FUSE
Fungal Systematics and Evolution
Volume 12
DECEMBER 2023
PAGES 81–89

doi.org/10.3114/fuse.2023.12.06

Phylloporia mutabilis sp. nov. from Benin, West Africa

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Key words:
Hymenochaetaceae
integrative taxonomy
new taxon
Phylloporia
polypore

Abstract: *Phylloporia* is a widespread genus of *Hymenochaetales* (*Basidiomycota*) with polyporoid basidiomata found mainly in the tropics. Species of *Phylloporia* are predominantly parasitic of woody plant hosts, while some species grow as saprotrophs. Data on the genus is still scarce for tropical Africa, where we expect a high diversity given the high plant diversity in this area. Two specimens of this genus were collected in Benin (West Africa) and analysed morphologically and phylogenetically based on a multigene dataset (ITS, LSU, *EF1α*). Strong support for a species new to science was found, described here as *Phylloporia mutabilis*. It differs from other *Phylloporia* species by stipitate, coriaceous basidiomata, earth coloured to dark brown when fresh and changing upon drying from golden to yellowish brown, the margin being large in young specimens, becoming narrower with maturity. Basidiomata of *Phylloporia mutabilis grow* on the soil under angiosperm trees in a dense dry forest, so its lifestyle (saprotrophic, parasitic or mycorrhizal) is not evident, and future ecological studies will be required to elucidate this aspect.

Citation: Olou BA, Krah F-S, Piepenbring M, Yorou NS (2023). *Phylloporia mutabilis sp. nov.* from Benin, West Africa. *Fungal Systematics and Evolution* **12**: 81–89. doi: 10.3114/fuse.2023.12.06
Received: 7 June 2023; **Accepted:** 22 July 2023; **Effectively published online:** 2 August 2023
Corresponding editor: P.W. Crous

INTRODUCTION

Phylloporia typified by *P. parasitica* is a polypore genus mainly distributed in the tropics (Murrill 1904, Ryvarden & Johansen 1980, Gilbertson & Ryvarden 1987, Wagner & Ryvarden 2002), with some species reported from temperate zones (Dai 2010, 2012, Ryvarden & Melo 2014, Bernicchia & Gorjón 2020). *Phylloporia* species mostly grow parasitically on living angiosperm trees or bushes, including roots, trunks, branches, petioles or leaves, with high levels of host specificity, causing white rot (Wagner & Ryvarden 2002, Zhou 2015a, Qin *et al.* 2018, Wu *et al.* 2019, Zhou *et al.* 2022). However, some species were recorded on dead wood (Ryvarden & Johansen 1980, Ferreira-Lopes *et al.* 2016, Wagner & Ryvarden 2002, Zhou & Dai 2012, Zhou *et al.* 2022) or with basidiomata on soil (Ipulet & Ryvarden 2005, Yombiyeni *et al.* 2015, Zhou 2015b, Chamorro-Martínez *et al.* 2022). The genus was described over a century ago (Murrill 1904) but it was rarely cited until the type specimen was re-examined and 12 species were recognised on the basis of morphological and phylogenetic data (Ryvarden 1972, Wagner & Ryvarden 2002). Species of *Phylloporia* differ from other polyporoid genera by annual or perennial, effused-reflexed, pileate or stipitate, soft corky to hard corky basidiomata, tomentose to velutinate pileal surface, a context mostly duplex with a black line between upper tomentum and lower contextual layer, a monomitic hyphal system in most species, generative hyphae with simple septa, absence of setal elements (with the exception of *Phylloporia mori*; Wu *et al.* 2020), and subglobose, ellipsoid or cylindric, hyaline to yellowish, fairly thick-walled basidiospores (Wagner & Ryvarden 2002, Zhou et al. 2022). From then on, *Phylloporia* gained more attention and currently 76 species are known worldwide (https://www.catalogueoflife.org). Fifteen species have been reported from tropical Africa, including two species from Benin (West Africa) (Olou *et al.* 2021). Given the parasitic nature of most species of *Phylloporia* and the high diversity of plants in Benin, *Phylloporia* species are probably more diverse than presently known. To explore this hidden diversity, we conducted surveys in Benin and collected two specimens corresponding morphologically to *Phylloporia*.

MATERIAL AND METHODS

Field collections

During a mycological survey in Benin from July to September 2021, two specimens belonging to the genus *Phylloporia* were collected in the dense dry forest of Pahou. The specimens were photographed in their natural environment using a Sony DSC-HX400V camera prior to recording. The geographical coordinates of each specimen were recorded. Small pieces of fresh basidiomata were placed in plastic bags half-filled with silica gel for subsequent DNA extraction. The remaining basidiomata were air or oven dried at 45–50 °C for 1–2 d depending on the consistency of the basidiomata. The dried basidiomata were then preserved in plastic bags for morphological study and deposited at the mycological herbarium of the University of Parakou (UNIPAR) in Benin.

