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Tropicoporus drechsleri (Hymenochaetales, Basidiomycota), a new species in the "*Inonotus linteus*" complex from northern Argentina

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Abstract

Morphological revision and phylogenetic analyses, based on nrITS and nrLSU, of specimens previously considered to be member of the "*Inonotus linteus*" species complex from in South America reveal a new species of *Tropicoporus*, here named *T. drechsleri*. It is a parasitic polypore restricted to the seasonally dry tropical forests of subtropical South America. Illustrations, taxonomic analyses and a discussion are presented, and a key to the *Tropicoporus* species in the Neotropics is provided.

Keywords: geographic distribution, host distribution, Hymenochaetaceae, polypore, taxonomy

Introduction

Tropicoporus L.W. Zhou, Y.C. Dai & Sheng H. Wu (2016: 341) (*Hymenochaetaceae* Donk) was segregated from *Inonotus s.l.* to accommodate some species of the "*Inonotus linteus*" complex, being characterized by producing annual to perennial basidiomata with resupinate, effused-reflexed to pileate habit, homogeneous to duplex context, a hyphal system that is dimitic or monomitic in the context and dimitic in the tubes, ellipsoid to subglobose, yellowish, slightly thick to thick-walled basidiospores and hymenial setae (Zhou *et al.* 2016).

According to the literature, there are eleven known species of *Tropicoporus* worldwide, of which *T. cubensis* (Y.C. Dai, Decock & L.W. Zhou) L.W. Zhou & Y.C. Dai (2016: 344) *T. dependens* (Murrill) L.W. Zhou, Y.C. Dai & Vlasák (2016: 344), *T. guanacastensis* L.W. Zhou, Y.C. Dai & Vlasák (2016: 343), *T. linteus* (Berk. & M.A. Curtis) L.W. Zhou & Y.C. Dai (2016: 344), *T. pseudolinteus* (Vlasák & Y.C. Dai) L.W. Zhou, Y.C. Dai & Vlasák (2016: 344), *T. sideroxylicola* (Vlasák & Y.C. Dai) L.W. Zhou, Y.C. Dai & Vlasák (2016: 344), *T. stratificans* G. Coelho & Yurchenko (2016: 147) and *T. tropicalis* (M.J. Larsen & Lombard) L.W. Zhou & Y.C. Dai (2016: 345) have a neotropical distribution, being registered either in tropical or subtropical climatic regions (Tian *et al.* 2013, Vlasák *et al.* 2013, Wu *et al.* 2015, Coelho *et al*. 2016, Zhou *et al.* 2016).

In subtropical South America, only *T. stratificans* and *T. linteus* are recorded to date (Ryvarden & Meijer 2002, Drechsler-Santos *et al.* 2008, Rajchenberg & Robledo 2013, Campos-Santana *et al.* 2015, Coelho *et al.* 2016, Grassi *et al.* 2016). *Tropicoporus linteus s.s.* is based on southern USA and Caribbean specimens, growing on *Quercus sp.* and *Tamarindus indica* L. (1753: 34) (Tian *et al.* 2013). However, southern South American collections with pileate basidiomata, grayish to blackish, cracked to rimose pilear surface, hyphal system varying from monomitic to dimitic, hymenial setae and subglobose to ellipsoid, yellowish, basidiospores have traditionally been identified as *Phellinus linteus* (Berk. & M.A. Curtis) Teng (1963: 762) or *Inonotus linteus* (Berk. & M.A. Curtis) Teixeira (1992: 126), and occur on several plant hosts (Drechsler-Santos *et al.* 2008, Rajchenberg & Robledo 2013, Campos-Santana *et al.* 2015).

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Recently, several studies demonstrated that latitude is strongly correlated with fungal diversity at large geographic scales (Zhou *et al.* 2011, Shi *et al.* 2013, Peay *et al.* 2016, Yahr *et al.* 2016), which is cause to review those specimens identified as *T. linteus* found in the Southern Hemisphere. Also, the literature on parasitic *Hymenochaetaceae* demonstrates that some level of host preference exists, what casts doubt on seemingly generalist taxa such as *T. linteus* (Tian *et al.* 2013 and references therein). In this context, the present study aimed to review the Argentinean collections previously identified as *T. linteus* to further the knowledge on the phylogeny and taxonomy of the "*Inonotus linteus*" complex in subtropical region of South America. This review revealed a new species of *Tropicoporus* which we describe in this paper.

Material & methods

Specimens were collected in the Chaco forests and seasonally dry tropical forests (SDTFs) of northern Argentina (Corrientes and Misiones Provinces) and kept at herbarium CTES. Herbaria acronyms followed Thiers B. (continuously updated).

Morphological studies:—Size, shape, and color of basidiomata (pilear surface, context, tubes and dissepiment) as well as characteristics of the tubes and pore surface (number of tube layers and pores per millimeter) were recorded. Colors were determined following Kornerup & Wanscher (1978). Microscopic examination was performed on freehand sections of specimens mounted in water, 5% potassium hydroxide solution (KOH), and Melzer's reagent (IK) (following Ryvarden 1991). All microscopic measurements (n = 40) and drawings were made in KOH. When giving the size range of the microscopic elements, 5% of the measurements were excluded from each end and are given in parentheses. The following abbreviations are used throughout the text: Q = the ratio of length/ width of basidiospores (Largent *et al.* 1977), L avg. = long average and W avg. = wide average. To describe the hyphal system, sections of tube trama and context of the basidiomata were carefully dissected under a stereomicroscope after incubation in 5 % (v/w) sodium hydroxide solution (NaOH) for 48h at 40°C (see Decock *et al.* 2010), and subsequently examined under optical microscopy.

DNA extraction, PCR and Sequencing:—Extraction of total genomic DNA from dried basidiomata followed the protocol of Doyle & Doyle (1987) modified by Góes-Neto *et al.* (2005). Primer pairs ITS8-F/ITS6-R and LR0R/LR7 (Dentinger *et al.* 2010, Moncalvo *et al.* 2000) were used to amplify the nrITS and nrLSU region, respectively, by a qualitative simplex polymerase chain reaction. Sanger Sequencing was performed with BigDye Terminator v.3.1 Cycle Sequencing Kit (Applied Biosystems, California, USA) following manufacturer procedures using the same primer pair for nrITS and primer pair LR0R/LR5 for nrLSU region. The sequencing was performed at FIOCRUZ-MG (Brazil) and the newly generated sequences and additional sequences downloaded from GenBank are listed in Table 2.

