
(G<=>T)	1.000000	1.000000
Bases freq.		
pi(A)	0.250335	0.264445
pi(C)	0.197077	0.190744
pi(G)	0.214423	0.303827
pi(T)	0.338165	0.240984
Bayesian		
	nrITS (means)	nrLSU (means)
m	0.028180	1.748761
alpha	72.537764	0.126495
pinvar	0.659067	0.896589
Substitution rates		
(A<=>C)	0.103705	0.168900
(A<=>G)	0.285210	0.124406
(A<=>T)	0.094778	0.064344
(C<=>G)	0.037408	0.086402
(C<=>T)	0.349477	0.491684
(G<=>T)	0.129422	0.064264
Bases freq.		
pi(A)	0.259546	0.260770
pi(C)	0.183644	0.192227
pi(G)	0.215210	0.303405
pi(T)	0.341600	0.243597

Tab. S6 Data from the ML and BA analyses on DATASET 4.

Alignment data		
Taxa	27	
Characters	1,528 (nrLSU 872; nrITS 656)	
Maximum Likelihood		

	nrLSU (means)	nrITS (means)
alpha	0.020000	0.020000
kappa	-	-
pinvar	0.501949	0.000100
Substitution rates		
(A<=>C)	2.485890	0.462603
(A<=>G)	2.823128	2.232116
(A<=>T)	0.636089	1.129946
(C<=>G)	2.688166	0.000000
(C<=>T)	7.827775	3.562190
(G<=>T)	1.000000	1.000000
Bases freq.		
pi(A)	0.265930	0.251216
pi(C)	0.189622	0.197205
pi(G)	0.303816	0.214489
pi(T)	0.240632	0.337090
Bayesian		
	nrLSU (means)	nrITS (means)
m	0.639088	1.479749
alpha	63.173411	35.720664
pinvar	0.919234	0.887111
Substitution rates		
(A<=>C)	0.155636	0.067736
(A<=>G)	0.159624	0.278402
(A<=>T)	0.059462	0.136599
(C<=>G)	0.152586	0.053711
(C<=>T)	0.402038	0.338224
(G<=>T)	0.070654	0.125328
Bases freq.		
pi(A)	0.263952	0.247810
pi(C)	0.191669	0.199165
pi(G)	0.303469	0.212699
pi(T)	0.240910	0.340327

Tab. S7 Data from the ML and BA analyses on DATASET 5 with MC4554.

Alignment data			
Taxa	11		
Characters	2,030 (nrITS 656; <i>rpb2</i> 794; <i>efl-α</i> 580)		
Maximum Likelihood			
	ITS (means)	<i>rpb2</i> (means)	<i>efl-α</i> (means)
alpha	0.020000	0.165882	0.565547
kappa	-	-	-
pinvar	0.000100	0.000100	0.000100
Substitution rates			
(A<=>C)	0.000000	4.484694	2.369845
(A<=>G)	1.998196	10.643969	5.437265
(A<=>T)	0.948063	1.490715	3.470129
(C<=>G)	0.586025	1.534028	0.432838
(C<=>T)	4.025090	33.104263	14.335476
(G<=>T)	1.000000	1.000000	1.000000
Bases freq.			
pi(A)	0.250507	0.251267	0.248698

pi(C)	0.197667	0.188622	0.283042
pi(G)	0.214256	0.289107	0.230471
pi(T)	0.337570	0.271005	0.237789
Bayesian			
	nrITS (means)	rpb2 (means)	efI- α (means)
m	0.313673	1.641393	0.898215
kappa	5.408371	-	-
pinvar	0.813523	0.676670	0.437331
Substitution rates			
(A<=>C)	-	0.089945	0.097892
(A<=>G)	-	0.202741	0.201184
(A<=>T)	-	0.034093	0.134969
(C<=>G)	-	0.033200	0.030970
(C<=>T)	-	0.608892	0.499278
(G<=>T)	-	0.031129	0.035709
Bases freq.			
pi(A)	0.245627	0.246237	0.252440
pi(C)	0.199434	0.192737	0.281534
pi(G)	0.212191	0.289667	0.229179
pi(T)	0.342748	0.271359	0.236848

Tab. S8 Data from the ML and BA analyses on DATASET 5 without MC4554.

