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Fulvifomes wrightii (*Hymenochaetales*), a new species related to *F. robiniae* from Argentina and Paraguay

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Abstract: Morphological revision and phylogenetic analysis based on nITS and nLSU of specimens previously considered to be a species related to *Fulvifomes robiniae* from South America revealed a new species of *Fulvifomes*, *i.e.* *Fulvifomes wrightii*. It grows on *Libidibia paraguariensis*, a *Fabaceae* distributed in the Chaco Region. The new species is characterised by a perennial, ungulate basidioma with a rimose pileal surface, 6–7 pores per mm, a homogenous context, indistinct stratified tubes and abundant crystals in tube trama and hymenia. Illustrations, taxonomic analyses and a key to the *Fulvifomes* species recorded from the Americas is provided.

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INTRODUCTION

Fulvifomes (Murrill 1914) is characterised by perennial basidiomata with or without a crust on the pileal surface, a monomitic to dimitic hyphal system, with or without dark lines in the context, and subglobose to ellipsoid, yellowish basidiospores, occasionally with a flattened side that turn darker in KOH solution (Zhou 2014, Salvador-Montoya *et al.* 2018, 2022). For many decades the genus was considered a synonym of *Phellinus* (*Phellinus s.l.*) or a subgenus of *Phellinus* (Dai 1999). However, molecular studies confirmed that *Fulvifomes* is a distinct taxon (Wagner & Fisher 2001, 2002). Wagner & Fischer (2002), Larsson *et al*. (2006) and Dai (2010) showed that *Fulvifomes* is closely related to *Aurificaria luteoumbrina* in their phylogenetic inferences. Currently, *Aurificaria* is considered a synonym of *Fulvifomes* (Zhou 2014). Ecologically, *Fulvifomes* includes species that grow on dead trunks and living angiosperm trees in temperate and tropical regions (Salvador-Montoya *et al*. 2018, Olou *et al.* 2019, Wu *et al.* 2022).

Fulvifomes robiniae (type species of the genus) is considered a parasitic polypore of *Robinia* species (recurrent host is *R. pseudoacacia*) in temperate North America (Salvador-Montoya *et al.* 2018). This species was related to *Fulvifomes rimosus* (Kotlaba & Pouzar 1978). However, Kotlaba & Pouzar (1978, 1979) showed *F. robiniae* and *F. rimosus* to exhibit morphological differences in the shape of pileal and pore surfaces, as well as in the size of basidiospores. Furthermore, *F. robiniae* was initially considered to have a variable morphology and wide geographic distribution in North and Central America (USA, Bahamas, Puerto Rico and Jamaica) (Kotlaba & Pouzar 1978, 1979, Gilbertson & Ryvarden 1987). Nevertheless, based on morphological, ecological and molecular data, Salvador-Montoya *et al.* (2018, 2022) have shown that specimens resembling *F. robiniae* from different parts of the Americas correspond to different entities.

During surveys in Paraguay and Argentina, specimens that resemble *F. robiniae* were collected in the Chaco Region of both countries. The aim of the present study was to taxonomically establish and describe a new species within the *F. robiniae* complex in the Chaco region in South America.

MATERIAL AND METHODS

Morphological studies

The specimens studied are deposited in the Fungarium of the Centro de Investigación y Extensión Forestal Andino Patagónico (HCFC) and Fungarium CTES. Morphological and microscopic procedures follow Robledo & Urcelay (2009). Colours were determined following Kornerup & Wanscher (1978). Spores were measured from sections from the tubes of basidiomata. For the spore measurements ImageJ software was used (González 2018). The following abbreviations were used: KOH = 5 % potassium hydroxide, IKI = Melzer's reagent, IKI– = neither amyloid nor dextrinoid, CB = cyanophilous, CB– = acyanophilous, L = mean spore length (arithmetic mean of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in L/W ratios among specimens studied, n = number of spores

