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# New insights on *Trametopsis* Tomšovský (Polyporales Gäum) based on phylogenetic evidences and morphological analyses of neotropical species

# NATALY GÓMEZ-MONTOYA<sup>1</sup>, ELISANDRO RICARDO DRECHSLER-SANTOS<sup>2,</sup> VALÉRIA FERREIRA-LOPES<sup>1,</sup> MICHAL TOMŠOVSKÝ<sup>3</sup>, CARLOS URCELAY<sup>1</sup> & GERARDO LUCIO ROBLEDO<sup>1,4\*</sup>

<sup>1</sup> Laboratorio de Micología, Instituto Multidisciplinario de Biología Vegetal, CONICET, Universidad Nacional de Córdoba, CC 495, CP 5000 Córdoba, Argentina.

<sup>2</sup> Laboratório de Micologia, Departamento de Botânica/CCB, PPGFAP, Universidade Federal de Santa Catarina, Florianópolis, CEP 88040-900, SC, Brazil.

<sup>3</sup> Faculty of Forestry and Wood Technology, Mendel University of Agriculture and Forestry in Brno, Zemědělska 3, CZ-613 00, Brno, Czech Republic.

<sup>4</sup> Fundación FungiCosmos, Av. General Paz 54, 4to piso, of. 4, CP 5000, Córdoba, Argentina.

\*corresponding author: glrobledo@yahoo.com

# Abstract

Based on molecular evidence and morphological analyses, a new species in the genus *Trametopsis* is revealed. *Trametopsis* aborigena sp. nov. is proposed and described from South America. Molecular phylogenetic analyses of ITS and LSU rDNA sequences suggest that *Trametopsis cervina* seems to encompass more than one species and confirm previous results showing that *Antrodiella brasiliensis* groups with *Trametopsis*. The morphological analyses of type specimens of *A. brasiliensis* and *A. luteocontexta* revealed a shared morphological pattern with *Trametopsis* and their combinations in *Trametopsis* are proposed. The circumscription of *Trametopsis* is discussed since all the studied specimens revealed a previously overlooked arrangement of characters, *i.e.*, cylindrical and slightly curved to allantoid basidiospores and a metachromatic hyphal system monomitic in the context and dimitic in the tubes.

Keywords: Argentina, phlebioid clade, polypores, taxonomy

# Introduction

The taxonomic and systematic arrangement of polypores has been traditionally proposed based on the study of north temperate to boreal mycotas (Gilbertson & Ryvarden 1986, 1987, Ryvarden & Gilbertson 1993, 1994, Fiasson & Niemelä 1984). When species and specimens from tropical regions became incorporated into the classification systems, traditional species and genera concepts were frequently challenged and re-circumscribed, and unexpected relationships arose with consequent changes in systematic arrangements. Examples of this can be found in different polypore groups, *e.g. Phellinus* Quél. (1886: 172) *s.l./Inonotus* P. Karst. (1879: 39) *s.l.* (Wagner & Fisher 2002, Drechsler-Santos *et al.* 2016), *Megasporoporia* Ryvarden & J.E. Wright (1982: 173) (Li & Cui 2013) and *Wrightoporia* Pouzar (1966: 173) (Chen *et al.* 2016).

Despite the efforts made towards finding monophyletic groups in the Polyporales some large clades include species that are traditionally kept in well-known polyphyletic genera such as *Ceriporiopsis* Domański (1963: 731) and *Antrodiella* Ryvarden & I. Johans. (1980: 256) or *Tyromyces* P. Karst. (1881: 17) in the "phlebiod clade". The revealed relationships in these groups are even more unexpected (*e.g.* Westphalen *et al.* 2016 a, b).