Phylogenetic analyses:—Sequences were manually edited using Geneious v. 6.1.8 (http://www.geneious.com, Kearse *et al.* 2012). New nrITS and nrLSU sequences were joined with sequences retrieved from GenBank (NCBI) (Table 2). The sequences used in this study represented species and genera covered by Wagner & Fischer (2002), Larsson *et al*. (2006), Vlasák *et al.* (2013), Tian *et al.* (2013), Wu *et al.* (2015), Coelho *et al*. (2016), Drechsler-Santos *et al*. (2016) and Zhou *et al.* (2016). Two distinct datasets were constructed: one composed only of nrITS sequences (with 33 specimens) and the other with combined nrITS + nrLSU sequences (with 37 specimens). Both datasets were aligned using MAFFT v.7 (Katoh & Standley, 2013), under the G-INS-i criteria, then manually inspected and edited using MEGA v.6 (Tamura *et al.* 2013). In order to compute the best fit model of nucleotide evolution, the nrITS dataset was subdivided into three data partitions, ITS1, 5.8S and ITS2, while the combined dataset was subdivided in four partitions: ITS1, 5.8S, ITS2 and LSU. *Inonotus compositus* Han C. Wang (2006: 137) and *I. hispidus* (Bull.) P. Karst. (1879: 39) were used as outgroup to the nrITS dataset, while *Fuscoporia senex* (Nees & Mont.) Ghob.-Nejh. (2007: 208) and *F. torulosa* (Pers.) T. Wagner & M. Fisch. (2001: 780) were used as outgroup for the combined dataset.

The best fit model of nucleotide evolution of each partition was selected with AIC (Akaike Information Criterion) using jModelTest2 v.1.6 (Darriba *et al.* 2012, Guindon & Gascuel 2003). Bayesian Inference (BI) and Maximum Likelihood (ML) phylogenetic analyses were applied to both datasets. BI was performed using MrBayes 3.1.2 (Ronquist & Huelsenbeck 2003) with two independent runs, each one beginning from random trees with four simultaneous independent chains, performing 1×10^7 mcmc generations, sampling one tree every 1×10^3 generation. The first 2.5×10^6 sampled trees were discarded as burn-in, while the remaining ones (all sampled after the average standard deviation of split frequencies reached < 0.01) were used to reconstruct a 50 % majority-rule consensus tree and calculate Bayesian posterior probabilities (BPP) of the clades. ML searches were conducted with RAxML-HPC v. 8.2.3 (Stamatakis 2014). The analysis first involved 100 ML searches, each one starting from one randomized stepwise addition parsimony tree, under a GTRGAMMA model, with all other parameters estimated by the software. Only the best scored likelihood tree from all the searches was kept to access the reliability of the nodes. Non-parametric bootstrapping replicates under the same model are computed, allowing the program to halt bootstrapping automatically by the autoMRE option. An additional alignment partition file to force RAxML software to search for a separate evolution model for each partition was used. J Model Test2 v.1.6, Mr Bayes 3.1.2 and RaxML-HPC v. 8.2.3 were used in CIPRES science gateway (Miller *et al.* 2010; http://www.phylo.org/). A node was considered significantly supported if it received a BPP ≥ 0.95 and/or BS ≥ 70%. The final alignment as well the resultant topologies were deposited in TreeBASE (http://purl.org/phylo/treebase/phylows/study/TB2:S21729?x-access-code=be8232d7ad02fca547b0b2b128df26c8&format=html).

TABLE 1. Comparison of morphological and ecological features of species of *Tropicoporus*.

Species	Basidioma	Pilear surface	Pores/ mm	Context	Hyphal System	Setae (µm)	Basidiospores		Substrata
							Size (µm)	Form	
T. boehmeriae (Wu *et al.* 2015)	R		7–9	H	D	13–25 × 5–9	(2–)2.2–2.9(–3) × 2–2.5(–2.7)	SG (-)	*Bo. nivea*
T. cubensis (Tian *et al.* 2013)	P	C	5–6	H	Mc/Dt	27–43 × 5–10	(4.0–)4.2–5.0 × 3.2–4(–4.3)	BE-E (-)	Angiosperm tree
T. dependens (Vlasák *et al.* 2013)	P	C	5–7	H	D	10–30 × 5–8	4–4.8(–5) × (3–)3.4–4	BE (-)	Angiosperm tree
T. drechsleri	P/I	C-Ri	4–5	Dp	Mc/Dt	16–42 × 4.5–9	(4–)4.5–5(–5.5) × (3–)3.5–4(–4.5)	BE-E (+)	*Co. americana*
T. excentrodendri (Zhou *et al.* 2016)	R-EF/I	Z	7–8	Dp	D	20–25 × 5–8	(3.2–)3.4–4(–4.2) × (2.7–)2.9–3.6(–3.8)	BE-SG (-)	*Ex. tonkinense*
T. guanacastensis (Zhou *et al.* 2016)	P	C	7–8	H	Mc/Dt	12–25 × 4–8	4.1–4.9(–5) × (3.1–)3.3–3.9(–4)	E (-)	Angiosperm tree
T. linteus (Tian *et al.* 2013)	P	C	5–7	H	Mc/Dt	22–30 × 4–7	4.8–5.5(–5.7) × (3.8–)3.9–4.6(–4.8)	BE-SG (-)	Angiosperm tree
T. pseudolinteus (Vlasák *et al.* 2013)	P	C-Ri	4–5	H	Mc/Dt	20–34 × 5–7	(4.7–)4.8–5.8(–6) × (3.3–)3.7–4.6(–4.9)	BE (-)	Angiosperm tree
T. rudis (Patouillard 1907; Zhou *et al.* 2016)	P	Ri	> 5	H		15–20 × 5	5 × 4	O	Base trunk
T. sideroxylicola (Vlasák *et al.* 2013)	P	C	2–3	H	D	27–35 × 6–8	6–7(–7.2) × (4.2–)4.4–5.1(–5.5)	BE-E (-)	*Si. obovatum*
T. stratificans (Coelho *et al.* 2016)	R		5–7	H	D	17–30 × 4.5–7	(3.5–)4–5(–6) × (3–)3.5–4(–4.5)	SG-E (-)	Angiosperm tree
T. tropicalis (Larsen & Cobb-Poulle 1990)	R		7–9	H	D	12–14 × 5–7	3–4.5 × 2.5–4	BE-SG	Angiosperm tree

EF = Efused-reflexed; P = Pileate; R = Resupinate; I = Imbricate; Ri = Rimose; C = Cracked; Z = Zonate; H = Homogeneous; Dp = Duplex; Mc/Dt = Monomitic in the context/Dimitic in the tubes; D = Dimitic; SG = Subglobose; BE = Broadly elipsoid; E= Elipsoid; O = Ovoid; Bo. = *Boehmeria*; Co. = *Cordia*; Ex. = *Excentrodendron*; Si. = *Sideroxylon*; (+) positive xantochroic reaction; (-) negative xantochroic reaction.

TABLE 2. List of species and GenBank accession numbers of taxa used in this study.

