Allophlebia, A New Genus to Accomodate *Phlebia Ludoviciana* (Agaricomycetes, Polyporales)

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Abstract

Allophlebia is proposed as a new genus in Meruliaceae based on morphological characters and molecular data. The genus is typified by *Peniophora ludoviciana* and the new combination *A. ludoviciana* is proposed. The genus is so far monotypic. The type species is characterized by a resupinate basidioma, a monomitic hyphal system with clamp connections, two types of cystidia (leptocystidia and metuloids), clavate basidia, and hyaline, thin-walled and ellipsoid basidiospores. A phylogeny for *Allophlebia* and related taxa was inferred from ITS and nLSU rDNA sequences and new information about the geographic distribution of *A. ludoviciana* is provided.

Introduction

Phlebia Fr. (Polyporales, Meruliaceae) was described by Fries in 1821 and intended for species with a hymenium composed of irregular veins and ridges. Fries (1828) pointed to *P. radiata* as the most typical member of his new genus and this species is now generally accepted as the type (Donk 1957). Species in *Phlebia sensu lato* usually have resupinate basidiomata that are ceraceous to subgelatinous in fresh specimens, and with a membraneous or coriaceous consistency when dry. The hymenial surface varies from smooth, tuberculate, phlebioid, odontoid, merulioid to poroid. The hyphal system is monomitic, rarely dimitic, with hyphae clamped and embedded in a more or less evident gelatinous matrix. Cystidia can be present or absent, basidia are clavate, narrow, with a basal clamp and disposed in a dense palisade, and basidiospores are allantoid to ellipsoid, smooth, thin-walled, IKI- and CB- (Eriksson et al. 1981; Bernicchia & Gorjón 2010). All species analyzed are saprobes on decaying wood (Nakasone 1990).

The original concept for *Phlebia* was successively considerably broadened (Donk 1931, 1957, Nakasone 1991, 1996, 1997, 2002, Nakasone & Burdsall 1984). However, this wider concept for *Phlebia* is clearly polyphyletic (Larsson et al. 2004, Binder et al. 2013, Floudas & Hibbett 2015, Justo et al. 2017). Several genera have been introduced or resurrected to accommodate species from *Phlebia*, e.g. *Cabalodontia, Crustodontia, Hermanssonia, Jacksonomyces, Lilaceophlebia, Mycoacia, Mycoaciella, Phlebiopsis, Scopuloides*, and *Stereophlebia*. Other *Phlebia* species have been moved to other genera, most notably to *Crustoderma* and *Resinicium*. After such removal and transfer of species and after adjustments for synonyms the genus still holds around 100 species, many of which are based on names for which there are no modern interpretation (www.mycobank.org). According to molecular data, *P. radiata*, the type species, and quite many other *Phlebia* species belong in Meruliaceae in Polyporales (Justo et al 2017), while a few are recovered in Hymenochaetales (Larsson 2007).

During studies of corticioid fungi from Northeast Brazil, specimens of *Phlebia ludoviciana* were collected. Molecular analyses showed that this species could not be placed in any of the phlebioid genera already described. Thus, the aims of this paper are to describe a new genus for *P. ludoviciana* and to discuss the geographical distribution of that species.

Material And Methods

Area and Morphological analysis

Field trips were undertaken in Northeast Brazil in the Atlantic Rainforest [Reserva Biológica de Pedra Talhada, (09º14'40"S, 36º25'35"W); Reserva Biológica de Guaribas (06º43'12"S, 35º10'55"W); Refúgio Ecológico Charles Darwin (07º49'42"S, 34º52'29"W), Reserva Particular do Patrimônio Natural (RPPN) Frei Caneca (08º42'41"S, 35º50'30"W), Reserva Biológica de Saltinho (8°44'16.9"S, 35°10'22,6"W)] and in montane forest (*Brejos Nordestinos*) in Caatinga; Reserva Ecológica Estadual Mata do Pau-Ferro (06°58'12"S, 35°42'15"W).

Specimens were identified based on macro- (measures, texture, consistency, shape and color of the basidiomata) and micro-morphology through slide preparations with 3% potassium hydroxide solution (KOH), stained with 1% aqueous phloxine. Melzer's reagent and Cotton Blue were used to analyze, respectively, dextrinoid and amyloid (IKI+/IKI-), and cyanophilous (CB+/CB-) reactions of the microstructures. Presence/absence of sterile structures and basidiospores were noted and measurements of at least 20 of them taken, when possible (Hjortstam et al. 1987; Watling 1969). The material was deposited in the Herbarium Pe. Camille Torrend (URM), Departmento de Micologia (UFPE), and in the Herbarium of the University of Oslo (O).