DNA extraction, amplification, and sequencing

We extracted the DNA from dried fragments of the *Phylloporia* sp. using the innuSPEED DNA Isolation Kits by Analytik Jena. The D1–D4 domains of the nuclear ribosomal large subunit of ribosomal DNA (LSU; 28S rDNA) is the DNA region mainly analysed in the context of previous studies on species delimitation in *Phylloporia*. Here, in addition to LSU, we amplified the internal transcribed spacer region of rDNA (ITS) and the translation elongation factor 1-alpha (*EF1α*). The primer pairs ITS-1F/ITS4 (White *et al.* 1990, Gardes & Bruns 1993), LR0R/LR5 (Vilgalys & Hester 1990), and EF1-983F/2218R (Rehner & Buckley 2008) were used to amplify the target DNA regions. The polymerase chain reaction (PCR) procedure, the PCR products purification, and Sanger sequencing followed Olou *et al.* (2020). Table 1 presents the accession numbers for all the sequences obtained in the context of the present study and obtained from GenBank for the phylogenetic analysis. The alignment used in the present study was deposited in TreeBASE (S30614).

Phylogenetic analyses

To study phylogenetic relationships, newly generated sequences were aligned with other sequences retrieved from GenBank. Thirty-seven ITS sequences were aligned with two ITS sequences generated in this study. In addition, 125 LSU sequences retrieved from GenBank and used by previous studies on *Phylloporia* (Olou *et al.* 2021, Wu *et al.* 2022, Zhou *et al.* 2022) were aligned together with two newly generated LSU sequences. Eighteen *EF1α* sequences were aligned with two newly generated sequences. Each region was aligned separately using the online mode of MAFFT v. 7 (Katoh *et al.* 2017). *Inonotus andersonii* and *Inonotus hispidus* were chosen as outgroups (Wu *et al.* 2019, Olou *et al.* 2021, Zhou *et al.* 2022). Multiple sequence alignments were inspected and some bases were manually adjusted using AliView v. 1.28 (Larsson 2014). One dataset of combined ITS-LSU-*EF1α* was assembled for the phylogenetic analysis. The best-fit evolutionary model was estimated for each partition using the standard model selection (Kalyaanamoorthy *et al.* 2017) implemented in IQ-TREE v. 1.6.12 (Minh *et al.* 2020, http://www.iqtree.org/) with the command line –m TESTONLY. Following this substitution model, the phylogenetic tree inference of Maximum likelihood (ML) and Bayesian Inference (BI) were performed to verify the phylogenetic position of the newly generated sequences. The ML was run using IQ-TREE v. 1.6.12 and the branch support was evaluated using the Ultrafast Bootstrap (UFBoot) (Hoang *et al.* 2018) with 5 000 replicates. The BI was executed using MrBayes v. 3.2.7 in command line mode (https://github.com/NBISweden/MrBayes) for five million generations until the standard deviation of split frequencies reached 0.01. Chain convergence was determined using Tracer v. 1.7.1 (http://tree.bio.ed.ac.uk/software/tracer/) and the first 25 % (5 000) trees were discarded as burn-in. The remaining trees were used to build the consensus tree using the Phylogenetic Tree Summarization (SumTrees) program within DendroPy v. 4.3.0. (Sukumaran & Holder 2010, https://github.com/jeetsukumaran/DendroPy). The topology of the species trees resulting from ML and BI analyses is congruent which enabled us to combine them. To combine both trees, the Phylogenetic Tree Summarization (SumTrees) program within DendroPy v. 4.3.0. (Sukumaran & Holder 2010, https://github.com/jeetsukumaran/DendroPy) was used to add the posterior probabilities (PP) of the BI on the ML tree. Then, the UFBoot values were added to the best tree obtained by ML that already had values of the posterior probabilities using IQ-TREE (Trifinopoulos *et al.* 2016). The resulting tree with (UFBoot /PP) is presented below and the support values of UFBoot and PP are indicated on each node.

Morphological examination

Macro- and microstructure descriptions were based on dried fungarium specimens of *Phylloporia* sp. Macro-morphological characters were described with the aid of a dissecting microscope. The colours of basidiomata were coded according to the Handbook of Colour of Kornerup & Wanscher (1981) and indicated in parentheses in the description. The microstructures were described using a LEICA DM2700M compound light microscope. For the microstructures, fine sections through the basidiomata were prepared for observation using a razor blade under a dissecting microscope and mounted in 10 % aqueous solution of potassium hydroxide (KOH). Melzer's reagent and Cotton Blue were used to test dextrinoid or amyloid and cyanophilic reactions. The following abbreviations are used: IKI = Melzer's reagent, IKI– = neither amyloid nor dextrinoid, CB = Cotton Blue, CB– = acyanophilous. The basidiospore size is given as length and width of the spores. For measurements we present the mean with standard deviation and minimum and maximum values in parentheses. The length (L), arithmetic average of all spore lengths, and the width (W), arithmetic average of all spore widths, were calculated. In addition, the ratio of length/width (Q) was calculated.