Alignment data			
Taxa	10		
Characters			
	2,030 (nrITS 656; rpb2 794; efI- α 580)		
Maximum Likelihood			
	nrITS (means)	rpb2 (means)	efI- α (means)
alpha	0.020000	0.165218	0.568013
kappa	-	-	-
pinvar	0.000100	0.000100	0.000100
Substitution rates			
(A<=>C)	0.000000	5.031898	2.657308
(A<=>G)	2.354623	11.931457	6.094762
(A<=>T)	1.126797	1.680865	3.891068
(C<=>G)	0.689360	1.753250	0.487765
(C<=>T)	4.777973	37.125924	16.064228
(G<=>T)	1.000000	1.000000	1.000000
Bases freq.			
pi(A)	0.250637	0.251267	0.248698
pi(C)	0.197964	0.188622	0.283042
pi(G)	0.213872	0.289107	0.230471
pi(T)	0.337526	0.271005	0.237789
Bayesian			
	ITS (means)	rpb2 (means)	efI- α (means)
m	0.326841	1.626866	0.903208
kappa	6.266991	-	-
pinvar	0.799317	0.672826	0.428971
Substitution rates			
(A<=>C)	-	0.087860	0.097460
(A<=>G)	-	0.205571	0.199814
(A<=>T)	-	0.034750	0.134400
(C<=>G)	-	0.033158	0.031244

(C<=>T)	-	0.607046	0.501559
(G<=>T)	-	0.031615	0.035522
Bases freq.			
pi(A)	0.246504	0.246148	0.252342
pi(C)	0.200354	0.192290	0.281535
pi(G)	0.210459	0.289576	0.229056
pi(T)	0.342683	0.271986	0.237067