		Genbank acession numbers	
Species name	**Voucher**	**nrITS**	**nrLSU**
Arambarria destruens	CIEFAPcc347	KP347538	KP347523
Fomitiporella sp.	Oe5	JF895466	JQ910908
Fomitiporella sp.	Oe6	JF895467	JQ910909
Fulvifomes fastuosus	CBS213.36	AY558615	AY059057
F. indicus	O25034	KC879262	KC879259
F. merrillii	TW	JX484013	JX484002
F. nilgheriensis	CBS209.36	AY558633	AY059023
F. rimosus	TW	JX484016	JX484003
F. robiniae	CBS211.36	AY558646	AY059038
Fuscoporia senex	KUC20110922-13	JX463658	JX463652
F. torulosa	759	AM269803	AM269865
Inocutis dryophila	SP25	AM269845	AM269783
Inonotus compositus	Wang 552	KP030781	KP030768
I. compositus	S45	EU282482	EU282484
I. pachyphloeus	Wu 0407_6	KP030785	KP030770
I. tenuissimus	Dai 12245	KC456242	KC999902
Phellinotus neoaridus	URM80362	KM211294	KM211286
P. piptadeniae	URM80322	KM211290	KM211282
Phellinus chaquensis	CTES568170	MG242440	MG242445
Phe. gabonensis	MUCL52070	HM635722	HM635686
Phe. lundellii	WEN1	KC551835	KC551859
Phe. tuberculosus	DP40	AM269806	AM906071
Phylloporia elegans	FLOR51179	KJ639050	KJ631409
Phy. flabelliforma	MUCL55569	KU198356	KU198349
Phy. gabonensis	MUCL55572	KU198354	KU198352
Sanghuangporus baumii	MPNU 7005	AF200230	AF458469
S. weirianus	CBS618.89	AY558654	AF458465
Sanghuangporus sp.	MUCL 47139	GU461973	GU462002
Sanghuangporus sp.	F915611	JX985739	JX985741
Tropicoporus boehmeriae	LWZ20140729-10	KT223640	-
T. boehmeriae	LWZ20140729-13	KT223641	-
T. cubensis	MUCL47113	JQ860324	-
T. cubensis	MUCL47079	JQ860325	KP030776
T. dependens	JV0409/12-J	KC778777	-
T. dependens	JV0409/20-J	KC778778	-
T. dependens	JV1207/3.4-J	KC778779	-
T. drechsleri	CTES570144	MG242437	MG242442
T. drechsleri	CTES570143	MG242436	MG242443
T. drechsleri	CTES570146	MG242438	MG242441
T. drechsleri	CTES570140	MG242439	MG242444
T. excentrodendri	KP030789	KP030789	-
T. excentrodendri	Yuan 6232	KP030790	-
T. excentrodendri	Yuan 6234	KP030791	-
T. guanacastensis	JV1407_103J	KP030792	-
T. guanacastensis	JV1408_25	KP030793	KP030778
T. guanacastensis	O19228	KP030794	-
T. linteus	JV1008/71	JQ860321	-
T. linteus	JV0904/64	JQ860322	-
T. linteus	JV0904/140	JQ860323	KP030780
T. pseudolinteus	JV0312/22.10-J	KC778780	-
T. pseudolinteus	JV 0402/35-K	KC778781	-
T. rudis	O915614	KP030796	-
T. rudis	O 915617	KP030797	-
T. sideroxycola	JV0409/30-J	KC778782	-
T. sideroxycola	JV1207/4.3-J	KC778783	-
T. tropicalis	UTHSC02-617	AY641432	-

continued on the next page...

TABLE 2. (Continued)

Species name	Voucher	Genbank acession numbers	
		nrITS	**nrLSU**
T. tropicalis	UAMH 10376	AY599487	-
T. tropicalis	IDR1300012986	KF695121	KF695122
T. stratificans	PHSPV2	KM199688	-
T. stratificans	PHSPV3	KM199689	-

Results

Molecular Phylogeny:—The final combined (nrITS+nrLSU) dataset included sequences from 37 fungal specimens, with 1676 characters (including introduced gaps), of which 872 were constant and 590 parsimony informative. The final nrITS dataset included sequences from 33 fungal specimens, with 790 characters (including introduced gaps), of which 456 were constant and 263 parsimony informative. The evolutionary models selected for nrITS dataset were TPM2+G (ITS1), TPM3+I (5.8S) and HKY+G (ITS2). For the combined dataset the selected models were TrN+I+G (ITS1), SYM+I+G (5.8S), HKY+G (ITS2), TIM2+I+G (LSU).