RESULTS

Molecular phylogeny

Two specimens of *Phylloporia* sp. recently collected in Benin (OAB0643 and OAB0666) were placed in a phylogenetic analysis of *Phylloporia* spp. Therefore, six sequences, namely two sequences of ITS rDNA, two of LSU rDNA, and two of the *EF1α* gene, were generated and combined with sequences retrieved from GenBank. The combined ITS, LSU, and *EF1α* alignment includes 128 sequences with 3 064 characters, of which 1 508 are distinct patterns, 959 are parsimony-informative, 326 singleton sites, and 1 779 constant sites. Three well supported major clades corresponding to the genera *Fomitiporella* (100/100), *Fulvifomes* (100/100), and *Phylloporia* (100/100) were recovered from the phylogenetic analyses inferred from the ITS-LSU-*EF1α* analysis (Fig. 1). Our newly generated sequences clustered together and form a distinct and well-supported clade (100/100) within *Phylloporia*, that is a sister clade of the bigger clade including *P. parasitica*, *P. flacourtiae*, and *P. littoralis*. As no further morphologically identical species of *Phylloporia* is known, we introduce them as a new species and provide a detailed description of this species.

Table 1. Species names, sample data, and GenBank accession numbers of sequences of *Phylloporia* spp. and closely related species of *Hymenochaetales* obtained in the context of the present study and those retrieved from GenBank.

Species	Voucher or Strain	Origin	ITS	LSU	*EF1α*	References
Fomitiporella resupinata	DMC76	Cameroon	KJ787822	JF712935	–	Zhou & Dai (2012)
Fomitiporella sinica	LWZ 20130809-5	China	KJ787819	KJ787810	–	Zhou (2014)
Fomitiporella tenuissima	Dai 12245	China	KC456242	KC999902	–	Yu *et al.* (2013)
Fomitiporella umbrinella	JV 0509/114	USA	KX181314	KX181336	–	Ji *et al.* (2017)
Fulvifomes fastuosus	CBS 213.36	Philippines	AY558615	AY059057	–	Wagner & Fischer (2002)
Fulvifomes robiniae	CFMR 2693	USA	KX065961	KX065995	–	Sayers *et al.* (2020)
Fulvifomes yoroui	OAB0097	Benin	MN017126	MN017120	–	Olou *et al.* (2019)
Inonotus andersonii	JV1209_66	USA	MN318443	MN318443	–	Sayers *et al.* (2020)
Inonotus hispidus	92-829	Germany	AY624993	AF311014	–	Wagner & Fischer (2001)
Phylloporia afrospathulata	MUCL 54511	Gabon	–	KJ743248	–	Yombiyeni *et al.* (2015)
	MUCL 53983	Gabon	–	KJ743249	–	Yombiyeni *et al.* (2015)
Phylloporia alyxiae	Chen 1182	Taiwan	–	LC514407	–	Wu *et al.* (2020)
	GC 1604-28	Taiwan	–	LC514408	–	Wu *et al.* (2020)
Phylloporia atlantica	JRF142	Brazil	–	MG738813	–	Wu *et al.* (2019)
	JRF151	Brazil	–	MG738814	–	Wu *et al.* (2019)
Phylloporia beninensis	OAB0107	Benin	–	MW244097	–	Olou *et al.* (2021)
	OAB0142	Benin	MW244094	MW244099	–	Olou *et al.* (2021)
	OAB0511	Benin	–	MW244096	–	Olou *et al.* (2021)
Phylloporia bibulosa	Ahmad27088	Pakistan	–	AF411824	–	Wagner & Ryvarden (2002)
Phylloporia boldo	CIEFAPcc532	Chile	–	MK193759	–	Rajchenberg *et al.* (2019)
	CIEFAPcc584	Chile	–	MK193758	–	Rajchenberg *et al.* (2019)
Phylloporia capucina	Robledo1610	Argentina	–	KJ651919	–	Sayers *et al.* (2020)
Phylloporia chrysites	MUCL 52862	Mexico	–	HM635667	–	Valenzuela *et al.* (2011)
Phylloporia chrysites	MUCL 52764	Mexico	–	HM635666	–	Valenzuela *et al.* (2011)
Phylloporia clariceae	FLOR:51258	Brazil	–	KJ631406	–	Ferreira-Lopes *et al.* (2016)
Phylloporia clausenae	Yuan 3528	China	–	KJ787795	–	Zhou (2015a)
	Cui8463	China	MH151186	MH165868	MH167424	Zhou (2015a)
Phylloporia crataegi	Dai18133	China	MH151191	MH165865	MH167431	Zhou & Dai (2012)
	Dai 11016	China	–	JF712923	–	Zhou & Dai (2012)
Phylloporia crystallina	JV2106/102	Ecuador	–	ON006467	–	Zhou *et al.* (2022)
Phylloporia cylindrispora	Yuan6144	China	–	KJ787798	–	Zhou (2015a)
	Yuan6148	China	–	KJ787797	–	Zhou (2015a)
Phylloporia cystidiolophora	Dai13953	China	–	MG738799	MH167438	Wu *et al.* (2019)
	Dai13945	China	–	MG738798	–	Wu *et al.* (2019)
Phylloporia dependens	Cui 13763	China	MH151190	KX242353	–	Chen *et al.* (2017)
Phylloporia elegans	FLOR:51179	Brazil	–	KJ631409	–	Ferreira-Lopes *et al.* (2016)
	FLOR:51178	Brazil	–	KJ631408	–	Ferreira-Lopes *et al.* (2016)
Phylloporia ephedrae	TAA 72-2	Turkmenistan	MH151184	AF411826	–	Wagner & Ryvarden (2002)
Phylloporia flabelliforma	MUCL 55570	Gabon	NR_154332	KU198350	–	Decock *et al.* (2015)
	MUCL 55569	Gabon	KU198356	KU198349	–	Decock *et al.* (2015)
Phylloporia flacourtiae	Yuan 6362	China	–	KJ787801	–	Zhou (2015a)
	Yuan 6360	China	–	KJ787800	–	Zhou (2015a)
Phylloporia fontanesiae	Cui12356	China	MH151188	MH165871	–	Zhou & Dai (2012)
	Li 199	China	–	JF712925	–	Zhou & Dai (2012)
Phylloporia fruticum	MUCL 52762	Mexico	–	HM635668	–	Valenzuela *et al.* (2011)
	ENCB TR&RV858	Mexico	–	HM635669	–	Valenzuela *et al.* (2011)
Phylloporia fulva	MUCL 54472	Gabon	–	KJ743247	–	Yombiyeni *et al.* (2015)