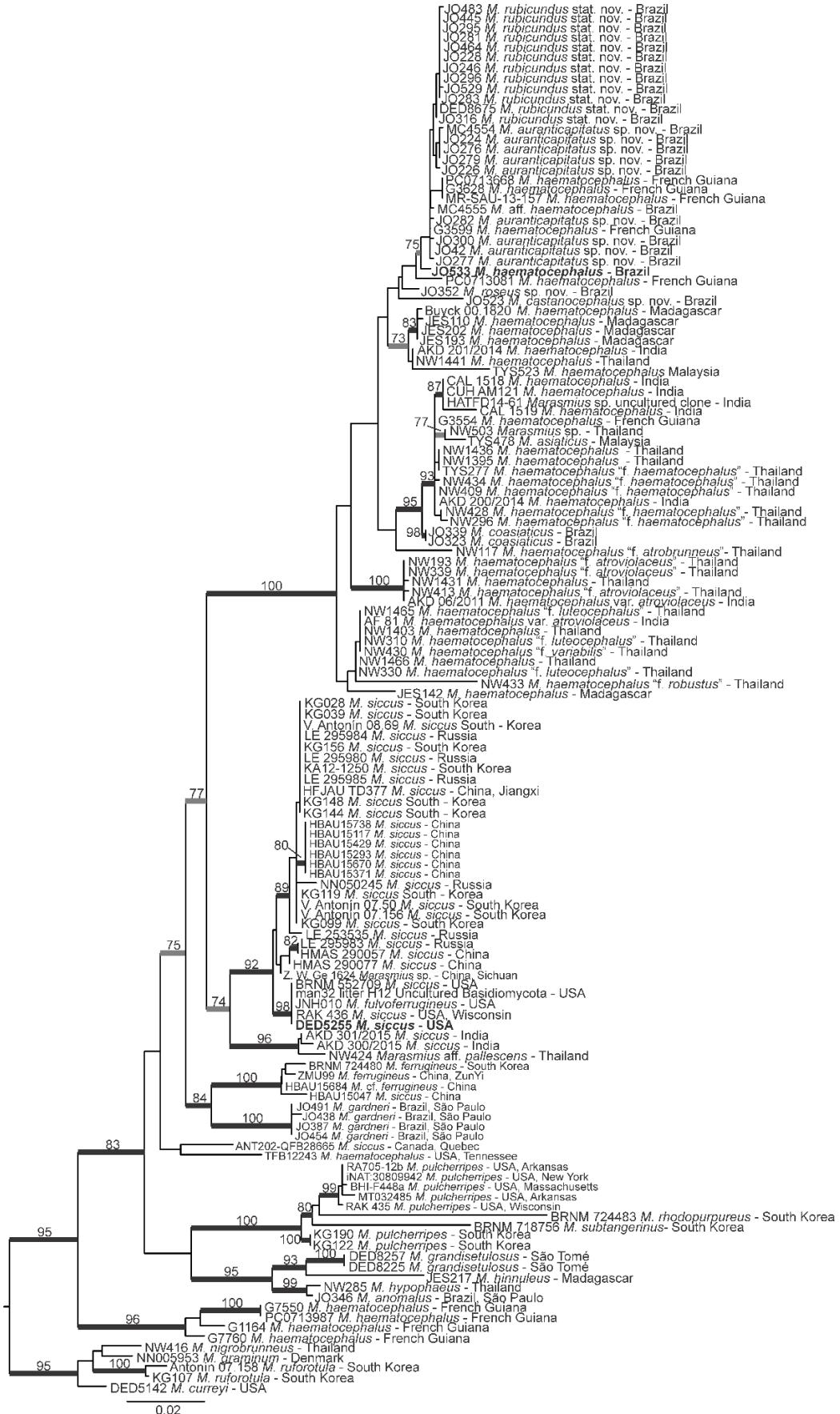


Fig. S4 Best-scored Maximum Likelihood Tree of nrITS+nrLSU DATASET 1 (-lnL: -6496.963232). Support values at the nodes consist of BS ≥ 70 . Thicker stems in black represent highly supported nodes, and those in grey partially supported nodes.



Fig. S5 50 % majority-rule tree of Bayesian analysis of nrITS+nrLSU DATASET 2a (-lnL: -3111.58). Support values at the nodes consist of PP ≥ 0.95 . Thicker stems in black represent highly supported nodes, and those in grey partially supported nodes.