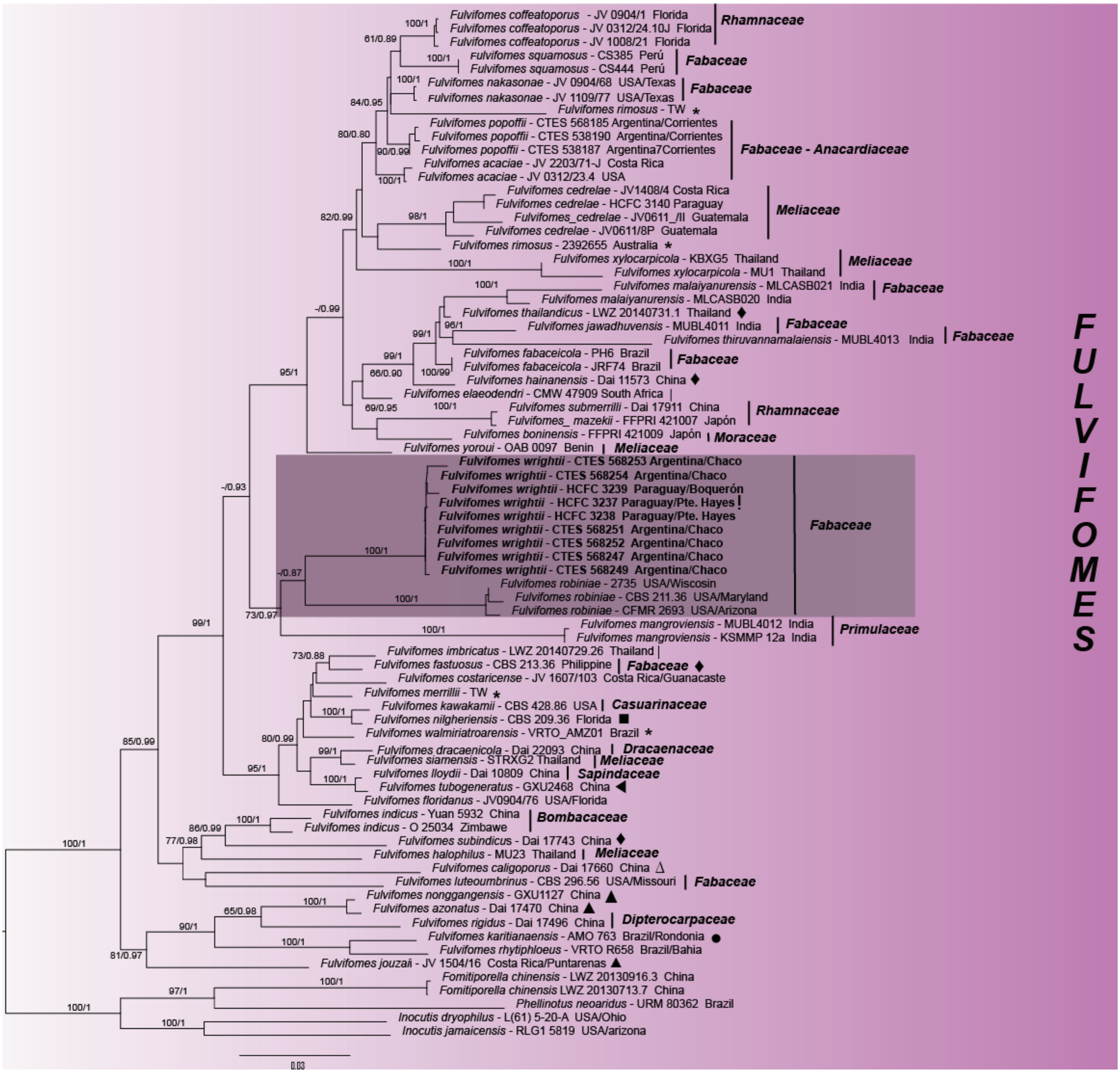

Fig. 1. Maximun likelihood (ML) tree of *Fulvifomes* based on dataset of ITS and nLSU sequences. Bayesian posterior probability above 0.80 and bootstrap values above 60 % are shown. Species studied in this work are in bold and the different substrates on which the species in the genus grow (! = type material; ♦ = angiosperm; ▲ = dead angiosperm; ◀ = living angiosperm; *= decaying wood; ● =dead deciduous wood; ■ dead trunk; Δ = unknown).

measured from a given number of specimens. The maps were prepared with QGIS 3.12 "Bucuresti" free software (https://www.qgis.org/en/site/).

Isolates

A fungal culture was obtained from the basidiomata by transferring small pieces from the context or tubes to Petri dishes containing 2 % malt extract agar (MEA) (Nobles 1965, Rajchenberg & Greslebin 1995) and deposited in the Culture Collection of Centro de Investigación y Extensión Forestal Andino Patagónico (CIEFAPcc).

DNA extraction, PCR amplification and sequencing

Extraction of total genomic DNA from dried basidiomata and culture followed the protocol of Doyle & Doyle (1990) modified by Tamari & Hinkley (2016). Primers pairs LR0R, LR5 and LR7 (Vilgalys & Hester 1990) were used to amplify nLSU sequences, while the ITS region was amplified using primers ITS1 and ITS4 (White *et al.* 1990). The PCR procedure for ITS and LSU followed Ji *et al.* (2017). For ITS the amplification was: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 54 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. For nLSU the amplification was: denaturation at 94 °C for 1 min, followed by 35 cycles of 94 °C for 30 s, 50 °C for 1 min and 72 °C for 1.5 min, with a final extension of 72 °C for 10 min. The PCR product was purified and sequenced in Macrogen Inc. (Republic of Korea).

Phylogenetic analyses

The new sequences obtained from each region were assembled and manually edited using the Bioedit program, Geneious v. 6.1.8 and CromasPro DNA Sequencing Software (Hall 1999, Treves 2010, Kearse *et al.* 2012). New nITS and nLSU sequences were added to sequences obtained from GenBank (NCBI) (Table 1). The sequences used in this work represent species endorsed by Ji *et al.* (2017), Salvador-Montoya *et al*. (2018, 2022) and Olou *et al*. (2019).

The dataset was aligned with Guidance (Sela *et al.* 2015), under L-INS-I criteria for nLSU region and Q-INS-I for ITS, then manually inspected and edited using the MEGA v. 6 program (Tamura *et al.* 2013) when needed. Potential ambiguously aligned segments were detected with the software Gblock v. 0.91b (Castresana 2000) for the nITS region. The combined dataset was constructed combining the nLSU and nITS regions and was subdivided into four data partitions: ITS1, 5.8S, ITS2 and LSU. *Phellinotus neoaridus, Fomitiporella chinensis*, *Inocutis dryophilus* and *Inonotus hispidus* were used as outgroups for phylogenetic inferences, based on works performed by Salvador-Montoya *et al.* (2018), Pildain *et al.* (2018) and Olou *et al*. (2019).

The best evolutionary model was selected with AIC (Akaike Information Criterion) with the jModelTest2 v. 1.6 on XEDE program in CIPRESS online (Darriba *et al.* 2012). Maximum likelihood (ML) and Bayesian inference (BI) were employed to perform phylogenetic analysis of the final combined dataset. Maximum likelihood was conducted with RaxMLv. 8.1 program (Stamatakis 2014) to find the best score trees with GTRGAMMA model for the single marker and the data set. The analysis first involved 1 000 independent ML searches each one starting from one randomised stepwise addition parsimony tree. The BI analysis was carried out in the Mr.Bayes v. 3.2.6 program (Ronquist & Huelsenbeck 2003) with two independent runs, each one starting from random trees with four independent simultaneous chains. A total of 8 000 000 million generations were made in total, sampling a tree every 1000 generations. The final alignment were deposited in TreeBASE (http://purl.org/phylo/treebase/phylows/study/TB2:S30336).