Table 1. (Continued).

Species	Voucher or Strain	Origin	ITS	LSU	*EF1α*	References
Phylloporia gabonensis	MUCL 55572	Gabon	KU198354	KU198352	–	Decock *et al.* (2015)
	MUCL 55571	Gabon	NR_154331	KU198353	–	Decock *et al.* (2015)
Phylloporia gutta	Dai16070	China	MH151183	MH165863	MH167423	Zhou & Dai (2012)
	Dai 4197	China	–	JF712927	–	Zhou & Dai (2012)
Phylloporia hainaniana	Dai 9460	China	–	JF712928	–	Cui *et al.* (2010)
Phylloporia homocarnica	Yuan 5766	China	–	KJ787804	–	Zhou (2015a)
	Yuan 5750	China	MH151195	KJ787803	–	Zhou (2015a)
Phylloporia inonotoides	MUCL 54468	China	–	KJ743250	–	Yombiyeni *et al.* (2015)
Phylloporia lespedezae	Dai17065	China	MH151179	KY242602	MH167419	Ren & Wu (2017)
	Dai17067	China	MH151180	KY242603	MH167420	Ren & Wu (2017)
Phylloporia littoralis	MUCL: 56145	Gabon	–	KY349141	–	Yombiyeni & Decock (2017)
	MUCL: 56144	Gabon	–	KY349140	–	Yombiyeni & Decock (2017)
	OAB0204	Benin	MW244095	MW244098	–	Olou *et al.* (2021)
Phylloporia lonicerae	Dai17900	China	MH151175	MG738802	MH167418	Qin *et al.* (2018)
Phylloporia lonicerae	Dai17899	China	MH151174	MG738801	MH167417	Qin *et al.* (2018)
	Dai17898	China	MH151173	MG738800	MH167416	Qin *et al.* (2018)
Phylloporia manglietiae	Cui 13709	China	MF410324	KX242358	MH167430	Chen *et al.* (2017)
Phylloporia minuta	FURB 55088	Brazil	–	NG_064479	–	Bittencourt *et al.* (2018)
Phylloporia minutipora	Dai16172	China	–	MH165873	MH167436	Zhou (2016)
	LWZ-2016	China	–	KU904466	–	Sayers *et al.* (2020)
	Dai 9257	China	–	KU904464	–	Sayers *et al.* (2020)
	Ipulet 706	Uganda	–	JF712929	–	Ipulet & Ryvarden (2005)
	MUCL 52865	Congo	–	HM635671	–	Valenzuela *et al.* (2011)
	Dai-21223	China	–	MZ437408	–	Wu *et al.* (2022)
Phylloporia montana	BDNA2409	Brazil	–	MG738811	–	Wu *et al.* (2019)
	BDNA2388	Brazil	–	MG738810	–	Wu *et al.* (2019)
Phylloporia mori	Wu 1105 2	Taiwan	–	LC514412	–	Wu *et al.* (2020)
	Wu 1105 3	Taiwan	–	LC514413	–	Wu *et al.* (2020)
Phylloporia moricola	Wu1807 1	China	–	LC589617	–	Wu *et al.* (2021)
	Wu1807 5	China	–	LC589618	–	Wu *et al.* (2021)
	Wu1807 6	China	–	LC589619	–	Wu *et al.* (2021)
Phylloporia murrayae	Wu 1404-4	Taiwan	–	LC514409	–	Wu *et al.* (2020)
	Wu 1404-5	Taiwan	–	LC514410	–	Wu *et al.* (2020)
Phylloporia mutabilis	OAB0643	Benin	OR096158	OR096136	OR161068	This study
	OAB0666	Benin	OR096159	OR096137	OR359376	This study
Phylloporia nandinae	Dai 10588	China	–	JF712930	–	Zhou & Dai (2012)
	Dai 10625	China	–	JF712931	MH167439	Zhou & Dai (2012)
Phylloporia nodostipitata	FLOR:51173	Brazil	KJ639057	KJ631412	–	Ferreira-Lopes *et al.* (2016)
	FLOR:51175	Brazil	–	KJ631413	–	Ferreira-Lopes *et al.* (2016)
Phylloporia nouraguensis	MUCL/FG-11-404	Guyana	–	KC136223	–	Decock *et al.* (2013)
	MUCL/FG-11-409	Guyana	–	KC136224	–	Decock et al. (2013)
Phylloporia oblongospora	Zhou179	China	MH151197	JF712932	–	Cui *et al.* (2010)
Phylloporia oreophila	CUI2219	China	MH151196	JF712933	–	Zhou & Dai (2012)
	Cui 9503	China	–	JF712934	–	Zhou & Dai (2012)
Phylloporia osmanthi	Yuan 5655	China	–	KF729938	–	Zhou (2015b)
Phylloporia parasitica	LR 19843	Argentina	KU198361		–	Decock *et al.* (2015)
Phylloporia pectinata	R.Coveny 113	Australia	–	AF411823	–	Wagner & Ryvarden (2002)
Phylloporia pendula	Cui 13691	China	–	KX242357	MH167426	Chen *et al.* (2017)