DNA extraction, PCR amplification and sequencing

Basidiomata fragments (30–50 mg) were removed, placed in tubes of 1.5 ml and stored at -20°C until DNA extraction. The method of DNA extraction followed Góes-Neto et al. (2005) and the reaction mix and parameters for PCR reactions of the ITS and LSU regions were according to Smith & Sivasithamparam (2000), using the primer pairs ITS4-ITS5 and LR0R-LR5, respectively (White et al. 1990, Moncalvo et al. 2000, Lima-Junior et al. 2014). The purification of PCR products was done with ExoSAP-IT™ PCR Product Cleanup Reagent (Thermo Fisher Scientific, USA), following the manufacturer's recommendations. The samples were sequenced at the Plataforma Tecnológica de Genômica e Expressão Gênica do Centro de Biociências (CB), UFPE, Brazil, in an ABI-310 Capillary Sequencer (PerkinElmer, Wellesley Massachusetts, USA). The cycle sequencing was carried out with the same primers of PCR reactions (Moncalvo et al. 2000). All obtained sequences were deposited in GenBank (National Center for Biotechnology Information, Bethesda, Maryland, USA). Attempts at sequencing RBP1, RBP2 and TEF resulted in only one low quality TEF sequence that could not be submitted to GenBank (available on request).

Phylogenetic analyses

The 2.0 Staden Package software was used for analyses and edition of electropherograms (Bonfield et al. 1995). These sequences were subjected to BLASTn search in NCBI to recover similar sequences from GenBank and used in the dataset to establish phylogenetic relationships (Table 1). Each gene region was aligned with the MAFFT v.7 online server using default settings (http://mafft.cbrc.jp/alignment/server/), then improved manually using MEGA 7.0 and combined to form the concatenated dataset (Kumar et al. 2016).

The ITS and LSU regions were first analyzed independently (data not shown). Since no important topological differences were detected, the regions were combined into a single matrix for the final analyses. The models of evolution were obtained from MEGA 7.0 (Kumar et al. 2016) and confirmed in TOPALi v2.5 (Milne et al. 2004) for each dataset. Phylogenetic analyses and tree construction were performed using Maximum Likelihood (ML) and confirmed in Bayesian Algorithm (BA). ML analysis was performed using MEGA 7.0 (Kumar et al. 2016) with 5000 bootstrap replications and based on GTR + G + I model. BA analyses were run in TOPALi v2.5 (Milne et al. 2004) with $5x10^6$ generations, also based on GTR + G model. Statistical support for branches was considered informative with Bayesian posterior probabilities (BPP) ≥ 0.80 and bootstrap (BS) values ≥ 70%. The trees were visualized with FigTree (Rambaut 2014) and the layouts were done in the software Microsoft PowerPoint.

Results

Five specimens were sequenced (URM 93082, URM 93251, URM 93329, O-F-110340, O-F-110341), generating five ITS and four LSU sequences (Table 1). These were combined with ITS and LSU sequences selected though BLAST searches against GenBank.

No strongly supported topological conflict was detected among the datasets analyzed (ITS, LSU and ITS + LSU) in the present study, thus only the combined analysis is presented here, performed mainly with ITS sequences since only that region is available for some key specimens. The combined dataset included 174 sequences (116 ITS and 58 LSU), with *Climacocystis borealis* (Fr.) Kotl. & Pouzar and *Junghuhnia nitida* (Pers.) Ryvarden as outgroup following Shan *et al*. (2018) (Table 1), and comprised 2138 characters including gaps.

The results of the phylogenetic analyses generated from ML and BA showed similar tree topologies and small or insignificant differences in statistical support values. Thus, the ML tree with bootstrap support values (BS) and posterior probabilities (PP) from Bayesian Inference of phylogeny (BI) was used to show the results of this study (Fig. 1).

The newly generated sequences are placed in a strongly supported clade (BS 99%, PP 0.99) with several samples of *A. ludoviciana* as well as other samples identified differently, previously deposited in GenBank. The *A. ludoviciana* clade is sister to a clade formed by *Phlebia ochraceofulva* and one unidentified sample and is genetically separated from the clade representing *Phlebia s.s*, typified by *P. radiata*, and from other described genera (Fig. 1).

Taxonomy

Allophlebia C.R.S. de Lira, Gibertoni & K.H. Larss., gen. nov.

Mycobank: MB 838838

Etymology—*Allophlebia* (Gk) = “allo-” other, different; “-phlebia” referring to genus *Phlebia*.

Description

Basidiomata resupinate, effused, adnate, ceraceous; hyphal system monomitic, all septa with clamps; thin-walled smooth leptocystidia and thick-walled encrusted cystidia present; basidia clavate, with four sterigmata; basidiospores ellipsoid, thin-walled, smooth, inamyloid, indextrinoid and acyanophilous.