RESULTS

Molecular phylogeny

The final combined database (28S + ITS1 + 5.8S + ITS2), had 68 sequences (including the new sequences), resulting in a total of 1 995 characters of which 628 were constant. The Jmodeltest results indicated that the best evolutionary model for each partition was TIM2+I+G, TrN+G, K80+I and TIM3+G for LSU, ITS1, 5.8S, ITS2, respectively.

The phylogenetic inferences based on the combined dataset showed that *Fulvifomes* was recovered as monophyletic (BS = 100/BPP = 1). Within *Fulvifomes*, the sequences of the new species formed a monophyletic group (BS = -/BPP = 0.87) closely related to *F. robiniae* (BS = 100/BPP = 1), but forming a distinct linage here named as *Fulvifomes wrightii* (Fig. 1).

Taxonomy

Fulvifomes wrightii M. Martínez, Salvador-Montoya & Rajchenb., ***sp. nov.*** MycoBank MB 848322. Figs 2, 3.

Typus: **Paraguay**, Pte. Hayes, Chaco Húmedo, residence "Frigorífico Concepción SA". Coord.: 23°26'39'' S57°27'54''W, on living stems of *Libidibia paraguariensis*, 18 May 2019, *M. Martínez, M. Vera & C. Insfrán, N° 415A,* CIEFAPcc 707 (**holotype** HCFC 3237).

Diagnosis: *Basidioma* perennial, ungulate, pileal surface rimose, dark gray, pore surface flat to convex, 6–7 pores/mm. *Context* homogenous. *Hyphal system* monomitic in the context and dimitic in tube trama. *Hymenia* with abundant crystals. *Basidiospores* subglobose to broadly ellipsoidal with a flattened side, (4.5–)5–6 × (4–)4.5–5 µm, thick-walled, yellow to brown in water, turning darker in KOH solution, on living trees of *Libidibia paraguariensis*.

Etymology: In honour of Dr. Jorge Eduardo Wright for his contributions to Paraguayan mycology.

Description: *Basidiomata* perennial, sessile, solitary, woody hard. *Pilei* dimidiate, ungulate to slightly applanate, projecting up to 100–143 mm long, 48–81 mm wide and 30–145 mm thick at the base. *Pileal surface* with brown tomentose zones (5E6 – 5F7), soon glabrous and black, dark grey (1F1) to greyish green (1C2 – 1D2), in juvenile specimens concentrically furrowed with small cracks, in the mature basidioma the pileal surface becoming radially to concentrically rimose, glabrous, margin slightly acute to obtuse, entire, brown reddish (6C7) to dark brown (6FA). *Hymenophore* poroid, flat to convex, brown (5E7 – 5E4), dark brown (6F8) to greyish brown (5E3); *pores* round to regular (5)6–7(8) per mm, (90–)100–190(–200) µm diam, dissepiments entire, (30–)40–170(–190) µm thick. *Tubes* indistinctly stratified, with whitish mycelial cords filling the more developed tubes, up to 105 mm long, brown (6E7). *Context* homogenous, golden brown (5D7), woody hard, up to 5–8 mm in juvenile specimen, almost lacking when mature. In KOH the context becomes reddish brown and, the tubes, dark brown.

Hyphal system monomitic in the context and dimitic in tube trama; generative hyphae thin- to thick-walled, branched, regularly simple-septate, (1.5–)2.5–4.5(–6) µm diam; *trama* with unbranched skeletal hyphae, 90–526 × (3–)3.5–4 um, lumen almost solid, tapering to the apex with 2–4 adventitious septa. *Generative hyphae* thin- to thick-walled, covered with small crystals, 1.5–4 µm diam, branched and simple septate. *Basidiospores* (4.5–)5–6 × (4–)4.5–5 µm, (L = 5.4 µm, W = 4.6 µm) Q = 1.10–1.25 (Q av. = 1.18), broadly ellipsoid to subglobose, with a flattened side, smooth and thick-walled, yellow to brown in water, dark brown in KOH, IKI–, CB–. Rhomboid and quadrangular crystals present in hymenia. *Basidia* and *cystidia* not observed.

Cultural characters: Growth slow, 0.5–3.5 cm in MEA in 25 d, at first mat somewhat compacted, then cottony, especially the central area, to somewhat homogeneously appressed, scant fluffy aerial mycelium to somewhat cottony present, pale yellow at first, then becoming deep yellow, margin irregular. Aerial hyphae composed of dominant generative hyphae, 1–4 µm diam, frequently branched, thickened in some sections and

Table 1. List of species, localities, sources and GenBank accession numbers of taxa used in this study.