While studying polypores in the Neotropics, specimens collected in Northwestern Argentina Yungas forests, and purportedly belonging to *Tyromyces*, revealed a particular arrangement of characters: the context composed of a monomitic hyphal system with both thin and sclerified clamped hyphae and the trama of the tubes dimitic with straight skeletal hyphae. In addition, hyphal walls showed a metachromatic reaction and basidiospores were cylindrical to allantoid. While this combination of characters did not match closely any described genus, molecular evidence (Blast analysis of the ITS marker) suggests that these specimens form an independent lineage strongly related to *Trametopsis cervina* (Schwein.) Tomšovský (2008: 8) and *Antrodiella brasiliensis* Ryvarden & de Meijer (2002:

40). On one hand *Trametopsis*, described to accommodate *Trametopsis cervina*, has been shown as related to some monomitic species of *Ceriporiopsis s.l., i.e. Ceriporiopsis resinascens* (Romell) Domański (1963: 732), *Ceriporiopsis pseudogilvescens* (Pilát) Niemelä & Kinnunen (2005: 83) and *Raduliporus aneirinus* (Sommerf.) Spirin & Zmitr (2006: 24) (Tomšovský & Homolka 2004, Tomšovský 2008, Tomšovský *et al.* 2010). On the other hand, *Antrodiella brasiliensis*, described from the Neotropical region, has been previously suggested to be phylogenetically related to the monotypic *Trametopsis* Tomšovský (2008: 7) (Miettinen *et al.* 2012), and morphologically closely related to the neotropical species *Antrodiella luteocontexta* Ryvarden & de Meijer (2002: 41). Morphological analysis of both species, *A. brasiliensis* and *A. luteocontexta* showed that they did not fit with the concept of *Antrodiella sensu stricto*. *Antrodiella s.s.* is circumscribed by the type species *Antrodiella semisupina* (Berk. & M.A. Curtis) Ryvarden (1980: 261) and related species (Miettinen *et al.* 2006; Miettinen & Ryvarden 2016).

The aim of this work was to evaluate the delimitation of *Trametopsis*, in order to corroborate whether the molecular evidence, suggesting a close relationship between *T. cervina*, *A. brasiliensis* and the new studied specimens of north west Argentina, correlates with a shared set of morphological diagnostic characters.

# Materials and methods

*Morphological studies*:—Studied specimens are preserved at CORD, FCOS, HF and MBM. Herbarium acronyms follow Thiers (2017) continuously updated. For the study of the specimens macroscopic observations were made on fresh and dried materials following Robledo & Urcelay (2009). Colors were determined according to Munsell (1975). Specimens were examined in Melzer's reagent (IKI), 3% potassium hydroxide (KOH), Phloxine, lactic acid Cotton Blue (CB, CB+ = cyanophilous) and Cresyl Blue (CrB, CrB+ = metachromatic) under the light microscope. Measurements of basidiospores and number of pores/mm followed a standard sampling of thirty measures per structure (n = 30), in presenting the size range of basidiospores, 5% of measurements were excluded from each end and are given in parentheses when relevant. Basidiospore morphology was described through a tridimensional plane, with a sporogram following Ferreira-Lopes *et al.* (2016). The following abbreviations were used for basidiospore measurements  $\mathbf{x}$  = arithmetic mean, Q = the ratio of length/width,  $\mathbf{Q}$  = arithmetic mean of Q ratio. The hyphal system structure was analyzed using the NaOH method (Decock *et al.* 2013) modified, handmade sections were incubated in warm (50°C) NaOH 3% solution for 20 to 24 hours and later mounted in NaOH 3% plus Congo Red. Country names abbreviations follow the United Nations Statistics Division Database 2014 (http://unstats.un.org/unsd/methods/m49/m49alpha.htm).

*DNA extraction, amplification and sequencing*:—DNA was extracted from dry basidiomata tissue using the CTAB method described in Ferreira-Lopes *et al.* (2016). To amplify ITS and LSU rDNA primer pairs ITS8-F / ITS6-R (Dentinger *et al.* 2010) and LROR / LR5 (Vilgalys & Hester 1990, Cubeta *et al.* 1991) were used respectively. PCR conditions were as described in Robledo *et al.* (2014). Sequencing reactions were performed with the same primer pairs.

*Phylogenetic analyses*:—New ITS and LSU sequences generated in this study have been deposited in GenBank® (http://www.ncbi.nlm.nih.gov) and were combined into a dataset with additional sequences gathered from GenBank® (Table 1). DNA sequences were initially aligned with Muscle v.3.6 (Edgar 2004), followed by manual inspection and correction in the data editor of BioEdit V7.0.1 (Hall 1999). Indels were coded as binary characters using the "simple indels coding method" (Simmons & Ochoterena 2000) implemented in the software Fast Gap 1.2 (Borchsenius 2009). The best fit Model of nucleotide evolution was found using jModelTest 2.1.3 (Darriba *et al.* 2012) according to the Akaike information criterion (Akaike 1974).