Type species: *Peniophora ludoviciana* Burt

Allophlebia ludoviciana (Burt) C.R.S. de Lira & K.H. Larss., comb. nov., Fig. 2a-f

Mycobank: MB 838839

Basionym: *Peniophora ludoviciana* Burt, Annals of the Missouri Botanical Garden 12 (3): 244 (1926)

Description: Nakasone et al. (1982).

Remarks: *Allophlebia* is so far monotypic. *Allophlebia ludoviciana* is characterized by a resupinate, ceraceous and golden yellow to deep orange basidioma (Fig. 2a-b), a smooth to minutely warted hymenophore without reaction in 3% KOH, and a monomitic hyphal system. Two types of cystidia can be observed: 1) Leptocystidia, narrowly obclavate to ventricose, hyaline and projecting above the hymenium, (35)45–70 × 5.5–7 µm (Fig. 2e), and 2) Cylindrical metuloids, heavily encrusted with hyaline crystals, with obtuse to slightly conical apex, immersed in the hymenium, 35–70 × 6–9 µm (Fig. 2f). The basidia are narrowly clavate and the basidiospores are ellipsoid, (4.5)5.5–6.5 × 2–2.5 µm, smooth, thin-walled, hyaline (Fig. 2f) and IKI- and CB-. *Allophlebia ludoviciana* and *Phlebia subochracea* are both bright yellow-orange when fresh and tan to light brown when dry. However, *P. subochracea* has longer and narrower basidiospores (5–7 × 1.5–2 µm) and lacks the metuloids found in *A. ludoviciana* (Nakasone et al. 1982).

Distribution: *Allophlebia ludoviciana* and specimens of this species identified differently were reported as saprobes, endophytes or as airborne basidiospores from Jamaica, Saint Lucia and United States of America (Nakasone et al. 1982, Ritttenour et al 2014), Cuba and Bermudas (Hjorstam & Ryvarden 2001), Mexico (Tapia & Chacón 2015), Ecuador, French Guyana, China and possibly Colombia (Fig. 1, Table 1). Here the presence in Brazil is confirmed (Fig. 1, Table 1). The Brazilian specimens studied by us were collected on decaying wood in Atlantic Rainforest (Southeast and Northeast Brazil) and montane forests in Caatinga (*Brejos Nordestinos*). In addition, there is a report of *A. ludoviciana* from the Southeastern Atlantic Rainforest identified as *Grammothelopsis puiggarii* (Table 1).

Material examined: Brazil: Alagoas, Quebrangulo, Reserva Biológica Pedra Talhada, leg. R.L.M. Alvarenga & A. Meiras-Ottoni, A., 6 June 2017, RC38 (URM93082), Ibid, leg. V. Xavier de Lima, 19 Sep. 2018, VXL550 (URM93250), Ibid, 20 Sep. 2018 VXL591 (URM93251); Paraiba, Areia, Reserva Ecológica Estadual Mata do Pau-Ferro, 29 April 2013, C.R.S. Lira 583 (URM 93329), Ibid. K.H. Larsson 16092 (O-F-110341), Ibid, Mamanguape, Reserva Biológica Guaribas, 30 May 2015, R.S. Chikowski 1300 (URM92973); Pernambuco, Cabo de Santo Agostinho, 7 June 2018, VXL155 (URM93249); Ibid, Igarassu, Refúgio

Ecológico Charles Darwin, 12 May 2017, R.S. Chikowski 1536 (URM93061), Ibid, Jaqueira, RPPN Natural Frei Caneca, 30 Sep. 2012 R.S. Chikowski 381 (URM92972), Ibid, 9 March 2013, R.S. Chikowski 548 (URM85875); São Paulo: Santos, Cananeia, Ilha do Cardoso, 2–5 Feb. 1987, L. Ryvarden 24695 (O-F-110338); São Paulo: São Paulo, Parque Estadual Fontes do Ipiranga, 16–24 Jan. 1987, K. Hjortstam 16335 (SP213701); Ibid L. Ryvarden 24141 (O-F-110339). Colombia: Magdalena, Parque Nacional Tayrona, Estacion de Gairaca, 12 June 1978, L. Ryvarden 15780 (O-F-918462). Ecuador: Orellana, Yasuni Nat. Park, Yasuni Research St., 9–12 Mar. 2002, L. Ryvarden 44743 (O-F-110340). USA: Iowa, Iowa City, 8 July 1934, D.P. Rogers 104 (O-F-504275); Louisiana, Plaquemines Parish, F. Edward Hebert Center, 26 July 1972, W.B. & V.G. Cooke 45633 (O-F-908538).