Species	Geographic Origin	Collection Reference	Substrate	GenBank accession number	
Fulvifomes azonatus	China/Yunnan	Dai 17470	Angiosperm	MH390395	MH390418
F. acaciae	Costa Rica	JV 2203/71-J	*Acacia* sp.	OP828596	OP828594
	USA	JV 0312/23.4	*Acacia* sp.	OP828597	OP828595
F. boninensis	Japón	FFPRI421009	*Morus boninensis*	LC315777	LC315786
F. caligoporus	China/Hainan	Dai 17660	On living angiosperm tree	MH390391	MH390421
F. cedrelae (as *F. centroamericanus*)	Guatemala	JV 0611/III	On living angiosperm tree	KX960764	KX960763
	Guatemala	JV 0611/8P	On living angiosperm tree	–	KX960757
	Costa Rica	JV 1408/4	On living angiosperm tree	KX960768	–
F. costaricense	Costa Rica/Guanacaste	JV 1607/103-J	Angiosperm	MH390386	MH390414
F. dracaenicola	China/Hainan	Dai 22093	*Dracaena cambodiana*	MW559804	MW559799
F. elaeodendri	South Africa	CMW 47909	*Elaeodendron croceum*	MH599132	MH599096
F. fastuosus	Philippines	CBS 213.36	*Gliricidia sepium*	AY059057	AY558615
	Thailand	LWZ 20140801-1	*Angiosperm*	KR905669	KR905675
F. floridanus	USA/Florida	JV 0904/76	*Lysiloma latisiliqua*	MH390388	MH390424
F. fabaceicola	Brazil/Pernambuco	JRF 74	–	MH048087	MH048097
	Brazil/Pernambuco	PH 6	–	MH048086	MH048096
F. fastuosus	Philippines	CBS 213.36	*Gliricidia sepium*	AY059057	AY558615
F. hainanensis	China	Dai 11573	*Angiosperm*	JX866779	KC879263
F. halophilus	Thailand	MU23	*Xylocarpus granatum*	JX104740	JX104693
F. imbricatus	Thailand	LWZ 20140729-26	*Angiosperm*	KR905671	KR905679
F. indicus	China	Yuan 5932	*Bombax ceiba*	JX866777	KC879261
	Zimbabwe	O 25034	Unknown	KC879259	KC879262
F. jouzaii	Costa Rica/Puntarenas	JV 1504/16-J	Angiosperm	MH390400	MH390425
F. jawadhuvensis	India	MUBL4011	*Albizia amara*	MW048886	MW040079
F. coffeatoporus	USA/Florida	JV0904/1	*Krugiodendron ferreum*	KX960765	KX960762
	USA/Florida	JV0312/24.10J	*K. ferreum*	KX960766	KX960760
	USA/Florida	JV1008/21	*K. ferreum*	KX960767	KX960761
F. karitianaensis	Brazil/Rondonia	AMO 763	–	MH048081	MH048091
F. kawakamii	USA	CBS 428.86	*Casuarina equisetifolia*	AY059028	–
F. merrillii	Taiwan	–	Unknown	JX484002	JX484013
F. mangroviensis	India	MUBL4012	*Aegiceras corniculatum*	MW048909,	MW040083
	India	KSM-MP12a	*A. corniculatum*	OM897221	OM897222
F. malaiyanurensis	India	CAL 1618	*Tamarindus indica*	MW048883	MF155651
F. nakasoneae	JV 0904/68	USA/Florida	Angiosperm	MH390373	MH390408
	JV 1109/77	USA/Texas	*Condalia hookeri*	MH390374	MH390409
F. nilgheriensis	USA	CBS 209.36	On dead deciduous wood	AY059023	AY558633
F. nonggangensis	China/Guangxi	GXU 1127	Angiosperm	MT571502	MT571504
F. popoffii	Argentina/Corrientes	CTES 568185	*Peltophorum dubium*	ON754378	ON754383
	Argentina/Corrientes	CTES 568187	*P. dubium*	ON754377	–
	Argentina/Corrientes	CTES 568190	*Schinopsis balansae*	ON754379	ON754384
	Argentina/Corrientes	CTES 568186	*P. dubium*	ON754376	ON754382
F. rhytiphloeus	Brazil/Bahia	VRTOR658	–	MT906624	MT908357
F. rigidus	China/Yunnan	Dai 17496	*Shorea chinensis*	MH390398	MH390432
F. rimosus	Taiwan	–	Unknown	JX484003	JX484016
	Australia	2392655	Unknown	–	MH628255
F. robiniae	USA/Maryland	CBS 211.36	*Robinia pseudoacacia*	AY059038	AY558646
	USA/Arizona	CFMR 2693	*R. neomexicana*	KX065995	KX065961

Table 1. (Continued).

Species	Geographic Origin	Collection Reference	Substrate	GenBank accession number	
	USA/Wisconsin	CFMR 2735	*R. pseudoacacia*	KX065996	KX065962
F. siamensis	Thailand	STRXG2	*Xylocarpus granatum*	JX104755	JX104708
F. squamosus	Peru/Piura	USM 258349	*Acacia macracantha*	MF479264	MF479269
	Peru/Piura	USM 258361	*A. macracantha*	MF479266	MF479267
F. subindicus	China/Hainan	Dai 17743	Angiosperm	MH390393	MH390435
F. submerrillii	China/Hubei	Dai 17911	On angiosperm stump	MH390371	MH390405
Fulvifomes sp.	Australia	MEL 2382673	Unknown	KP013036	KP013036
F. thailandicus	Thailand	LWZ 20140731-1	Angiosperm	KR905665	KR905672
F. tubogeneratus	China/Guangxi	GXU 2468	On dead trunk	MT580800	MT580805
F.thiruvannamalaiensis	India	MUBL4013	*Albizia amara*	MZ221600	MZ221598
F. xylocarpicola	Thailand	KBXG5	*Xylocarpus granatum*	JX104716	JX104669
	Thailand	MU1	*X. granatum*	JX104718	JX104671
F. yoroui	Benin/Collines	OAB 0097	*Pseudocedrela kotschyi*	MN017120	MN017126
F. wrightii	Paraguay/Pte.Hayes	HCFC 3237	*Libidibia paraguariensis*	OQ924554	OQ807188
	Paraguay/Pte.Hayes	HCFC 3238	*L. paraguariensis*	OQ924556	OQ807189
	Paraguay/Boquerón	HCFC 3239	*L. paraguariensis*	OQ924555	–
	Argentina/Chaco	CTES 568247	*L. paraguariensis*	OQ924562	OQ807190
	Argentina/Chaco	CTES 568252	*L. paraguariensis*	OQ924561	OQ807191
	Argentina/Chaco	CTES 568254	*L. paraguariensis*	OQ924557	OQ807195
	Argentina/Chaco	CTES 568251	*L. paraguariensis*	OQ924560	OQ807192
	Argentina/Chaco	CTES 568249	*L. paraguariensis*	OQ924559	OQ807193
	Argentina/Chaco	CTES 568253	*L. paraguariensis*	OQ924558	OQ807194
F. waimiriatroarensis	Brazil/Amazonas	VTROAMZ01	Unknown	OK086356	OK086370
Fomitiporia chinensis	China	LWZ 20130713-7	Deciduous wood	KJ787808	KJ787817
F. chinensis	China	LWZ 20130916-3	Deciduous wood	KJ787809	KJ787818
Inonotus hispidus	Spain	S45	*Vitis vinifera*	EU282484	EU282482
I. porrectus	USA/Missouri	CBS 296.56	*Gleditschia triacanthos*	AY059051	AY558603
Inocutis dryophilus	USA/Ohio	L(61)5-20-A	*Quercus prinus*	AM269846	AM269783
I. jamaicensis	USA/Arizona	RLG 15819	*Q. arizonica*	KY907703	–
Phellinotus neoaridus	Brazil/Pernambuco	URM 80362	*Caesalpiania sp.*	KM211286	KM211294