Bayesian Inference (BI), Maximum Parsimony (MP) and Maximum Likelihood (ML) were applied to the data set. Bayesian analyses were conducted using MrBayes version 3.2.6 (Ronquist *et al.* 2011) with two independent runs, 5 million Metropolis-coupled Markov chain Monte Carlo (MCMCMC) generations with four chains, sampling trees every 1000th generations. The log-likelihood scores of sample points against generation time were plotted using TRACER version 1.6 (Rambaut *et al.* 2014) to determine when the run reached stationarity. Node support was tested by posterior probabilities (PP), obtained from a 50% majority rule consensus tree after deleting 25% of the trees. Individual datasets, including Indels matrix, were combined in a Nexus file comprising 24 entries representing 11 putative species. *Irpex lacteus* (Fr.) Fr. (1828: 142) was selected as the outgroup (Miettinen *et al.* 2012). Nodes with Bayesian Posterior Probability (BPP)  $\geq$  0.95 were considered strongly supported, while nodes with 0.94  $\geq$  BPP  $\geq$  0.7 were considered moderately supported. Maximum Parsimony was performed with TNT (Goloboff *et al.* 2008)

through New Technology Search with the following heuristic algorithms: Sectorial search, Ratchet, Drift and Tree fusing, additional parameters were set as default. The most parsimonious tree was resampled through 100 Bootstrap replications, additional parameters were set as default. Nodes with Bootstrap (BS)  $\ge$  95% were considered strongly supported, while nodes with 94%  $\ge$  BS $\ge$  70% were considered moderately supported. Maximum likelihood (ML) searches were conducted with PhyML (Guindon *et al.* 2010) under the TN93+I+G model with all model parameters estimated by the program. Heuristic searches were performed with Best of NNI and SPR, with random initial tree by BioNJ. Nodes with SH-like support (SH)  $\ge$  0.9 were considered strongly supported, while nodes with  $0.9 \ge$  SH  $\ge$  0.7 were considered moderately supported. Additional parameters were set as default.

Taxon	GenBank Accesion Number			
Voucher reference - Origin	ITS	LSU		
Ceriporiopsis resinascens				
BRNM706968 - CZE	EU30896	EU368501		
BRNM 710169 - CZE	FJ496675	FJ496698		
BRNM 712508 - CZE	FJ496674	FJ496697		
Ceriporiopsis pseudogilvescens				
BRNM 686416 - SVK	FJ496679	FJ496703		
Niemela 7447 - FIN	FJ496680	FJ496700		
Niemela 7477 - FIN	FJ496681	FJ496699		
Emmia latemarginata ( <b>O</b> )				
LE222701 - RUS	KF856498	KF856498		
LE254426 - RUS	KF856508	KF856508		
Flavodon flavus				
FP150441 - JAM	JN710543	JN710543		
MEL:2382923 - AUS	KP012792	KP012792		
Gloeoporus dichrous				
FP 151129 - USA	KP135058	KP135213		
KUC20131001 30 - KOR	KJ668541	KJ668394		
Gloeoporus pannocinctus				
BRNM 709972 - CZE	EU546099	FJ496708		
Irpex lacteus				
Nilson 421 - SWE	JN710547	JN710547		
Olofsson 421 - SWE	JX109852	JX109852		
Raduliporus aneirina				
HHB-15629 - USA	KP135023	KP135207		
TAA181186 - EST	FJ496683	FJ496704		
BRNM706970 - CZE	EU340895	EU368503		
Trametopsis brasiliensis				
Meijer3637 - BRA (T)	JN710510	JN710510		
Trametopsis cervina				
PRM 900574 - CZE	AY684175	AY855907		
TJV 93 216T - USA	JN165020	JN164796		
MG299 - IRN	KU213592	KU213594		
MG300 - IRN	KU213595			
Trametopsis aborigena				
Robledo1236 - ARG (T)	KY655336	KY655338		
Robledo1238 - ARG	KY655337	KY655339		

**TABLE 1.** List of taxa, specimens and sequences used in the phylogenetic analyses. O= Outgroup; T= Type. Newly generated sequences for this study are in boldface. Country names abbreviations follow the United Nations Statistics Division Database.