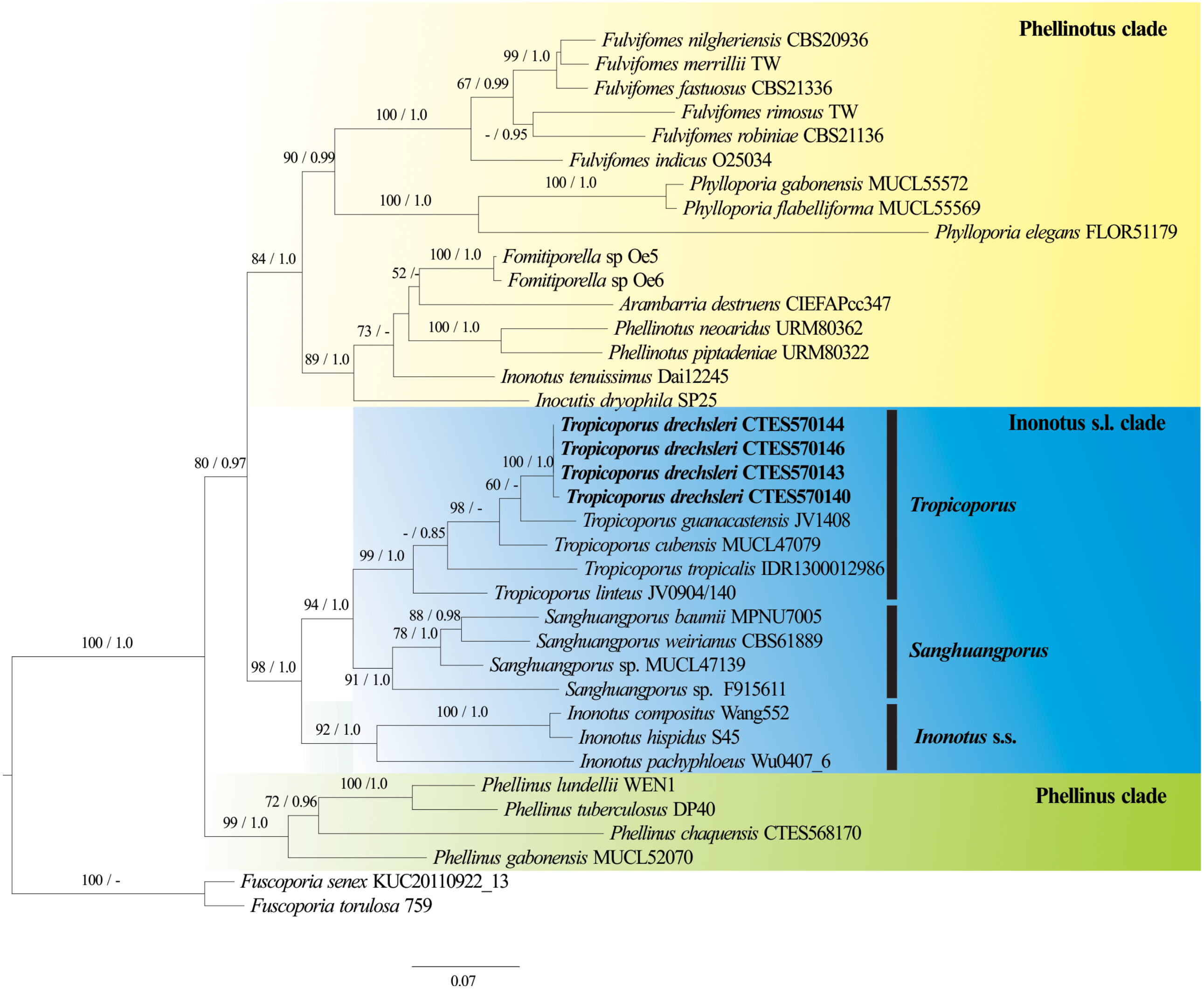

FIGURE 1. Maximum likelihood (ML) tree of *Tropicoporus* and related genera based on dataset of nrITS and nrLSU sequences. Bayesian posterior probability above 0.7 and Bootstrap values above 50 % are shown.

The combined topology (Fig. 1) shows three main clades. The first (phellinotus clade), is well supported (84% BS, 1.0 BPP) and is composed of *Fulvifomes* Murrill (1914: 49), *Phylloporia* Murrill (1904: 141), *Fomitiporella* Murrill (1907: 12), *Arambarria* Rajchenb. & Pildain (2015: 759), *Phellinotus* Drechsler-Santos, Robledo & Rajchenb. (2016: 222) and some residual lineages. The second main clade corresponds to *Inonotus s.l.* (98% BS, 1.0 BPP), including

Inonotus P. Karst. (1879: 39), *Sanghuangporus* Sheng H. Wu, L.W. Zhou & Y.C. Dai (2016: 340) and *Tropicoporus*. Within *Tropicoporus*, the studied specimens formed a well-supported terminal branch separated from *T. linteus* (100% BS, 1.00 BPP). Finally, the third clade is *Phellinus* Quél. (1886: 172) (99% BS, 1.0 BPP). The nrITS topology (Fig. 2) reconstructs the phylogenetic relationships of the genus *Tropicoporus*, and corroborates the studied specimens as a lineage separate from *T. linteus* (100% BS, 1.00 BPP), having as sister clade an assemblage composed of *T. dependens*, *T. guanacastensis* and *T. cubensis* (100% BS, 1.00 BPP).

Since the studied specimens clustered together in an independent, well-supported lineage, besides presenting morphological distinctions from all other known *Tropicoporus* species, they are described as a new species of *Tropicoporus* from the Southern Hemisphere.

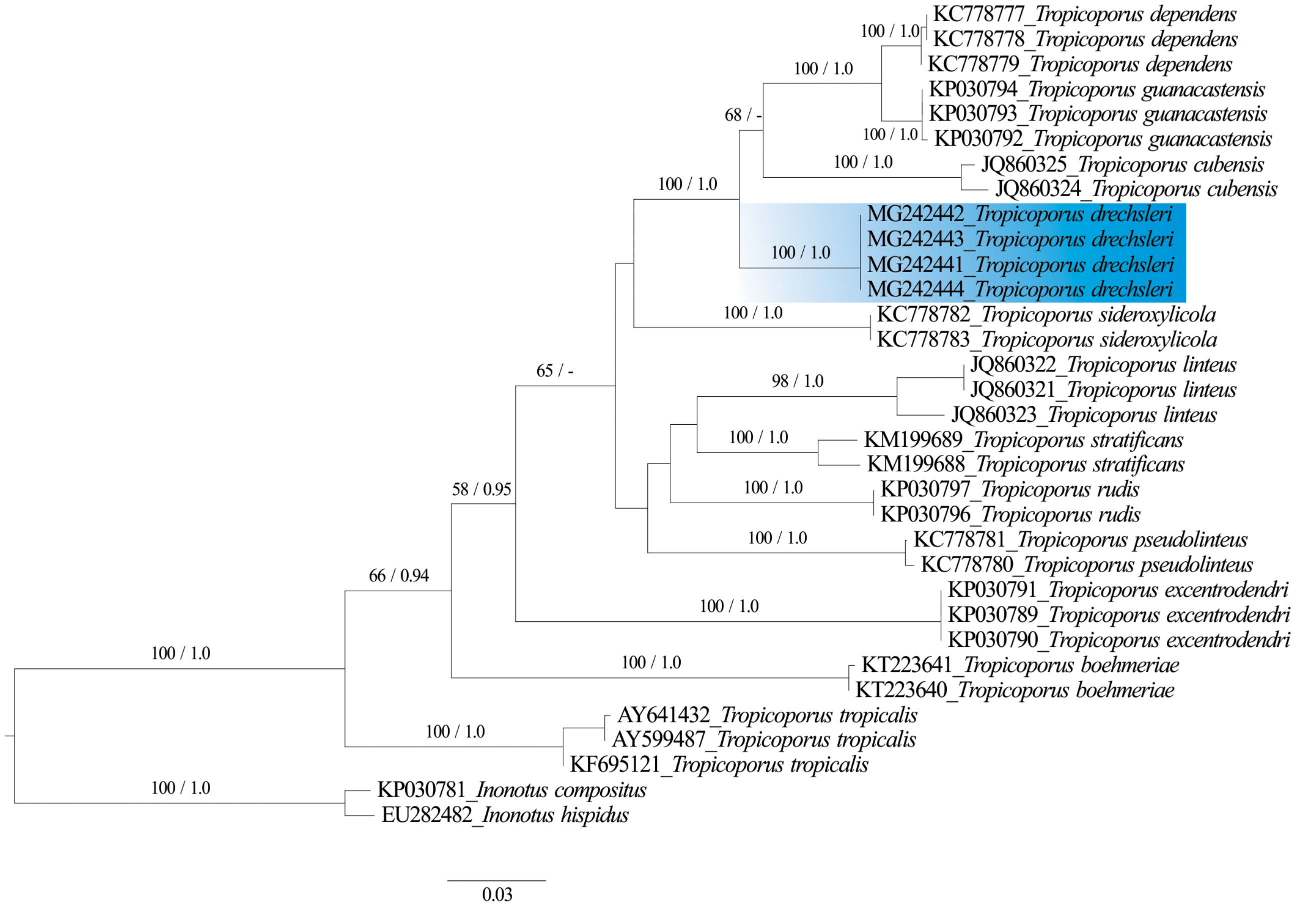

FIGURE 2. Maximum likelihood (ML) tree of *Tropicoporus* based on dataset of nrITS sequences. Bayesian posterior probability above 0.7 and Bootstrap values above 50 % are shown.