with some cytoplasmic contents, regularly septate. Fibre hyphae present, not dominant, little branched, 2.5–3.5 µm diam, lumen almost solid. Chlamydospores abundant, globose, ellipsoid, terminal and intercalated 3.7–11.9 × 4.7– 9.9 µm. The hyphae are pale yellow in water, turning reddish on contact with KOH (Fig. 4).

Habitat and Distribution: Basidiomata are found on living trees of *L. paraguariensis* (*Fabaceae*). This polypore is distributed in the Chaco region of Paraguay and Argentina (Fig. 5).

Specimens examined: **Argentina,** Chaco, Presidencia de la Plaza, Capitán Solari, Parque Nacional Chaco, on living tree of *L. paraguariensis*, 29 Mar. 1990, *O.F. Popoff* 693 (CTES 568261); *ibid*., on living tree of *L. paraguariensis*, 17 Sep. 2016, *C.A. Salvador-Montoya et al*. 715, 717 and 716 (CTES 568247, 568254 and 568252, respectively); *ibid*., on living tree of *L. paraguariensis*, 18 Sep. 2016, *C.A. Salvador-Montoya & O.F. Popoff* 723, 724, 725, 726 and 727 (CTES 568250, 568249, 568253, 568251, 568248, respectively); *ibid*., on living tree of *L. paraguariensis* (*as Caesalpinia melanocarpa*), Jun. 1947, *Wright, C. Iaconis & J.A. Stevenson* (BACF 53440 as *Fomes dependens*); *ibid*., Apr. 1949, *Martinoli* (BACF 53441, as *Fomes dependens*). **Paraguay,** Pte. Hayes, Chaco Húmedo, residence "Frigorífico Concepción SA", 23°26'39''S 57°27'54''W, on living tree of *L. paraguariensis*, 18 May 2019, *M. Martínez, M. Vera & C. Insfran* 415A (HCFC 3237, **holotype**); *ibid*., 18 May 2019, M. *Martínez, M. Vera & C. Insfran* 415B (HCFC 3238); *ibid*., 16 Nov. 2018, M. *Martínez, B. De Madrignac & Cristian* 393 (HCFC 3239).

Additional specimens examined: *Fulvifomes robiniae*: EE. UU. Ohio #223 (*ex* NY, **lectotype** *fide* Lowe) (BACF 27561, **isotype**). *Fulvifomes aff. robiniae*: **Tayikistan**, Tadzhik SSR, Nurek, on living *Pistacia vera*, 25 Apr. 1980, *E. Parmasto* 102813 (BAFC 28043, as *Phellinus robiniae*).

Fig. 2. *Fulvifomes wrightii sp. nov*. **A–I.** Basidiomata: A. CTES 568247; B. CTES 568248; C. CTES 568252; D. CTES 568250; E. CTES 568251; F. CTES 568249; G. CTES 568254; H. CTES 568253; I. HCFC 3238; J. HCFC 3237 (holotype). **K, L.** Pore surface. **M–O.** Basidiospores: M. In water; N. In Melzer's reagent; O. In 5 % KOH. Scale bars: A–D = 2cm; E, F = 1 cm; G = 5 cm; H = 2 cm; I = 5 cm; J = 1cm; K, L = 3 cm; M–O = 5 µm.