# Results

*Molecular analyses*:—The complete alignment of the ITS region included 664 positions, including gaps, whereas the LSU region included 571 positions including gaps. For both Maximum Parsimony and Maximum Likelihood, LSU and ITS were used as a combined data set which included 1214 positions, including gaps, where 304 sites are variables

and 273 are parsimony-informative. For TNT and PhyML, gaps and missing data were treated differently. TPM 2 uf+G was chosen as the best-fit substitution model to the ITS dataset in the Bayesian Inference, with the following base frequencies A (0.2485), C (0.2058), G (0.2108), T (0.3349) and a gamma distribution shape parameter of 0.36. The nucleotide substitution rates estimated according to this model were A/G=11.5270, A/T=2.0948, C/G=1.0000, C/T=11.5270 and G/T=1.0000. TrN+I was chosen as the best-fit substitution model to the LSU dataset in the Bayesian Inference, with the following base frequencies A (0.2855), C (0.1774), G (0.2711), T (0.2661), proportion of invariable sites of 0.6580. The nucleotide substitution rates estimated according to this model were A/C=1.0000, A/G=4.3499, A/T=1.0000, C/G=1.0000, C/T=13.2583, G/T=1.0000.

The two independent runs of Bayesian analysis converged to stable values after 5000000 generations (average standard deviation of split frequencies = 0.003689; average potential scale reduction factor = 1.000), a total of 30% of the sampled trees were discarded as burn-in. The remaining trees were used to construct the 50% majority-rule consensus trees (Figure 1). In the MP analysis, the heuristic searches resulted in one most parsimonious tree with score 783, Consistency Index (CI) =0.788 and Retention Index (RI) =0.906. In the ML analysis the size of the most likely tree was =0.57377 (Log-likelihood = -4079.81865). The BI, MP and ML analysis resulted in identical topologies, therefore only the BI tree is shown in Figure 1; support values for all analyses are given above the branches.

The new specimens from the north west Argentinian Yungas forests grouped in a strongly supported clade (BPP = 1.0/ SH=0.93/ BS =100) constituting an independent phylogenetic lineage which we describe below as a new species, *Trametopsis aborigena*. This new species is placed between *Trametopsis cervina* and *Antrodiella brasiliensis*; these three taxa formed a strongly supported clade (BPP=1/ SH=0.96/ BS =100) hereafter recognized as *Trametopsis*. *Trametopsis cervina* specimens grouped with moderate support suggesting that they encompass more than one species.

*Trametopsis* is closely related to *Ceriporiopsis pseudogilvescens / Ceriporiopsis resinascens* clade (BPP=0.99/ SH=1/ BS =100), *Raduliporus aneirinus* clade (BPP=1/ SH=1/ BS =100) and *Gloeoporus dichrous* (Fr) Bres. (1913: 74)/ *Gloeoporus pannocinctus* (Romell) J. Erikss. (1958: 136) clade (BPP=1/ SH=1/ BS =100). This group of related taxa has been recovered repeatedly by several works on the phlebioid clade (Binder *et al.* 2013, Miettinen *et al.* 2012, Tomšovský *et al.* 2010, Zhao & Cui 2014, Zmitrovich & Malysheva 2014).



**FIGURE 1.** Best-scored tree representing the phylogenetic relationships based on ITS and LSU rDNA. Bayesian Inference, Maximum Parsimony and Maximum Likelihood support values are given above the branches.