Taxonomy

Tropicoporus drechsleri Salvador-Montoya & Popoff *sp. nov.* (Figs. 3, 4)

Mycobank:—MB823698

Holotype:—ARGENTINA. Chaco: Primero de Mayo, Colonia Benítez, Reserva Natural Educativa Colonia Benítez, 27.318220 S, 58.949756 W, 67 m, on living tree of *Cordia americana* (L.) Gottschling & J.S. Mill. (2006: 364), 22 March 2016, *C.A. Salvador-Montoya 681* (CTES 570140).

Diagnosis:—Basidioma perennial, pileate, rimose, hymenophore poroid, (3–)4–5(–6) pores/mm, context with a thin dark line. Hyphal system monomitic in the context and dimitic in the tubes, setae subulate or ventricose. Basidiospores broadly ellipsoid to ellipsoid with a flattened side, (4–)4.5–5(–5.5) × (3–)3.5–4(–4.5) µm, thick-walled, yellowish, chestnut to ferruginous in KOH, on living tree of *Cordia americana*.

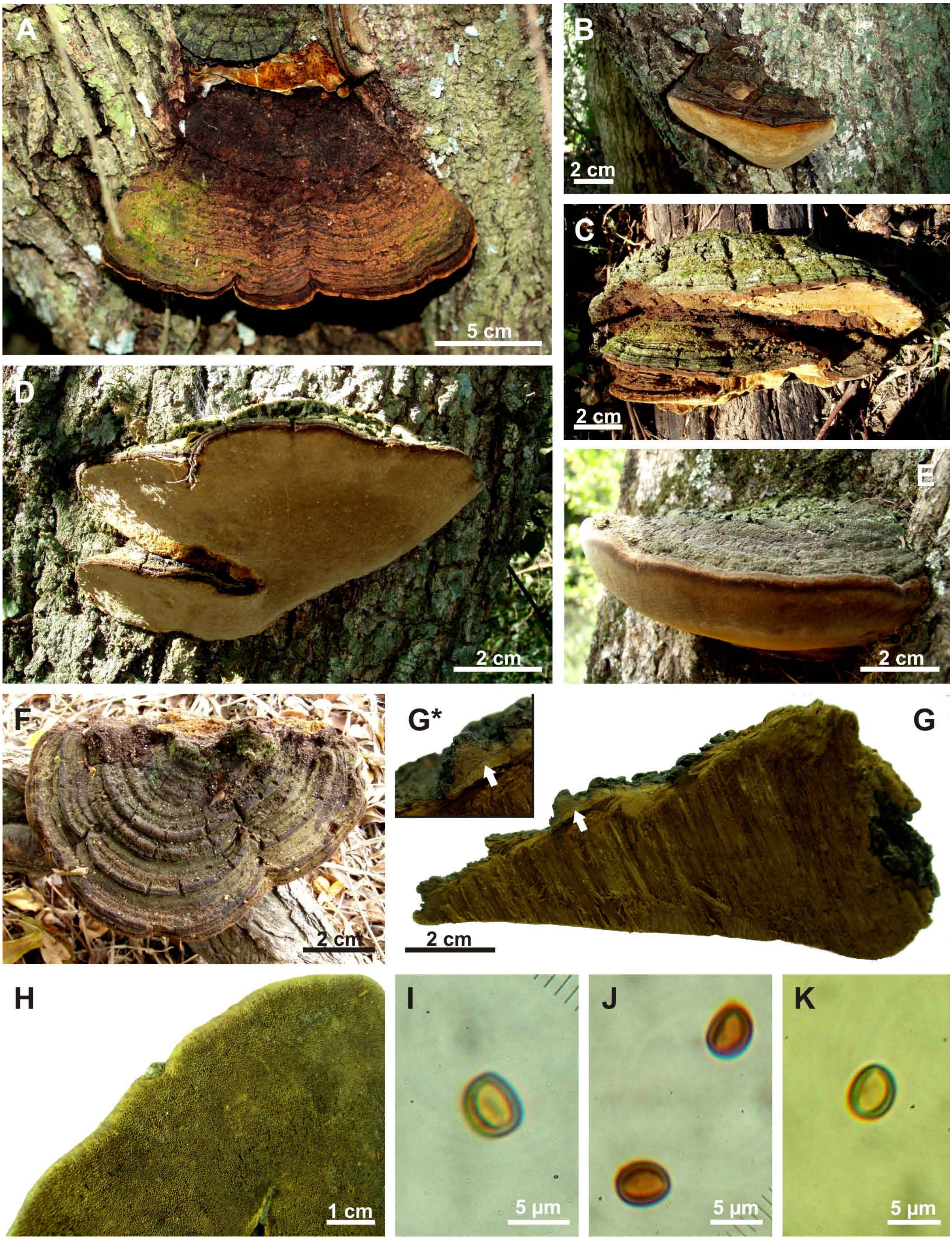

FIGURE 3. Macroscopic features of *Tropicoporus drechsleri*. **A–E)** Basidiomata (paratypes): A) CTES568148, B) CTES570143, C) CTES570142, D) CTES570144, E) CTES570146. **F–K)** CTES570140 (holotype): F) basidioma, G) context duplex, in details (G*) with dark line near to pilear surface, and indistinctly stratified tubes, H) pores surface. **I–K)** basidiospores: I) in water, J) in KOH 5% (xantochroic reaction), K) in Melzer reagent. Photos by: Carlos A. Salvador-Montoya.