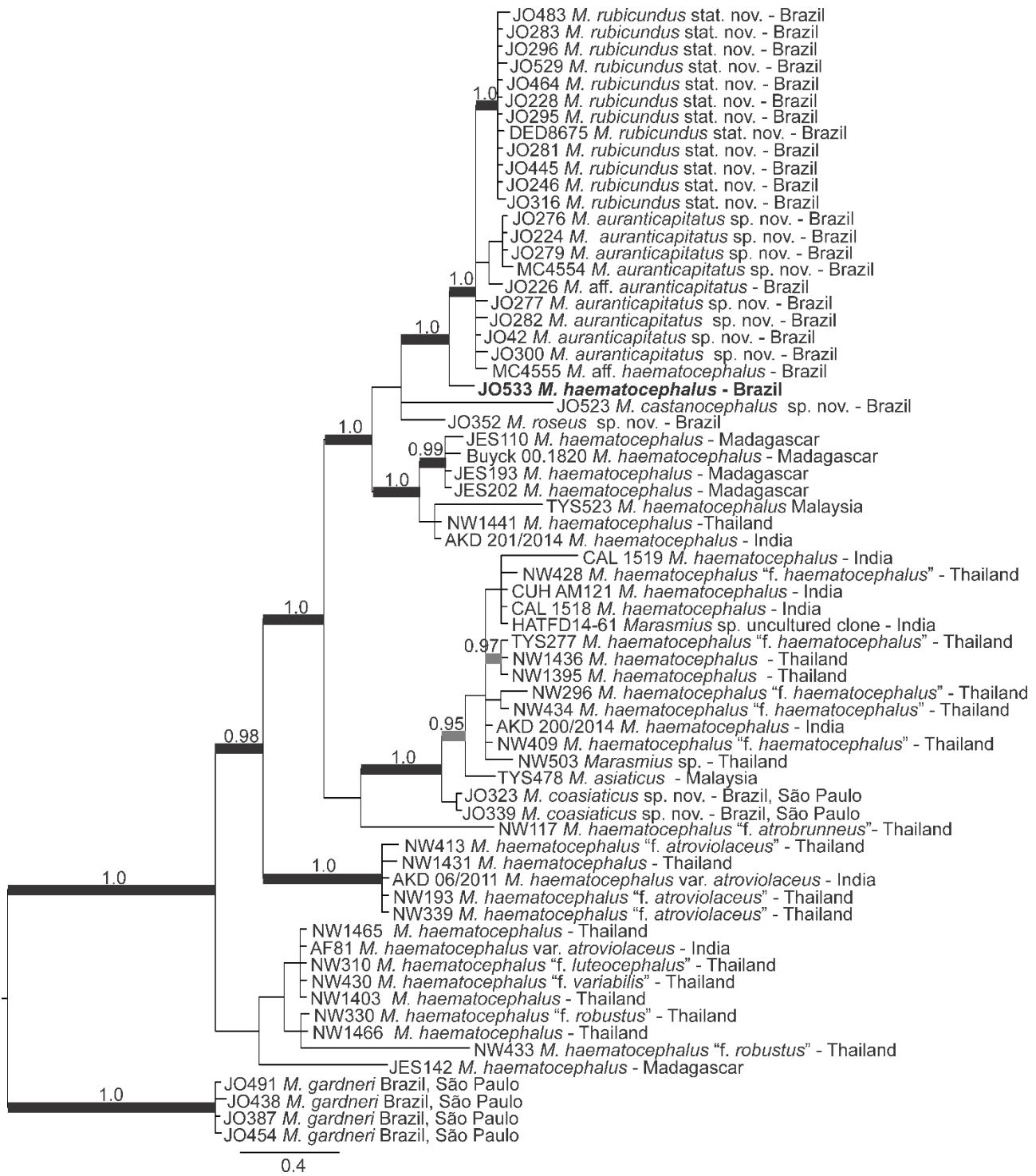


Fig. S6 50 % majority-rule tree of Bayesian analysis of nrITS+nrLSU DATASET 2b (-lnL: -3656.52). Support values at the nodes consist of PP ≥ 0.95 . Thicker stems in black represent highly supported nodes, and those in grey partially supported nodes.

Additional specimens figures: Reserva Biológica de Paranapiacaba (RBP); Parque Estadual das Fontes do Ipiranga (PEFI); Parque Estadual da Cantareira (PEC); Parque Estadual Turístico do Alto Ribeira (PETAR).



Fig. S7 Color pictures of fresh basidiomata of *Marasmius rubicundus* from RPB: (up) JO223, JO228, JO230, JO246, (bottom) JO281, JO283, JO295, JO316, JO318. Scale bar = 10 mm.



Fig. S8 The most ruby pink strain of *Marasmius rubicundus* (JO281) from RPB. Scale bar = 10 mm.



Fig. S9 *Marasmius rubicundus* from PEFI: JO330, JO335, JO338, JO380. Scale bar = 10 mm.



Fig. S10 *Marasmius rubicundus* from PEC: JO445, JO446, JO481, JO483, JO492, JO516. Scale bar = 10 mm.



Fig. S11 *Marasmius rubicundus* from PETAR: JO529. Scale bar = 10 mm.

Synonyms under *Marasmius haematocephalus*?

Below, the species listed as synonym of *Marasmius haematocephalus* in Singer (1976), Pegler (1983), Antonín (2007), Tan *et al.* (2009), and Wannathes *et al.* (2009).

Marasmius rhodocephalus Fr., Nova Acta Regiae Soc. Sci. Upsal ser. 3, 1: 31. 1851.

MycoBank MB#155861

Status: Legitimate; current name.

Type: Unknown.

Origin: Mexico.

Protologue:

Pileo membranaceo convexo plano sulcado persistenter roseo-rubro, margine integro, stipite setiformi glabro nitido fuscopallido basi simplici insititio, lamellis adnatis aequalibus pauci valde distantibus pallidis.