# Taxonomy

Detailed morphological analyses of the new northwestern Argentinian specimens, the type specimens of *A. brasiliensis* and *A. luteocontexta* and original specimens of *T. cervina* corroborated a morphological homogeneity. Therefore, the new species *Trametopsis aborigena* and the new combinations *Trametopsis brasiliensis* and *Trametopsis luteocontexta* are presented here. Since the following combination of characters: a hyphal system structure monomitic in the context and dimitic in the trama of the tubes, with metachromatic reaction of hyphal walls and cylindrical slightly curved to allantoid thin-walled basidiospores, constitutes a diagnostic feature of *Trametopsis* as defined phylogenetically here (including *T. aborigena*, *T. brasiliensis*, *T. luteocontexta*), it is necessary to make the following emendation:

*Trametopsis* Tomšovský *emend.* Gómez-Montoya, Robledo & Tomšovský Czech Mycol. 60(1): 7 (2008) Type species: *Trametopsis cervina* Tomšovský, Czech Mycol. 60(1): 8 (2008)

Basidiomata annual, sessile pileated to effused-reflexed or rarely resupinate, usually in imbricate clusters; pilear surface smooth, glabrous to strigose, pinkish buff to cinnamon or clay colour, usually zonate sometimes azonate; pore surface concolorous with upper surface, darkening when dry; pores angular, irregular, daedaloid to irpicoid, dissepiments becoming thin and lacerate, usually large 1–4 per mm; context fibrous, azonate. Hyphal system dimitic, hyphal walls metachromatic, negative in Melzer's reagent and CB. Context monomitic with clamped, thin-walled, thick-walled to sclerified generative hyphae, forming short or rather long intercalary segments. Trama of the tubes dimitic with hyaline, thin-walled generative hyphae and thick-walled skeletal hyphae. Basidia clavate. Fusoid cystidioles occasionally present. Basidiospores cylindrical and slightly curved to allantoid, hyaline, thin-walled, negative in Melzer's reagent and CB.

Remarks:—the combination of the microscopic characters of *Trametopsis* perfectly fits the description of *Trametes cervina* by Jahn (1983, *cf.* figure 8–9), for which three types of hyphae are described: a) thin-walled, hyaline, clamped generative hyphae with numerous oil drops and often with short branches; b) thick-walled clamped generative hyphae with a thin lumen and intercalary segments of thick-walled to mostly solid, in between thin walled hyphae and c) thick-walled skeletal hyphae.

*Trametopsis aborigena* Gómez-Montoya & Robledo *sp. nov.* (Figure 2A–D, 3A–C, F, 4) MycoBank: MB820105

Typification:—ARGENTINA. Salta: Dpto. Sta. Victoria Oeste, Parque Nacional Baritú, Lipeo (to Baritú), 1222 m. a. s. l., 22° 26' 21.6" S, 64° 44' 7.8" W, on dead tree, 6 May 2007, *Robledo 1236* [FCOS41, CORD(C)00005352] GenBank accession numbers ITS: KY655336, LSU: KY655338.

Etymology:---from latin "aborigines"= aboriginal, native to the area.

Description:—*Basidiomata* annual, sessile, pileate, effused-reflexed to occasionally resupinate, pileus dimidiate and broadly attached, applanate and lightly convex, occasionally imbricate, each pileated portion up  $5 \times 1.5 \times 0.5$  cm, the small resupinate part under the pileus effused up  $10 \times 5 \times 0.2$  cm. *Pilear surface* light pale brown (7.5YR 7/6–8/4) toward the base and close to the substrate, changing to pale yellowish (10YR 8/3–8/4) [or some specimens strong brown (5YR 5/8)] near the margin, velutinate towards the base, with yellowish red (2.5YR 4/8) to dark yellowish brown (7.5YR 8/3–8/4) radial veins composed of hyphal fascicles and branching to the margin. Margin yellowish (7.5YR 7/6), in section round in the pileate portion, irregular in the effused portion, up 1 mm wide. *Pore surface* pale brown (7.5YR 7/6–8/4) to pale yellow (10YR 8/3–8/4). Pores angular, irregular, 1–3 per mm, some pores are fused giving a daedaloid appearance. Dissepiments irregular in height, lacerate to slightly irpicoid. *Context* homogeneous, whitish (10YR 8/1), fibrous, up to 0.4 cm thick at the base in the pileate portion, 0.1 cm thick in the effused portion. *Tube layer* not stratified, white (10YR 8/1) to pale yellow (10YR 8/3–8/4), up to 0.1 cm thick at the base (Figure 2).