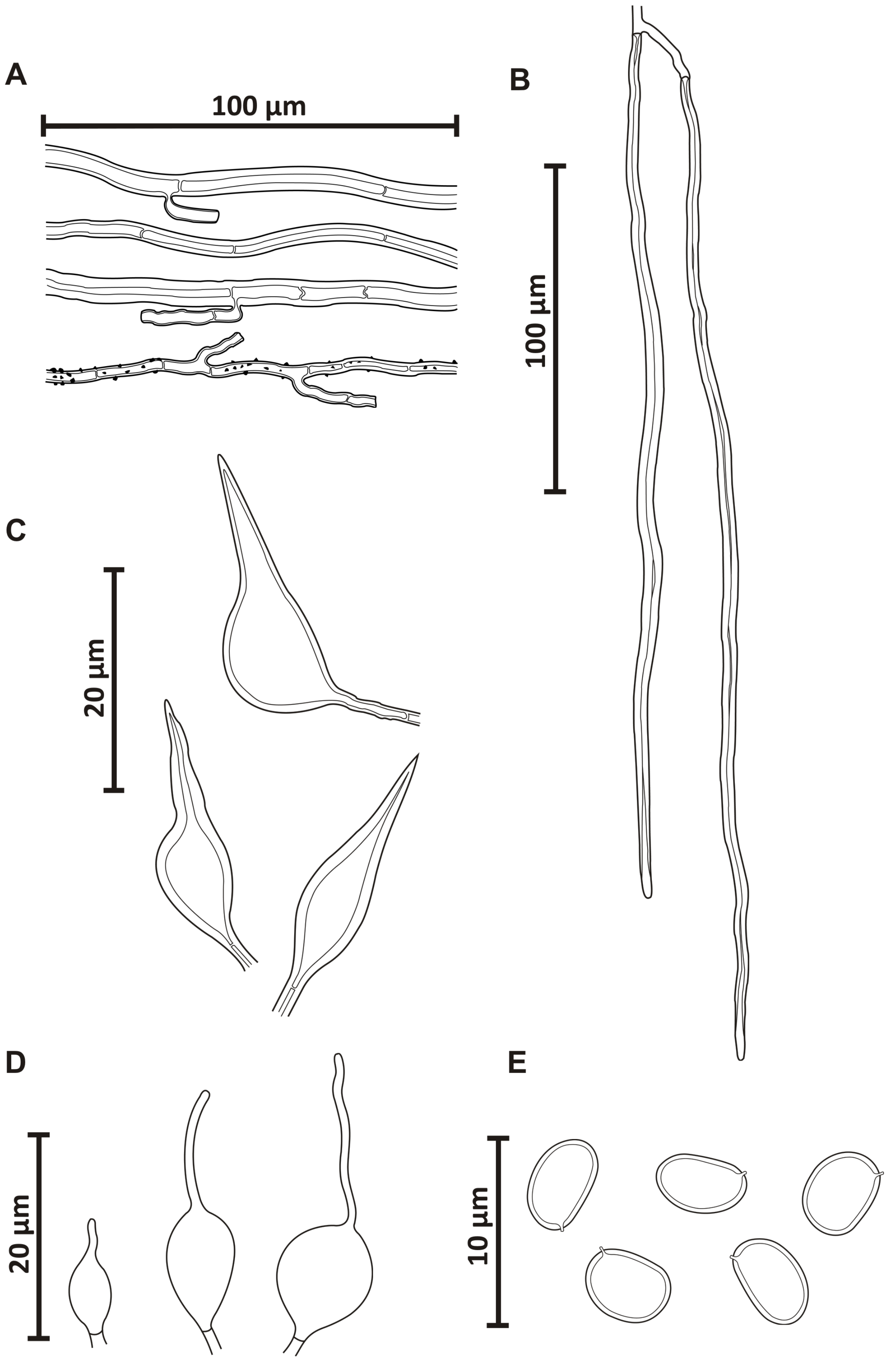

FIGURE 4. Microscopic features from holotype (CTES570140). A) Thin- to thick-walled, occasionally covered by crystals, generative hyphae, B) skeletal hyphae of tubes, C) subulate to ventricose hymenial setae, D) narrowly lageniform to lageniform cistidia, E) broadly ellipsoid to ellipsoid with ventral side flattened, thick walled, basidiospores. Drawings by: Carlos A. Salvador-Montoya.

Description:—*Basidioma* perennial, pileate, sessile, broadly attached, applanate, triquetrous to ungulate, solitary, imbricate, up to 131 mm long, 90 mm wide and 50 mm thick, woody hard; *pilear surface* pubescent at first, concentrically zonated with some radial fissures, brown (5E7 to 5F7), later becoming concentrically sulcate and radially deeply cracked, rough and dark brown (5F4), when well developed and mature, becoming rimose, radially and concentrically deeply sulcate, glabrous, very dark gray (1F1); *margin* entire, round, sharp, thin to thick, pubescent and yellowish brown (5D6) to brown (5E6); *pore surface* dark brown (5F7), pores rounded, regular, (3–)4–5(–6)/mm, with (100–)110–340(–400) µm in diam., dissepiments entire, (30–)40–130(–170) µm thick; *context* up to 21 mm thick at the base in well-developed specimens, fibrous, azonate, brown (5E7), with an inconspicuous thin dark line near the pilear surface, crust thin and dark gray to black; *tubes* indistinctly stratified with whitish mycelia strands usually filling the old tubes, brittle, up to 42 mm long, dark brown (5E7).

Hyphal system monomitic in the context and dimitic in the tubes; context dominated by generative hyphae, 6 µm in diam., simple septate, branched, thin-walled to gradually thick-walled, occasionally septate, some resemble to binding-like hyphae; trama of tubes with thin to slightly thick-walled generative hyphae, simple septate, branched, occasionally covered by crystals towards the dissepiment edge, and unbranched skeletal hyphae, thick-walled with a visible to solid lumen, (104–)162–430(–456) µm long × (2–)3.5–4.5(–5) µm in diam. (L avg. = 282.75 µm, W avg. = 3.85 µm), tapering to the apex where the wall is thin and three adventitious septa are present; *setae* frequently arising from the subhymenium, subulate and ventricose, (15–)16–42(–43) µm long × (3.5–)4.5–9(–12) µm diam., occasionally with a regular heel running parallel to the tube wall, slightly thick-walled to almost solid; *cystidioles* narrowly lageniform to lageniform, (7–)8–24(–31) µm long × (2.5–)3–6.5(–7) µm diam., thin-walled, hyaline, frequently at the dissepiment edge; *basidia* clavate, (9–)10–16(–17) µm long × (3–)4.5–5.5(–7.5) µm wide, hyaline, with four sterigmata; *basidiospores* broadly ellipsoid to ellipsoid, with a flattened side, (4–)4.5–5(–5.5) × (3–)3.5–4(–4.5) µm (L avg. = 4.76 µm, W avg. = 3.56 µm), Q = 1.13–1.50 (Q avg. = 1.34), thick-walled, smooth, pale yellow in water, turning chestnut to ferruginous brown in KOH (xanthocroic reaction), IKI-.

Etymology**:**—*drechsleri*, in honor of Dr. Elisandro Ricardo Drechsler-Santos, enthusiastic mycologist and dedicated mentor, who continuously contributes to increase the knowledge of the neotropical wood-decaying fungi.

Habitat and distribution:—Basidiomata found at the base of trunk and branches of living *Cordia americana*, in seasonally dry forests of subtropical regions in South America.

Remarks:—*Tropicoporus drechsleri* is characterized by applanate to ungulate, imbricate, basidiomata, a rimose and black pilear surface, large pores (4–5/mm) and a context with an inconspicuous dark line. When mature, *T. drechsleri* resembles *T. sideroxylicola* and *T. dependens* by presenting a cracked to rimose, gray to black, pilear surface, besides the binding-like hyphae in the trama, but differs from these two species by having a duplex context. In addition, *T. dependens* presents 5–7 pores/mm and *T. sideroxylicola* presents 2–3 pores/mm and a dimitic hyphal system throughout (Table 1). *Tropicoporus drechsleri* is similar to *T. excentrodendri* L.W. Zhou & Y.C. Dai (2016: 341) by having imbricate basidiomata and a duplex context with a black line, but the latter differs by presenting 7–8 pores/mm and a dimitic hyphal system (Table 1). In northeast Argentina, *T. drechsleri* can be confused with *Phellinus chaquensis* (Iaconis & J.E. Wright) J.E. Wright & Blumenf. (1984: 416). Both species present ungulate basidiomata with a black and rimose pilear surface, as well as subulate hymenial setae. However, *P. chaquensis* differs by presenting smaller pores (6–7 pores/ mm), a homogeneous context, a dimitic hyphal system, smaller setae (11–24 × 4–7 µm) and globose to subglobose, hyaline to pale yellow in KOH, basidiospores (Q = 1.00–1.25). Furthermore, *Phellinus chaquensis* has been reported growing on *Astronium balansae* Engl. (1881: 45), *Caesalpinia paraguariensis* (D. Parodi) Burkart (1952: 26) and species of *Schinopsis* Engl. (1876: 403) (Iaconis & Wright 1953, Robledo & Urcelay 2009, Luna *et al.* 2012, Rajchenberg & Robledo 2013), while *T. drechsleri* is only parasitic on *Cordia americana*.