Table 1. (Continued).

Species	Voucher or Strain	Origin	ITS	LSU	*EF1α*	References
	Cui 13876	China	–	KX901670	MH167427	Chen *et al.* (2017)
Phylloporia perangusta	Dai18139	China	MH151169	MG738803	MH167413	Wu *et al.* (2019)
Phylloporia pseudopectinata	Cui 13746	China	–	KX242355	MF977778	Chen *et al.* (2017)
	Cui 13749	China	–	KX242356	MH167429	Chen *et al.* (2017)
Phylloporia pulla	Cui 5251	China	–	KU904468	–	Zhou (2016)
	Dai 9627	China	–	KU904469	–	Zhou (2016)
Phylloporia radiata	LWZ-2016a	China	–	KU904470	–	Zhou (2016)
Phylloporia rattanicola	Dai18233	China	–	MG738807	–	Wu *et al.* (2019)
	Dai18235	China	MH151172	MG738808	MH167415	Wu *et al.* (2019)
Phylloporia ribis	82-828	Germany	–	AF311040	–	Wagner & Ryvarden (2002)
Phylloporia rinoreae	MUCL: 56283	Gabon	–	MN243144	–	Jerusalem *et al.* (2019)
	MUCL: 57328	Gabon	–	MN243146	–	Jerusalem *et al*. (2019)
Phylloporia rubiacearum	Chen 3583	Taiwan	–	LC514416	–	Wu *et al.* (2020)
	Chen 3584	Taiwan	–	LC514417	–	Wu *et al.* (2020)
Phylloporia rzedowskii	MUCL 52859	Mexico	–	HM635673	–	Valenzuela *et al.* (2011)
	MUCL 52860	Mexico	–	HM635674	–	Valenzuela *et al.* (2011)
Phylloporia sumacoensis	JV2109/73	Ecuador	–	ON006468	–	Zhou *et al.* (2022)
Phylloporia solicola	JRF145	Brazil	–	MG738815	–	Wu *et al.* (2019)
Phylloporia sp.	Robledo1220	Argentina	–	KC136225	–	Sayers *et al.* (2020)
	ISA007	Brazil	–	KJ743265	–	Sayers *et al.* (2020)
Phylloporia spathulata	Chay456	Mexico	–	AF411822	–	Ferreira-Lopes *et al.* (2016)
Phylloporia splendida	Dai6282	China	–	MG738805	–	Wu *et al.* (2019)
	Cui8429	China	–	MG738804	–	Wu *et al.* (2019)
Phylloporia tabernaemontanae	*Dai 18852*	Australia	–	MZ437409	–	Wu *et al.* (2022)
	Dai 18853	Australia	–	MZ437410	–	Wu *et al.* (2022)
Phylloporia terrestris	Yuan 5738	China	–	KC778784	–	Zhou (2015b)
	He2359	China	MH151189	MH165869	–	Zhou (2015b)
Phylloporia tiliae	Yuan 5491	China	–	KJ787805	–	Zhou (2013)
Phylloporia ulloai	MUCL 52866	Mexico	–	HM635677	–	Valenzuela *et al.* (2011)
	MUCL 52867	Mexico	–	HM635678	–	Valenzuela *et al.* (2011)
Phylloporia weberiana	Dai 9242	China	–	JF712936	–	Sayers *et al.* (2020)
Phylloporia yuchengii	YG 051	Uzbekistan	–	KM264325	–	Gafforov *et al.* (2014)