*Hyphal system* monomitic in the context and dimitic in the trama of the tubes, IKI-, CB-, metachromatic; contextual generative hyphae clamped,  $3.0-4.5 \mu m$  wide, of two types, a) hyaline and thin walled with numerous oil drops, and b) pale yellowish thick-walled with a thin lumen, often with short lateral solid branches, intercalary segments of thick-walled, mostly solid, in between thin-walled hyphae, thick-walled hyphae dominate the context giving a dimitic appearance, trama of the tubes with clamped generative hyphae mostly thin-walled, skeletal hyphae thick-walled with



**FIGURE 2.** Macroscopic features of *Trametospis* species. *Trametopsis aborigena* A–D [HOLOTYPE FCOS41, CORD(C 00005352], A) Pileus, B) Context, C) Reddish veins pileal surface, D) Pores. *Trametopsis cervina* E–G (FCOS-39), E) Pileus, F) Context, G) Pores. *Trametopsis brasiliensis* H–J (HOLOTYPE, HF C3637), H) Pileus, I) Context, J) Pores. *Trametopsis luteocontexta* K–M (HOLOTYPE, MBM 180795), K) Pileus, L) Context, M) Pores. Bars = 0.5 cm. Photos by: Nataly Gómez-Montoya and Gerardo Robledo



**FIGURE 3.** Microscopic characters of *Trametopsis aborigena* A–C, F [HOLOTYPE FCOS41, CORD(C) 00005352]. A–C) Clamped generative hyphae, F) Basidiospores. *Trametopsis cervina* D–E, G (FCOS39) D) Generative hyphae clamped, E) Metachromatic, clamped generative hyphae, G) Basidiospores. *Trametopsis.brasiliensis* (HOLOTYPE, HF C3637) H) Basidiospores. *Trametopsis luteocontexta* (HOLOTYPE, MBM 180795) I) Basidiospores. Bars = 5 μm. Photos by: Nataly Gómez-Montoya

a wide lumen, to 900  $\mu$ m long, 3.9  $\mu$ m wide in the main part, ending with rounded apices. *Cystidia* absent. *Basidia* clavate, with basal clamp, hyaline, thin-walled, 19–22 × 5–6  $\mu$ m, with four sterigmata. *Basidiospores* subalantoid in equatorial lateral view and cylindrical in equatorial adaxial view and equatorial abaxial view, thin-walled, hyaline, IKI-, 5–7 (–7.5) × 1–2.5  $\mu$ m,  $\mathbf{x} = 6.3 \times 1.7 \,\mu$ m, Q =3.5–4.2,  $\mathbf{Q} = 3.9$ .

Ecology and distribution:—growing on fallen branches, so far known from the Yungas Mountain Rain Forests in NW Argentina. For a detailed description of the Yungas forests and its polypore diversity see Robledo & Rajchenberg (2007) and references therein.

Remarks:—*Trametopsis aborigena* is characterized by pileate basidiomata, with yellowish red to dark yellowish brown radial veins on the pilear surface, angular and irregular pores 1–3 per mm and suballantoid to cylindrical basidiospores,  $5-7 \times 1-2 \mu m$ . Macromorphologically, it resembles *T. cervina*, however the basidia and basidiospores of *T. cervina* are larger than those of *T. aborigena* (Table 2).

Specimens examined:—ARGENTINA. Salta: Dpto. Sta. Victoria West, Parque Nacional Baritú-Lipeo-(to Baritú), elevation 1222 m. a. s. l., 22° 26' 21.6" S, 64° 44' 7.8" W, growing on dead tree, 6 May 2007, *ROBLEDO 1238*. [FCOS42, CORD (C)00005353]

Additional specimens examined:—*Trametopsis cervina*: CZECH REPUBLIC. Valašské Meziříčí, Oznice village, 49. 4380556° N, 017.9066667° E, growing on wood of *Fagus sylvatica*, 22 October 2010, leg. *V. Tomešová*, det. M. Tomšovský (FCOS-39); Ibid., Moravian Karst Protected Nature Area, Habrůvka Bučina National Nature Reserve,49.3192028°N, 16.6944983° E, growing on a fallen *Fagus sylvatica*, 14 January 2016, leg. *J. Hrabáková*, det. M. Tomšovský (FCOS-40).