Ad ramos radicesque emortuos ad Mirador, regni Mexican. *Liebm.*

Proximis intermedius, colore pilei elegantissimo roseo-rubro persistente (nec expallente, nec in sicci obscurato), praecipue diversus, forte varietas! Stipes uncialis l. parum ultra, omnino setae forma et substantia, fuscescens, sed micore argenteo vibrans; basis primo albido-villosa, mox nuda, haud dilatata. Pileus 2–3 lin. latus, secus lamella profunde sulcatus, ceterum laevis et glaber. Lamellae venis haud connexae, sed postice junctae. *M. pyrrhocephalus* Berk. Dec. n. 118 mycelio albo et stipites piloso longius recedit.

Note: It is curious why Fries did not consider it similar to *M. haematocephalus* nor determined it as such but proposed a new species. However, the pileus transitioning from pink to red may relate this closer to *M. rubicundus* rather than *M. haematocephalus*. It could be even *M. cf. pallidens* (JO426) with shorter spores. The veined lamellae are unusual to these species. No type material seems preserved and, unless new collections from the original location matching the protologue be found, the species should be regarded as poorly known. Based on the fine-tuned concept of *M. haematocephalus* in this study, this should be regarded as a different species. Spegazzini (1926) named a collection from the Cordoba hills, Argentina, as *M. rhodocephalus* with basidiospores compatible in size with the *M. haematocephalus* complex. Whether this was authentic for *M. haematocephalus* or for *M. rhodocephalus*, it cannot be known.

Marasmius semipellucidus Berk. & Broome, J. Linn. Soc., Bot. 14: 36. 1873.

MycoBank MB#203401

Status: Legitimate; current name.

Type: Kandy district, Peradeniya, on dead twigs, Nov. 1867, Thwaites 101p.p. (Holotype K(M) 99650).

Origin: Sri Lanka.

Protologue:

Pileo campanulato sulcato spadiceo; stipite sursum pellucido, deorsum opaco, toto striato; lamellis albis (nº. 101 in part).

On dead twigs &c.

Pileus 1–2 lines across; stem ½ an inch high.

Differs from other species with which it might be confounded in the upper part of the stem being pale and pellucid.

Notes: The pileus (2.116–4.232 mm diam.) color is light brown or chestnut brown and the stipe is about 12.7 mm long with a translucent pale apex. Based on the fine-tuned concept of *M. haematocephalus* in this study, the synonymy is unsupported. If not conspecific as a primordium, this seems identical to *M. davidi* Antntín (≡ *M. helvolus* var. *brunneolus* Berk. & Broome) which has a hyaline stipe then brown from base upwards (Pegler 1986), or “*M. haematocephalus* ‘f. *luteocephalus*’” (Wannathes *et al.* 2009). Therefore, along with the geographic origin, it is distinct from *M. castanocephalus*.

Marasmius sanguineus Cooke & Massee, Grevillea 17: 59. 1889.

MycoBank MB#195404

Status: Legitimate; current name.

Type: Laion Forest, on dead leaves, 06 Jul 1888, Ramage (Holotype K(M) 108858).

Origin: Dominica.

Protologue:

Pileo convexo, membranaceo, sanguineus (1–1 ½ cm diam.) glabro, laevi; stipite elongato, glabro, pallido (4 cm long), lamellis paucis, distantissimis, ventricosis, adnexis, pileo concoloribus.

On dead leaves. Laion Forest, Dominica. West Indian Exploration Committee (Ramage).

Allied to *Marasmius rhabarbarinus* Berk.

Notes: Indeed, this seems compatible to the fine-tuned concept of *M. haematocephalus* in this study except for the ventricose lamellae concolorous with the pileus (marginate). This should be regarded as a different species and seems not conspecific with *M. auranticapitatus*, *M. castanecephalus*, *M. coasiaticus*, *M. roseus*, or *M. rubicundus*.

Marasmius atropurpureus Murrill, N. Amer Fl. 9: 262. 1915.

MycoBank MB#207221

Status: Legitimate; current name.

Type: Bahama Islands, New Providence, Lake Cunningham, on dead leaves and sticks, 08 Sept 1904, E.G. Britton 612 (Holotype NY[FH, MICH]).