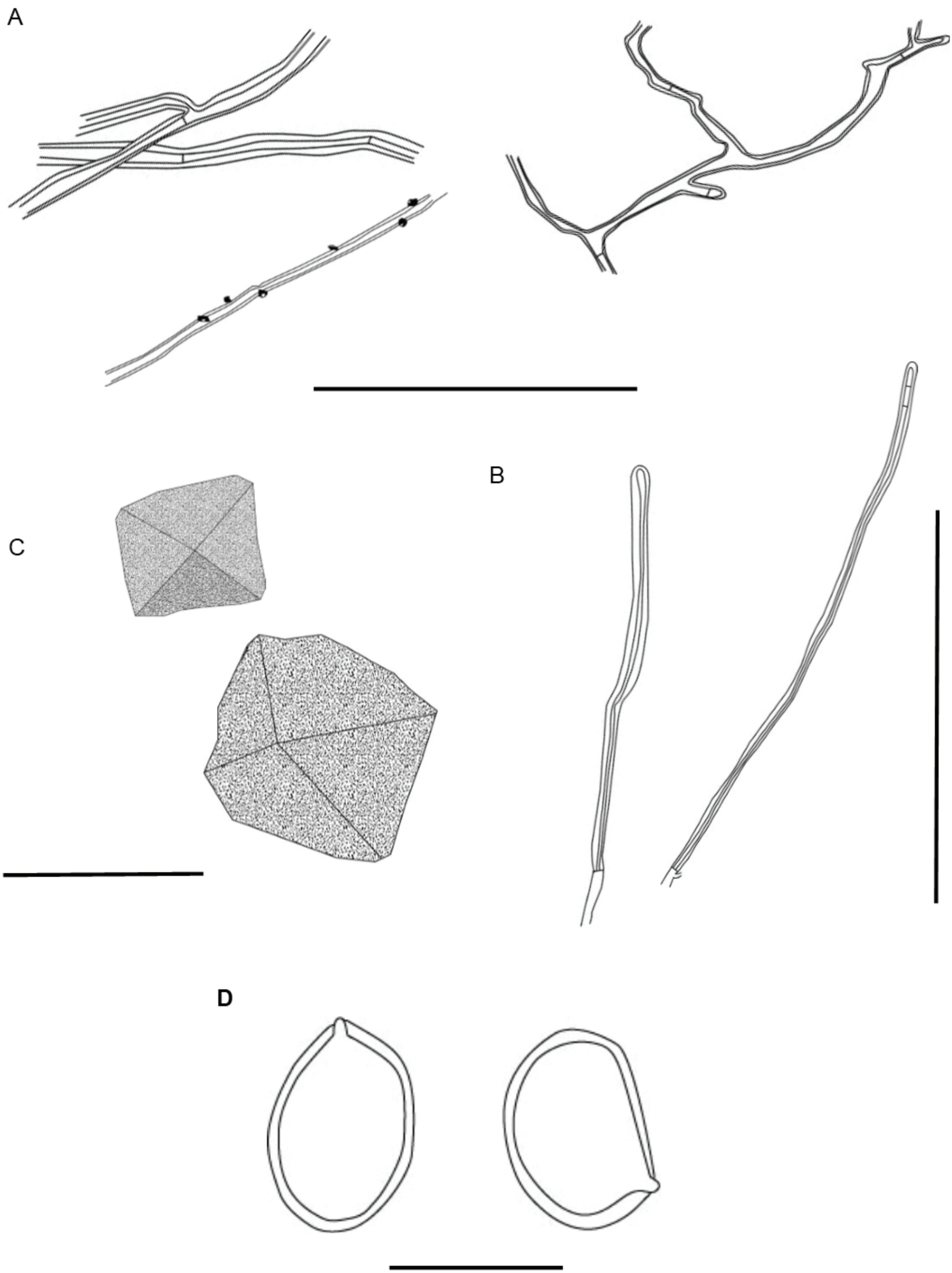

Fig. 3. Microscopical features of *Fulvifomes wrightii*. **A.** Thin- to thick-walled generative hyphae of the context. **B.** Skeletal hyphae from the tubes. **C.** Crystals. **D.** Basidiospores. Scale bars: A = 100 µm; B = 100 µm; C = 15 µm; D = 10 µm.