Material examined:—ARGENTINA. Chaco: Primero de Mayo, Colonia Benítez, Reserva Natural Educativa Colonia Benítez, 27.317883S, 58.950140W, 67 m, on living tree of *C. americana*, 22 March 2016, *C.A. Salvador-Montoya et al. 678* (CTES 570139), *ibid.*, 27.317825S, 58.950217W, 64 m, on living tree of *C. americana*, 10 August 2016, *C.A. Salvador-Montoya et al. 690* (CTES 570141), *ibid.*, 27.318040S, 58.950260W, 65 m, on living tree of *C. americana*, 10 August 2016, *C.A. Salvador-Montoya et al. 693* (CTES 570142), *ibid.*, 27.318019S, 58.950898W, 63 m, on living tree of *C. americana*, 10 August 2016, *C.A. Salvador-Montoya et al. 696* (CTES 570143), *ibid.*, 27.317932S, 58.950447W, 64 m, on living tree of *C. americana*, 10 August 2016, *C.A. Salvador-Montoya et al. 697* (CTES 570144), *ibid.*, 27.317766S, 58.949756W, 64 m, on living tree of *C. americana*, 10 August 2016, *C.A. Salvador-Montoya et al. 699* (CTES 570145); Presidencia Victorino de la Plaza, Capitán Solari, Parque Nacional Chaco, 26.810987S, 59.604804W, 85 m, on living tree of *C. americana*, 18 September 2016, *C.A. Salvador-Montoya et al. 728* (CTES 570146). Corrientes: Itatí, Yacareí, on *C. americana*, 4 February 1990, *O. Popoff 624* (CTES 568153). Formosa: Bermejo, Reserva Natural Formosa, 24.310806S, 61.809753W, 180 m, 8 May 2012, *N. Niveiro* *et al. 2711* (CTES 570147). Misiones: San Ignacio, Reserva Privada Osununú, 27.278808S 55.578079W, 153 m, on living undetermined tree, 12 June 2016, *O. Popoff 5021* (CTES 570148), *ibid.*, 27.280278S 55.575806W, on living tree of *C. americana*, 5 May 2017, *E.R. Drechsler-Santos et al. DS2106* (CTES 568152); Puerto Iguazú, Parque Nacional Iguazú, 25.684722S, 54.447778W, on dead trunk, 21 March 2017, *C.A. Salvador-Montoya et al. 793* (CTES 568147), *ibid.*, 25.671514S, 54.448792W, on living tree of *C. americana*, *C.A. Salvador-Montoya et al.798* (CTES 568146), *ibid.*, 25.684167S, 54.446944W, on living tree of *C. americana*, 24 March 2017, *C.A. Salvador-Montoya et al. 803* (CTES 568149), *ibid.*, 25.671514S, 54.448792W, on living tree of *C. americana*, 1 May 2017, *E.R. Drechsler-Santos et al. DS2009* (CTES!568148), *id.* 2 May 2017, *E.R. Drechsler-Santos et al. DS2052* (CTES 568150); Parque Nacional Salto Encantado, 27.062442S, 54.841475W, 5 May 2017, *E.R. Drechsler-Santos et al. DS2076* (CTES 568151).

Additional specimens examined:—*Phellinus chaquensis*: ARGENTINA. Chaco: Presidencia Victorino de la Plaza, April 1949, *J. Martinoli s.n.* (LPS 18519, holotype; LPS 31379, cotype); Presidencia Victorino de la Plaza, Parque Nacional Chaco, 26.808023S, 59607415W, on living tree of *Schinopsis balansae*, 17 September 2016, *C.A. Salvador-Montoya et al. 711* (CTES 568157), *id. C.A. Salvador-Montoya 712* (CTES 568158), *id. C.A. Salvador-Montoya 713* (CTES 568159); *ibid*., 26.813535S, 59.606830W, on living tree of *S. balansae*, 17 September 2016, *C.A. Salvador-Montoya et al. 718* (CTES 568160), *id. C.A. Salvador-Montoya et al. 719* (CTES 568161); *ibid*., 26.813535S, 59.606830W, on living tree of *S. balansae*, 18 September 2016, *C.A. Salvador-Montoya et al. 721* (CTES 568162), *id. C.A. Salvador-Montoya et al. 722* (CTES 568163); Primero de Mayo, Reserva Natural Educativa Colonia Benítez, 27.317883S, 58.950140W, on dead trunk, 22 March 2016, *C.A. Salvador-Montoya 679* (CTES 568170); *ibid.*, on dead trunk, 10 August 2016, *C.A. Salvador-Montoya et al. 689* (CTES 568156). Corrientes: San Cosme, Ruta provincial 98, 27.557784S, 58.594431W, on living tree of *S. balansae*, 21 April 2016, *C.A. Salvador-Montoya et al. 687* (CTES 568154), *id. C.A. Salvador-Montoya et al. 688* (CTES 568155).

Discussion

In subtropical South America, *T. linteus* was recorded growing on *Anadenanthera colubrina* (Vell.) Brenan (1955: 182), *Allophylus edulis* (A. St.-Hil., A. Juss. & Cambess.) Hieron. ex Niederl. (1890: 180), *Aspidosperma quebracho-blanco* Schltdl. (1861: 137), *Peltophorum dubium* (Spreng.) Taub. (1892: 176), *Ocotea suaveolens* (Meisn.) Benth. & Hook. f. ex Hieron. (1881: 437), *Nectandra saligna* Nees & Mart. (1833: 48) and *C. americana* (Rajchenberg & Robledo 2013), as *Phellinus linteus*. However, our morphological and molecular analyses corroborate those collections on *C. americana* as a separate, non-related lineage from *T. linteus*, here described as a new species, *T. drechsleri* (Figs. 1, 2). Further studies on specimens collected on different plant hosts shall confirm their identities, either expanding the distribution of *T. linteus s.s.* or revealing undescribed species. Morphologically, *T. drechsleri* mainly differs from *T. linteus* by having a duplex context and a xanthocroic reaction of the basidiospores wall (Fig. 3G, G*, I-K; Table 1). Furthermore, *T. drechsleri* occurs in seasonally dry forests of subtropical region in South America, while *T. linteus s.s.* was delimited from collections in the tropical forest of Florida (USA) and Central America (Tian *et al*. 2013).