Origin: Bahamas.

Protologue:

Pileus conic to bell-shaped or hemispheric, not expanding, slightly umbonate, very thin and membranous but entirely opaque, gregarious, about 5 mm broad, rarely larger; surface beautifully colored, atropurpureus or subvinosous with a darker-purple center, smooth, glabrous, not striate, at least not until dry, minutely rugose under a lens, margin entire or slightly undulate, concolorous; lamellae narrow to medium, distant, about 12 in number, white, not interveined, adnate, attached to a collar, the edges of which, as well as the edges of the young lamellae, is dark-purple like the pileus; stipe long, slender, filiform, smooth, glabrous, polish, avellaneous, at times with a slight brownish tint, slightly whitish-myceloid at the base, about 4–5 cm long and 0.5 mm thick.

Type collected on fallen dead leaves and sticks at Lake Cunningham, New Providence, Bahama Islands, September 8th 1904, Elizabeth G. Britton 612 (herb. N.Y. Bot. Gard.).

Distribution: Known only from the type locality.

Notes: This seems synonym of the previous with marginate but narrow to medium lamellae. The pileus color also recalls *M. haematocephalus*, but the lamellae are divergently marginate. Because of the stipe with basal mycelium, it is likely that the author misused the term collar for the lamellae. It is quite unsupported to be conspecific with *M. auranticapitatus*, *M. castanecephalus*, *M. coasiaticus*, *M. roseus*, or *M. rubicundus*.

Marasmius vinosus Beeli, Bull. Soc. Roy. Bot. Belgique 60: 158. 1928.

MycoBank MB#281782

Status: Illegitimate., Art. 53.1.

Type: Holotype -, M^{me} Goossens, n° 106–107, -.

Origin: Republic of the Congo.

Protologue:

Pileo pellucido, convexo-plano, plicato, glabro levi, vinoso, centro plicatoque atro, 1–2 cm. lato; stipite cylindrico fistuloso, glabro levi, concolore, 2.5–3 × 0.05–0.1cm.; lamellis exadnato liberis, distantibus, latis, albidis; carne in stipitem rosea.

Chapeau mince-pellucide, convexe-plan, plissé, glabre et lisse, rouge vineux arête des plis et centre plus sombre, 1–2 cm. diam.; pied cylindrique, fistuleux, glabre et lisse, concolore, 2,5–3 × 0,05–0,1 cm.; lameles adnexes-libres très distantes, larges, blanches; spores non observées; chair du pied rosée.

Groupés sur du bois mort dans la forêt sèche.

Eala, avril, mai et octobre 1923(M^{me} Goossens, n° 106–107). Nom indigène: Bekolacongoli.

Notes: This seems conspecific with *M. haematocephalus* based on the fine-tuned morphological concept, but the origin from tropical Africa may place this along with strains in Shay *et al.* (2017) and/or Antonín (2007) and Dutta (2017). However, the name is illegitimate due to competing homonymy with the next one.

Marasmius vinosus Speg., Anal. Mus. nac. B. Aires, Ser. 3 12: 264. 1909.

MycoBank MB#166300

Status: Legitimate, current name.

Type: Holotype -, Spegazzini, Apr. 1906, on rotten branch: Tucumán.

Origin: Argentina.

Protologue:

Diag. Calopus, gregarius parvulus, pileo subcentrico convexulo glabro obscure vinoso, hymenio candido, lamellis paucis veniformibus distantibus concoloribus, stipite brevi atro-vinoso glabro v. subpruinuloso sporisque subbellipsoideis mediocribus hyalinis.

Hab. Ad ramos dejectos putrescentes in Parque Roca, Tucumán, Apr. 1906.