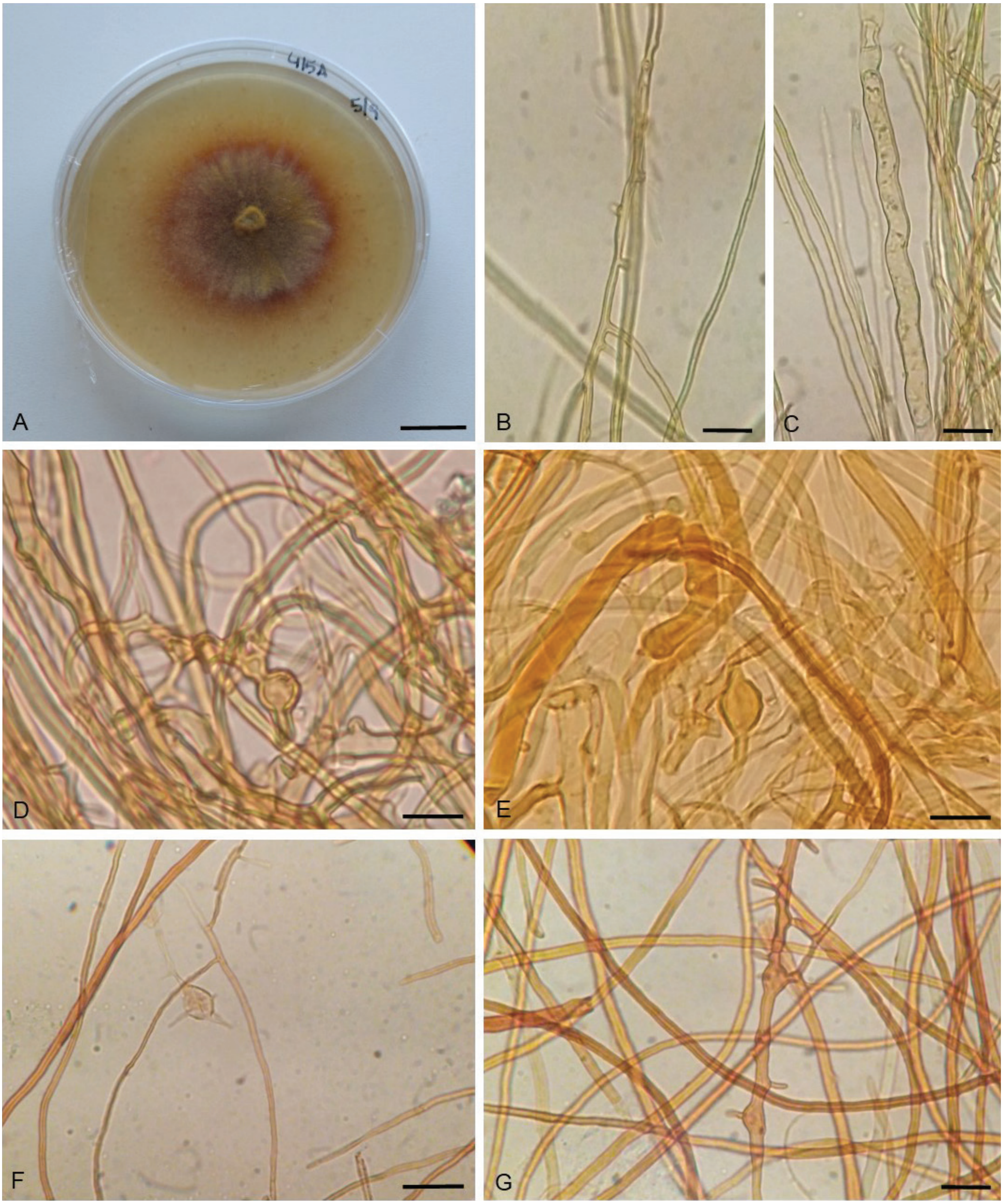

Fig. 4. *Fulvifomes wrightii.* Macro- and microscopic cultural features. **A.** Mycelial mat, **B, C.** Generative hyphae, in water. **D–F.** Ellipsoid and globose chlamydospores, in KOH. **G.** Fiber hyphae, in KOH. Scale bars: A = 2 cm; B, C = 5 µm; D–F = 15 µm; G = 5 µm.

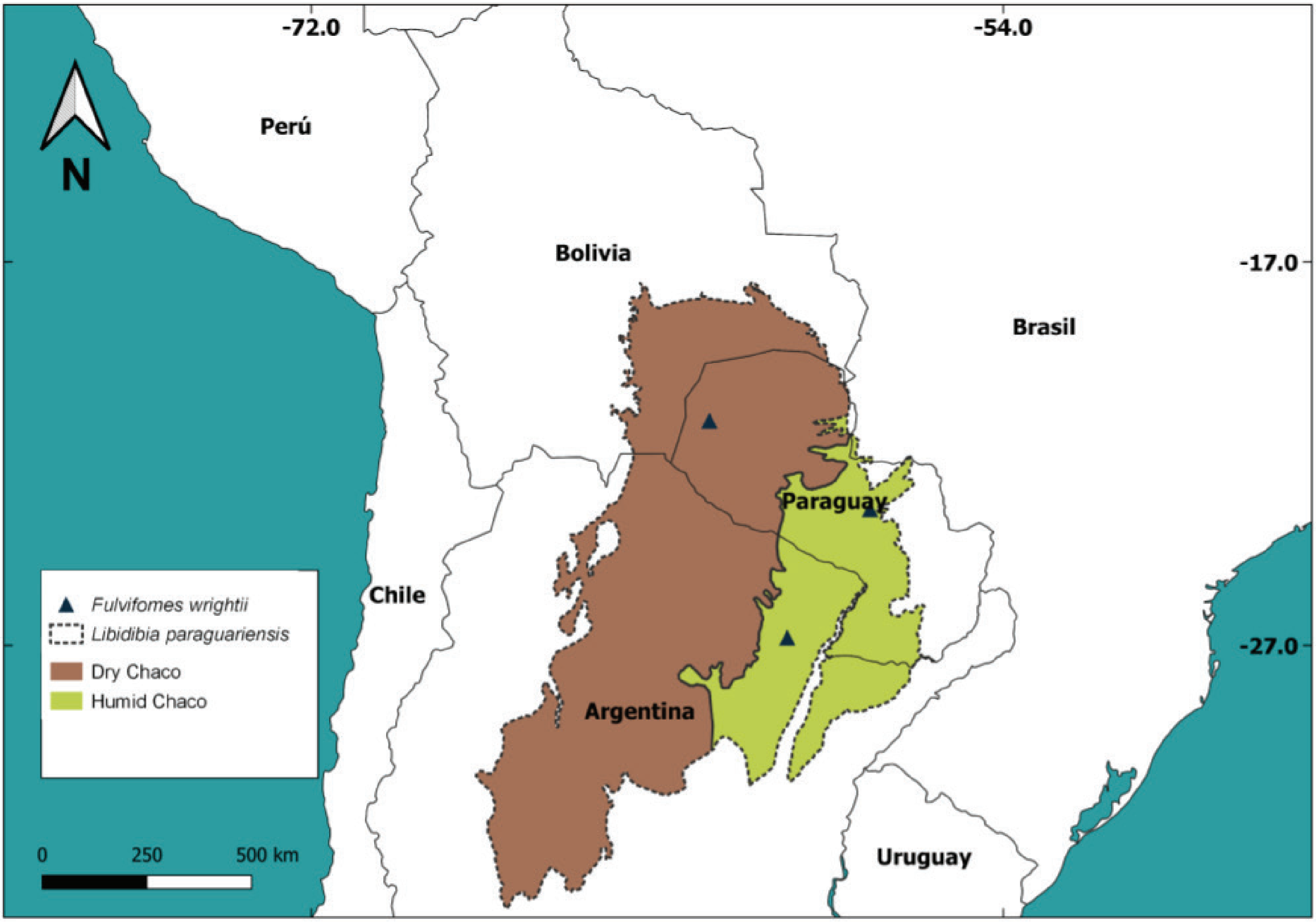

Fig. 5. Map of the geographic distribution of specimens of *Fulvifomes wrightii* and the host *Libidibia paraguariensis* in subtropical region (the black lines represent the estimated distribution of the host).