**FIGURE 4.** Microscopic features of *Trametopsis aborigena* [HOLOTYPE FCOS41, CORD(C) 00005352]. A) Sporogram from the basidiospores in equatorial and polar view, (el = equatorial lateral view; ead = equatorial adaxial view; eab = equatorial abaxial view; dp = distal polar view and pp = proximal polar view). B) Basidia, C) Thick and thin-walled generative hyphae from the context, D) Skeletal hyphae in the trama of the tubes. Drawings by Nataly Gómez-Montoya.

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Species	Basidiospores			Basidia	Pores
Specimens / Reference	Size (µm)	x	Q		Size (p/mm); shape
Trametopsis brasilensis					
Ryvarden & Meijer (2002)	4.5–5.5(–6) × 1.8–2.2			15–20 × 4–5	1–2; angular; partly split to sinuous
HF C3637 ( <b>T</b> )	5-5.5(-6) × 2.0-2.5 (3.0)*	5.3 × 2.3	2.3	15–16 × 4–5	1–2; angular; irregular, fused, sinuous to lamellate
MBM 084739 ( <b>PT</b> )	5-6.5 × 1.8-2.5 *	5.8 × 2.2	2	n/s	1–2; angular; irregular, fused, sinuous to lamellate
	Arithmetic average of specimens	5.6 × 2.3	2.2		
Trametopsis cervina					
Tomšovský (2008)	(5.5–)6–9(–10) × (1.7–) 2–3			20–25 × 5–7	Irregular; daedaloid to irpicoid.
Jhan (1983)	(5.5–) 6–7.5 (–8) × (1.7–) 2–2.3(–2.6)			n/d	1-2(-3); lacerate, daedaloid to irpicoid
Gilbertson & Ryvarden (1987)	7–9 (–10) × 2.5–3			20-30 × 6-7	1; irregular, lacerate; daedaloid to hydnoid
FCOS-39	6-8 × 1.5-3*	6.8 × 2.1	3.4	21–23 × 6–7	2–4; angular, irregular, lacerate
FCOS-40	6-8.5 × (1.5-)2-3*	7.3 × 2.5	3.0	n/s	1.5–3; round to angular, irregular, lacerate and of lamellar appearance towards the base
	Arithmetic average of specimens	7.5 × 2.5	3.2		
Trametopsis aborigena	<u>_</u>				
Robledo 1236 (T)	5-7 × 1-2.0*	6.1 × 1.5	4.2	(15-)19-22 × (4-)5-6	3–4; angular, irregular, fused to daedaloid
Robledo1238	6–7(–7.5) × 1.5–2.5*	6.5 × 1.9	3.5	n/s	2–4; angular, irregular, fused to daedaloid
	Arithmetic average of specimens	6.3 × 1.7	3.9		
Trametopsis luteocontexta					
Ryvarden & Meijer (2002)	3.0-3.5(-4) × 1.4-2.0			15-18 ×4-5	1–2; round to angular, irregular
MBM 180795 (T)	4.5–5.0 × (1.0–)1.5–2.0*	4.8 × 1.6	2.3	n/s	1–2(–3.0); round to angular, entire, irregular

**TABLE 2.** Comparative table between *Trametopsis* species, based on specimen studied and literature. T= type, PT= paratype, n/d= no described, n/s= not seen, \* size range based on 30 measurements.

*Trametopsis brasiliensis* (Ryvarden & de Meijer) Gómez-Montoya & Robledo *comb. nov.* (Figures 2 H–J, 3H). Mycobank: MB820117

Basiomyn: Antrodiella brasiliensis Ryvarden & de Meijer, Synopsis Fungorum 15: 40, 2002 (HF!)

Remarks:—The study of the type and paratype specimens showed a context composed of thin to thick-walled clamped generative hyphae; in the tubes, generative hyphae are thin-walled and skeletal hyphae are thick-walled to solid with a wide lumen. Basidiospores are allantoid,  $5-5.5(-6) \times 2.0-2.5$  (3.0) µm, slightly larger than originally described [4.5-5.5 (-6) × 1.8-2.2 µm]. Pores are angular, irregular, with some pores fused, sinuous to lamellate (Table 2).

Specimens examined:—BRAZIL. Paraná, Colombo, Embrapa Florestas, 900 m. a. s. l., growing on decayed dicotyledonous branch, 28 May 1999, HF C3637 (holotype). Ibid., Campina Grande do Soul, Parque Marumbi, ombrophilus forest, on decayed dicotyledonous branch, 1000 m.a.s.l., 7 May 1992, *A de Meijer* 2248, MBM 084739.