Obs. Pilei convexuli leniter excentrici (10–20 mm dm.) membranáeo-subcarnosuli non pellucidi tenacelli glaberrimi obsolete laxeque radiatim striati, centro plus minusve umbilicati, margine recti integerrimi, lividi v. cyaneo-

rubescentes; lamellae simplices angustae, fere plicaeformes, integerrimae non furcatae, spatis laevibus non rugosis; stipes e nodulo parum manifesto, saepius leniter pruinuloso, exsurgentem, recti v. curvuli teretes (5–15 mm lngr. × 0,5–1 mm dm.), pileo obscuriores, glaberrimo opaci tenaces sed non rigidi nec lognosi; basidia clavulata (20–25 × 10 µm) sterigmatibus 2 longiusculis coronata, cystidiis clavulatis appendice cylindracea non v. vix breviore ornatis commixta; sporae ex ovato subnaviculares (8–14 × 4–7 µm) saepius biguttulatae laeves hyalinae.

Notes: This species is not close to *M. haematocephalus*.

Cryptic species

In this study, *cryptic species* means *clusters of alike-identical morphospecies with evidence of phylogenetic divergence in the time-space as the result of speciation, hidden by insufficient data or short evolutionary time*. This biological phenomenon produces a great bias in morphology-based analyses. In fungi, morphological innovations are usually preceded by differential reproduction and genetic variation/isolation (Taylor *et al.* 2000, 2006). Species in these clusters are devoid of striking (if any), diagnosable morphological distinction (overlapping variation of characters) as recently genetically isolated species are not expected to present immediate phenotypic differences, although over time they should (Taylor *et al.* 2000). Morphological stasis, adaptive convergence under stabilizing selection, or non-adaptive convergence and parallelism may be behind this phenomenon. In this analysis, cryptic species may form mono-, para- or polyphyletic relationships (main paper body, Figs. 1–3). Despite definition in Bickford *et al.* (2007), a conceptual inconsistency about what cryptic species is defined remains under debate (Struck *et al.* 2018). Some advocate that cryptic species not only diverged recently, but also in sympatry or were reproductively isolated (Stebbins 1950; Paterson 1991). Other add that they are only distinguishable with molecular data (Sáez & Lozano 2005; Van Campenhout *et al.* 2016; Horsáková *et al.* 2019). Sáez & Lozano (2005) understand “cryptic species” as a synonymous of “sibling species” (Mayr 1942), sharing an immediate common ancestor, then sister species. Or, in cases where key distinctions are found after detailed comparison of morphological and non-morphological (i.e. ecological, biochemical, etc.) features, the taxa would be pseudo-cryptic or pseudo-sibling species (Sáez & Lozano 2005). Also, crypticity reflecting different degrees how cryptic species manifest into semi-cryptic, pseudo-cryptic, sibling and hyper-cryptic levels brings even more debate on this phenomenon (Korshunova *et al.* 2017, 2019). Zúñiga-Reinoso *et al.* (2015) recommend more caution with the use of the term “cryptic species” where, once differences in criterious morphometrics are found, two or more species formerly considered cryptic loose this status (i.e. pseudo-cryptic species). Horsáková *et al.* (2019) suggest two criteria to find “fully cryptic” species: i) being separated by highly supported reciprocally monophyletic clades in multiple independent genetic markers; ii) no suggestive evidence of hybridization between the cryptic species. The study highlights the importance of the integrative taxonomy combining as more evidence of various sorts of data as possible. Balasundaram *et al.* (2015), studying a species complex in *Serpula* (Boletales, Fungi), defended the use of multiple loci to detect cryptic species in Fungi as did Horsáková *et al.* (2019) in a study with *Euconulus* (Gastropoda: Stylommatophora). Balasundaram *et al.* (2015) evaluated the phylogenetic informativeness power (PI) of ten genetic makers (*tub*, *hsp*, *rpb2*, *tef1*, *gpd*, ITS, COX, LSU, mtSSU, SSU, ordered by the PI) to resolve cryptic species based on the bootstrap support average and nodes that they could support in their phylogenetic trees. In this context, Struck *et al.* (2018) approach this concept proposing a framework in order to shift from pattern-base to process-driven research to understand this phenomenon. This framework has two premises: 1) cryptic species have to be distinguishable as statistically separable and diverged genotypic clusters of individuals that do not form diagnostic morphological clusters; 2) the temporal dimension of cryptic species of statistical lower degrees of phenotypic (morphology) disparity than non-cryptic relatives given similar divergence time estimates from their more recent common ancestors.

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