Taxonomy

Phylloporia mutabilis Olou, ***sp. nov.*** MycoBank MB 849082. Figs 2, 3.

Etymology: *mutabilis* (Latin), referring to the colour of basidiomata, changing as it dries.

Typus: **Benin**, Atlantic Province, dry dense forest of Pahou near Ouidah city, 6°23′2.97″N, 2°9′15.90″E, alt. 33.1 m, on soil under angiosperm of dry dense forest, 8 Jul. 2021, *leg. B.A. Olou*, OAB0643 (**holotype** UNIPAR, OAB0643). Holotype sequences: ITS OR096158, LSU OR096136, and *EF1α* OR161068.

Diagnosis: *Phylloporia mutabilis* differs from known species of *Phylloporia* by the combination of the following characteristics: *Basidiomata* stipitate, caespitose, coriaceous, pileus surface and margin with bands of white and dark brown colours in fresh specimens, margin large in young specimens and becoming narrower with maturity, earth coloured to dark brown when fresh and golden brown to yellowish brown after drying. *Pilei* semi-circular to circular, up to 5 cm wide and 2 mm thick at base. *Setae*, *cystidia* and *cystidioles* absent. *Basidia* 9–12 × 4–6 µm. *Basidiospores* ellipsoid to subglobose, 2.7–3.8 × 2–2.9 µm.

Description: *Basidiomata* eccentrically to laterally stipitate, caespitose, two to several pilei rising from a common base, coriaceous, without odour or taste. Pilei semi-circular to circular, up to 5 cm wide and 2 mm thick at base. *Pileal surface* tomentose, shiny when fresh, earth coloured (5F2) to dark brown (6F8) when fresh and golden brown (5D7) to yellowish brown (5E8) when dry, concentrically zonate; margin entire, yellowish white, with a distinct groove between the margin and the central part of the pileal surface. *Pore surface* golden yellow (4C6); pores angular, 6–8 per mm, slightly decurrent on stipe. Context up to 1.5 mm thick, duplex, the lower context woody,

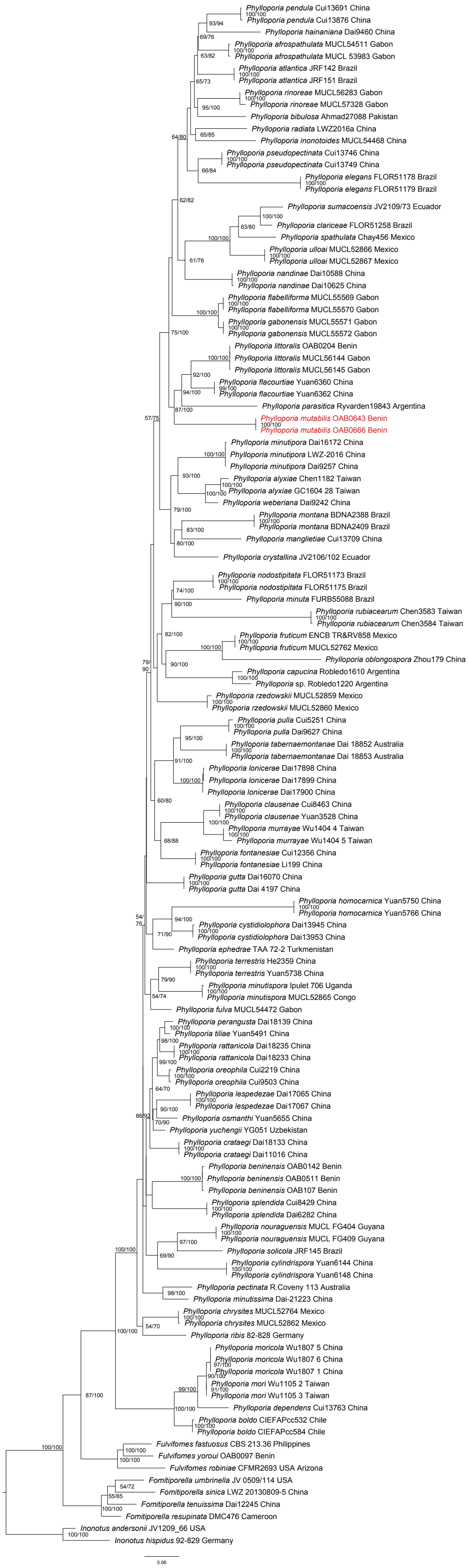

Fig. 1. Summarised tree from the Maximum likelihood (ML) and Bayesian analysis (BI) analyses of the combined ITS-LSU- EF1α dataset of *Phylloporia* and closely related genera. Branch support values given as UFBoot/PP. Newly generated sequences are highlighted in red. The sequence names are followed by voucher or strain number and country of origin.