*Trametopsis luteocontexta* (Ryvarden & de Meijer 2002) Gómez-Montoya, Robledo & Drechsler-Santos *comb. nov.* (Figures 2K–M, 3I).

Mycobank: MB820118

Basionym: Antrodiella luteocontexta Ryvarden & de Meijer, Synopsis Fungorum 15: 41, 2002 (MBM!).

Remarks:—The study of the type specimen showed that the context present generative hyphae thin-walled to thick-walled, both with clamps; in the tubes, generative hyphae thick-walled to thin-walled, both with clamps and skeletal hyphae thick-walled to solid with a wide lumen. Basidiospores are cylindrical,  $4.5-5.0 \times (1.0-)1.5-2.0 \mu m$ , larger than originally reported [ $3.0-3.5(-4) \times 1.4-2.0$ ]. Pores are round to angular, irregular, entire, 1-2(-3) per mm.

Specimens examined:—BRAZIL. Paraná, Curitiba, Parque Barigui, in mixed ombrophilous forest, 900 m. a. s. l., growing on decayed dicotyledonous branch, *A. de Meijer* 2574, 5 March 1993, MBM 180795.

#### Key to the Trametopsis species known worldwide

•	1 1	
1	Pilear surface zonate, strigose to velutinate, basidiomata robust, up 8 cm wide	
1'	Pilear surface azonate, smooth and glabrous to pubescent, basidiomata smaller up 2 cm wide	
2	Northern Hemisphere species, basidiospores 7.0-10 µm lengh and wider than 2.0-3.0 µm	Trametopsis cervina
2'	Neotropical South American species, basidiospores samller, $5.0-7.0 \times 1.0-2.0 \ \mu m$	Trametopsis aborigena
3	Basidiospores $4.5-6.0 \times 1.8-2.5 \mu m$ , markedly bent to allantoid	Trametopsis brasiliensis
3'	Basidiospores $3.0-5.0 \times 1.4-2.0 \mu m$ , slightly bent	Trametopsis luteocontexta
		-

#### Discussion

Phylogenetic analyses showed that the previously monotypic genus *Trametopsis* involves at least three species, including two species from the neotropical region. These species, *i.e. T.cervina*, *T. aborigena*, *T. brasiliensis* and *T. luteocontexta*, share a set of relevant morphological characters, but have some particular features that distinguish and differentiate them (*cfr.* remarks above and Table 2).

Our phylogenetic analyses include original sequences/specimens of *T. cervina* used to evidence the concept of *Trametopsis* as an independent genus. In addition, sequences of *Trametopsis cervina* from other regions of the Northern Hemisphere, *i.e.* North America, Europe, and Asia (Iran, Middle East) were included (Table 1). Our analyses suggest that *T. cervina* seems to be represented by more than one species. Specimens from Iran have strictly resupinate basidiomata (Ghobad-Nejhad & Langer 2016), which is unusual in Central European specimens. Specimens from USA seem to have larger pores and a more hairy pilear surface (Gilbertson & Ryvarden 1987) than European specimens. In the literature, North American specimens have larger basidiospores than European specimens (Table 2) (Jahn 1983, Gilbertson & Ryvarden 1987, Tomšovský 2008). Since the type specimen of *T. cervina* comes from North America (North Carolina, USA), further studies including wider sampling might reveal that *T. cervina* encompasses more species from different continents.

The genus *Trametopsis* is closely related to *C. pseudogilvescens, C. resinascens* and *R. aneirinus*. These taxa are kept in different genera mainly by their morphological differences (Kinnunen & Niemelä 2005, Tomšovský *et al.* 2010). Morphological analyses of the hyphal system of *Trametopsis spp.* showed that they present monomitic and dimitic structures in the context and trama of the tubes, respectively. Some aspects of this noteworthy feature were previously observed by Jahn (1983). This hyphal system structure was confirmed here for specimens of *T. cervina* from Europe and *T. brasiliensis* and *T. luteocontexta* from Brazil supporting the emendation of the genus proposed here.

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