Discussion

When combining *Peniophora ludoviciana* to *Phlebia*, Nakasone et al. (1982) grouped this species with *P. brevispora*, *P. subochracea* and *P. subserialis* in the section Leptocystidiophlebia based on morphology and culture characteristics. Our results, however, show that although *P. ludoviciana* is close to *P. subochracea*, *P. brevispora* and *P. subserialis* are distantly related from each other and from *P. ludoviciana* and *P. subochracea* (Fig. 1), similar to the findings of other studies. Floudas & Hibbett (2015) included *P. brevispora* (HHB7030) and several samples identified as *P. subserialis* and *P. subochracea* (EU 118656) in their analyses. *Phlebia brevispora* is placed in the *Phlebia s.s.* clade, while the samples identified as *P. subserialis* are placed in three different clades, one corresponding to *A. ludoviciana* (HQ607954, HM997135, HQ377286, KP135343, HQ248219, FD427, HHB9768) and sister to *P. subochracea* (EU118656), one close to *P. nothofagi* and *P. fuscoatra* (AF141631), currently belonging to *Mycoacia*, and the last one belonging to the *Phanerochaete* clade (AY219365, JN017928, HHB-5796). Justo et al. (2017) did not include *P. subserialis* in their study, but *P. ludoviciana* (FD-427) is placed in a clade with *P. subochracea* I (HHB8715), both representing *A. ludoviciana* and sister to *P. subochracea* II (HHB8494), an undescribed species of *Allophlebia*, all of them distantly related from *P. brevispora* (FBCC1463 or HHB7030, not detailed in their Fig. 5) and from *P. radiata*. Shen et al. (2018) did not include *P. brevispora* in their analyses, but *P. ludoviciana* (FD-427) is again sister to *P. subochracea* (HHB8715), both corresponding to *A. ludoviciana* and distantly related from *P. radiata* and the sample identified as *P. subserialis* (AF141631).

In our study, the *Allophlebia* clade is genetically separated from the *Phlebia s.s.* clade (BS = 87/PP = 0.96, with *P. radiata*) as well as from other genera in Meruliaceae and from remaining sequenced species of *Phlebia* recovered outside of Meruliaceae. It is strongly supported as a monophyletic group (99) (Fig. 1), in accordance with the recommendations by Vellinga et al. (2015). The new genus may also include Fungal sp. (TP2) from Thailand (Klomklieng et al. 2014) and *P. ochraceofulva* FBCC295 with unknown origin (Kuuskeri et al. 2015), but they represent isolates without vouchers, which prevents morphological studies.

The sequences of *A. ludoviciana* generated in our study clustered with 17 sequences from the USA and French Guiana and 14 other sequences that also represent *A. ludoviciana*, but were identified differently:

P. aff argentina from French Guiana, *P. subserialis* from Brazil, China, Ecuador, the USA and possibly from Colombia, *Phlebia* cf. *subserialis* from the USA and *Grammothelopsis puiggarii* from Brazil and possibly China, as well as unidentified fungal samples from the USA and Mexico (Table 1), forming a distinct, strongly supported clade (BS = 99/PP = 0.99) (Fig. 1). *Phlebia argentina* (Speg.) Rajchenb. & J.E. Wright, originally collected on *Salix humboldtiana* in Argentina, is characterized by membraneous basidiomata and one kind of cystidia, strongly encrusted metuloids projecting beyond the hymenium (Rajchenberg & Wright 1987). The type of *P. subserialis* is from France and sequences from there and other European countries, as well as one sequence of material from India (Table 1), are distantly placed in the phylogenetic tree (Fig. 1). In addition, *P. subserialis* has narrower leptocystidia (3–4 µm), lacks encrusted cystidia, and has longer, sub-allantoid basidiospores [6–7(-8) x 2-2.5 µm] (Bernicchia & Gorjón, 2010). Thus, specimens of *P. subserialis* reported in the Americas should be reevaluated (Nakasone et al. 1982). *Grammothelopsis puiggarii* is a species characterized by large, angular pores (1–2 per mm), large, dextrinoid, thick-walled basidiospores and dextrinoid skeletal hyphae (Rajchenberg & Wright 1987). This species is currently placed in Polyporaceae and the sequences clustering with *A. ludoviciana* are clearly misidentified.

This study improved the circumscription and the knowledge about the distribution of a species previously placed in *Phlebia*. The results also indicate that *Phlebia s.s.* is still in need of rearrangement and for these taxonomical approaches including morphology, DNA analyses and geographical data are strongly encouraged.

Declarations

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Conflicts of interest/Competing interests (include appropriate disclosures) – Not applicable

Ethics approval - Not applicable

Consent to participate - Not applicable

Consent for publication - Not applicable

Availability of data and material – All material is deposited in Herbarium URM and O. The sequences is deposited in GenBank. Data will be available online after the acceptance of the manuscript in http://www.splink.org.br/ and https://www.ncbi.nlm.nih.gov/genbank/.