Fig. 2. Basidiomata of *Phylloporia mutabilis* (OAB0643). **A.** Fresh basidiomata in the field. **B.** Basidiomata after drying. Scale bars = 1 cm.

golden brown, up to 1.4 mm thick, upper context very narrow, up to 0.1 mm thick, the two parts separated by a black line. *Tubes* golden yellow, woody, up to 1 mm long at the base and in the middle of basidiomata, narrow toward the margin. Stipe yellow brown, cylindrical or more frequently flattened, up to 4 cm long and 1 cm in diam., duplex, inner part woody, outer part as tomentum, corky, the two parts separated by a black line. *Hyphal system* monomitic; generative hyphae septate without clamps. Contextual hyphae golden yellow, thick-walled, septate without clamps, unbranched, CB–, 4–7 µm diam. *Tramal hyphae* golden yellow to golden brown, thick-walled, unbranched, septate without clamps, CB–, 2.5–4.5 µm diam. Setae, cystidia, and cystidioles absent. *Basidia* with four sterigmata, 9–12 × 4–6 µm; basidioles similar to basidia. *Basidiospores* broadly ellipsoid to subglobose, yellowish, thick-walled, smooth, IKI–, CB–, (2.6–) 2.7–3.8(–4.1) × 2.0–2.9(–3.1) µm, L = 3.2 µm, W = 2.4 µm, Q = 1.33 (n = 54/1).

Ecology and distribution: Basidiomata grow on the soil under angiosperm trees in a dense dry forest. This species is currently only known from the type locality in southern Benin.

Additional specimen examined: **Benin**, Atlantic Province, dense dry forest of Pahou in Ouidah, 6°23′2.97″N, 2°9′15.90″E, alt. 33.1m, on soil under angiosperms of dense dry forest, 8 Jul. 2021, *leg*. B.A. Olou, OAB0666 (UNIPAR).

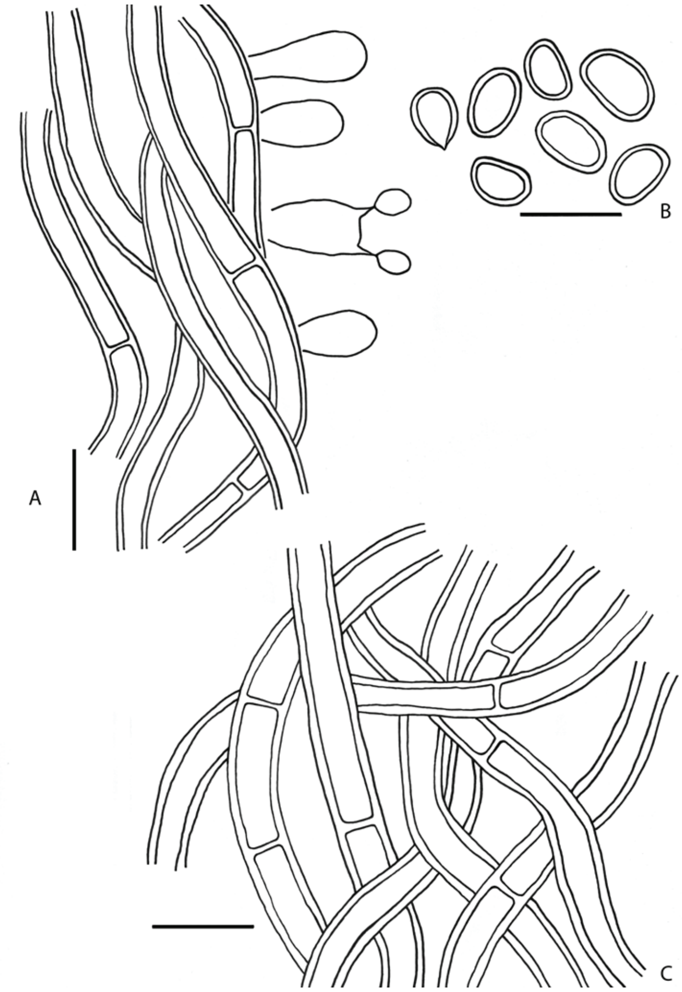

Fig. 3. *Phylloporia mutabilis* (OAB0643). **A.** Hyphae of the trama close to a pore and basidia, one basidium with young basidiospores. **B.** Basidiospores. **C.** Contextual hyphae. Scale bars: A, C = 10 µm; B = 5 µm.