DISCUSSION

Fulvifomes wrightii is characterised by its perennial ungulate basidiomata with rimose and dark grey pileal surface, a convex pore surface with 6–7 pores per mm, indistinctly stratified tubes, the homogenous context, a dimitic hyphal system that is restricted to the tubes (*viz*., monomitc in the context), and hymenia and tube trama with abundant crystals in well-developed specimens (Fig. 3). *In vitro*, the culture has chlamydospores (Fig. 4).

Fulvifomes wrightii resembles *Fulvifomes robiniae* by the shape of basidiomata and basidiospores. However, *F. robiniae* has a cracked and dark brown pileal surface, a flat pore surface with 5–6 pores per mm, and lacks crystals in the hymenium (Gilbertson & Ryvarden 1987, Salvador-Montoya *et al*. 2018). Additionally, *F. robiniae* has a geographic distribution in temperate zones of the USA, growing mainly on living trees of *Robinia pseudoacacia* (Kotlaba & Pouzar 1978, Salvador-Montoya *et al.* 2018), a *Fabaceae* that is native in North America (IPNI 2022). Outside the Americas, *R. pseudoacacia* is a naturalised and invasive species in the temperate regions of Europe, as well as in Asia and Southern Africa (Capdevila-Argüelles *et al.* 2011). Regarding *F. wrightii*, it is found in the subtropical region of South America, growing on living trees of *L. paraguariensis* [common name is "Guayacán", considered the South American ebony tree according to Aronson & Toledo (1992)]. *Libidibia paraguariensis* is considered endemic to the Chaco region and is distributed in north and central Argentina, southern Bolivia, Brazil (specifically in Matto Grosso do Sul state), Paraguay (Giménez *et al.* 2017). According to Mereles (2005), *L. paraguariensis* appears in xerophytic forests in the Chaco region, and grows in structured, floodable and asphyxiated soils. Nevertheless, Imaña-Encinas *et al*. (2019) mention it as a tree species of the humid Chaco, conditioned by topographic gradients and floods.

Fulvifomes wrightii also resembles *F. cedrelae, F. rimosus*, *F. popoffii* and *Phellinus chaquensis*. Nevertheless, *F. cedrelae* differs by smaller basidiospores (5–5.5 × 4–4.5 µm) and by growing on *Meliaceae* where it induces a heart-rot (*e.g. Cedrela fissilis, C. odorata* and *Swietenia mahagoni*) (Salvador-Montoya *et al.* 2018, 2022). Regarding *F. rimosus*, it has larger pores (4–5 pores/mm) (Kotlaba & Pouzar 1978). In the case of *F. popoffii*, this species has a rimose pileal surface, a flat pore surface with 5–6 pores/mm and grows on living trees of *Peltophorum dubium* (Salvador-Montoya *et al*. 2022). Finally, *P. chaquensis* differs from *F. wrigthii* by its smaller pores (6–7 pores/mm), presence of hymenial setae and by growing on standing trees of *Astronium balansae*, *L. paraguariensis* and species of *Schinopsis* (Luna *et al.* 2012, Rajchenberg & Robledo 2013, Salvador-Montoya *et al.* 2018).

Key to species of *Fulvifomes* in America

1 Pileal surface rimose[1] 2
1 Pileal surface fissured, cracked or squamulate[2] 9

2 Hyphal system dimitic throughout the basidioma 3
2 Hyphal system monomitic in the context and dimitic in the tubes 4

3 Tubes distinctly stratified, spores cyanophilous, pores 9–10 per mm ..... *F. jouzaii*
3 Tubes indistinctly stratified, spores acyanophilous, pores 3–5 per mm ..... *F. rimosus*

4 Basidioma triquetrous, on *Polygonaceae* ..... *F. minutiporus*
4 Basidioma ungulate, another host 5

5 Pores (5–)6–7(–8) per mm 6
5 Pores 3–4 per mm 8

6 Crystals lacking, context with indistinct dark lines ..... *F. cedrelae*
6 Crystals present in the hymeniun and tubes, context without black lines 7

7 Growing on *Peltophorum dubium* and *Schinopsis balansae* ..... *F. popoffii*
7 Growing on *Libidibia paraguariensis* ..... *F. wrigthii*

8 Tubes stratified, basidiospores ellipsoid ..... *F. fabaceicola*
8 Tubes indistinctly stratified, basidiospores subglobose to globose ..... *F. coffeatoporus*

9 Tubes distinctly stratified, dimitic hyphal system throughout the basidioma 10
9 Tubes indistinctly stratified, dimitic hyphal system restricted to the tubes 11

10 Pores 7–9 per mm ..... *F. rhytiphloeus*
10 Pores 4–7 per mm ..... *F. grenadensis*

11 Context with black lines 12
11 Context without black lines 13

12 Basidiospores ellipsoid, chlamydospores present ..... *F. kawakamii*
12 Basidiospores subglobose, chlamydospores absent ..... *F. costaricense*

13 Pilear surface squamulate, on *Acacia macracantha* ..... *F. squamosus*
13 Pilear surface cracked with crusted or scrupose zone, host different 14

14 Growing on *Robinia pseudoacacia* ..... *F. robiniae*
14 Growing on *Acacia* 15

15 Basidiospores broadly ellipsoidal, 5–6 × 4–5 µm ..... *F. acaciae*
15 Basidiospores ellipsoid, 4–5 × 3–4 µm 16

16 Pileal surface glabrous ..... *F. karitianaensis*
16 Pileal surface velutinate ..... *F. waimiriatroariensis*

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[1]Rimose: having a surface covered with a network of cracks radial-concentrically and small crevices.
[2]Fissured: having long irregularly, narrow cracks or openings.

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