Code availability - Not applicable

Authors' contributions - All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by all authors. The first draft of the manuscript was written

by Carla Rejane de Sousa Lira and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript. Karl-Henrik Larsson and Tatiana B. Gibertoni provided funds and supervised this research.

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Tables

Table 1 Sequences of Meruliaceae used in this study with vouchers, locality and GenBank accession numbers for the ITS and LSU regions. The sequences in bold were generated in this study.

Species	Voucher/Locality	Locality	GenBank Access Number	
			ITS	LSU
Allophlebia ludoviciana	URM 93082	Brazil	MN044657	-
A. ludoviciana	URM 93251	Brazil	MN044659	MN044661
A. ludoviciana	URM 93329	Brazil	MN044658	MN044660
A. ludoviciana	O-F-110340	Ecuador	MT974604	MT982121
A. ludoviciana	O-F-110341	Brazil	MT974603	MT982120
Climacocystis borealis (Fr.) Kotl. & Pouzar	KHL13318	Estonia	JQ031126	-
Climacodon septentrionalis (Fr.) P. Karst.	RLG-6890	USA	KP135344	-
Crustodontia chrysocreas (Berk. & M.A. Curtis) Hjortstam & Ryvarden	HHB-3946	USA	KP135357	-
C. chrysocreas	FCUG2827	USA	KY948764	-
C. chrysocreas	KUC20121123-24	South Korea	KJ668482	KJ668335
C. chrysocreas	CLZhao 851	China	MG231783	-
Fungal sp.	MX417	Mexico	JQ919918	-
Fungal sp.	TP2	Thailand	KF860888	-
Geesterania carneola (Bres.) Westphalen & Rajchenberg	MCW 388/12	Brazil	KY174999	KY174999
Geesterania davidii Westphalen & Rajchenberg	MCW 370/12	Brazil	KY174997	KY174997
Grammothelopsis puiggarii (Speg.) Rajchenb. & J.E. Wright	RP 134	Brazil	KP859299	KP859308
G. puiggarii	WZ-143	China (?)	MN856289	-
Hydnophlebia canariensis Telleria, M. Dueñas & M.P. Martín (Type)	MA-Fungi 86622	Spain	KF528103	KF528103
H. canariensis	MA-Fungi 86623	Spain	KF483013	KF528104
H. gorgonea Telleria, M. Dueñas & M.P. Martín	MA Fungi 86659	Cape Verde	KF483049	KF528140
H. gorgonea	MA Fungi 86658	Cape Verde	KF483048	KF528139

Species	Voucher/Locality	Locality	GenBank Access Number	
			ITS	LSU
H. meloi Telleria, M. Dueñas & M.P. Martín	MA Fungi 86654	Cape Verde	KF483044	KF528135
H. omnivora (Shear) Hjortstam & Ryvarden	ME-497	USA	KP135332	KP135218
H. omnivora	KKN-112	USA	KP135334	KP135216
H. subchrysorhiza Hai X. Ma & S.H. He	Cui 16185	China	MK860722	MK860739
Junghuhnia nitida (Pers.) Ryvarden	KHL11903	Sweden	EU118638	EU118639
Luteoporia albomarginata F. Wu, Jia J. Chen & S.H. He (Type)	Dai 15229	China	NR154126	NG060338
L. albomarginata	Dai 15240	China	KU598874	KU598879
Mycoacia fuscoatra (Fr.) Donk	KHL13275	Estonia	JN649352	JN649353
M. fuscoatra	HHB-10782	USA	KP135365	KP135265
M. nothofagi (G. Cunn.) Ryvarden	BP:106925	Hungary	KX349908	-
M. nothofagi	KHL13750	France	GU480000	GU480001
M. nothofagi	AH31887	Spain	GQ259416	-
Mycoacia uda (Fr.) Donk	Kropp1	USA	KY948764	-
M. uda	CBS 224.56	France	MH857593	MH869142
Phlebia acanthocystis Gilb. & Nakasone	KUC20131001	South Korea	KJ668484	KJ668337
P. acanthocystis	FP150571	USA	KY948767	KY948844
P. acerina Peck	CLZhao 1582	China	MH114855	-
P. acerina	CBS 125860	Australia	MH863815	MH875278
P. aff argentina	G6894	French Guiana	MN994783	-
P. ailaoshanensis C.L. Zhao	CLZhao 3879	China	MH784918	MH784928
P. ailaoshanensis	CLZhao 3882	China	MH784919	MH784929
P. albida Fr.	GB 1833	Spain	KY948748	KY948889
P. albida	CBS 214.67	USA	MH858951	MH870641
P. albomellea (Bondartsev) Nakasone	FP-101843	USA	AY219369	-