Tropicoporus drechsleri resembles *Phellinus chaquensis*, however, the type of hyphal system and the xanthocroic reaction in the basidiospores wall are distinctive between the two species. The two polypores species are distributed in Chaco forests (Fig. 5), being *P. chaquensis* distributed up to the foothills of Yungas in Argentina, growing on *A. balansae*, *C. paraguariensis* and species of *Schinopsis* (Iaconis & Wright 1953, Robledo & Urcelay 2009, Luna *et al*. 2012, Rajchenberg & Robledo 2013). *Tropicoporus drechsleri* extends its distribution from northeast Argentina, in the Misiones floristic group of the seasonally dry tropical forests (SDTFs) (Fig. 5) (Särkinen *et al*. 2011, Dryflor *et al.* 2016). Correlatively, *C. americana* is a tree species naturally distributed from Bolivia, Paraguay, southern Brazil, northern Argentina, and northern Uruguay (Martínez-Crovetto 1963, Lombardo 1964, Klein 1985, López *et al*. 1987, Killean *et al*. 1993, Dimitri *et al*. 2000), and recorded in Chaco forests and the south and south-west regions of subtropical seasonal forests in South America (Oliveira-Filho *et al*. 2016). Furthermore, *T. drechsleri* belongs to a lineage distinct to *P. chaquensis* (Fig. 1) and being parasitic presumably follows the distribution of its plant host.

Tropicoporus is characterized by having colored basidiospores (Wu *et al.* 2015, Coelho *et al*. 2016, Zhou *et al.* 2016). However, the examined materials of *T. drechsleri* showed basidiospores yellowish in water, becoming chestnut to ferruginous in 5% KOH solution. The xanthocroic reaction in the wall of basidiospores is also observed in species of the "Phellinotus clade" (*Hymenochaetaceae*), as *Arambarria destruens* Rajchenb. & Pildain (2015: 759), *Phellinotus neoaridus* Drechsler-Santos & Robledo (2016: 224) and *P. piptadeniae* (Teixeira) Drechsler-Santos & Robledo (2016: 224) (Rajchenberg *et al*. 2015, Drechsler-Santos *et al*. 2016), although these taxa lack setal elements. We conclude, based on the materials revised of *T. drechsleri*, *Tropicoporus* included one species with basidiospores with a flattened side, a yellowish natural color, that present a xanthocroic reaction (i.e., becoming chestnut to ferruginous brown in KOH solution).

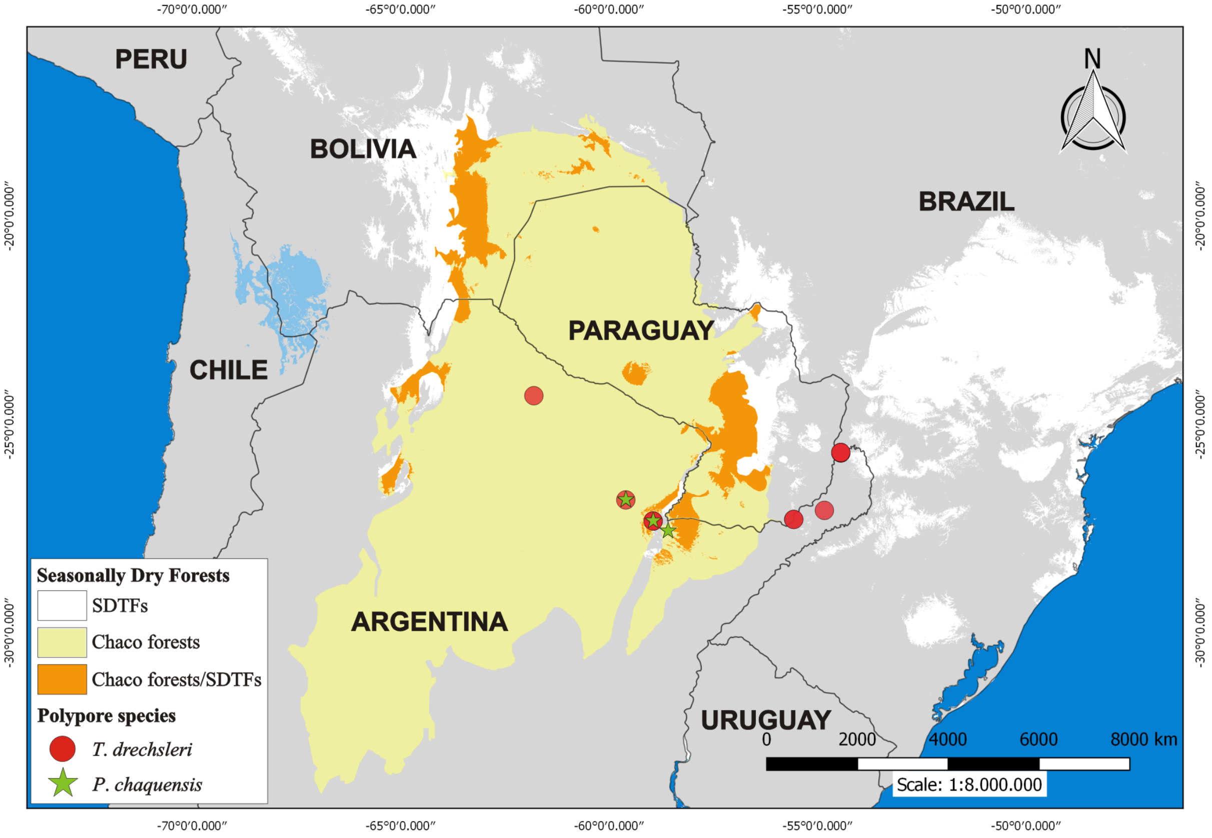

FIGURE 5. Map of the geographic distribution of specimens of *Tropicoporus drechsleri* and *Phellinus chaquensis* in subtropical region of South America.

Key to species of *Tropicoporus* in the neotropical region

1. Basidiomata resupinate 2
   Basidiomata pileate 3
2. Pores 5–7 per mm, tube layers stratified .... *T. stratificans*
   Pores 7–9 per mm, tube layers non stratified .... *T. tropicalis*
3. Basidiomata with a duplex context .... *T. drechsleri*
   Basidiomata with a homogenous context 4
4. Hyphal system dimitic throughout 5
   Hyphal system monomitic in the context and dimitic in the tubes 6
5. Pores 2–3 per mm .... *T. sideroxylicola*
   Pores 5–6 per mm .... *T. dependens*
6. Pores 4–5 per mm .... *T. pseudolinteus*
   Pores >5 per mm 7
7. Pores 7–8 per mm, hymenial setae <25 µm long .... *T. guanacastensis*
   Pores 5–7 per mm, hymenial setae up to 43 µm long 8
8. Basidiospores subglobose to broadly ellipsoid, <4 µm wide .... *T. cubensis*
   Basidiospores broadly ellipsoid to ellipsoid, >4 µm wide .... *T. linteus*

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