DISCUSSION

Sequences generated from two specimens of *Phylloporia mutabilis* were added to the phylogeny of the genus *Phylloporia*. Our phylogenetic analyses of combined ITS-LSU-*EF1α* dataset reveal that sequences of *Phylloporia mutabilis* form a distinct clade which has a sister clade, including *P. littoralis*, *P. flacourtiae*, and *P. parasitica*. The three latter species differ from *P*. *mutabilis* by resupinate or pileate-sessile basidiomata (Murrill 1904, Yombiyeni & Decock 2017, Zhou 2015a).

Among the 76 known *Phylloporia* species, 10 species have pileate-stipitate basidiomata like *P. mutabilis*. Of these 10 species, seven, namely *P. afrospathulata*, *P. elegans*, *P. minutispora*, *P. nodostipitata*, *P. spathulata*, *P. solicola* and *P*. *terrestris* are not phylogenetically closely related to the new species. The remaining three species, *P. rajchenbergii*, *P. ryvardenii* and *P. verae-crucis* were not included in the phylogenetic analyses because their sequences are not available (Chamorro-Martínez *et al.* 2022)

Phylloporia rajchenbergii differs from *P. mutabilis* by its lateral stipitate basidiomata, a reddish brown pileus, polygonal to elongate and smaller pores, 14–16 per mm (Chamorro-Martínez *et al.* 2022).

Phylloporia ryvardenii differs from *P. mutabilis* by its neotropical origin, the lack of black in the context and stipe, and smaller spores, 10–12 per mm (Chamorro-Martínez *et al.* 2022).

Phylloporia veracrucis differs from *P*. *mutabilis* by its larger ellipsoid basidiospores, 4.5 × 3.5 µm (Wagner & Ryvarden 2002) (smaller in *P*. *mutabilis*, 3.8 × 2.9 µm). In addition, *P*. *veracrucis* is only known from Mexico (North America) (Wagner & Ryvarden 2002) while *P*. *mutabilis* is known from Benin (West Africa). *Phylloporia mutabilis* is newly described here and its distribution will have to be reassessed once more collections become available.

Phylloporia rajchenbergii, *P*. *ryvardenii* and *P*. *veracrucis* were reported to be related to *P. spathulata* (Wagner & Ryvarden 2002, Chamorro-Martínez *et al.* 2022). *Phylloporia spathulata* was reported from tropical Africa (Ryvarden & Johansen 1980), but the species was considered to have a neotropical distribution by Ferreira-Lopes *et al.* (2016). In addition, the sequences of *P*. *spathulata* did not match with those of *P*. *mutabilis*, so it is obvious that *P*. *mutabilis* and *P*. *spathulata* are two different species. Records of *P. spathulata* from tropical Africa need to be examined microscopically and phylogenetically as these specimens might represent another species.

The lifestyle of *P*. *mutabilis* is not known. Its basidiomata were found on soil and its mycelium could develop on the roots of nearby living trees or on dead wood debris buried in the soil. It might also have a mycorrhizal lifestyle like some species of *Coltricia*. Future studies on the ecology of terrestrial *Phylloporia* species will shed light on our understanding of the lifestyle of terrestrial *Phylloporia* species.

The description of *P. mutabilis* brings the diversity of *Phylloporia* in Benin to three species, namely *P*. *beninensis*, *P*. *littoralis* and *P*. *mutabilis*. *Phylloporia beninensis* and *P*. *littoralis* are recorded from woodlands with open canopy in central and northern Benin (dry habitats) and these species are characterised by pileate-sessile or effused-reflexed basidiomata attached to wood. *Phylloporia mutabilis* is the only species recorded from a dense dry forest with a closed canopy in southern Benin (wet habitat) and is characterised by pileate-stipitate basidiomata on soil. Although it is still too early to draw this conclusion, our data seem to indicate that species in dry habitats are characterised by pileate-sessile basidiomata and species in wet habitats by pileate-stipitate species. Previous studies have shown that morphological traits of the basidiomata are linked to microclimate (Krah *et al.* 2022). Similarly, the size of the basidiomata, its colour, lightness and toughness are linked to harsh microclimatic conditions (Krah *et al.* 2019, Bässler *et al.* 2021). However, at present we know little about whether the presence or absence of the stipe in a basidioma can be linked to habitat types or microclimatic adaptations. Further mycological surveys on *Phylloporia* in Benin will increase the diversity of species of *Phylloporia* and this will facilitate ecological studies to answer these outstanding questions.

ACKNOWLEDGEMENTS

This research was funded by The German Federal Ministry of Education and Research, BMBF (grant No. 01D20015). Boris Armel Olou also received support from the Mohamed Bin Zayed Species Conservation Fund (grant No. 192520581) for the field work.

Conflict of interest: The authors declare that there is no conflict of interest.

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