Species	Voucher/Locality	Locality	GenBank Access Number	
			ITS	LSU
P. albomellea	no voucher	USA	L43378	-
P. aurea (Fr.) Nakasone	FCUG2767	Turkey	HQ153409	-
P. aurea	CFMR:DLL2011-100	USA	KJ140614	-
P. brevispora Nakasone	BAFC-633	Argentina	HM208154	JX863667
P. brevispora	FBCC1463	Finland (?)	LN611135	LN611136
P. centrifuga P. Karst.	HHB-9239	USA	KP135380	KP135262
P. centrifuga	CBS 125890	Sweden	MH864088	MH875547
P. cf. martiana	OMC1242	USA	KY948765	-
P. cf. subserialis (Bourdot & Galzin) Donk	HHB-8715	USA	KY948770	KY948846
P. cf. subserialis	MS42b	USA	KJ831936	-
P. coccineofulva	HHB-11466sp	USA	KY948766	KY948851
P. floridensis Nakasone & Burds.	HHB-7175	USA	KP135384	-
P. floridensis	FP-102562	USA	KP135386	-
P. leptospermi (G. Cunn.) Stalpers	CBS 126031	New Zealand	MH863894	MH875355
P. leptospermi	TTT1607	New Zealand	HQ153413	-
P. lindtneri (Pilát) Parmasto	GB501	Norway	KY948772	KY948847
P. livida (Pers.) Bres.	MG103	Finland	HQ153415	-
P. livida	FP135046	USA	KY948758	KY948850
P. livida subsp. tuberculata Hallenb. & E. Larss.	FCUG2716	Russia	HQ153417	-
P. livida subsp. tuberculate	TTT1418	New Zealand	HQ153419	-
P. lividina Hjortstam	HHB-4160	USA	KY948755	KY948849
P. lividina	HHB-9721	USA	KY948756	-

Species	Voucher/Locality	Locality	GenBank Access Number	
			ITS	LSU
P. ludoviciana (Burt) Nakasone & Burds.	FD-427	USA	KP135342	-
P. ludoviciana	G1085	French Guiana	MF061328	-
P. nantahaliensis Nakasone & Burds.	HHB-2816	USA	KY948777	KY948852
P. nitidula (P. Karst.) Ryvarden	Nystroem 020830	Sweden	EU118655	-
P. nitidula	T 407	Canada	KY948747	-
P. ochraceofulva (Bourdot & Galzin) Donk	FBCC295	Sweden	LN611116	-
P. radiata Fr.	Champ-81	France	KX449485	-
P. radiata	AFTOL-ID 484	USA	AY854087	AF287885
P. rufa (Pers.) M.P. Christ.	CFMR:5445	USA	KX065955	KX065989
P. rufa	CBS 126034	New Zealand	MH863896	MH875357
P. serialis (Fr.) Donk	FCUG2868	USA	HQ153429	-
P. setulosa (Berk. & M.A. Curtis) Nakasone	AH31879	Spain	GQ259417	-
P. setulosa	HHB-6891	USA	KP135382	KP135267
P. subochracea (Alb. & Schwein.) J. Erikss. & Ryvarden	KGN 162 – 95	Sweden	EU118656	-
P. subserialis (Bourdot & Galzin) Donk	JSP 01–10	Brazil	KR093857	-
P. subserialis	CY097	USA	HQ607954	-
P. subserialis	UFMGCB 2216	Brazil	HM997135	-
P. subserialis	UFMGCB 1883	Brazil	HQ377286	-
P. subserialis	KRT Iso 21	USA	MN430941	-
P. subserialis	HHB-9768	USA	KP135343	-
P. subserialis	PCT.28	Colombia (?)	HQ248219	-
P. subserialis	HHB-5324	USA	AB084620	-

Species	Voucher/Locality	Locality	GenBank Access Number	
			ITS	LSU
P. subserialis	CK463	USA	MH474313	MH483585
P. subserialis	CBS 211.54	France	MH857296	MH868828
P. subserialis	GB-240	Sweden	AY219365	-
P. subserialis	V2EF16a	France	KT692553	-
P. subserialis	FBCC426	Finland	LN611120	-
P. subserialis	6829 (PUN)	India	KP715568	-
P. subserialis	PV352i	Ecuador	MH003356	-
P. subserialis	LSU0936	USA	MT000447	-
P. subserialis	BRPCT8	China	MT658054	-
P. subserialis	WZ-325	China	MN856437	-
P. subserialis	WZ-245	China	MN856367	-
P. subserialis	WZ-238	China	MN856360	-
P. subserialis	WZ-90	China	MN856249	-
P. subserialis	-	Portugal	FJ791134	-
P. tremellosa (Schrad.) Nakasone & Burds.	KUC20121123	South Korea	KJ668481	KJ668334
P. tremellosa	CBS 217.56	France	MH857589	MH869138
Phlebiporia bubalina Jia J. Chen, B.K. Cui & Y.C. Dai (Type)	Dai 13168	China	KC782526	KC782528
Phl. bubalina	Dai 15231	China	KU598876	KU598881
Sarcodontia crocea (Schwein.) Kotl.	BRNM:761841	Czech Republic	KX831471	KX831473
Sarcodontia crocea	BRNM:721609	Czech Republic	KX831470	KX831472
Scopuloides sp.	FP-150473	USA	KP135355	-
S. hydnoides (Cooke & Massee) Hjortstam & Ryvarden	KHL11916	Sweden	EU118665	EU118665
S. hydnoides	FBCC423	Finland	LN611119	LN611119
S. rimosa (Cooke) Jülich	HHB-7042	USA	KP135350	KP135282

Species	Voucher/Locality	Locality	GenBank Access Number	
			ITS	LSU
S. rimosa	11G092	South Korea	LC387824	MK158344
S. rimosa	RLG-5104	USA	KP135351	KP135283
Uncultured fungus	CMH524	USA	KF800613	-

Figures

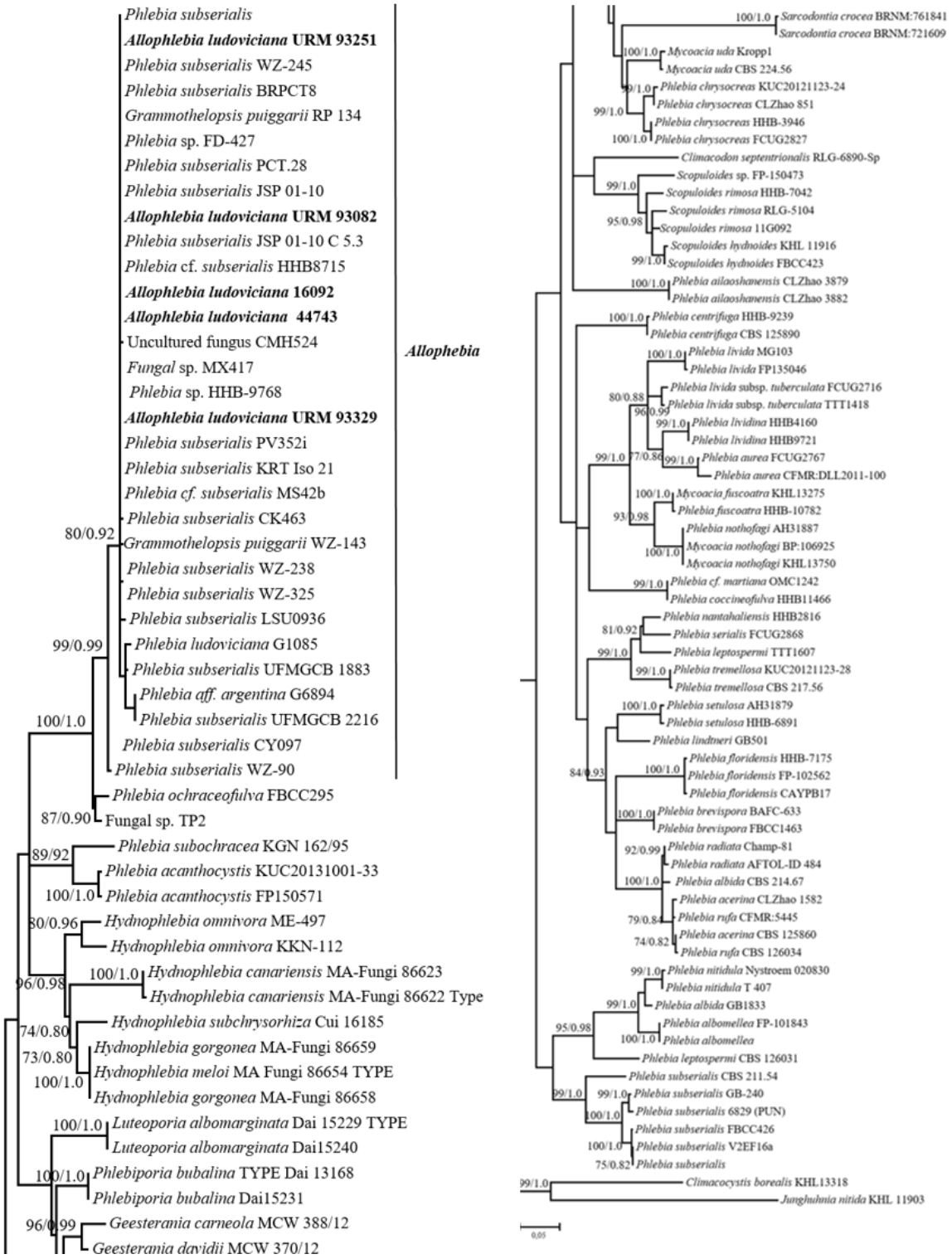

Figure 1

Phylogenetic reconstruction of sequences of Meruliaceae specimens inferred from a combined dataset of ITS and nLSU. Parsimony bootstrap generated by ML (higher than 60%) and BA posterior probabilities (higher than 0.70) are showed along the branches, respectively. The sequences in bold were generated in this study

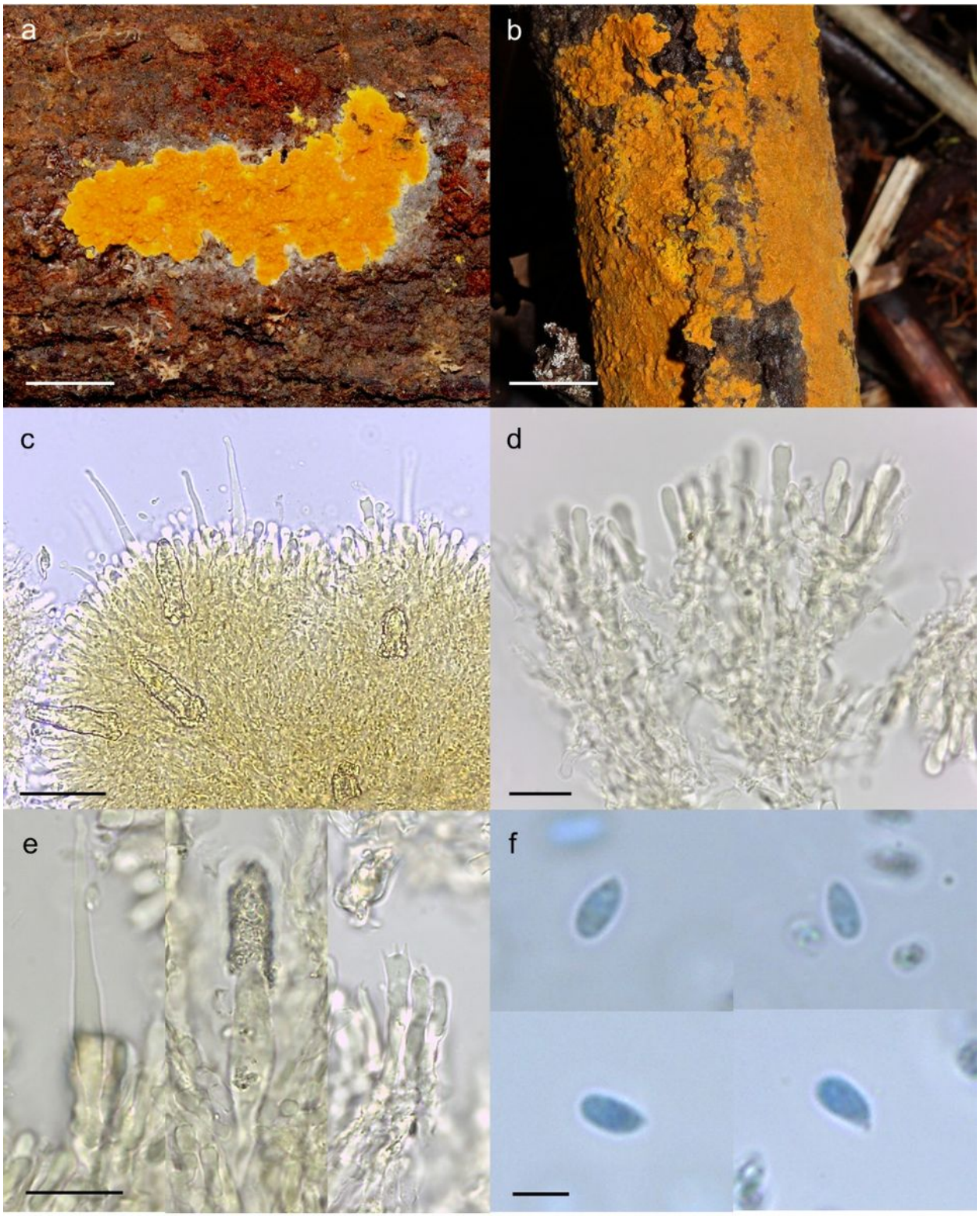

Figure 2

Allophlebia ludoviciana. a-b. Fresh specimens (a. URM 93249, b. URM 93251); c. Leptocystidia; d. Basidia; e. Metuloids; f. Basidiospores. Bars: a, b, c = 1 cm; c = 50 µm; e, f = 20 µm